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Sunday, July 15, 2012

Late-Breaking Original Research

LB1 Identification of a genomic region associated with severe combined immunodeficiency in pigs. E. H. Waide*[1], C. K. Tuggle[1], D. M. Thekkoot[1], N. Boddicker[1], R. R. R. Rowland[2], C. R. Wyatt[2], and J. C. M. Dekkers[1], *[1]Iowa State University, Ames, [2]Kansas State University, Manhattan.*

Severe combined immunodeficiency (SCID) is a genetic defect caused by a recessive mutation in one of several genes and has been identified in humans, horses, and dogs, and artificially created in rats and mice. SCID mice have been extensively used to study immune mechanisms, cancer progression and treatment, autoimmune diseases, and vaccination strategies. We recently reported the first discovery of SCID in pigs based on the postmortem examination of 4 related piglets from a selection line of Yorkshire pigs, which showed severely underdeveloped immune systems, later characterized as being devoid of B and T cells. Repeat matings of the 2 sires and 4 dams of these piglets produced 6 additional litters with confirmed SCID piglets in an approximately 20 to 25% frequency. Piglets with SCID appear normal up to weaning but deteriorate quickly after weaning, typically because of respiratory disease. Affected piglets have been shown to sustain human tumor growth, consistent with SCID. To identify the genomic region associated with this defect, 20 affected piglets, 50 unaffected littermates, the 6 parents, and 96 normal ancestors were genotyped using the Illumina Porcine SNP60 Beadchip. The dfam option of PLINK was used to identify a 5.6-Mb region that is associated with the defect ($P = 2.7 \times 10^{-7}$). The region contains a strong candidate gene associated with the immune system. Haplotype phasing analyses using phase (2.1.1) identified 2 distinct haplotypes that are associated with the recessive defect. Single SNP testing in the region confirmed BeadChip data and co-segregation of the region with the SCID phenotype. Sequencing of the region is underway to identify the causative mutation. This novel finding of SCID in pigs and the associated genetic test are important from several perspectives: (1) this defect may be present in commercial populations, as the line that produced the SCID pigs was originally derived from the US Yorkshire population, and (2) SCID pigs will be valuable for infectious disease research in pigs and as a biomedical model for humans. EHW is a Fellow supported by USDA NIFA National Needs grant #2010-38420-20328.

Key Words: pigs, immune system, genetics

LB2 Characterization of genetic variation within the somatotropic axis in DNA pools of beef and dairy cattle divergent for milk production, size, fertility, and immune response. M. P. Mullen*[1,2], C. Creevey[3], D. P. Berry[4], M. S. McCabe[2], D. J. Howard[1], D. A. Magee[5], M. C. Lucy[6], D. E. MacHugh[5,7], and S. M. Waters[2], *[1]Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Teagasc, Athenry, Co. Galway, Ireland, [2]UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland, [3]Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Teagasc, Grange, Co. Meath, Ireland, [4]Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Cork, Ireland, [5]UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland, [6]Department of Animal Sciences, University of Missouri, Columbia, [7]UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin 4, Ireland.*

The somatotropic axis is well established as a key regulator of postnatal growth and development in mammals with direct effects on agro-economic traits in livestock. The identification of genetic variants affecting performance within this axis is therefore an attractive goal. The aim of this study, using a pooled DNA approach coupled with target enrichment and high-throughput sequencing, was to identify polymorphisms and estimate allele frequencies across 83 candidate genes of the somatotropic axis in (1) dairy bulls of high or low genetic merit for milk protein percent, carcass weight, calving interval, somatic cell count, and tuberculosis susceptibility; and (2) beef bulls representing 6 beef cattle breeds. DNA samples from (1) 750 Holstein-Friesian bulls divided into 10 groups (n = 75) divergent (high and low) for genetic merit for each trait; and (2) 300 beef cattle (n = 50 per breed), were pooled using equimolar quantities from each animal to construct 16 Illumina sequence libraries. A custom Agilent Technologies SureSelect Target Enrichment System was used to selectively capture and enrich approximately 2 Mb of coding, intronic, and regulatory sequences from the 83 targeted genes. These enriched libraries were then sequenced using an Illumina Genome Analyzer II. In total, 7,450 SNPs and 995 indels were identified across all pools. Thirty-five percent (n = 2,637) of SNPs were located within 5′ and 3′ UTRs. Fifty-nine percent (n = 4,351) were intronic and 6% (n = 462) were exonic, including 223 non-synonymous substitutions (NSS) with 11 mutations resulting in a stop codon gain or loss. Significant (≥2-fold; $P < 0.01$) allele frequency differentials between the 5 low and high genetic merit groups were observed for 878 SNPs including 55 NSS (3 stop gain/loss). This study has identified novel variation and allele frequency differentials within key genes involved in growth and development, metabolism and health in cattle, potentially harboring heritable variation in performance and contributing to differences between breeds in somatotropic axis regulation and control.

Key Words: DNA pools

LB3 Imputation of microsatellite alleles from dense SNP genotypes for paternal verification. M. C. McClure[1], T. S. Sonstegard[1], G. R. Wiggans[1], A. Van Eenennaam[2], K. Weber[2], C. Penedo[2], and C. P. Van Tassell*[1], *[1]USDA-ARS, Beltsville, MD, [2]University of California, Davis.*

Microsatellite (MS) markers have recently been used for parental verification and are still the international standard despite higher cost, error rate, and turnaround time compared with single nucleotide polymorphism (SNP)-based assays. Despite domestic and international interest from producers and research communities, no viable means currently exist to verify parentage for an individual unless all familial connections were analyzed using the same DNA marker type (MS or SNP). This requirement is a major limitation for historic animals where a DNA source does not exist due to culling, death, or change in ownership of animals. Moreover, the additional cost of MS genotyping is difficult to justify when increasing numbers of commercial dairy cows are SNP genotyped and nearly every dairy sire is SNP genotyped. A simple and cost-effective method was devised to impute MS alleles from SNP haplotypes within breeds. This approach has been verified

(>98% accurate) for imputing the International Society of Animal Genetics (ISAG) recommended panel of 12 MS for cattle parentage verification across 479 dairy cattle representing 4 dairy breeds (Brown Swiss, Guernsey, Holstein, and Jersey). Some MS-haplotype associations held true across these phylogenetically diverse breeds, implying that some combinations were present before modern breed formations and have been preserved across breeds. Results from the dairy breeds were used to impute MS in 117 beef animals from 7 breeds (Belgian Blue, Devon, Angus, Maine-Anjou, Charolais, Dexter, Texas Longhorn, Ankole). While the beef MS imputation call rate was lower (69%), of those called the imputation was still fairly accurate (78%) although for most loci multiple (2–4) alleles were imputed. MS markers are currently the international standard parentage verification for exported semen; this work represents a tool to quickly migrate toward SNP based verification in 1 generation. Finally, these imputation methods can be implemented in any species with available high-density SNP genotypes flanking MS allele genotype.

Key Words: microsatellite, SNP, impute

LB4 Improvement of feed efficiency through diet and breed-dependent genetic polymorphisms.

N. V. L. Serão,* J. E. Beever, D. B. Faulkner, and S. L. Rodriguez-Zas, *University of Illinois at Urbana-Champaign.*

The consideration of different production systems in genome-wide association studies may provide insights into the effects of markers interacting with other factors. The objective of this study was to identify SNPs with diet and breed-dependent associations for feed efficiency traits in beef cattle. A total of 1,321 steers obtained from 5 ranches (2005 to 2008) were used in this study. Animals from 5 breeds, using Angus (AN) and Simmental (SM; purebred Angus [AN], 3/4AN, 1/2AN:1/2 SM, 3/4 SM and purebred SM) were fed with 5 diets, with different ingredients, and levels of total energy and non-degradable fiber. Traits analyzed were: average daily gain (ADG), dry matter intake (DMI), residual feed intake (RFI), residual average daily gain (RADG) and residual intake and gain (RIG). For RFI, DMI was predicted using ADG, back-fat depth (BF), rib-eye area (REA) and mid-test metabolic weight (MW), whereas for RADG, ADG was predicted using DMI, BF, REA and MW. The sum of RADG and −1*RFI defined RIG. Associations were performed using Qxpak5 v.5, in a model including the fixed effects of individual SNPs, breed, diet, breed/diet by SNP interaction, initial weight (covariate), and the random effects of contemporary group (29 levels), and additive polygenic effect. A total of 33 and 26 SNPs interacting with, respectively, breed and diet, were significantly associated ($P < 0.0001$), in which 10 markers were overrepresented across all traits. In addition, 19 markers are harbored on gene regions. The SIPA1L1 gene showed diet-dependent effect for RFI. Higher efficiency is observed in animals presenting "CC" genotypes when fed diet with medium energy and non-degradable fiber content, compared with those fed a low-energy diet containing stored wet distiller grains. For the PTPRT gene, the additive effect for allele "A" was 0.3143 g higher in 3/4 AN steers compared with SM for RADG. This indicates that 3/4 AN steers present higher gain than SM steers with similar intake. Our results show the importance of identifying diet and breed-dependent genomic markers to be used for selection on different production systems.

Key Words: genome-wide association study, residual feed intake, residual average daily gain

LB5 Mixed rumen microbes respond to excess carbohydrate by synthesizing glycogen and spilling energy.

T. J. Hackmann,* K. L. Backus, and J. L. Firkins, *The Ohio State University, Columbus.*

Some pure cultures of rumen bacteria respond to excess carbohydrate by storing it as glycogen, but others respond by spilling energy. Whereas pure culture studies suggest possible responses of mixed cultures to excess carbohydrate, the response of mixed cultures has not been directly studied. We determined whether mixed rumen microbes direct excess carbohydrate toward glycogen synthesis, energy spilling, or both. Batch cultures of mixed microbes were prepared by centrifuging rumen fluid from 4 dairy cows and washing with N-free buffer. Cultures were maintained under anaerobic conditions (39°C) and contained prokaryotes, protozoa, and fungi. Cultures were dosed with 5 or 20 m*M* glucose. Heat production, free glucose, cell protein, and glycogen were measured using calorimetry, glucose-oxidase peroxidase, bicinchoninic acid, and anthrone. Glycogen was measured enzymatically in preliminary experiments, but these measurements led to lower recovery of cell components than when glycogen was measured using anthrone. Heat production was partitioned across (i) baseline endogenous metabolism (heat production before dosing glucose), (ii) glycogen synthesis (assuming 100 kJ/mol glucose residues accumulated in glycogen), and (iii) energy spilling [total heat production minus (i) and (ii)]. For cultures dosed with 5 m*M* glucose, endogenous metabolism and glycogen synthesis accounted for all (101.4 ± 7.1%) heat production; no spilling occurred ($P \geq 0.152$). For cultures dosed with 20 m*M* glucose, endogenous metabolism and glycogen synthesis accounted completely for heat production, but only initially. Energy spilling became detectable ($P \leq 0.05$) by approximately 30 min, and it eventually accounted for as much as 29.8% of heat production in one culture. After glucose was exhausted, cultures dosed with 20 m*M* glucose degraded glycogen rapidly and continued to spill energy, showing spilling may be mediated by rapid glycogen degradation. As in some pure cultures, mixed cultures can spill some energy. However, mixed cultures respond to excess carbohydrate predominantly by glycogen synthesis, without spilling, when the excess is small.

Key Words: rumen microbes, glycogen, energy spilling

LB6 Fine mapping and discovery of recessive mutations that cause abortions in dairy cattle.

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Five haplotypes that never become homozygous (HH1, HH2, HH3, JH1, and BH1) were previously confirmed to have recessive effects on dairy cow conception rate. Inheritance is now routinely traced and reported. Regions suspected to contain the mutations were narrowed to 3.2 Mb for HH1 and 0.8 Mb for JH1 where source and crossover haplotypes do not become homozygous. Only crossovers between BovineSNP50 (50k) genotyped animals and a 50K parent are used in narrowing the suspect region. Because pedigrees extend many generations, crossovers of crossovers are used both to designate carrier status and in fine mapping. Sequence data then revealed the causative mutation for HH1 in the APAF1 gene on BTA5 and for JH1 in the CWC15 gene on BTA15. These 2 genes are conserved across many species, but a single nucleotide mutation in each stops the translation of DNA to protein and causes

loss of homozygous embryos and fetuses. Frequency of heterozygous animals among those genotyped is 4.5% for HH1 and 23.4% for JH1. Accuracy of detecting the fertility haplotypes using the BovineLD (LD) chip with 6,909 markers was tested by reducing 50K genotypes to LD for 1,000 animals (500 heterozygous and 500 normal) and then imputing back to 50K. Concordance was 100% between status from the LD imputed and the 50K genotypes, but can be poorer if imputation is not done first or if pedigrees are incomplete. To improve accuracy for such animals and to allow laboratories to determine status without imputation, nearby markers were selected that had lowest frequency within breed for alleles that were present in each fertility haplotype. The best 40 markers per haplotype provided high concordance without requiring pedigrees or imputation and were added to the LD chip by GeneSeek in the Genomic Profiler. For animals genotyped with other chips, inheritance of several previously known recessive defects can also be determined with 95 to 100% accuracy and used in selection and mating programs. If sequence data reveals causative mutations for the remaining fertility haplotypes, these can be added to future chips so that the nearby markers are no longer needed.

Key Words: haplotype, crossover, mutation

LB7 Maternal dietary energy source during gestation affects expression of imprinted genes in fetal tissues in sheep. X. Lan, R. Gambra, M. A. Berg, E. J. Cretney, H. Khatib, and A. E. Radunz,* *University of Wisconsin-Madison, Madison.*

Mature pregnant multiparous Polypay ewes (n = 14) were used in a randomized complete block design to evaluate the effects of maternal dietary energy source during mid- to late-gestation on gene expression in maternal placental tissue and fetal tissue. From d 67 ± 3 of gestation until necropsy (d 130 ± 1), ewes were fed 1 of 3 diets formulated to contain 3.52 Mcal ME/d. The primary energy sources were from alfalfa haylage (HL; fiber), corn (CN; starch), or dried corn distillers grains (DG; protein, fat, fiber). At necropsy, cotyledons were removed and a sample was flash-frozen. Fetuses were dissected and samples were collected from the perirenal and subcutaneous adipose depots as well as longissimus dorsi (LD) muscle. Total RNA was extracted from tissues and used to synthesize cDNA. Expression profiles of 9 ovine imprinted genes (H19, IGF2R, GRB10, MEG8, IGF2, PEG1, PEG3, DLK1, and DIO3) were estimated in placental tissue and the fetal LD using qRT-PCR. No significant differences between sex and treatment were detected among the imprinted genes. In fetal LD tissue, expression of DLK1 ($P = 0.03$) and PEG 1 ($P = 0.04$) were greater in fetuses from dams fed CN vs. HL or DG and expression of IGF2R was greater ($P = 0.01$) in fetuses from dams fed HL vs. CN or DG. Expression of DIO3 in fetal LD tissues from dams fed CN tended ($P = 0.09$) to be greater than fetal LD from dams fed HL or DG although it did not reach significance level. The DLK1 and DIO3 genes are found in a cluster of imprinted genes that is highly conserved in mammalian species. Interestingly, this cluster contains the mutation responsible for the callipyge phenotype (muscle hypertrophy) in sheep. To the best of our knowledge, this is the first report of the effects of maternal diet on gene expression in the callipyge region.

Key Words: fetal programming, imprinted genes, sheep

LB8 Potential for post-extraction algal residue to replace cottonseed meal as a protein supplement to grazing cattle. M. L. Drewery,* J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

Algal biomass has been identified as a second-generation biofuel. Significant quantities of the co-product, post-extraction algal residue (PEAR) result from conversion to biofuel. After extraction, PEAR is concentrated in protein, suggesting it may replace cottonseed meal (CSM) as a protein supplement. Our objectives were to determine the optimal level of PEAR supplementation to steers consuming low-quality forage and compare effects of supplementation on N metabolism and forage utilization to a CSM control. Five steers (BW = 198 kg) arranged in a 5 × 5 Latin square had ad libitum access to oat straw (4% CP). Treatments were infused ruminally once daily and included PEAR (18% CP) at 0, 50, 100, and 150 mg of N/kg of BW daily and CSM (43% CP) at 100 mg of N/kg of BW. Increased provision of PEAR stimulated total digestible organic matter intake (TDOMI) quadratically ($P = 0.05$) from 0.9 to 1.6 kg/d for 0 and 100 mg of N/kg of BW of PEAR, respectively. Organic matter digestibility (OMD) increased quadratically ($P < 0.01$) with supplementation, from 47 to 51% for 0 and 100 mg of N/kg of BW PEAR, respectively. At isonitrogenous levels of PEAR and CSM, TDOMI was similar ($P = 0.22$) as was OMD ($P = 0.50$). Negative N balance was observed with all treatments except PEAR provided at 100 or 150 mg of N/kg of BW. Steers consuming straw without supplemental protein lost 13.6 g of N/d. Nitrogen balance was greatest (1.84 g of N/d) when PEAR was provided at 100 mg of N/kg of BW. There were no significant differences between PEAR and CSM supplementation for plasma urea-N, ammonia, or VFA concentrations. Ammonia concentrations increased quadratically ($P = 0.05$) in response to increased supplemental PEAR, from 0.99 to 1.92 m*M* for 0 and 150 mg of N/kg of BW of PEAR. Overall, comparison of PEAR and CSM at isonitrogenous levels suggests there are no significant differences in forage intake, digestion, or N balance, suggesting cattle provided PEAR utilize forage in a similar manner to those supplemented CSM. These observations indicate PEAR may replace CSM as a protein supplement in forage-based cattle operations.

Key Words: post-extraction algal residue, supplementation

Sunday, July 15, 2012

SYMPOSIA AND ORAL SESSIONS
ASN-ADSA®-ASAS Preconference: Regulation of Nutritional Intake and Metabolism

1 Role of the central melanocortin system in appetite regulation and nutrient homeostasis. B. L. Panaro and R. D. Cone,* *Department of Molecular Physiology and Biophysics, Vanderbilt University School of Medicine, Nashville, TN.*

The central melanocortin system has long been implicated as a key regulator of energy homeostasis. The melanocortin-4 receptor (MC4R) integrates various homeostatic signals to control body weight through altering food intake and energy expenditure. Inhibition of MC4R signaling causes obesity in all vertebrate species tested, from fish to humans. The most notable differences caused by MC4R deficiency are hyperphagia and decreased energy expenditure, both of which contribute to the obesity observed in humans and mice. There is substantial evidence that MC4R deficient mice overconsume high-fat diets compared with obese controls, in a single food choice model. Previous rodent studies have investigated this feeding behavior in single-diet paradigms without offering another diet choice. Surprisingly, under 2-choice diet paradigms featuring a high-fat or high-sucrose diet paired with standard chow, MC4R deficient mice invariably have a lower preference for palatable high-fat and high-sucrose diets compared with wild-type littermates. Furthermore, while dietary preference for high fat or high sucrose seems to be attenuated in the MC4R deficient mice, the drive for hyperphagia is consistently enhanced by dietary variety, as a result of increased consumption of standard chow. Together, these food preference observations suggest a role for MC4R in the processing of food-directed behaviors, with reduced MC4R signaling leading to hyperphagia in an environment presenting a variety of foods. The mechanisms that guide these behaviors are largely uncharacterized, though we hypothesize that MC4R regulates dietary behaviors through both central and peripheral contributions to gut-brain communication. For example, in additional to hypothalamic sites of action, MC4R may also affect food intake indirectly through effects on gut motility, and even effects on enteroendocrine cell function.

2 The regulation of hepatic glucose uptake in vivo. A. Cherrington,* *Vanderbilt University School of Medicine, Nashville, TN.*

In the postprandial state, the liver takes up and stores glucose to minimize the fluctuation of glycemia. Elevated insulin concentrations, an increase in the load of glucose reaching the liver, and the oral/enteral/portal vein route of glucose delivery (compared with the peripheral intravenous route) are factors that increase the rate of net hepatic glucose uptake (NHGU). The entry of glucose into the portal vein stimulates a "portal glucose signal" that not only enhances NHGU but concomitantly reduces muscle glucose uptake to ensure appropriate partitioning of a glucose load. This coordinated regulation of glucose uptake is likely neurally mediated, at least in part, since it is not observed following total hepatic denervation. Moreover, there is evidence that both the sympathetic and the nitrergic innervation of the liver exert a tonic repression of NHGU that is relieved under feeding conditions. Further, the energy sensor AMPK appears to be involved in regulation of NHGU and glycogen storage. Consumption of a high fat and fructose diet impairs NHGU and glycogen storage, in association with a reduction in glucokinase protein and activity. An understanding of the impact of nutrients themselves and the route of nutrient delivery upon liver carbohydrate metabolism is fundamental to the development of therapies for impaired postprandial glucoregulation.

3 Active and reactive amino acid homeostasis during feeding, lactation, and disease. G. E. Lobley,* *Obesity and Metabolic Health Division, Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen, UK.*

Amino acids (AA) are critical responders and regulators during both anabolism and catabolism. In response to either acute or chronic intake AA are partitioned between oxidation and protein gain. Trans-hepatic studies suggest the utilization of ingested AA is driven primarily by the anabolic process while AA oxidation of any excess restores homeostasis. This mechanism provides a simple (and universal) means to regulate inter-tissue metabolism. Feeding exerts 2 aspects on AA metabolism. First, pattern of supply (e.g., meal or continuous) can influence net protein anabolism. In the neonate, intermittent supply gives greater efficiency whereas in the elderly single large meals may be preferred. Second, protein (AA) is the most satiating macronutrient and is used in many weight loss strategies. Satiety may be regulated through release of gut hormones that provide state of "hunger" (e.g., ghrelin) or "fullness" (e.g., PYY) signals. These may be released in response to either protein per se or to free AA. Uptake of AA by specific organs is linked to both direct (e.g., muscle growth, milk protein output) and indirect (e.g., precursors for other AA, gluconeogenesis, energy) needs. Infection increases the demands for specific AA to produce key proteins or peptides. Therefore, AA supply needed during disease differs from requirements for normal physiological processes and the deleterious effects of inflammation may be offset by extra provision of specific AA, such as glutamine, threonine and cysteine. AA or their metabolites can also indicate health status. For example, a key role played by methionine (Met) is to supply C-1 groups that methylate macromolecules involved in metabolic regulation. When either Met or other factors of the methionine cycle are limited, this results in hyperhomocysteinemia, an independent risk factor for several diseases. Kinetic studies in rodents have shown that less than 20% of tissue homocysteine flows through plasma and that uptake by key tissues, including heart, may link to disease progression. AA, both separately and as part of protein, play key roles in maintaining mammalian health and well-being.

4 Adipose and endocrine integration of metabolism. P. E. Scherer,* *UT Southwestern Medical Center, Dallas, TX.*

During the progression from the lean to the obese state, adipose tissue undergoes hyperplasia as well as hypertrophy in an attempt to cope with the increased demand for triglyceride storage. This requires a high degree of plasticity at both the cellular and at the tissue level. Even though adipose tissue as a whole seems to be a relatively static tissue containing many adipocytes that turn over slowly, these cells are embedded in an environment that can rapidly adapt to the needs of expanding and newly differentiating adipocytes. The extracellular matrix of adipose tissue faces unique challenges with respect to adjusting to the need for remodeling and expansion. In parallel, the vasculature has to adapt to altered requirements for nutrient and oxygen exchange. A decrease in the plasticity of these processes leads to metabolic dysfunction. Furthermore, to maintain a healthy, non-inflamed phenotype, complex regulatory mechanisms are in place to ensure adipocytes and stromal vascular cells efficiently crosstalk to allow adipose tissue to expand upon increased demand for storage of triglycerides. Therefore, we propose a model of stepwise adipose tissue dysfunction that is initiated by rapid expansion of existing adipocytes to accommodate triglycerides during excess caloric intake. This leads very quickly to an acute, and eventually chronic, state of hypoxia in adipose tissue. Changes during the expansion process also affect adipocyte-derived secretory factors (adipokines), such as adiponectin. Adiponectin promotes insulin sensitivity, decreases inflammation, and promotes cell survival. Its levels are frequently downregulated in the obese state. We have recently demonstrated that adiponectin potently stimulates a ceramidase activity associated with its 2 receptors, adipoR1 and adipoR2, and enhances ceramide catabolism and formation of its anti-apoptotic metabolite, sphingosine-1-phosphate (S1P). Our observations suggest a novel role of adipocyte-derived factors that have beneficial systemic effects, with sphingolipid metabolism as its core upstream component.

5 Heat stress and post-absorptive metabolic perturbations.

L. H. Baumgard*[1] and R. P. Rhoads[2], [1]*Iowa State University, Ames,* [2]*Virginia Polytechnic Institute and State University, Blacksburg.*

Environmental-induced hyperthermia compromises efficient animal production by marginalizing efforts to reduce food production inputs while negating the contribution of animal genetics toward performance endpoints. Modification of farm infrastructure has yielded modest success in mitigating heat stress-related losses yet heat stress remains arguably the costliest issue facing progressive livestock producers. Reduced output (e.g., milk yield, muscle growth, egg production) during heat stress was traditionally thought to result from decreased nutrient intake (a classic biological response shared by all animals during environmental-induced hyperthermia). Recent observations by our group challenges this belief, indicating 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 changes such as 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 heat stress. 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 heat stress 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 our work has characterized similar events between growing and lactating ruminants, growing pigs and adult rodents. Ultimately, these changes result in the reprioritization of fuel selection during heat stress, which appears to be primarily responsible for reduced animal productivity during the warm summer months.

6 Linoleic acid and inflammation: Evidence-based research from human clinical studies.

K. L. Fritsche*[1] and G. H. Johnson[2], [1]*University of Missouri, Columbia,* [2]*Johnson Nutrition Solutions, Kalamazoo, MI.*

The authors conducted a systematic review of randomized controlled trials that permitted the assessment of dietary linoleic acid (LA) on biological markers of chronic inflammation among the healthy non-infant population was conducted. A search of the English and non-English literature using MEDLINE, the Cochrane Controlled Trials Register, and EMBASE was conducted to identify relevant articles. Fifteen studies (8 parallel and 7 crossover) met inclusion criteria. None of the studies reported significant findings for a wide variety of inflammatory markers including C-reactive protein, fibrinogen, plasminogen activator inhibitor type 1, cytokines, soluble vascular adhesion molecules or tissue necrosis factor-α. The only significant outcome measures reported for higher LA intakes were greater excretion of prostaglandin E2 and lower excretion of 2,3-dinor-thromboxane B2 in one study 1 and higher excretion of tetranorprostanedioic acid in another. However, both authors observed that these effects were not an indication of increased inflammation. It is concluded that virtually no evidence is available from randomized, controlled intervention studies among healthy, non-infant humans to show that variations in the level of LA in the diet affects in vivo inflammation in healthy humans.

7 Microbial hydrogen metabolism in colonic health and disease.

H. R. Gaskins,* *University of Illinois, Urbana-Champaign.*

In mammals, dietary fiber (polysaccharides, oligosaccharides, lignin and associated plant substances) and other nutritional components not absorbed in the upper digestive tract reach the colon where they are fermented by the cooperative metabolism of a complex microbiota. Fermentation products include short chain fatty acids (SCFAs; acetate, propionate and butyrate) and gases including molecular hydrogen (H_2). Colonic SCFAs, which are present at high concentrations (>100 m*M*), serve as the primary energy source for epithelial cells and modulate cell fate through influences on differentiation, growth arrest, and apoptosis. The H2 produced during fermentation is either excreted or used as a source of electrons by 3 groups of H_2-consuming microorganisms (hydrogenotrophs); the acetogens (generating acetate), methanogens (methane) and sulfate reducing bacteria (SRB; hydrogen sulfide, H_2S). Hydrogenotrophic organisms are present at much lower densities than are fermentative bacteria. However, in the absence of microbial H_2 consumption, the H_2 partial pressure rapidly reaches a level that thermodynamically inhibits further fermentation. Methane and sulfide production have been recognized as major pathways for H_2 disposal in the colon, but various factors such as colonic pH, sulfate availability, transit time, and microbial composition may influence which of these mechanisms predominates. Our research seeks to better understand the nature of the hydrogenotrophic microbiota and the extent to which end products of their metabolism vary among individuals and contribute to chronic inflammation and colorectal cancer. Of particular interest are SRBs and host epithelial responses to their toxic end product H_2S. Host and microbial aspects of our related working hypothesis will be described and data presented from recent studies that demonstrate the prevalence of hydrogenotrophs in the human colonic mucosa and their responsiveness to diet.

8 Characterizing the cellular mechanisms of postprandial thermogenesis in skeletal muscle.

B. A. Henry* and I. J. Clarke, *Department of Physiology, Monash University, Victoria, Australia.*

Thermogenesis is the dissipation of energy through specialized heat production. This process contributes to 10–15% of total energy expenditure in lean individuals. Thermogenesis is well characterized in brown adipose tissue, but whether other tissues are thermogenic is contentious. To characterize this in sheep we developed a model of postprandial thermogenesis, whereby sheep were entrained to a meal-feeding regimen with food restricted to a set meal time. We demonstrate increased skeletal muscle heat production at the onset of feeding and that central infusion of leptin upregulates this. Furthermore, central administration of leptin increases the expression of uncoupling protein (UCP) 2 and 3, but not UCP1 in skeletal muscle. The increase in UCP3 is associated with a switch to uncoupled respiration in isolated mitochondria. Thus, leptin-induced heat production in skeletal muscle is concomitant with the induction of thermogenesis. In addition to mitochondrial function, we examined changes in calcium cycling. Meal-feeding increased heat production as well as the expression of ryanodine receptor 1 (RyR1) mRNA and sarcoplasmic Ca^{2+}-dependent ATPase (SERCA) 2 protein in skeletal muscle. Thermogenesis in muscle, therefore, is facilitated via both mitochondrial uncoupling as well as calcium cycling pathways. Finally, we characterized differences in thermogenesis in animals predisposed to obesity. To do this we utilized two unique models, the genetically lean and obese sheep as well as a model of cortisol responsiveness. We show that animals characterized as high cortisol responders (HR) have greater propensity to obesity when fed a high energy diet compared to low cortisol responders (LR). Resistance to obesity in the LRs is preceded by a higher thermogenic response in muscle. This contrasts the genetically lean and obese animals, where lean animals have increased thermogenesis in adipose tissue, but not muscle. In conclusion, we show that skeletal muscle heat production is associated with altered mitochondrial function and enhanced calcium cycling. Furthermore, innate differences in thermogenesis (either muscle or fat) predispose animals to weight gain and obesity.

Triennial Reproduction Symposium: Impediments to Fertility in Domestic Animals

9 The obstacle course to successful establishment of pregnancy in domestic livestock species. M. D. Utt and M. L. Day,* *Department of Animal Sciences, The Ohio State University, Columbus.*

Research in reproductive biology over the past century has provided valuable knowledge and technologies that have and will be used to increase the likelihood of creating a successful pregnancy in domestic livestock species. However, maximal reproductive efficiency has not been achieved in any of these species. Successful establishment of pregnancy is a complex series of interrelated events that can be impaired at the gamete level through fetal development. The gametes contain genetic information and other factors necessary for creating viable offspring, but genetic and/or developmental deficiencies of gametes and the gonadal environment in which they reside may influence embryonic and fetal development. When sperm are deposited in the female reproductive tract at an appropriate time relative to ovulation, fertilization rate is relatively high, and differences therein are related to compensable and uncompensable sperm traits and/or sperm transport. Following fertilization, developing embryos reside in the oviduct before moving into the uterus. The oviductal and uterine environments are influenced by estrogen and progesterone before and after ovulation, and embryonic development may be affected by fluctuations in concentrations of either or both steroids. Latent effects of estrogen and progesterone on the uterus may impact the lifespan of the corpus luteum (CL) and/or embryonic development through maternal recognition of pregnancy (MRP) and the preimplantation period. Regardless of species, MRP consists of embryonic-derived signals that inhibit destruction of the CL and consequently the conceptus. Defective interactions among the conceptus, uterus, and CL can subsequently lead to failure in MRP. After MRP, embryonic or fetal loss is still possible due to uterine deficiencies, environmental effects, or combinations thereof. Many of the aforementioned obstacles to pregnancy may be exacerbated by production and metabolic stress; therefore, lactating dairy cattle are an appropriate model to study the spectrum of factors that impede attainment of optimal reproductive efficiency.

Key Words: pregnancy, deficiency, embryo

10 Sperm characteristics that limit success of fertilization. W. L. Flowers,* *North Carolina State University, Raleigh.*

The theoretical relationship between male fertility and sperm characteristics resembles a positive, asymptotic equation. When numbers of spermatozoa are low, fertilization rates are low. As the number of sperm cells increase, so does fertility. This response gradually diminishes until a plateau is reached and additional spermatozoa do not affect male fertility. Variation clearly exists among males in how their fertility responds to increasing spermatozoa both in terms of the slope of the positive portion of the curve and the point at which it reaches a plateau. These differences in male fertility patterns often are attributed to differences in the quality of their sperm cells. Sperm characteristics can be qualitative or quantitative and measure individual or functional properties. Qualitative assessments such as motility and morphology deal with population dynamics, and as they increase so does fertilization rate to a point. Hence, qualitative characteristics probably are responsible for variations along the linear portion of male fertility curves. Quantitative evaluations such as amounts of plasma membrane proteins or acrosin activity estimate aspects of all sperm cells produced by males and most likely mainly influence the level at which fertilization rates reach their plateau. Individual and functional characteristics of sperm can be qualitative or quantitative and affect male fertility patterns accordingly. Intuitively, functional traits such as sperm binding should provide a better indication of fertilization than individual ones such as motility. However, correlations of both types with fertility are very similar. Reasons for this may be related to how characteristics of sperm cells are influenced by the female reproductive tract after insemination. For example, capacitation patterns of spermatozoa in some boars are different in vitro than in vivo. If this relationship holds true for other traits, development of tests that account for this variation are necessary to address a critical need for understanding sperm characteristics that limit fertility.

Key Words: livestock, fertility, spermatozoa

11 The ovarian follicular reserve in ruminants: What regulates its formation and size? J. E. Fortune,* M. Y. Yang, and J. J. Allen, *Cornell University, Ithaca, NY.*

Primordial follicles have an oocyte arrested in first prophase of meiosis and a layer of flattened granulosa cells. These nongrowing follicles comprise the follicular reserve, the source of growing follicles until reproductive senescence. Indirect evidence indicates that the size of the follicular reserve in adult women is a measure of their reproductive potential. Therefore, it is of interest to elucidate the mechanisms that regulate follicle formation and factors that may enhance or diminish the size of the primordial pool. In species such as cattle, sheep, and humans, follicle formation and the establishment of the follicular reserve occur during fetal life. We use fetal bovine ovaries as a model to study the regulation of follicle formation and acquisition of the capacity to activate (initiate growth). Our results suggest a critical role for fetal ovarian steroids in the timing of follicle formation and differentiation of newly formed primordial follicles to a stage where meiosis has arrested in prophase I and ability to activate has been acquired. Current studies are focused on the regulation of fetal ovarian steroidogenesis by gonadotropins, steroids, and growth factors. We hypothesize that factors that interfere with production and/or action of fetal steroids may affect the size of the follicular reserve and perhaps the reproductive potential of the ensuing adult. Because domestic animals may be exposed to forage containing estrogenic compounds and to other environmental estrogens, the effects of endocrine disrupting chemicals on follicle formation and capacity to activate are potentially important. Nutrition may be another influence on the size of the follicular reserve. In adult cattle, the number of follicles in follicular waves has been correlated with their fertility and nutritional restriction during the first 110 d of bovine pregnancy was associated with fewer follicles in waves (vs. controls) when daughters reached maturity. Although there is much to be learned about the regulation of follicle formation in cattle and its relationship to fertility, this stage of ovarian development may be very important to adult reproductive potential.

Key Words: ovarian follicle, ovary, cattle

12 Influence of follicle characteristics at ovulation on early embryo survival. T. W. Geary*[1], M. F. Smith[2], M. D. MacNeil[1], M. L. Day[3], G. A. Bridges[4], G. A. Perry[5], F. M. Abreu[3], J. A. Atkins[2], K. G. Pohler[2], E. M. Jinks[3], and C. A. Roberts[1], *[1]USDA-ARS, Fort Keogh, Miles City, MT, [2]Division of Animal Sciences, University of Missouri, Columbia, [3]Department of Animal Science, Ohio State University, Columbus, [4]Department of Animal Science, University of Minnesota, Grand Rapids, [5]Department of Animal and Range Sciences, South Dakota State University, Brookings.*

Reproductive losses are significant in domestic animals and represent huge economic inefficiencies in livestock production. Across livestock species, embryonic mortality is the greatest contributor to reproductive losses. In most livestock species, early pregnancy diagnosis is an impediment to making significant progress to alleviate these losses. Perhaps unfairly, the female of each livestock species receives the blame for the majority of pregnancy failures. Research has focused on production of an optimal follicle that leads to ovulation of a highly fertile oocyte and production of steroids responsible for preparation of the female reproductive tract for pregnancy. Most studies have used hormonal manipulation of the estrous cycle and ovulation to identify factors affecting pregnancy success. Physiological maturity of the ovulatory follicle includes numerous reproductive processes and events obligatory for pregnancy establishment and maintenance. In sows, mares, and beef and dairy cows, oocytes derived from larger follicles were more competent, as assessed by in vitro development, than oocytes from smaller follicles. In cattle, ovulatory follicle size was highly correlated with serum estradiol concentration, and estradiol supplementation at AI improved pregnancy rates of cows ovulating smaller follicles. Greater ovulatory follicle size and more rapidly growing follicles at GnRH-induced ovulation were positively associated with fertilization success; while ovulatory follicle size, but not follicle growth rate, was positively associated with recovery of a viable embryo on d 7 in beef cows. In mares, age related changes in follicular signaling appear to play a large role in oocyte quality and fertility. This presentation focuses on follicular characteristics involved in early embryo survival, including follicle/oocyte maturation as affected by ovulatory follicle age, size, hormonal environment, and so on, and their effects on pregnancy establishment and maintenance. There is a strong relationship between the ovulatory follicle and steroid production related to early embryo development and pregnancy establishment.

Key Words: follicle, fertility, embryo survival

13 Deficiencies in the uterine environment and failure to support embryo development. G. A. Bridges,* *University of Minnesota, Grand Rapids.*

Pregnancy failure in cattle can result from failure to fertilize the oocyte or embryonic loss during gestation. Although fertilization failure occurs, embryonic mortality has a greater contribution to pregnancy failure. A variety of factors contribute to embryonic loss and it may be exacerbated in certain animals including high-producing lactating dairy cows and in some cattle in which estrous synchronization and timed AI was performed. Asynchronous follicular dynamics during timed AI protocols can induce ovulation of immature follicle that produce insufficient estradiol and a corpus luteum that potentially produces reduced progesterone concentrations compared with cows induced to ovulate mature follicles. In lactating dairy cows, circulating concentrations of steroids are reduced due to elevated feed intake causing increased liver blood flow and increased steroid catabolism in the liver. In each of these classes of animals that have decreased steroid concentrations, fertility is reduced compared with females that ovulate mature follicles at timed AI or to nonlactating dairy animals. Recent research in beef cows induced to ovulate immature follicles and lactating dairy cows suggest that deficient uterine function is the primary factor responsible for infertility in these animals. Failing to provide adequate concentrations of estradiol before ovulation results in prolonged effects on expression and localization of uterine genes and proteins that participate in regulating uterine functions during early gestation. Furthermore, progesterone concentrations during early gestation affect embryonic growth, interferon-tau production, and uterine function. Therefore, an inadequate uterine environment induced by insufficient steroid concentrations before and after ovulation could cause early embryonic death either directly by failing to provide an adequate uterine environment for embryo survival, adhesion, and implantation, or indirectly by failing to support appropriate embryonic growth which could lead to decreased conceptus size and malfunction of the process of maternal recognition of pregnancy.

Key Words: fertility, uterus, steroids

14 Interactions of the embryo, uterus and corpus luteum for sustenance of embryos. T. R. Hansen,* A. Q. Antoniazzi, J. J. Romero, R. L. Ashley, and R. C. Bott, *Animal Reproduction and Biotechnology Laboratory, Department of Biomedical Sciences, Colorado State University, Fort Collins.*

Interferon-tau (IFNT) from the ruminant conceptus disrupts oxytocin signaling and pulsatile release of prostaglandin F2α (PGF) in the endometrium through prevention of upregulation of the estradiol receptor, and consequently oxytocin receptor, which occurs during luteolysis. Microarray analysis revealed upregulation of several hundred genes in bovine endometrium and peripheral blood cells, and in ovine corpus luteum (CL) in response to early pregnancy that were mostly interferon-stimulated genes (ISG). For this reason, we hypothesized that IFNT not only protects pregnancy through paracrine action on release of endometrial PGF, but also has endocrine action through induction of resistance of the CL to lytic actions of PGF during early pregnancy. Antiviral activity, an indicator for type I IFN, increased in uterine vein blood on d 15 of pregnancy in sheep and was blocked through preadsorption with anti-IFNT antibody, providing evidence that IFNT was present in uterine vein blood. A specific (no cross-reactivity with other type I or II IFN) and sensitive (100 pg/mL) radioimmunoassay for IFNT was developed and used to detect IFNT in uterine vein blood from d 15–16 pregnant sheep. Global mass spectrometry was used to demonstrate presence of IFNT in uterine vein serum from a d 15 pregnant ewe. The ISG were upregulated in CL by d 14 of pregnancy and were localized primarily to large luteal cells, but also to small luteal cells in ewes. Culture of isolated ovine large and small luteal cells as well as mixed luteal cells with low (100 pg/mL) levels of IFNT caused upregulation of ISG. Endocrine delivery of IFNT (200 µg/d) using miniosmotic pumps into the uterine vein for 7 d (d 10–17 of estrous cycle) caused a delay in return to estrus beyond 32 d. Finally, systemic delivery (subcutaneous or jugular vein) of 20 µg of IFNT/d using miniosmotic pumps starting on d 10 of the estrous cycle, followed 24 h later by a challenge with PGF injection resulted in protection of the CL through d 13 based on serum progesterone profiles. It is inferred from these studies that IFNT protects early pregnancy in ruminants through paracrine action on the endometrium and also through endocrine action on the CL and peripheral blood cells in context of enhancing luteal resistance to PGF and the maternal ability to combat viral infections, respectively. USDA-NIFA-AFRI 2011-67015-20067.

Key Words: corpus luteum, endometrium, pregnancy

15 Limitations in uterine and conceptus physiology that lead to fetal losses.

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Conceptus losses in livestock occur throughout gestation. Clearly, the uterus and embryo/placenta/fetus play interconnected roles in these losses, the details of which depend on the period of gestation and the species. Studies in sheep and pigs have indicated that the uterine glands are essential for full fertility, based on experiments where gland development was reduced through the use of exogenous hormones. In sheep and cattle, normally the uterus is well able to support more than a single fetus, although these species differ in the consequences of multiple births. When 2 conceptuses are present, the placentas of cattle often anastomose, putting one fetus at risk if the other is lost. One likely reason this does not occur in sheep is because sheep embryos undergo intrauterine migration, similar to pigs. In pigs, the equidistant separation of conceptuses is likely to be essential for optimizing conceptus survival, as is the simultaneous and uniform elongation of blastocysts that occurs during the time of maternal recognition of pregnancy. Other studies in pigs have indicated that the size of the uterus influences litter size and therefore fetal losses. In response to crowded intrauterine conditions in the pig, increased conceptus losses begin to occur between d 30 and 40 of pregnancy, and further losses occur sporadically during later gestation. There is evidence that improved fetal erythropoiesis can reduce these losses. Reports also indicated that profound changes in placental development occur under crowded intrauterine conditions that may contribute to losses during late gestation. Reductions in placental stroma formation may compromise the ability of the pig placenta to adapt to reduced uterine space. Consistent with this, both hyaluronan and hyaluronidase activity are decreased in the placentas of small compared with large fetuses. These results suggest that improvements in placental stroma formation could improve placental ability to compensate for reduced intrauterine space, resulting in increased placental function and reduced fetal losses during late gestation. USDA is an equal opportunity provider and employer.

Key Words: placenta, erythropoiesis, hyaluronan

16 The spectrum of factors that impede pregnancy in dairy cows.

R. L. A. Cerri*[1], J. E. P. Santos[2], W. W. Thatcher[2], and J. L. M. Vasconcelos[3], *[1]University of British Columbia, Vancouver, BC, Canada, [2]University of Florida, Gainesville, [3]Sao Paulo State University, Botucatu, SP, Brazil.*

The fertility problem in dairy cows is complex and multifactorial but can be divided into 2 major categories: 1) failure to submit cows for insemination, and 2) extensive embryonic and fetal losses. Numerous factors influence these 2 categories (e.g., heat stress, energy balance, cow comfort, health, ovarian dynamics and uterine environment). In the past 10 yr, however, the trend in daughter pregnancy rate has been positive based on USDA data through 2010. This improvement is likely a direct effect of the intensive use of timed AI (TAI) programs, which improved submission rates and, to some extent, pregnancy per AI because of physiological optimization of the reproductive programs. Recently, the use of activity monitors in North American herds has improved submission rates, thereby reducing pharmacological interventions. Although fertilization rate is relatively high (80%), only around 40% of fertilized embryos result in a pregnancy at 60 d after insemination. Early and late embryonic losses are still an unsolved problem in lactating dairy cows and are partly explained by changes in ovarian and uterine physiology. More time between follicle emergence to ovulation concomitantly with decreased concentrations of circulating progesterone and estradiol, reduce embryo quality and create a suboptimal uterine environment that negatively affects pregnancy. Metabolic and health disorders also play major roles as they affect around 40 to 50% of cows in early lactation. Pregnancy per AI exceeds 50% in cows not affected by any clinical periparturient disorder. A pool of knowledge has been acquired regarding the interactive cellular and molecular mechanisms of the conceptus and endometrium within the periattachment period. However, additional research is needed to unveil the effects of steroid and metabolic hormones, health disorders, and among-cow differences in molecular mechanisms pivotal to successful pregnancy. Genetic selection and applied and basic technologies to improve submission rates and reduce pregnancy losses, without affecting milk production, will likely remain at the forefront to improve reproductive efficiency in modern dairy cows.

Key Words: dairy cows, estrous detection, pregnancy loss

Monday, July 16, 2012

POSTER PRESENTATIONS
Animal Health I

M1 Immunological and metabolic responses of Holstein and Jersey cows according to body condition score change prepartum. R. C. Chebel, L. G. D. Mendonça, P. R. B. Silva, and J. G. N. Moraes,* *Department of Veterinary Population Medicine, University of Minnesota, St. Paul.*

Objectives of this experiment were to evaluate the immune and metabolic responses of Holstein (H) and Jersey (J) cows according to body condition score (BCS) change (BCSC) prepartum. Data from 2 experiments were used. Experiment 1 was conducted with Holstein cows (n = 29) and experiment 2 was conducted with Jersey cows (n = 68). Cows received BCS on d −22 ± 7 and 1 ± 1 (calving = d0) and were classified as having lost (L) and as having not lost (NC) BCS prepartum. Blood was sampled on d −7, 0, 7, and 14 for determination of neutrophil phagocytosis (PHAGO) and oxidative burst (OXID) and expression of CD18 and L-selectin and concentrations of NEFA and glucose. Data were analyzed by Chi-squared and ANOVA for repeated measures. Percentages of H (65.5%) and J (51.5%) cows losing BCS prepartum were similar (P = 0.20). The interaction between breed and BCSC was associated with most of the innate immunity parameters evaluated because among J cows BCSC was not associated with innate immunity parameters (P > 0.10). On the other hand, HL cows had reduced PHAGO (57.8 ± 3.6 vs NC = 73.9 ± 4.8%; P < 0.01) and OXID (93.2 ± 0.7 vs 96.0 ± 0.9%; P = 0.02) than HNC cows. The interaction between breed and BCSC tended (P = 0.09) to be associated with intensity of OXID because HL cows had reduced OXID intensity than HNC cows (15857 ± 3052 vs 24770 ± 3782; P = 0.07). There was a tendency for the interaction between breed and BCSC to be associated with percentage of neutrophils positive for CD18 (P = 0.08) because HL cows tended to have reduced percentage of neutrophils expressing CD18 than HNC cows (74.1 ± 2.0 vs NC = 80.2 ± 2.5%; P = 0.06). Concentration of NEFA was associated with BCSC (L = 0.533 ± 0.038, NC = 0.429 ± 0.044mmol/L; P = 0.03) but was not associated with the interaction between breed and BCSC (P = 0.99). On the other hand, glucose concentration was not associated with BCSC (P = 0.50) or with the interaction between breed and BCSC (P = 0.62). Immunological parameters peripartum were differently affected by BCS loss prepartum in Holstein and Jersey cows.

Key Words: peripartum cow, body condition score, immunological parameter

M2 Treatment outcomes for clinical mastitis caused by *E. coli* in a Wisconsin dairy herd. M. J. Fuenzalida*[1], W. Oliveira[1], J. Gaska[2], and P. L. Ruegg[1], [1]*Department of Dairy Science, University of Wisconsin, Madison,* [2]*Gaska Dairy Health Services, Columbus, WI.*

The objective of this study is to describe the effect of intramammary antimicrobial treatment (ceftiofur) on milk yield, and somatic cell (SCC) reduction during a 42-d follow-up period. Clinical mastitis (CM) occurring in a single quarter (n = 133) was diagnosed between May 2011 and January 2012. Average milk yield was 42.3 kg/d, parity was 2.5, logSCC 1.95, and DIM was 162. Explanatory variables considered in the models were DIM, parity, previous cases of CM, previous SCC, and previous milk yield after treatment. Of 133 cases of clinical mastitis caused by *E. coli*, 75 were not treated and 58 received intramammary ceftiofur. PROG GENMOD was used for analyzing the binary outcomes (yes/no for SCC reduction, yes/no for milk yield reduction) and PROC GLM SAS 9.2 was used to analyze the continuous variable milk yield. Milk yield after occurrence of the case was 42.4 and 41.5 for treated and not treated cows, respectively but was not significantly affected by treatment (P = 0.48). One unit increase in logSCC was associated with 2.7 kg/d reduction in milk production. Occurrence of a previous case of CM was associated with about 4 kg/d less milk production. Treatment was not associated with SCC reduction (OR = 1.84, CI 0.32–10.31) or change in milk yield (OR = 0.78, CI 0.27–2.21). In this farm, treatment of CM caused by *E. coli* did not improve milk production or SCC compared with no treatment. Supported by AFRI Competitive Grant no. 2010–85122–20612

Key Words: clinical mastitis, SCC, milk yield

M3 Differential expression of the hepatic and adipose transcriptome in peripartal Friesian cows with endometritis. H. Akbar*[1], J. M. Khan[1], S. Meier[2], C. Burke[2], S. McDougall[3], M. Mitchell[4,5], S. L. Rodriguez-Zas[1], R. E. Everts[1], H. A. Lewin[1], J. R. Roche[2], and J. J. Loor[1], [1]*University of Illinois, Urbana,* [2]*DairyNZ Limited, Hamilton, New Zealand,* [3]*Cognosco, Animal Health, Morrinsville, New Zealand,* [4]*Liggins Institute, University of Auckland, Auckland, New Zealand,* [5]*University of Queensland Centre for Clinical Research, Brisbane, St. Lucia, Australia.*

Inflammation of the endometrial lining of the uterus (endometritis) often develops in dairy cows soon after calving. Afflicted animals can develop chronic infections of the uterus due to pathogenic bacteria. This disease causes poor reproductive performance, decreased energy balance, lower milk yield, and potentially hepatocellular damage. The objective of the current study was to uncover molecular changes induced by endometritis using expression profiling of liver and adipose transcriptomes. Postpartal liver and adipose tissue samples were harvested at slaughter from healthy (NUI; n = 6) cows or cows with endometritis (UIN; n = 6) at 29 d postpartum. Endometritis was defined as > 6% of uterine fluid nucleated cells being polymorphonuclear (PMN) cells; healthy cows had ≤ 1% PMN. Transcriptome expression was performed via bovine microarray (~13,000 oligonucleotides) and RT-PCR. Functional analysis of differentially expressed genes (DEG; P < 0.05, fold-change cut off ≥ or ≤ 1.5 UIN vs. NUI) was carried out using the dynamic impact approach (DIA) with the KEGG pathway database. A total of 97 DEG from liver (35 downregulated, 62 upregulated) and 144 from adipose (82 downregulated, 62 upregulated) were used for functional analysis. In liver, endometritis induced activation of selenoamino acid metabolism, complement and coagulation cascades, glycosphingolipid biosynthesis, and toll-like receptor signaling pathway. Bioinformatics analysis also revealed an inhibition of fatty acid oxidation, PPAR signaling, SNARE interactions in vesicular transport, and N-glycan biosynthesis. Functional analysis of adipose uncovered as the most induced pathways nicotinamide metabolism, glycosaminoglycan biosynthesis, and basal transcription factors. The most-inhibited pathways in adipose were taurine and hypotaurine metabolism, pantothenate and CoA biosynthesis, and TCA cycle. Quantitative PCR of liver tissue further revealed a marked increase in superoxide dismutase-2 (SOD2) and glutathione peroxidase (GPX1) expression in UIN, suggesting a greater state of oxidative stress in those animals. Overall, these preliminary results suggest that uterine infection after calving induces molecular alterations in peripheral tissues.

Key Words: uterine infection, transition cow, genomics

M4 A comparison of two antibiotics on growth performance in beef cattle treated for bovine respiratory disease (BRD). N. O. Minton*[1], L. L. Hawkins[2], and M. S. Kerley[1], [1]*University of Missouri, Columbia,* [2]*Bayer HealthCare, Animal Health, Shawnee Mission, KS.*

Therapy for bovine respiratory disease (BRD) commonly occurs throughout the receiving period. Proper treatment of BRD is critical to cattle performance throughout the feeding phase. We hypothesized differences in growth performance occur among different antibiotics used for treatment of BRD. Naïve crossbred steers (n = 102) were monitored for BRD over a 45-d growth study. Steers were randomly assigned to antibiotic treatments which consisted of either enrofloxacin (ENR; n = 51) (Baytril 100 Bayer HealthCare, Animal Health) or florfenicol + flunixin (F+F; n = 51) (Resflor Gold Merck Animal Health).Within treatment steers were categorized as no treatment (control), single treatment (ST), relapse (RL) or chronic. Steers were randomly assigned to 2 pens with treatment evenly distributed within pen. Two consecutive BW were recorded at treatment initiation, d 28, and d 45. Individual FI using the GrowSafe feed intake system and visual assessment were used to identify cases of BRD. Rectal temperatures of $\geq$40°C were diagnosed with BRD and treated with predetermined antibiotic. Control steers represent non treated steers. Chi-squared distribution determined morbidity and relapse rate were not different among ENR and F+F. ENR had greater percentages of chronics (6.2% vs. 2.1%; $P < 0.001$) with lower mortality rate (2.1% vs. 7.2%; $P < 0.001$) than F+F; respectively. IBW was not different among all categories between both ENR and F+F. ADG, F:G and total BW gain were not different between control steers and ENR ST and RL steers. ENR ST and RL steers tended to be more efficient than either category of F+F steers ($P = 0.11$). ENR ST steers had greater ADG (1.76+0.11 vs. 1.37+0.11; $P < 0.05$), FBW (333.63+6.77 vs. 311.86+6.77; $P < 0.05$) and BW gain (77.5+4.96 vs. 60.30+4.96; $P < 0.05$) than ST F+F steers. DMI as a percent of BW was not different on treatment day as well as 3 d before and after treatment of BRD between ST ENR and F+F steers. We conclude utilizing enrofloxacin for therapy of BRD corresponds to an increase in growth performance and feed efficiency during the receiving period in comparison to florfenicol + flunixin.

Key Words: health, feedlot, beef

M5 Feedback on data entry errors effect on the maintenance of accurate and consistent dairy health records. S. K. Giebel*[1], J. R. Wenz[1], S. A. Poisson[1], C. S. Schneider[2], and D. A. Moore[1], [1]*Department of Veterinary Clinical Sciences, Washington State University, Pullman,* [2]*College of Agricultural and Life Sciences, University of Idaho, Moscow.*

Maintenance of data quality is not a one-time effort; it requires continuous auditing and evaluation to ensure quality. One reason for this is that health data entry is not standardized in dairy management software (DMS), like reproductive records. The purpose of this study was to evaluate the time needed for producers to implement and maintain health data entry protocols. Forty-three dairies enrolled in a demonstration project on consistent and accurate health records, 51% from Eastern Washington (EWA), 26% from Western Washington (WWA), and 23% from Idaho (ID), with an average herd size of 2,683 cows (range 366–9,880). Producers were provided with error reports weekly until the percentage of errors dropped below 5.1% for 2 consecutive reports, at which point the dairy was considered graduated. All dairies continued to receive monthly error reports until January 2012. Reports provided feedback on data entry in comparison to their customized health event data recording protocols. The first report averaged 20.5% errors with a range of 0.0 to 81.3%. It took an average of 9 reports before a dairy graduated to monthly reporting, with a range of 4 to 21. Of those herds that contributed at least 3 mo to the study post graduation, nearly 50% never relapsed (relapse = error rate >5%) but if they did, it most commonly occurred in the first month post graduation. The average months to relapse was one (range 0–6). The error rate on the last report averaged 4.7% with a range of 0.0–16.6%. If the herd was using the Protocol function in Dairy Comp 305 or the Rx-Plus function in DHI-Plus before the start of the project, months to relapse was shorter than those that did not ($P = 0.01$). Median time to relapse was longer for large herds (>1950 cows) compared with smaller herds (4 vs. 2 mo; $P = 0.06$). Median time to relapse was 4 mo for EWA, 2 mo for WWA and 2.5 mo for ID ($P = 0.04$). For those producers less comfortable with computer use, there was a tendency for the rate of relapse to be faster compared with those more comfortable ($P = 0.08$). Dairies can implement and maintain consistent and accurate health records when provided with regular feedback.

Key Words: data recording protocols, dairy management software, dairies

M6 Impact of water and feed deprivation on physiological parameters in steers. J. A. Daniel*[1], P. H. Walz[2], J. A. Carroll[3], T. H. Elsasser[4], and B. K. Whitlock[5], [1]*Berry College, Mount Berry, GA,* [2]*Auburn University, Auburn, AL,* [3]*USDA-ARS Livestock Issues Research Unit, Lubbock, TX,* [4]*USDA-ARS Bovine Functional Genomics Laboratory, Beltsville, MD,* [5]*University of Tennessee, Knoxville.*

A report in rats demonstrated that dehydration as the result of 8 d of water deprivation increased leakage of endotoxin from the intestine (Zurovsky and Barbiro, 2000; Exp. Toxicol. Pathol. 52:37–42). Given the large number of bacteria in the rumen of cattle, a much shorter period of water deprivation may result in increased leakage of endotoxin and subsequent changes in the physiologic parameters. Therefore, the purpose of this study was to determine the effect of water and feed deprivation on physiologic parameters in steers. Holstein steers (n = 4) fitted with indwelling jugular and hepatic vein cannulas received a 72-h period of water and feed deprivation followed by reintroduction of water and feed for a 24-h period (96 h total) or a 96-h period with ad libitum water and hay access (control) in a switch back design with a 3-wk wash-out period between repetitions. Blood samples were collected and rectal temperatures (RT) were recorded every 6 h for a total of 96 h. Body weights were recorded every 12 h. Data were tested for effects of treatment, time, treatment × time interaction and replication using procedures for repeated measures with JMP software (version 7; SAS Institute Inc.). Water and feed deprivation increased packed cell volume at 30, 54, 60, and 66 h relative to control steers ($P < 0.05$). Total protein in the serum was increased at 48, 54, 66, 72, and 78 h in water and feed deprived steers compared with control steers ($P < 0.05$). The average body weight of water and feed deprived steers was less than control steers at 36, 48, 60, and 84 h ($P < 0.05$), and percent of body weight loss was greater in water and feed deprived steers at 24, 36, 48, 60, 72, and 84 h than control steers ($P < 0.05$). Rectal temperature of water and feed deprived steers was lower than control steers at 6, 12, and 66 h, and RT of water and feed deprived steers was higher than control steers at 72 h ($P < 0.05$). These results suggest that water and feed deprivation negatively affect steers before typical indicators of dehydration (packed cell volume and total protein) are altered.

Key Words: steers, water, feed

M7 Implementation of health data entry protocols effect on time for data management.

S. K. Giebel*[1], J. R. Wenz[1], S. A. Poisson[1], C. S. Schneider[2], and D. A. Moore[1], [1]*Department of Veterinary Clinical Sciences, Washington State University, Pullman,* [2]*College of Agricultural and Life Sciences, University of Idaho, Moscow.*

Producers want to be assured that it will not add time to the process of data management when implementing protocols for consistent and accurate dairy health data entry. Research done on data capture and entry into dairy management software (DMS) program is limited and dated. The purpose of this study was to assess the time taken to capture and enter health data before and after implementation and maintenance of data entry protocols. Twenty-three dairies enrolled in the demonstration project were used to evaluate the time taken to capture health data and enter it into their DMS program. Information was collected on the general flow of data from cow to computer during 2 visits, one before implementation of accurate and consistent health records and one 4 mo after maintenance. The difference in time, for data capture and entry, between the first and second visit was categorized as increased, decreased or no change. There were 22 dairies with complete data for the capture of health information. On average, it took dairy personnel 21.8 (range 2.3–65.8) seconds per cow to capture information at the first visit. After data entry protocol maintenance, it took an average of 17.6 (range 1.0–46.6) seconds per cow. Using a sign test, herds were more likely to either take less or the same amount of time for data capture between visits ($P < 0.001$). There were 18 dairies with complete data for entry of health information. On average, it took dairy personnel 4.6 (range 0.6–12.8) seconds per cow to enter data into the computer at the first visit. After protocol maintenance, it took an average of 3.3 (range 0.3–9.7) seconds per cow. Using a sign test, herds were more likely to either take less or the same amount of time for data entry between visits ($P < 0.01$). The only factors that appeared to influence data capture were related to on-farm protocols such as recording all hospital cow numbers in the parlor and the frequency of data capture in the parlor. Implementation of health data entry protocols for more accurate and consistent records did not add time to the process of data management.

Key Words: data capture, data entry, dairy management software

M8 Transcriptome analysis of liver tissue from calves infected with bovine viral diarrhea virus and *Mannheimia haemolytica.*

R. L. Mills*[1,2], L. Carlos-Valdez[2], L. O. Burciaga-Robles[2], D. Stein[2], D. L. Step[2], R. W. Fulton[2], U. DeSilva[2], and C. R. Krehbiel[2], [1]*Austin Peay State University, Clarksville, TN,* [2]*Oklahoma State University, Stillwater.*

Bovine respiratory disease (BRD) negatively affects animal growth and performance, leading to less desirable carcass characteristics. To understand the effects of BRD on liver gene expression, 16 crossbred steers (280.8 ± 32.5 kg) were divided into 2 treatment groups: the control group (CON) received an intratracheal dose of isotonic saline; an infected group (INF) was exposed to a PI-BVDV calf for 72 h followed by intratracheal inoculation with *Mannheimia haemolytica* serotype A (MH). Liver biopsies were taken before exposure to both pathogens (PRE), 12 (12H), and 24 h (24H) following bacterial inoculation. Total RNA was extracted and oligonucleotide microarray hybridization performed on PRE and 24H sampling times ($n = 6$). Significance for the microarray was set at fold change greater than |2| and $P < 0.001$. Quantitative RT-PCR was performed to examine gene expression at the indicated time points with significance set at $P < 0.05$. Pathway analysis was conducted using Ingenuity Pathway Analysis. Microarray analysis found 44 genes were induced and 45 genes were suppressed following 24h of dual infection. Pathway analysis revealed lipid metabolism, molecular transport, cellular assembly and organization, carbohydrate metabolism, and small molecule biochemistry were the molecular and cellular functions most affected. PCR showed that β-site APP-cleaving enzyme 1 (BACE1) was increased 2.3-fold in INF compared with CON ($P < 0.05$). S100 calcium binding protein A8 (S100A8) transcripts increased 28.9-fold in INF versus CON ($P < 0.001$), increased more than 21-fold in 12H and 24H above PRE ($P < 0.01$), and exhibited an infection × time interaction with INF-12H and INF-24H showing mRNA increases of 44- and 42-fold above CON-PRE, respectively ($P < 0.01$). Fatty acid desaturase 2 (FADS2) was suppressed 73.2-fold in INF relative to CON ($P = 0.05$) and tended to be downregulated 29.5- and 95.1-fold at 12H and 24H versus PRE ($P = 0.09$). Gene expression changes in liver are indicative of hepatic inflammation, which may suggest calves with BRD are susceptible to the development of fatty liver.

Key Words: beef cattle, bovine respiratory disease, gene expression

M9 See abstract #100

M10 Changes in biomarkers of the nitrooxidative stress response and prolactin signal transduction elements to *E. coli* infection in the mammary gland.

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Key features of the mammary gland (MG) response to *E. coli* infection (INFec) include (a) the cellular generation of reactive oxynitrogen molecules (Roxn) derived from nitric oxide (NO) and superoxide anion ($O_2^{-\bullet}$) and (b) loss of responsiveness to lactogenic hormone signaling. Of significance to the MG is the damage done to mammary epithelial cells (MEC) by Roxn generated by MEC and neutrophils (PMN). The aim of this study was to determine the time course of production and cellular localization of biomarkers of the Roxn pathway and to quantify changes in PRL receptor (PRLr)-janus kinase-2 (JAK-2) signaling. As applied across the 4 quarters of the MG, 5 multiparous lactating Holstein cows received treatments consisting of PBS or 400 cfu *E. coli* administered 12 or 24 h before euthanasia. MG tissues (lobulo-alveolar) were prepared for immunohistochemical (IHC) localization of biomarker antigens. IHC biomarkers for the Roxn pathway elements consisted of 3′-nitrotyrosine (3-NT, cellular protein nitration) as well as inducible (i) and constitutive (e) isoforms of nitric oxide synthase (NOS, NO generation), and xanthine oxidase (XO, $O_2^{-\bullet}$ generating capacity). Prolactin (PRL) signal transduction elements markers were PRLr, JAK-2, and nitrated JAK-2 (ntJAK, Roxn-inactivated JAK-2). Antigenic markers were quantified by image analysis of digitally captured micrographs. Mean pixel densities of all antigenic determinants were affected by time and/or cell type ($P < 0.02$). Infiltrating PMN were present only at 24 h. The 3-NT increase peaked in MEC (4.6-fold) at 12h and in PMN (3.7-fold) at 24 h. Both iNOS and eNOS increased in MEC at 12 and 24 h but only iNOS was increased in PMN at 24 h. XO increased 118% in MEC at 12 h ($P < 0.04$) but normalized by 24h. PRLr was decreased by 29 ($P < 0.03$) and 54% ($P < 0.01$) in MEC at 12 and 24 h, respectively. JAK-2 was decreased 84% ($P < 0.02$) at 24 h, respectively. ntJAK was increased 22- ($P < 0.005$) and 4-fold ($P < 0.05$) at 12 and 24 h, respectively. The

data indicate that changes in these measured cellular responses to INFec occur in the MG as a function of time and cell type.

Key Words: mammary gland, infection, biomarker

M11 Associations among subclinical hypocalcemia, neutrophil function, and incidence of uterine disease in dairy cows of low or high risk of developing metritis. N. Martinez*[1], F. S. Lima[1], R. S. Bisinotto[1], L. F. Greco[1], E. S. Ribeiro[1], F. Maunsell[2], K. N. Galvão[2], C. A. Risco[2], and J. E. P. Santos[1], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*Department of Large Animal Clinical Sciences, University of Florida, Gainesville.*

Objectives were to establish relationships among subclinical hypocalcemia (SCH) and concentrations of energy metabolites, neutrophil (PMN) function and incidence of uterine diseases in dairy cows considered to be of low (LRM; normal calving) or high-risk (HRM; calving problems) of developing metritis. In this prospective cohort study, HRM cows (n = 55) were matched with LRM (n = 55) based on parity and day of calving. Rectal temperature (RT) and vaginal discharge were monitored in the first 12 DIM. Metritis was defined as fetid, watery vaginal discharge, and puerperal metritis (PuMet) was defined as metritis concurrent with RT ≥ 39.5°C. Blood was sampled at 0, 1, 2, 3, 4, 7, and 12 DIM and analyzed for Ca, NEFA and BHBA. Neutrophil function was measured at 0, 1, and 3 DIM. Serum Ca ≤ 8.59 mg/dL in at least one day within the first 3 DIM defined SCH based on receiver operator characteristic analysis (AUC = 0.77; $P < 0.01$). Data were analyzed using PROC GLIMMIX of SAS. Cows with SCH had fewer ($P < 0.01$) circulating blood PMN (3.0 vs. 4.5 $\times 10^3$ PMN/μL) in the first 3 DIM, and reduced ($P < 0.05$) proportion of PMN with oxidative burst (32.4 vs. 42.5%) and phagocytosis (61.3 vs. 73.1%) at 3 DIM compared with normocalcemic (NC) cows. The mean RT of cows increased ($P < 0.01$) when metritis was associated with SCH (39.0°C) compared with cows with metritis and NC (38.7°C). Among HRM cows, those with SCH had greater ($P < 0.05$) incidence of metritis and PuMet [77.8% (35/45) and 53.5% (24/45)] compared with NC cows [(20.0% (2/10) and 10.0% (1/10)]. Among LRM cows, those with SCH had greater ($P < 0.05$) incidence of metritis and PuMet [40.7% (11/27) and 29.6% (8/27)] compared with NC cows [(14.3% (4/28) and 0.0% (0/28)]. Metritis did not influence concentrations of NEFA or BHBA; however, cows with SCH had greater ($P < 0.01$) NEFA (704.6 vs. 426.8 μM) and BHBA (9.9 vs. 7.7 mg/dL) concentrations compared with NC cows. These findings indicate that cows with SCH have impaired innate immunity and increased incidence of uterine diseases compared with NC cows regardless of calving problems.

Key Words: subclinical hypocalcemia, neutrophil function, metritis

M12 Hepatic and peripheral interferon responses to bovine respiratory disease in feedlot steers. J. O. Baggerman,* C. A. Gifford, and C. R. Krehbiel, *Oklahoma State University, Stillwater.*

Bovine respiratory disease (BRD) is the most economically important disease in the feedlot industry. Several pathogens contribute to BRD, yet the mechanism by which these pathogens evade immune response remains unclear. Conflicting evidence suggests that the interferon (IFN) response is impaired by BRD pathogens while others have shown robust IFN response in BRD-infected animals. We hypothesize that the IFN response is muted in cattle that exhibit sustained BRD infection. Liver biopsies were collected and RNA isolated from control calves (CONT, n = 6); calves treated once for BRD (1TRT, n = 6); treated twice for BRD (2TRT, n = 6); or treated 3 times for BRD (3TRT, n = 6). Expression of Interferon Stimulated Gene-15 (*ISG15*) and Myxovirus resistance protein 1 (*MX1*) mRNA levels was quantified. Relative to CONT, *MX1* mRNA levels increased ($P < 0.05$) over 7-fold in liver biopsies from 1TRT, but were similar ($P > 0.10$) to CONT for 2TRT and 3TRT. Likewise, *ISG15* mRNA levels were 40-fold greater ($P < 0.05$) than CONT for 1TRT, but 2TRT and 3TRT were similar to CONT. To determine if the IFN response is impaired with sustained BRD infection as suggested by the changes in gene expression in liver biopies, *MX1* mRNA levels in peripheral blood leukocytes (PBL) was evaluated from chronically infected calves (CHRON, n = 3) and controls (CONT, n = 3). Additionally, peripheral blood mononuclear cells (PBMC) were isolated from CHRON (n = 6) and CONT (n = 6) calves. For each animal, PMBC were isolated and plated into 6 well plates (4 million cells/mL; 4 wells/animal). Two wells served as a control and 2 wells were treated with human interferon-α (Sigma-Aldrich; 2.5 ng/mL) for 8 h before harvest for mRNA extraction. In PBL samples, *MX1* mRNA levels were similar ($P > 0.10$) in CHRON and CONT2 indicating that the type I interferon response was not active. However, in PBMC challenged with IFN, *MX1* mRNA increased approximately 100-fold in both CHRON and CONT2 groups compared with their own non-treated controls. Results demonstrate that the IFN response is reduced in calves treated multiple times for BRD, but the IFN pathway is still responsive to exogenous IFN. Thus, IFN might be a viable treatment alternative in calves that remain sick after 1 to 2 treatments for BRD.

Key Words: bovine respiratory disease, interferon, interferon stimulated genes

M13 Meta-analysis of *Trypanosoma* prevalence in livestock in the Americas. Z. J. Simoni[1], H. E. Rodulfo[1], M. De Donato*[1,2], M. I. Takeet[3], S. O. Peters[2,4], and I. G. Imumorin[2], [1]*IIBCA, Universidad de Oriente, Cumana, Venezuela,* [2]*Dept. Animal Science, Cornell University, Ithaca, NY,* [3]*Dept. Veterinary Microbiology & Parasitology, Federal University of Agriculture, Abeokuta, Nigeria,* [4]*Dept. Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria.*

Cattle tripanosomosis is a hemoparasitic disease caused by species of *Trypanosoma*, transmitted through dipterans of the genus *Tabanus*, in Central and South America. *T. evansi* and *T. vivax* are species that infect horses and cattle, respectively. They have been reported in at least 10 South American countries, including Colombia, Venezuela, Bolivia, Peru, and Brazil. We surveyed data on prevalence and clinical signs reported for *T. vivax* in water buffalo and cattle in these countries. Studies of genetic characterization indicate that the circulating species in South America is very similar to *T. vivax* from West Africa. *T. vivax* has been known to produce economic losses in the livestock industry, causing mortality, poor weight gain, lower fertility, abortion, and low production of milk and colostrums, in addition to costs associated with control (drugs and veterinary fees). *T. evansi* can cause a serious anemic disease in horses, camels, dogs and elephants. In South America, species such as capybara, coati, and wild rats have been found infected by *T. evansi*, without showing clinical alterations, thus, being considered as natural reservoirs. Recent studies have demonstrated that *T. evansi* has an aberrant kADN without maxicircles and the genetic analysis of kADN have shown that strains from equids of Africa, Asia y South America have similar sequences in the minicircles. *T. theileri* has been found in cattle in South and North America, and although this species is considered non-pathogenic, its pathogenicity has been linked to coinfection with other hemoparasites or subjected to severe stress. *T. equiperdum* has been reported in South and Central America in horses, but its form of transmission is by sexual intercourse, associated with important clinical symptoms. The effects of these *Trypanosoma* species on livestock throughout this region especially in isolated rural areas with attendant consequences on the economy of small to medium size producers are highlighted.

Key Words: trypanosomosis, livestock, parasite

M14 Cytokine production of isolated CD4+ T-cells from high and low immune responder dairy cows during the peripartum period. M. A. Paibomesai* and B. Mallard, *University of Guelph, Guelph, Ontario, Canada.*

The peripartum period is one of transition and high stress for dairy cows. It is associated with higher incidents of both metabolic and pathogenic disease. Both antibody (AMIR; IL-4 dominated) and cell mediated (CMIR; IFNγ dominated) immune responses (IR) play a key role in the maintenance of health in cattle protecting against extracellular and intracellular pathogens. These processes are induced and maintained by CD4+ T-helper cells, which undergo specific shifts in population and function in response to parturition effects. The aim of this study was to determine the effects of parturition on cytokine production of CD4+ T-cells isolated from highAMIR/lowCMIR (hiAMIR) and highCMIR/lowAMIR (hiCMIR) cows. Previously IR phenotyped cows were selected based on hiAMIR (n = 12) and hiCMIR (n = 11) responses to test antigens. Isolated CD4+ T-cells collected at 28 d prepartum, 4 d postpartum, and 21 d postpartum from these groups were stimulated with the mitogen, Concanavalin A (ConA) and incubated for 24hrs. Cell culture supernatants were collected and IL4 and IFNγ concentrations were quantified by ELISA and analyzed using ANOVA. There was no difference in IL4 concentration across all time points for hiCMIR cows and an increase of IFNγ ($P = 0.0223$) was observed between 4 d postpartum (3366 pg/mL) and 21 d postpartum (7755 pg/mL). There was a decrease of IL4 ($P = 0.0474$) from 28 d prepartum (496 pg/mL) to 21 d postpartum (212 pg/mL) in hiAMIR cows and no difference observed for IFNγ concentration in this group. There was a difference between hiAMIR and hiCMIR groups at 21 d postpartum with hiCMIR isolated T-cells producing more IL4 than hiAMIR group ($P = 0.0161$) and a tendency to produce more IFNγ ($P = 0.0591$). In conclusion, it is evident that T-helper cells isolated from hiAMIR and hiCMIR show different responses to parturition effects in terms of cytokine production. These differences could be in response to biases in CMIR and AMIR in these 2 groups and was most notable at 21 d from parturition.

Key Words: peripartum period, cytokines, T-helper cells

M15 Space allowance influences Holstein bull calf innate immunity after castration. L. E. Hulbert[1], M. S. Calvo*[1], M. A. Ballou[2], K. C. Klasing[1], and F. M. Mitloehner[1], [1]*Department of Animal Science, University of California, Davis,* [2]*Animal and Food Sciences, Texas Tech University, Lubbock.*

Objectives were to determine if space allowance in wooden hutches influences the innate immune responses of Holstein bull calves after castration. Calves were randomly assigned at 4 d of age to either conventional (Cnv; 0.46 m^2 space; n = 18), medium (Med; 0.70 m^2space; n = 17), or large (Lrg; 1.39 m^2 space; n = 18) hutches. Calves were surgically castrated at 24 d. Peripheral whole blood (WB) samples were collected at −1, 1, 5, and 12 d relative to castration. All calves had increased plasma cortisol 1 d after castration ($P \leq 0.01$). Plasma haptoglobin (Hap) increased from pre-castration concentrations 1 d after castration in all calves, but Med-calves had greater Hap 5 d after castration compared with pre-castration ($P \leq 0.05$). Cnv-housed calves had greater Hap concentrations than Med- and Lrg-housed calves, especially at 12 d after castration ($P \leq 0.05$). The day before castration, Cnv-calves had the greatest WB killing (WBK) of *E. coli*, but 1 d after castration, WBK in Cnv-calves decreased to percentages lower than Med- or Lrg-calves ($P \leq 0.05$). Within 12 d after castration, WBK in Cnv-calves returned to similar percentages as pre-castration. The Lrg-calves had the least Tumor Necrosis Factor (TNF)-α concentrations from WB stimulated with endotoxin 1 d after castration ($P \leq 0.05$), but Lrg-calve TNF-α increased at 5 d after castration to concentrations greater than 1 d before castration ($P \leq 0.05$). Percentage of neutrophils undergoing phagocytosis and oxidative burst to *E. coli* tended ($P = 0.06$) to decrease in Lrg-calves following castration, with the least percentage at 12 d after castration. Lrg-calves also had suppressed intensity of neutrophil oxidative burst compared with the other calves ($P \leq 0.01$). Modifying wooden hutches to the maximum space did not seem to positively influence calf innate immune function during castration, when there is a great risk of infection.

Key Words: free-space, inflammation, stress

M16 Effects of *Bacillus cereus* var. *toyoi* (Toyocerin) on the immune system of calves. A. Aris*[1], A. Serrano[1], M. Terré[1], G. Jiménez[3], M. Castillo[3], and A. Bach[1,2], [1]*Department of Ruminant Production, IRTA, Caldes de Montbui, Spain,* [2]*Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain,* [3]*Rubinum SA, Rubí, Spain.*

Bacillus cereus var. *toyoi* (Toyocerin) has shown beneficial effects on the immune system of pigs and poultry, but it has not been studied on cattle. The objective of this experiment was to evaluate the effects of Toyocerin on the immune system of calves. Twenty-four Holstein calves (75.2 ± 1.87 kg of BW and 77 ± 0.7 d of age), were randomly distributed according to BW in 2 groups: 12 calves were assigned to a conventional concentrate feed (CTR), and the other 12 calves were fed the same concentrate feed supplemented with 2×10^8cfu *Bacillus cereus var. toyoi*/kg concentrate (TOY). Animals were vaccinated at d 0 with IBRaxion vaccine (Mérial) against infectious bovine rhinotracheitis (IBR) and re-vaccinated at d 20 of the study. On d 0 and 56, blood samples were taken to assess the antibody titer against IBR vaccine. Animals were killed at 60 to 67 d of the study. Before sacrifice, a blood sample was obtained to evaluate the proliferation capacity of peripheral blood mononuclear cells (PBMC). Immediately after sacrifice, animals were abdomen opened, and the whole gastrointestinal tract was removed. Jejunal fragments were sampled to analyze IgA and cytokines expression by qPCR. Data were analyzed by ANOVA using the treatment as the main effect. There were no differences in PBMC proliferation between the 2 treatments. The TOY calves tended ($P = 0.07$) to present a greater antibody response than CTR calves (92.5 ± 1.50% vs. 82.5 ± 3.50%, respectively); whereas no differences in IgA expression were observed at jejune level. Calves in the TOY group showed a clear increase ($P < 0.05$) in the expression level of Th2 cytokines such as IL-10 ($3.12 \times 10^{-3} \pm 0.8x10^{-3}$) in comparison to calves in the CTR group ($1.37 \times 10^{-3} \pm 0.3 \times 10^{-3}$), which would explain the observed improvement in humoral response to vaccination. On the other hand, the levels of Th1 cytokines related to cellular response, such as IL-12 and IL-1β, were numerically lower in TOY group than in CTR group. In conclusion, these preliminary results indicate that Toyocerin exerts a positive effect on the modulation of the immune response in calves.

Key Words: *Bacillus toyoi*, immune response, probiotic

M17 Space allowance influences the innate immune responses of Holstein calves during weaning. L. E. Hulbert*[1], M. S. Calvo[1], M. A. Ballou[2], K. C. Klasing[1], and F. M. Mitloehner[1], [1]*Department of Animal Science, University of California, Davis,* [2]*Animal and Food Sciences, Texas Tech University, Lubbock.*

Objectives were to determine if increased space allowance in wooden hutches influences the innate immune responses of Holstein bull calves during weaning. Calves were randomly assigned at 4 d of age to either conventional (Cnv; 0.46 m^2 space; n = 18), medium (Med; 0.70 m^2 space; n = 17), or large (Lrg; 1.39 m^2 space; n = 18) hutches. Calves were fed 227 g as-fed milk replacer (MR) twice daily (am and pm) until weaning and offered a calf starter ad libitum throughout the experiment. Weaning was initiated at age 53 d by removal of the pm MR feeding and was completed at age 64 d by removal of the am MR. Peripheral whole blood (WB) samples were collected before the am MR at age 53, 57, 64, 67 and 71 d. At age 67 and 71 d, all calves had increased circulating cortisol and neutrophil:lymphocyte and decreased Interferon- γ secretion from WB stimulated with phytohemagglutinin, compared with pre-weaning measures ($P \leq 0.01$). Also, at age 67 and 71 d, Med-calves had greater tumor necrosis factor-α secretion from WB stimulated with endotoxin than the other treatments ($P \leq 0.05$). In all calves, plasma urea nitrogen (UN) was increased at age 67 d compared with pre-weaning ($P \leq 0.01$) and was greatest among Cnv-calves ($P \leq 0.05$). Plasma haptoglobin (Hap) increased from pre-weaning in Cnv- and Med-calves ($P \leq 0.01$), but did not change over time among Lrg-calves. In addition, Lrg-calves had the least WB killing of *E. coli* at age 64 d ($P \leq 0.05$) and had less neutrophil phagocytosis and oxidative burst responses to heat-killed *E. coli* at age 53 and 64 d compared with the other calves ($P \leq 0.05$). Weaning was stressful for all calves, especially after the second bottle was removed. However, a moderate increase in space allowance for calves housed in wooden hutches may be beneficial to innate immune responses during weaning, while the largest increase in space allowance may negatively affect innate immunity.

Key Words: free-space, wean, inflammation

M18 Group-housed Holstein bull calves have decreased innate immune responses compared to individually housed calves after surgical castration. L. E. Hulbert[1], M. S. Calvo[1], R. A. Kurzbard*[1], M. A. Ballou[1], K. C. Klasing[1], and F. M. Mitloehner[1], [1]*Department of Animal Science, University of California, Davis,* [2]*Animal and Food Sciences, Texas Tech University, Lubbock.*

Objectives were to (1) determine if housing calves in groups of 3 (Group; n = 9 pens) or individually (Indv; n = 18) influences the innate immune responses of Holstein bull calves following surgical castration and (2) determine whether the innate immune responses of grouped calves is influenced by their ADG ranking within a pen (low = 0.80 ± 0.116; mid = 1.27 ± 0.116; or high = 1.68 ± 0.116 kg/d. All calves were surgically castrated at 24 d of age. Peripheral whole blood (WB) samples were collected at −1, 1, 5, and 12 d relative to castration. At 12 d after castration, all calves had greater plasma cortisol than pre-castration measures ($P < 0.01$). In Indv calves, neutrophil:lymphocyte (N:L) did not change after castration ($P > 0.10$), but N:L increased in Group calves 1 d after castration ($P \leq 0.05$). In addition, 12 d after castration, Group calves had greater plasma haptoglobin (Hap) than Indv-calves ($P < 0.01$). In contrast, before castration Indv-calves had greater WB killing (WBK) of *E. coli* than Group calves ($P \leq 0.05$) and the day after castration, WBK decreased in Indv calves to percentages lower than Group-calves ($P \leq 0.05$). Within 12 d after castration the WBK of Indv calves had returned to pre-castration measures ($P \leq 0.05$). At 5 and 12 d after castration, all calves had increased tumor necrosis factor (TNF)-α concentrations in WB stimulated with endotoxin compared with pre-castration ($P < 0.01$). Over the entire study period, neutrophil oxidative burst response to heat-killed *E. coli* was lower in Group calves compared with Indv calves ($P \leq 0.05$). Mid-ranked Group calves had higher interferon-γ secretion from whole blood cultures stimulated with phytohemagglutinin 1 and 12 d after castration than either the high- or low-ranked calves ($P \leq 0.05$). These data suggest that group housing calves in wooden hutches during castration may negatively influence innate immune function. However, group-housing had the least negative effect on immune function in mid-performing calves.

Key Words: bovine, grouping, stress

M19 A transient receptor potential channel 4 (TRPC4) gene to study response to gastrointestinal nematode infection in parasite-resistant goats. M. M. Corley* and J. Ward, *Virginia State University, Petersburg.*

Gut expulsion of a variety of mammalian (human, sheep, and mice) nematodes requires mechanisms that enhance gut contractions and glycoprotein hyper-secretion to allow detachment of the nematode from the gut wall. *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 transient receptor potential cation channels (TRPC) allows membrane depolarization and entry of calcium into the cell, thereby resulting in smooth muscle contraction. Deletion of TRPC4 in mice greatly reduces intestinal motility and contractility. To date, the relationship between gene expression of TRPC4 and the response to GIN infection has not been assessed in goats or any other species. This study evaluated gene expression of TRPC4 in selected pasture exposed parasite resistant goats. Intestinal tissues were harvested from goats exhibiting susceptibility and resistance to *H. contortus*. Primers were designed from conserved regions of TRPC4 human, bovine, mouse and rat nucleotide sequence alignments. Total RNA was extracted from homogenized goat intestinal tissues and real time RT-PCR (qRT-PCR) was performed to determine TRPC4 gene expression. The qRT-PCR results showed that TRPC4 was upregulated ($P < 0.05$) in goats naturally susceptible to *H. contortus* infection. Breed and gender differences ($P < 0.05$) in TRPC4 expression were observed. Overall, there was a strong positive ($P < 0.05$) correlation between TRPC4 gene expression and FAMACHA eye color chart scores and fecal egg counts, and strong negative correlation ($P < 0.05$) with packed cell volume in goats. These data indicate that TRPC4 may be useful in elucidation of the relationship between gastrointestinal contractility and the response to gastrointestinal nematode infection in goats as well as other species.

Key Words: goat, gastrointestinal nematode, TRPC4

M20 Use of selected blood parameters to identify markers of heat-sensitivity in Angus and Romosinuano heifers. R. Chaffin,* B. A. Scharf, J. S. Johnson, J. Bryant, D. Kishore, P. A. Eichen, and D. E. Spiers, *University of Missouri, Columbia.*

A study was performed to determine blood parameter differences in heat-sensitive Angus (ANG) and heat-tolerant Romosinuano (RO) heifers in response to heat stress. Eighteen month-old ANG (n = 11; 306.7 ± 25.9 Kg BW) and RO (n = 10; 312.9 ± 32.0 kg BW) heifers were maintained in the Brody Environmental Center (University of Missouri-Columbia) at cycling thermoneutral air temperature (TN, 18.5–23.5°C) for 7 d, followed by either continued maintenance at TN or exposure to heat stress (HS, 18.5–38°C) for the remaining 12 d of the study. Heifers received melengestrol acetate (0.5mg/animal/day) to suspend reproductive cycling. Blood samples were obtained via jugular venipuncture at TN (d 5), early HS (EH, d 10), and late HS (LH, d 17), and analyzed for a variety of parameters. Rectal temperature (Tcore) was measured with a thermistor thermometer 6 times daily. On d 5, average Tcore did not differ between breeds ($P = 0.89$). During EH and LH, Tcore was significantly higher in ANG overall ($P = 0.001$), and higher among HS ANG than other groups (~1°C, $P = 0.025$). Though insignificant, Tcore tended to rise continually between EH and LH among HS ANG (~0.4°C) while falling in HS RO (~0.3°C). RO had lower triglycerides (TAG) than ANG on d 5 ($P = 0.028$). On d 10 and 17, RO still exhibited lower TAG than ANG ($P = 0.004$), with no effect of HS on either breed. Cholesterol (CHO) was not different between ANG and RO on d 5 ($P = 0.36$), but ANG showed higher levels of CHO than RO during treatment ($P = 0.04$), with HS exposure causing a further reduction below TN level ($P = 0.02$). On d 5, RO had higher alkaline phosphatase (ALP) than ANG ($P = 0.012$), as well as on d 10 and 17 ($P = 0.004$). In general, HS lowered ALP on d 17 from the pretreatment level ($P = 0.05$). These results suggest that blood TAG and ALP levels may serve as markers for detecting potential heat-sensitivity before stress, while blood CHO and ALP levels may be useful markers for heat-sensitivity in beef heifers during stress.

Key Words: heat stress, Angus, Romosinuano

M21 Variation in innate immune parameters in Holstein calves is influenced by housing environment and physiological period.

M. D. Sellers,* D. L. Hanson, A. R. Pepper-Yowell, C. J. Cobb, and M. A. Ballou, *Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

Objective was to determine if housing environment and physiological state influence the proportion of variation in innate immune parameters due to time, between calves, and within calves during the neonatal, weaning, and commingling periods in Holstein calves. Ninety-nine calves (2 ± 1 d old) were randomly assigned to 5 treatments: 1, 2, or 3 calves/pen indoors (IN1, n = 21; IN2, n = 20; IN3, n = 18), and 1 or 3 calves/pen outdoors (OUT1, n = 21; OUT3, n = 20). Weaning started on d 43 with removal of PM milk, and was completed when starter consumption was 800 g/d. Calves were commingled on d 91 by randomizing all calves into outdoor group hutches (n = 5 calves/hutch). Peripheral blood samples were collected during neonatal (d 3, 10, 21), weaning (d 45, 47, 53), and commingling (d 91, 94, 99) periods and analyzed for neutrophil oxidative burst (OB) capacity when cocultured with an *Escherichia coli*, neutrophil L-selectin expression, whole blood secretion of tumor necrosis factor-α (TNF) when cocultured with lipopolysaccharide, and plasma concentration of haptoglobin. For each treatment within a period, variation was partitioned using Type III sums of squares estimates and reported as eta-squared, or the proportion of variation attributable to a given effect compared with total variation. Sources of variation included: variation due to time (DAY), between-calf (BET) and residual (RES). Values are reported as ranges or means across treatments. During the neonatal period, OUT3 calves had a larger BET proportion than OUT1 calves for neutrophil L-selectin expression (0.44 vs. 0.20) and OB capacity (0.54 vs. 0.29), and plasma haptoglobin (0.25 vs. 0.16). During weaning, OUT1 calves had higher BET proportions than OUT3 calves (0.56 vs. 0.23) for haptoglobin. The BET accounted for more variation across treatments during weaning when compared with the neonatal period for TNF secretion (0.57 vs. 0.40), percent of cells OB positive (0.64 vs. 0.51), and OB capacity (0.66 v 0.43). Proportion of variation due to DAY was lower during weaning than during the neonatal period (0.13 vs. 0.39). The BET variation for percentage of neutrophils positive for OB decreased during commingling compared with weaning (0.45 vs. 0.64). Differences in housing environment and physiological period influence proportion of residual variation, variation between calves, and variation due to time.

Key Words: calf, housing, immune

M22 Intravaginal administration of lactic acid bacteria modulated innate immune responses of periparturient dairy cows.

Q. Deng, J. F. Odhiambo, T. Lam, S. M. Dunn, and B. N. Ametaj,* *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

Dairy cows are characterized by a suppressed immunity around parturition, which increases their susceptibility to uterine infections. The goal of this investigation was to evaluate innate immune responses of transition dairy cows administered intravaginally with a mixture of lactic acid bacteria (LAB). In total, 152 pregnant Holstein cows were randomly assigned, based on parity and BCS, into 3 groups 2 wk before the expected day of calving. Cows received intravaginally a mixture of LAB or carrier (sterile skim milk) once per week at −2, −1, and +1 wk relative to the day of calving as following: treatment 1 (TRT1) - 2 consecutive LAB and 1 carrier dose; treatment 2 (TRT2) - 3 consecutive LAB doses; control (CTR) - 3 consecutive carrier doses. LAB were a mixture of *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138, and FUA3140 stored in sterilized skim milk. The LAB were infused intravaginally with a sterile insemination pipette at 10^8 to 10^9 cfu per dose. Blood samples were collected from the tail vein before each treatment and once per wk up to +8 wk. A subset of serum samples from 32 cows were used to analyze TNF-α, haptoglobin, and lipopolysaccharide-binding protein (LBP) by ELISA. Results demonstrated that both probiotics and parity had an effect on the concentration of TNF-α in serum. The concentrations of TNF-α were 231, 706, and 326 pg/mL in TRT1, TRT2, and CTR, respectively ($P < 0.05$). Primiparous cows had lower concentrations of TNF-α than multiparous cows (189 vs. 654 pg/mL) ($P < 0.01$). The interaction between TRT and parity showed a tendency to affect the concentration of TNF-α ($P < 0.1$). Concentrations of haptoglobin in serum were 407, 262, and 390 µg/mL in TRT1, TRT2, and CTR, respectively ($P > 0.05$). There was an interaction of TRT and parity on concentrations of haptoglobin ($P < 0.05$) in the serum, although no effect ($P > 0.05$) of treatments was obtained. Concentrations of LBP in the serum were 7,878, 7,500, and 8,337 ng/mL in TRT1, TRT2, and CTR, respectively ($P > 0.05$). Serum concentrations of both haptoglobin and LBP changed with wk ($P < 0.01$). Overall, intravaginal application of LAB modulated innate immune responses in transition dairy cows.

Key Words: dairy cows, lactic acid bacteria, innate immunity

M23 Intravaginal administration of a mixture of lactic acid bacteria lowered the incidence of clinical diseases in transition dairy cows.

Q. Deng, J. F. Odhiambo, T. Lam, S. M. Dunn, and B. N. Ametaj,* *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

Infertility is the main cause of culling of dairy cows in Canada causing dairy industry more than $667 million in losses during 2010. More than 35% of the cows in a herd are affected by various forms of reproductive tract infections. Infertility is highly related to bacterial infections of the uterus immediately after calving and uterine infections are highly associated with other periparturient diseases. The objective of this study was to evaluate whether intravaginal infusion of a mixture of lactic acid bacteria (LAB) would affect the incidence of clinical diseases in transition dairy cows. 152 pregnant Holstein cows were assigned randomly to

3 groups 2 wk before the expected day of calving, based on their parity and BCS. Cows received intravaginal LAB around parturition as follows: treatment 1 (TRT1) - 2 consecutive LAB and 1 carrier (1 mL of sterile skim milk) dose; treatment 2 (TRT2) - 3 consecutive LAB doses; control (CTR) - 3 consecutive carrier doses. LAB used were a mixture of 3 lactic acid bacteria including *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138, and FUA3140 stored in sterilized skim milk and infused at 10^8 to 10^9 cfu per dose. Cows were checked twice per week after parturition for retained placenta (RP), vaginal purulent discharges, left displaced abomasum (LDA), and lameness. Results indicated an overall incidence rate of vaginal purulent discharges of 25%. Within those cows, 24% were in TRT1, 26% in TRT2, and 50% in CTR ($P = 0.05$). RP had an overall incidence rate of 7.9%. Within the cows with RP, 17% were in TRT1, 33% in TRT2, and 50% in CTR ($P = 0.07$). LDA exhibited an overall incidence rate of 4.0%. Within the cows having LDA, 17% were in TRT1, 50% in TRT2, and 33% in CTR ($P = 0.07$). The overall incidence rate of lameness was 10.5%. Within those lame cows, 31% were in TRT1, 44% in TRT2, and 25% in CTR ($P = 0.02$). It should be pointed out that a major reason for lameness was mechanical injury. In conclusion, intravaginal administration of LAB lowered the incidence of vaginal purulent discharges and RP in periparturient dairy cows.

Key Words: dairy cow, lactic acid bacteria, disease incidence

M24 Acute phase response intensity is related to the metabolic and immunologic statuses of early postpartum dairy cattle.

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Objective was to describe the relationship between the intensity of the acute phase response and the metabolic and immunologic statuses of early postpartum, multiparous cows. Peripheral blood was collected from 240 Holstein cows, 2–8 DIM and 2nd-8th parity from 8 dairies across 5 d (n = 6 cows/dairy/day). Plasma concentrations of haptoglobin were measured colorimetrically and cows were classified as low (1st quartile), moderate (2nd and 3rd quartiles), or high (4th quartile) responders. Metabolic measurements included plasma β-hydroxybutyrate (BHBA) concentrations. Immunologic measurements included total leukocyte counts and differentials, neutrophil L-selectin expression, neutrophil oxidative burst capacity when cocultured with *Escherichia coli*, as well as the secretion of tumor necrosis factor-α and interferon-γ when diluted whole blood was cocultured with lipopolysaccharide and phytohemagglutinin, respectively. All data are reported as Low, Moderate, and High, respectively. Haptoglobin concentrations ranged from 0.42 to 1.04, 1.05–3.50, and 3.51–10.47 adjusted optical density. High cows had greater BHBA concentrations ($P < 0.05$; 509, 548, and 645 ± 57.8 μ*M*), elevated rectal temperatures ($P < 0.01$; 101.3, 101.4, and 101.7 ± 0.14°C), and neutropenia ($P < 0.01$; 3.5, 3.3, and $2.2 \pm 0.34 \times 10^6$ cells/mL). In addition, the innate immune responses of High cows were stimulated as evident by increased secretion of tumor necrosis factor-α ($P < 0.05$; 570, 562, and 732 ± 72.5 pg/mL), expression of L-selectin on neutrophils ($P < 0.01$; 71, 72, and 119 ± 10.0 mean fluorescence intensity), and neutrophil oxidative burst capacity ($P < 0.05$; 117, 123, and 146 ± 11.7 mean fluorescence intensity). In contrast, the secretion of interferon-γ was suppressed in both the Moderate and High cows ($P < 0.01$; 707, 420, and 309 ± 102.8 pg/mL). These data indicate that a stronger acute phase response during the early postpartum period is characterized by increased concentrations of ketone bodies, activated innate immune responses, and a suppressed adaptive immune response.

Key Words: immune, metabolic, transition cow

M25 Isolation and analysis of transient receptor potential channel (TRPC) genes in goats: Implications for study of gastrointestinal nematode infection.

M. M. Corley and J. Ward,* *Virginia State University, Petersburg.*

Transient receptor potential cation channels (TRPC) are involved in several cellular functions. The TRPC channels function as calcium cation channels that cause membrane depolarization and entry of calcium into the cell, thereby resulting in smooth muscle contraction. Specifically, it has been shown that TRPC4 and TRPC6 deletions in mice, impairs intestinal motility and contractility. Goats are plagued with the gastrointestinal nematode *Haemonchus contortus*, that costs the small ruminant industry billions of dollars per annum in livestock loss and drug treatment. The ability of the intestine to expel worms is dependent on many factors, one of which is intestinal contractility. Although the role of TRPC 4 and 6 has been identified as crucial in intestinal contractility in mice, the TRPC 4 and 6 genes have not been isolated in goats, nor evaluated in *H. contortus* infection. Therefore, the objective of this study was to identify and characterize the TRPC4 and TRPC 6 genes of goats. Total RNA was isolated from homogenized intestinal tissue and purified. Reverse transcriptase PCR (RT-PCR) was performed using cross species primers designed from the human, bovine, mouse and rat TRPC4 and 6 gene alignments. The RT-PCR products were visualized via agarose gel electrophoresis. The expected bp RT-PCR products were observed (388 and 350 bp, respectively), indicating successful amplification of the goat TRPC 4 and 6 cDNA. The cDNA PCR products were sequenced. The goat TRPC showed 98, 92, 91, and 90% sequence homology to the bovine, horse, pig, and human TRPC genes, respectively, and 88 and 87% homology to rat and mouse TRPC. Identification and analysis of goat TRPC 4 and 6 genes will help to elucidate the involvement of TRPC genes in the response to *H. contortus* infection in goats.

Key Words: goat, gastrointestinal, TRPC genes

Breeding and Genetics: Fertility and Early-Life Traits

M26 The relationship of herd-average conception rates and calving interval with sire predicted transmitting ability for three fertility traits. E. S. Benner and C. D. Dechow,* *Penn State University, University Park.*

The objective of this study was to determine the relationship of sire predicted transmitting ability (PTA) for fertility with reproductive performance in low and high fertility Holstein herds. First service conception rate (FSC; 42,389 records), services per conception (SPC; 29,924 records), and calving interval (CI; 28,113 records) were the herd fertility traits. Herds with a FSC of $\geq$28.4% and a CI of $\leq$13.8 mo were classified as high fertility, whereas herds with <28.4% FSC and >13.8 mo CI were classified as low fertility. Records were further stratified into high genetic groups of daughter pregnancy rate (DPR) if sire DPR was ≥ -0.6, high cow conception rate (CCR) if sire CCR was ≥ -0.7, and high heifer conception rate (HCR) if sire CCR was ≥ -0.4. Records with from cows with sire PTA below those levels were classified as belonging to the low genetic group for each trait. Fertility traits were evaluated in ASREML and the effect of DPR, CCR, and HCR genetic groups were evaluated separately. The model included fixed effects for lactation number, herd group (high or low fertility), genetic group (high or low sire PTA), and the interaction of herd and genetic groups. Age within lactation number, herd-calving-cluster, and error were the random effects. The effect of herd group was highly significant for all traits. The effect of DPR genetic group, CCR genetic group, and HCR genetic group was also significant for all traits ($P < 0.05$). FSC was 3.9% and 3.1% higher for the high CCR and DPR genetic groups, respectively, than the corresponding low genetic groups. SPC decreased by 0.07 services for the high HCR genetic group, 0.10 services for the high DPR genetic group, and 0.14 services for the high CCR genetic group. CI decreased from 1.6 d (HCR) to 5.1 d (DPR) in the high genetic groups. The interaction of DPR or CCR genetic group with herd fertility group was not significant for any trait. The interaction of HCR genetic group effect and herd fertility was significant for FSC ($P < 0.05$). FSC was 17% for both high and low HCR group in low fertility herds, but increased from 32% for low HCR group to 34% for the high HCR group in high fertility herds. In conclusion, this study provides evidence that selection for high fertility can improve reproductive performance in both favorable and adverse fertility herds.

Key Words: daughter pregnancy rate, conception rate, fertility

M27 Effect of body condition score at open period on reproductive traits of dairy cows in Hokkaido. J. Hirose,* Y. Masuda, and M. Suzuki, *Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan.*

Body condition score (BCS) is a useful indicator for farmers to evaluate negative energy balance (NEB) of dairy cows. During postpartum period, severe NEB in a cow tends to lower reproductive performance. This suggests that if BCS is scored before conception farmers may be able to predict fertility. The objective of this study was to investigate the relationship between BCS at open period and fertility traits. Reproductive and lactation records collected by the Hokkaido Dairy Milk Recording and Testing Association, and type records collected by Holstein Cattle Association of Japan (Hokkaido Branch) were used. From this data set, only primiparous cows recorded between 2007 and 2009 were extracted. The fertility traits used were days open (DO), days from calving to first service (DFS), and number of services (NS). DO and DFS were analyzed using the GLM procedure of SAS and the LOGISTIC procedure of SAS was used for NS analysis. BCS was scored on a scale of 1 to 9, where 1 = thin and 9 = fat. These scores were then divided into 5 classes: 1 to 3, 4, 5, 6, and 7 to 9. The months of calving were divided into 4 seasons: January to March = spring, April to June = summer, July to September = fall and October to December = winter. BCS, dairy milk yield, protein to fat ratio (P/F), the square of P/F, age of calving, and season were included as fixed effects in all models. As a result, individuals in BCS class 1 showed significantly delayed DO (+11.27 d) and DFS (+11.86 d) compared with BCS class 3 ($P < 0.05$). In contrast individuals in BCS class 4 and 5 were estimated to have a fewer NS (0.15 and 0.23 times) than BCS class 3. The optimal P/F range was found and it significantly decreased DO, DFS, and NS, but spring and summer had significantly adverse effects on these traits. Cows with a younger calving age had significantly shorter DO and DFS. The effects of calving seasons and milk production are associated with fertility traits; however, cows with a medium to high BCS also showed the same tendencies. The BCS at the open period may be an important indicator of when to start the reproductive cycle.

Key Words: body condition score, reproductive trait, dairy cows

M28 Cyclicity and fertility of Holstein, Jersey, and crossbred cows in a fall-calving, pasture-based dairy. K. Glosson* and S. Washburn, *North Carolina State University, Raleigh.*

With the decline in fertility in dairy herds over many years, use of crossbreeding is one practice that may improve reproduction. At the Center for Environmental Farming Systems Dairy Unit in Goldsboro, North Carolina, 143 cows were studied in a fall-calving (Oct. to Jan.), pasture-based dairy. The 2010–2011 herd included 15 Jerseys (JJ), 12 Holsteins (HH), 37 crosses of JH or HJ (F1), 39 crosses >50% Jersey (JX), and 40 crosses >50% Holstein (HX). Milk samples collected at 10-d intervals around 30, 60, and 90 d postpartum were tested for progesterone, to determine cyclic status. Any milk sample with progesterone concentration at >1.0 ng/mL or an observed estrus were used to confirm that a cow was cyclic. Cows were observed for estrus and inseminated via AI from Jan 1, 2011 through April 30, 2011. Data for percentages of cows cycling at 30, 60, and 90 d after calving and for those pregnant to first insemination and within the 120-d breeding season are included in the table as raw data means. More JJ, JX, and F1 cows were cyclic at 30 d postpartum compared with HX or HH. Differences in cyclic status were less at 60 d and all cows were cyclic by 90 d postpartum. Conception rates at first service and pregnancy percentages for the 120-d breeding season were generally higher for crossbred cows than for JJ and HH. However, the number of observations was low for both purebred groups. The data in this study are consistent with the potential for improved reproduction for crossbred dairy cows.

Table 1. Cyclicity and fertility of crossbred dairy cows

	Breed types				
Item	JJ	JX	F1	HX	HH
Number	15	39	37	40	12
Cyclic at 30 d (%)	60.0	59.0	62.2	35.0	41.7
Cyclic at 60 d (%)	100	97.4	89.2	72.5	91.6
Cyclic at 90 d (%)	100	100	100	100	100
Pregnant at 1st service (%)	33.3	46.2	56.8	50.0	41.7
Pregnant within 120-d season (%)	46.7	71.8	78.4	70.0	50.0

Key Words: fertility, progesterone, crossbred

M29 Genomic differences between highly fertile and sub-fertile Holstein dairy heifers. A. E. Navarrette*[1], C. A. Gill[1], T. E. Spencer[2], and T. R. Bilby[1,3], [1]*Department of Animal Science, Texas A&M University, College Station,* [2]*Department of Animal Sciences, Washington State University, Pullman,* [3]*Texas Agrilife Research and Extension, Stephenville.*

Reduced fertility in dairy cattle remains a major economic loss to dairy producers. Identifying dairy cattle with superior genetic potential for fertility would increase dairy farm profitability. Blood samples were taken and DNA extracted from dairy heifers (n = 40) on 2 commercial dairies in Texas. Heifers were classified into 2 groups based upon services per conception (SPC); those animals with a single SPC were determined to be highly fertile (n = 20) and heifers with greater than or equal to 4 SPC were classified as sub-fertile (n = 20), representing the 2 tails of the population distribution. Whole genome association analysis was performed utilizing a 777K high-density (HD) single nucleotide polymorphism (SNP) chip. Genomic data were evaluated utilizing a whole genome association analysis toolset (PLINK) and 570,620 SNP were available for analysis with a total of 39 samples being analyzed. Forty-four SNP were determined to be associated with fertility ($P \leq 10^{-5}$) and were located on *Bos taurus* chromosomes (BTA) 2, 4, 9, 19, and 26. The SNP and ranges between SNP were analyzed using BLAST-Like Alignment Tool (BLAT), and SNP were associated with 5 candidate genes for reproduction. The SNP on BTA 2 were located within the region coding for the non-imprinted Prader-Willi/Angelman syndrome 2 (NIPA2) gene and cytoplasmic fragile X mental retardation 1 (FMR1) interaction protein 1 (CYFIP1). In addition, 3 SNP on BTA 9 were located near monofunctional C1-tetrahydrofolate synthase (MTHFD1L). A difference in allele frequency was observed between the 2 groups for SNP located on BTA 19 in proximity to 2 genes, zinc finger 18 (ZNF18) and mitogen activated protein kinase 4 (MAP2K4). The SNP associated with 3 genes and one microRNA, which were significant but had no known role in reproduction, were elaC homolog 2 (ELAC2), vacuolar protein sorting 41 homolog (VPS41), glutaredoxin 3 (GLRX3), and microRNA 744 (MIR744). The NIPA2, CYFIP1, MTHFDIL, ZNF18, and MAP2K4 genes have all been linked to reproduction in various species and may play a role in fertility in dairy cattle. Further studies are needed to ascertain the involvement of these and other genes related to fertility in dairy cattle.

Key Words: dairy, genomics, SNP

M30 The quality and yield of embryos from Holstein dairy cows in relation to inbreeding. J. Bezdicek*[1], A. Makarevich[2], R. Holasek[2], E. Kubovicova[2], Z. Hegedusova[2], and F. Louda[2], [1]*Agroresearch Rapotin, Ltd., Vikyrovice, Czech Republic,* [2]*Research Institute for Cattle Breeding, Ltd., Vikyrovice, Czech Republic.*

The effect of inbreeding depression on reproduction traits in livestock is very important. There are several reproduction traits that reveal inbreeding depression, such as service period and age at first calving. The aim of this study was to evaluate the effect of inbreeding level (F_X) on yield and quality of embryos from Holstein cows. The data involve cows used for embryo transfer in the years 2010–2011 at farms in the Czech Republic. The value of F_X ranged from 3.125 to 6.25%. In total, 648 embryos were recovered from 87 donors by flushing of the uterus with Complete flush solution. Of these donors, 21 were inbred (163 embryos collected) and 66 non-inbred cows (485 embryos collected). The data were analyzed using StatSoft Inc. Statistica 10 with descriptive statistics and *t*-tests. Of 485 embryos flushed from 66 non-inbred cows (4.9 embryos per flushing; $s_X = 4.5$) 322 embryos (66.4%) were transferred to recipients. The number of unfertilized embryos was 114 (23.5%) with average of 1.7 embryos per flushing ($s_X = 2.2$) and 49 embryos (10.1%) were degenerated with average of 0.7 embryos per flushing ($s_X = 1.3$). Of 163 embryos collected form 21 inbred cows 107 embryos were transferable (65.6%) with average of 5.1 embryos per flushing ($s_X = 5.2$), 39 embryos were unfertilized (23.9%) with average of 1.9 embryos per flushing ($s_X = 2.0$) and 17 embryos were degenerated (10.5%) with average of 0.8 embryos per flushing ($s_X = 1.7$). There were no statistically significant differences between the inbred and non-inbred cows (*t*-test), although in some cases the records from inbred cows were poorer (number of transferable embryos, unfertilized embryos, degenerated embryos). The significant (negative) correlation was found only between F_X and the total number of collected embryos ($r = -0.50$; $P < 0.05$). There was also non-significant correlation between F_X and number of embryos suitable for transfer (−0.41). In conclusion, the inbred cows with a lower degree of F_X showed insignificantly slightly poorer yield and quality of embryos.

Key Words: embryo transfer, inbreeding

M31 Antioxidants in bovine semen cryopreservation. M. F. Duarte-Junior, L. K. Hatamoto-Zervoudakis,* J. T. Zervoudakis, P. P. Tsuneda, P. H. D. Gomes, F. M. Wingert, F. A. P. B. Arguello, and W. A. S. Marinho, *Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil.*

The present study aimed to determine if the addition of vitamins E and C to bovine semen extender reduces damage caused by cryopreservation and oxidative stress, and preserves fertility after the freeze-thawing process. We used 16 Nelore bulls (*Bos taurus indicus*) aged between 2 and 3 years, with proven fertility and without pathology in the reproductive tract. Each ejaculate was split into 3 equal groups and diluted in Tris-based extender containing vitamin E (tocopherol acetate, 10 mmol), vitamin C (ascorbic acid, 0.45mg/ml), and no additive (control). Diluted semen was chilled for 4 h to 4°C and placed into 0.5 mL chilled straws at a concentration of 25×10^6 sperm/straw. Straws were cooled for 10 min to −95°C in nitrogen vapor, followed by storage in liquid nitrogen until laboratory analysis. Frozen straws were then thawed individually at 37°C for 20 s in a water bath for the evaluation. Spermatic characteristics (motility, viability, abnormality and acrosomal integrity) and oxidative stress (lipid peroxidation) were assessed for each sample. No significant differences ($P > 0.10$) were observed in sperm motility, viability and abnormality, and oxidative stress among the groups. Addition of vitamin E to extender provided better acrosomal membrane integrity ($P < 0.10$) when compared with controls (94.34% ± 0.57 vs. 92.04% ± 2.69), however the addition of vitamin C (93.04% ± 2.98) did not protect acrosomal membranes as compared with other groups. Extender supplemented with vitamin E protected acrosomal membranes against freeze-thaw-induced damages and improved measures of bovine semen quality. Further studies are required to obtain more concrete results on the determination of lipid peroxidation and antioxidant capacities of vitamin E in cryopreserved bovine semen

Key Words: vitamin E, vitamin C, oxidative stress

M32 Extender supplementation with vitamin E and cryopreservation of bull sperm. P. P. Tsuneda, L. K. Hatamoto-Zervoudakis,* J. T. Zervoudakis, L. C. M. Soares, M. F. Duarte-Junior, P. H. D. Gomes, and F. M. Wingert, *Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil.*

The objective were evaluation of bovine semen extender supplementation with vitamin E improved viability and quality sperm. Were used

5 young Nelore bulls. Each ejaculate retreated 2 aliquots which were subsequently diluted with lactate extender (Lactato-based extender) and another Lactato extender supplemented with 50.0 m*M* of vitamin E in concentration of 100 × 10^6/mL viable spermatozoa. The diluted aliquots were chilled to 5°C for 4 h, then packaged into 0.5-mL straws and maintained for 20 min up to 5 cm in nitrogen vapor and after immersed in liquid nitrogen. Thawing was performed at 36°C for 30 s, immediately after thawing were evaluated sperm motility, sperm viability and oxidative stress (lipid peroxidation). There was no statistical effect in spermatozoa motility and viability ($P = 0.2133$, $P = 0.3696$, respectively). The supplementation of extender with vitamin E increased oxidative stress ($P = 0.0001$) suffered by spermatic cell during the process of freezing and thawing. Spermatozoa cryopreserved in a medium not supplemented showed a less oxidative stress (180.362 ± 64.858 ng/mL) compared with spermatic cells cryopreserved in extender supplemented (736.851 ± 112.662 ng/mL). It is concluded that extender supplementation with 50 mmol of vitamin E was not effective in protecting spermermatic cell against damage caused by freezing and thawing processes.

Key Words: fertility, spermatozoa, antioxidant

M33 Multibreed genetic evaluation of calving ease and birth weight using a threshold-linear model in Brangus.

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Multibreed genetic evaluation (MBE) was implemented for calving ease (CE) and birth weight (BW) using a threshold-linear model applied to data from the International Brangus Breeders Association. Data included 60,586 CE records with 2 categories (1: easy; 2: difficult) and 500,278 BW records from 1975 to 2011. The pedigree file contained 735,925 animals. Calving ease priors for heterosis and unknown parent group within breeds (breed effects) were obtained by scaling the BW heterosis and breed effects 2%; however, external EPD for CE were not available. External BW EPD priors from the American Angus Association for Angus sires were fit in the analysis. (Co)variance components and MBE for CE and BW were estimated with a threshold-linear model. The model included fixed effects of contemporary group (age-sex-herd), age of dam and heterosis breed contribution, and direct and maternal genetic random effects. The EPDs were compared with those from the current (C-) MBE for BW in Brangus. Of all CE records, 94.5% indicated easy calving. Direct and maternal heritability estimates were 0.23 and 0.18 for CE and 0.46 and 0.16 for BW, respectively. Genetic correlations between CE and BW were 0.87 for direct effects and 0.45 for maternal effects. Genetic correlations between direct and maternal effects were −0.19 for CE and −0.50 for BW. By setting the oldest age group for Angus breed as the mean base in MBE (87.5% in probability scale), predicted breeding values for CE were converted to a probability scale. The EPD was calculated as a deviation from the mean. For 17,847 sires with at least one progeny for birth weight, the correlation of direct EPD between BW in this study and in the C-MBE was 0.96. The correlation between BW in the C-MBE and CE in this study was −0.85. The correlation between BW and CE in this study was −0.90. For maternal EPD, the correlation between BW in this study and in the C-MBE was 0.87. The correlation between BW in the C-MBE and CE in this study was −0.18. The correlation between BW and CE in this study was −0.08.

Key Words: multibreed evaluation, calving ease, Brangus

M34 Expression profiling of testicular sense and antisense RNA transcripts of Brahman bulls.

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This study was designed to identify the extent to which both sense and antisense RNA transcripts were expressed in testis from postpubertal *Bos indicus* bulls as part of a bovine epigenetics project. Concurrent incidences of sense and antisense gene transcription were investigated by microarray analysis. Total RNA was extracted from testicular parenchymal tissue of sixteen 18-mo-old Brahman bulls immediately after slaughter at the departmental abattoir. A random subset of 4 of the 16 RNA samples was used in a microarray experiment. Expression microarrays were designed to assess transcription across the whole bovine genome without emphasis on known gene loci. Therefore, the 60-mer oligo probe-set from a commercial bovine whole-genome comparative genomic hybridization array was printed in expression format (Agilent Technologies, Santa Clara, CA). A total of 171,533 unique probes distributed approximately evenly across the genome were printed on the array (slide A). A second array was designed in which the reverse complement of each of the 171,353 probes was printed (slide B). Cy3-labeled cRNA from each of 4 bulls was hybridized to 4 pairs of microarrays. Expression was detected for 16,738 probes on slide A, and 20,853 probes on slide B. Transcription was detected in both directions for 2,229 unique oligo sequences. To confirm the microarray results for sequences expressed as both sense and antisense transcripts, nested primers were used to directly prime reverse transcription reactions and amplify PCR products so that sense and antisense transcription could be compared for 8 genes by quantitative real-time RT-PCR (qRT-PCR). Gene expression was measured by qRT-PCR of RNA from tissue from all 16 bulls. By relative quantification analysis, similar patterns of expression were observed across animals for a given gene. The relative abundance of sense to antisense transcript quantity was gene dependent, and appeared to be differentially expressed within genes, but not across animals. In summary, we observed that approximately 10% of expressed transcripts in testis are expressed bi-directionally. These data provide a foundation for examining how non-coding transcripts attenuate and regulate gene expression in the bovine testis.

Key Words: antisense RNA, *Bos indicus*, testis

M35 Model comparison for genetic parameter estimation of birth and weaning weight traits in beef cattle.

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Assumptions of normality in most animal breeding applications may make inferences vulnerable to the presence of outliers. Heavy-tail densities are viable alternatives to normal distribution and provide robustness against unusual or outlying observations when used to model the densities of residual effects. Our objective is to compare estimates of genetic parameters of fitting normal with heavy-tail distributions (Student's *t* and Slash) for residuals in univariate data of birth and weaning traits in beef cattle. A total of 17,019 birth and weaning weight records from 1998 through 2010 at the Rex Ranch were analyzed. Models included fixed effects of contemporary group and sire breed, while animal and maternal effects were random. The posterior mean and median estimates of the 2 heritabilities, and the genetic correlation using the Markov Chain Monte Carlo algorithms were similar to each other across models, implying that the posterior densities were symmetric and unimodal. Results revealed that posterior means for degrees of freedom were 6.78 and 4.89 in Student's t error model and 2.23 and 1.80 in slash error model for birth and weaning weight. Posterior means of direct and maternal heritabilities for birth weight were slightly smaller in Student's t when compared with the Normal model. The smallest values were found in the Slash model. For weaning weight, posterior means of direct and maternal heritabilities were highest in Normal models, followed by Slash and the least values were found in Student's t error model. Evaluation of 95% posterior probability interval showed that the genetic correlation between additive and maternal effects were not significant for birth weight but they were significant for weaning weight.

Key Words: genetic parameters, robust models, heavy-tailed distributions

M36 Genetic parameters of the reproductive traits in Nelore beef cattle. C. C. P. Paz*[1,2], H. L. Moreira[2], M. E. Buzanskas[3], L. El Faro[1], R. B. Lôbo[2,4], and D. P. Munari[3], [1]*SAA/APTA, Ribeirão Preto, SP, Brazil,* [2]*USP/FMRP, Ribeirão Preto, SP, Brazil,* [3]*UNESP/FCAV, Jaboticabal, SP Brazil,* [4]*ANCP, Ribeirão Preto, SP, Brazil.*

The scrotal circumference (SC) and age at first calving (AFC) are traits easily measured and the most important as indicative of precocity in bovine. Genetic parameters for birth weight (BW), age at first calving (AFC), gestation length (GL) and scrotal circumference (SC) were estimated using records of the 109,185 animals of the Nelore breed participating in a cattle breeding program of the Brazil. The gestation length was analyzed as cow trait (GLcow) and as calf trait (GLcalf). Estimation of genetic parameters was performed using the restricted maximum likelihood method (REML) for animal models, using the WOMBAT software. The mixed model used for BW and GLcalf was $y = Xb + Z1a + Z2m + e$, in which y is the vector of the dependent variable; X is the incidence matrix for fixed effects, thereby associating the elements of b and y; b is the fixed-effects vector (contemporary group); Z1 and Z2 is the incidence matrix for direct and maternal random effects, thereby associating the elements of a and y; a is the random-effects vector for direct additive genetic effects; m is the random-effects vector for maternal genetic effect and e is the residual-effects vector. For SC, AFC and GLcow, the maternal genetic effect was not included in the mixed model. For BW and GL, a linear and quadratic effect of the covariate dam age was considered. Heritability estimates were moderate for BW (0.30 + 0.02), AFC (0.20 + 0.02), GLcow (0.20 + 0.01), GLcalf (0.49 + 0.05) and SC (0.41 + 0.02). Genetic correlation estimates between BW and AFC, GLcow, GLcalf, SC were 0.36, 0.31, 0.13, 0.07 respectively, between AFC and GLcow, GLcalf, SC were 0.19, 0.28, −0.40, respectively, between GLcow and SC was 0.02 and between GLcalf and SC was −0.21. These results suggest that selection for AFC and GL could improve female reproductive efficiency. The direct selection for SC and GLcalf could be better than the selection for AFC due to higher heritability estimate. The gestation length analyzed as calf trait (GLcalf) could be included in the selection index of the Nelore Brazil Program.

Key Words: genetic associations, heritability, precocity

M37 Genetic trends for growth-related traits and calving ease of Simmental beef cattle. H. M. Saad*[1], W. Shafer[2], and R. M. Enns[1], [1]*Department of Animal Sciences, Colorado State University, Fort Collins,* [2]*American Simmental Association, Bozeman, MT.*

Genetic change in a trait, over time, is primarily driven by the genetic variability, accuracy of selection, generation interval, and selection intensity and, in multiple trait selection programs, by genetic correlations with other traits of interest. Given modern genetic evaluation tools, and reproductive tools such as artificial insemination, selection intensity is a primary driver of genetic improvement. The main goal of this study was to quantify the selection pressure placed on growth and calving ease in the American Simmental Association (ASA) registry as part of a larger project to evaluate birth weight or calving ease EPD in selection programs. Data consisted of 2,540,928 records, from 1980 to 2011, from ASA. Data included maternal calving ease EPDs (CEM) and direct EPDs and accuracies for birth weight (BW), weaning weight (WW), yearling weight (YW), and calving ease (CED). To compare genetic trends on an equal scale, mean EPDs by year were converted to standard deviation units (sdu). Based on preliminary analysis indicating a change in selection pressure since the importation of Simmental genetics, genetic trend for all studied traits can be divided into 2 parts, that occurring from 1980 to 1991 (period 1) and that from 1992 to 2011 (period 2). Results show that mean EPDs for BW in period 1 increased by 0.017 ± 0.0004 sdu/year, which indicates that breeders put more emphasis on growth and correspondingly experienced increasing birth weight. During this period, mean EPDs for CED showed little change (0.0017 ± 0.0003 sdu/year), while mean EPDs for CEM increased by 0.023 ± 0.001 sdu/year. During period 2, the rate of genetic change of mean EPDs for BW dropped dramatically (−0.024 ± 0.001 sdu/year) while mean EPDs for CED increased by 0.019 ± 0.0007 sdu/year. As result, the rate of increase in mean EPDs for YW slowed (0.007 ± 0.0006 sdu/year) while that for WW did not show any change (0.00016 ± 0.0007 sdu/year). These results suggest selection emphasis differed between periods, with breeders selecting against BW in period 2 which resulted in a slower genetic change in growth-related traits compared with had they selected directly for calving ease.

Key Words: Simmental, genetic trend, calving ease

M38 Estimates of genetic parameters for female fertility traits of Canadian Simmentals. J. Jamrozik*[1], S. McGrath[2], R. A. Kemp[2], B. Holmquist[3], and S. P. Miller[1], [1]*CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada,* [2]*RAK Genetic Consulting Ltd., Lethbridge, AB, Canada,* [3]*Canadian Simmental Association, Calgary, AB, Canada.*

Calving to first insemination (CFI) (probability that a cow will successfully produce a calf from her first service) and days to calving (DC; interval between the first exposure to the bull and calving) defined separately for heifers and multi-parity cows were analyzed with a 4-trait linear animal model. The data were 108,206 records on 56,879 Canadian Simmental females with AI and Natural Service breeding records collected from 1974 to 2010. The model included fixed effects of year-season of breeding, age of cow by season of breeding, and age of cow's dam. Random effects were contemporary group, service sire by year of breeding (for CFI only), animal genetic, and cow permanent environmental (PE) effects for repeated records of multi-parity cows.

Bayesian methods were used to estimate posterior distributions of covariance components and genetic parameters. Estimates (SD) of heritability were low, ranging from 1.8% (0.29) for CFI in heifers to 3.7% (0.44) for DC in multi-parity cows. Interval trait (DC) had slightly higher heritabilities compared with CFI; both traits expressed in older cows were more heritable than corresponding traits for heifers. Contemporary group contributed up to 56% of the total variance for DC in heifers. Service sire and the PE were relatively larger (smaller) sources of variation compared with additive genetic (contemporary group) effects. All traits were highly genetically correlated: from 0.68 for CFI in heifers and multi-parity cows to 0.91 for DC in heifers and multi-parity cows. Environmental correlations ranged from −0.72 between CFI and DC in heifers to 0.91 for DC in heifers and multi-parity cows. Correlations smaller than 1 and heterogeneous variances indicated that CFI and DC expressed different aspects of female fertility in beef cattle, and fertility of heifers and multi-parity cows seemed to be different traits genetically. All 4 traits could be used in a form of selection index in Canadian Simmentals to breed for better fertility. Genetic progress, however, would be challenging given low values of heritability, and accurate EPD of bulls would require large numbers of progeny.

Key Words: female fertility, beef cattle, genetic parameters

M39 Polymorphisms in FSH-β ESR and BF genes and their relationship with reproductive traits in Yorkshire pigs. C. Liu[1], J. Shen[1], S. Zhu[1], W. Shi[2], and Y. Yu*[1], *[1]China Agricultural University, Beijing, China, [2]Animal Husbandry and Veterinary Station of Beijing, Beijing, China.*

The objectives were to provide the molecular basic information of sow reproduction traits for a Yorkshire breeding farm in Beijing, China. We investigated 3 SNPs in swine follicle stimulating hormone β (FSH-β; Zhao et al., 1999), estrogen receptor (ESR; Rothschild et al., 1996) and properdin (BF; Chen et al., 2009) genes and analyzed their relationship with reproductive traits in the Yorkshire population. A total of 251 Yorkshire sows were randomly selected from the breeding farm in Beijing suburb, China. High quality genomic DNA were extracted from the hair follicles for each pig. PCR-RFLP procedure was used for genotyping of the 3 genes. Associations of the SNPs with 3 reproductive traits, total number born (TNB), number born alive (NBA), and litter birth weight (LBW), were analyzed with mixed GLM model (SAS 9.1). The effects of parity, season, herd, and genotype were included in the model. The dominant genotype for FSH-β, ESR, and BF in the population were BB, AB and CC, respectively. Parity, season, and genotypes significantly affected the reproductions traits of the sows. At the first parity, the sows with AB genotype in FSH-β gene had significantly higher NBA and LBW than AA ($P < 0.05$), and significantly higher NBA than BB genotype ($P < 0.05$). The sows with CC genotype of BF gene were 1.70 kg higher in LBW than the CT sows ($P < 0.05$). The sows with combined genotype of AB-BB-CC for FSH-β, ESR, and BF genes was found significantly higher TNB, NBA and BLW than the AB-AA-CT sows ($P < 0.01$). As for the multiparity, the sows with AB and BB genotypes of FSH-β gene showed significantly higher LBW than the AA sows ($P < 0.05$). The key reproductive traits of the Yorkshire population were significantly influenced by single gene effect of FSH-β. Combined effects of multigenes should be considered in the association study on pig reproduction traits.

Key Words: BF, ESR and FSH-β, pig reproduction traits

M40 Genetic parameters for lifetime number of piglets born alive and length of productive life using a linear censored model. C. Y. Chen*[1], A. C. Clutter[2], and S. Tsuruta[3], *[1]Newsham Choice Genetics, Chesterfield, MO, [2]Agricultural Research Division, University of Nebraska, Lincoln, [3]Department of Animal and Dairy Science, University of Georgia, Athens.*

The objective of this study was to estimate genetic parameters for lifetime number of piglets born alive (LNBA) and length of productive life (LPL) using a single-trait linear model accounting for censoring. Records of 8,899 Large White females from a single farm collected between 2003 and 2011 were used. LNBA was defined as the number of piglets born alive produced during the lifetime of the sow. LPL was defined as the number of days from first farrowing to last farrowing in natural logarithm scale. Censored records represented 25% of the data. The average number of litters per sow was 5.0. Analyses were carried out with 3 approaches: a linear model excluding censored data (M1), a linear model ignoring censoring (M2), and a linear censored model (M3). Fixed effects included year_quarter based on entry date as contemporary group. Random effects were animal additive genetic effects. The effect of the 3 approaches on EBVs were evaluated for sows with parity < 4 (n = 3,391) and sows with parity > = 4 (n = 5,508). For LNBA, estimates of heritability were 0.13, 0.18, and 0.12 for models 1, 2, and 3. For LPL, estimates of heritability were 0.05, 0.07, and 0.07. Correlations between EBVs for LNBA were 0.97 for M1–2, 0.94 for M1–3, and 0.97 for M2–3 for sows with parity < 4. The same estimates were 0.94, 0.93, and 0.98 for sows with parity > = 4. For LPL, correlations were 0.95, 0.94, and 0.99 for M1–2, M1–3, and M2–3 for sows with parity < 4 and 0.94, 0.94, and 0.99 for sows with parity > = 4. Analysis accounting for censoring has lowest heritability due to increased residual variance and decreased genetic variance for LNBA whereas analysis excluding censored data has lowest estimate of heritability for LPL. Excluding censored data seemed to have larger effects on the estimation of breeding values than ignoring censoring. The effect of model choice on estimation of breeding values for LNBA was larger for sows with larger parity.

Key Words: censored data, genetic parameter, lifetime prolificacy, pigs

M41 Genome-wide association study of age at puberty in swine. J. F. Schneider,* D. J. Nonneman, R. T. Wiedmann, and G. A. Rohrer, *USDA, ARS, U. S. Meat Animal Research Center, Clay Center, NE.*

Age at puberty (AP) is an economically important trait in swine production. Reducing AP provides opportunities to lower the cost of gilt development, reduce age at first farrowing, increase litter size, and improve sow longevity. This analysis was designed to identify quantitative trait loci (QTL) associated with AP. Heat detection with boar contact began at 140 d of age and ended at 230 d of age. Seven hundred 50 7 gilts representing generations 5–8 of a Landrace-Duroc-Yorkshire cross reached puberty during 7 breeding seasons and were genotyped using a 60k chip. SNP were removed that met criteria including minor allele frequency <0.05, call rates <0.95, and unknown location. Five animals were removed with call rates <0.95 or that failed a Mendelian test. Bayesian methods were used to analyze 41,848 SNP. Prior estimates of variances were taken from MTDFREML with heritability = 0.32. The genomic variance priors were estimated by a preliminary run of BayesC using estimates from MTDFREML as priors. A previous estimate of Pi = 0.99 was confirmed by BayesCPi. Final BayesC using a burnin of 1000 iterations and a total chain length of 51,000 produced an estimate of 0.16 for the proportion of phenotypic variances explained by genetic markers (genomic heritability). A total of 94 QTL (5 consecutive SNP) were selected for statistical testing based on QTL variance. Testing identified 72 significant QTL including 25 at $P < 0.001$, 32 at $P < 0.005$, and 15 at the $P < 0.01$ level. QTL were found on all chromosomes analyzed (SSC) except 17. Chromosome 2 (SSC2) contained the most QTL with 9, followed by SSC1, SSC3, and SSC7 with 6, and SSC6, SSC10, SSC12, and SSC15 with 5 QTL each. These regions correspond to previously identified QTL (http://www.animalgenome.org/cgi-bin/QTLdb/SS/index accessed 2/06/2012). The results of this analysis demonstrate that opportunities exist to introduce QTL into genetic improvement programs designed to reduce AP. USDA is an equal opportunity provider and employer.

Key Words: puberty, swine, QTL

M42 Survival in crossbred lambs: Individual, maternal, heterosis, and breed effects.

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Early mortality in lambs causes substantial economic loss and animal welfare concerns and it is considered a major production limitation. The present study was a genetic analysis of lamb survival from a crossbred population involving 14 breeds to assess factors affecting death of lambs in 5 different periods of life. Data from 7,990 lambs, defined as a binary trait (dead or alive) in 5 different periods (until 1 d, 2 to 30 d, 2 to 60 d, 2 to 90 d and 2 to 120 d of age) were analyzed with a logistic version of the Dickerson full genetic model. Factors considered in the model predictor included sex of lamb, birth type (1, 2,…, 5), birth month, dam age, individual and maternal breed composition, individual and maternal heterosis (assuming the same magnitude for all pairwise combinations of breeds), and the random individual and maternal additive genetic effects. Results revealed that the effect of F1 individual heterosis resulted in a significant reduction in the probability of death in all 5 periods of life: −3.71% ($P = 0.08$), −6.12% ($P = 0.01$), −7.28% ($P = 0.02$), −8.24% ($P = 0.01$) and −11.26% ($P = 0.002$). These results suggest the importance of using crossbred animals for increased survival. Maternal heterosis did not have a significant effect in survival in most periods (except the 2 to 30 d period), probably because all animals in the study were artificially raised on milk replacer. The East Friesian maternal effect caused a significant increase in the probability of death in all periods from 2 to 120 d of age (ranging from 11.29 to 14.45%). These results highlight the importance of splitting maternal and heterosis effects from the effect of breed itself when analyzing survival data. All individual breeds with a significant effect on survival caused a decrease in the probability of death relative to the Lacaune breed, but the size of this decrease varied greatly among breeds and periods. Heritability for lamb survival tended to be low in all periods ranging from 0.04 to 0.13 and the maternal component was almost null (<0.04).

Key Words: crossbred, lamb, survival

M43 Efficiency of breeding Pantaneiro bulls by libido test.

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Pantaneiro cattle have been a genetic resource of the Brazilian Pantanal region for nearly 3 centuries. They are well adapted to the soil and climate of the region, reproducing naturally. However, with the arrival of zebu cattle in the region in the 1930s, breeders began indiscriminately crossbreeding these 2 breeds and attributed the merit only for zebu cattle. Currently, the Pantaneiro population is threatened in the region by substitution from zebu cattle. However, Pantaneiro bulls are well known for high libido, showing optimal reproductive performance in natural mating. This study aimed to evaluate potential breeding efficiency of Pantaneiro bulls using libido tests, to characterize the breed with the hopes of its conservation. We used 6 adult bulls aged 3–8 years, who underwent libido tests lasting 20 min/test, using 3 females in a prostaglandin-induced heat in each test. Each bull was tested 6 to 11 times, totaling 56 libido tests with 18.6 h of observation. During the libido test, all sexual behaviors of interest were noted. Scoring was from 0 to 10 where zero = bull showed no sexual interest in females and 10 = the bull made 2 or more services, followed by sexual interest, including mounts, attempted mounts, and services. The results showed that all 6 bulls evaluated had grade 10. All bulls showed interest in a female within 17 s and the first service occurred within 5 min. During the 20 min test the following behaviors were observed: smelling/licking of the vulva (8×), Flehmen Reflex (3.5×), mounting tentative with hands suspended (7×), active pursuit (7×), complete mount (1.5×), exposure of the penis (9×), and sexual interest in more than one female (6.5×). These were all behaviors associated with full mounting. These bulls were shown to be direct in their approaches to mounting and held 2 mounts (n = 2), 4 mounts (n = 3), or 5 mounts (n = 1) during 20 min of observation. These results suggest that Pantaneiro bulls have a high libido and that breeding efficiency would be high if this excellent performance is also carried out in natural matings in the field during the breeding season.

Key Words: animal conservation, beef cattle, animal genetic resource

M405 See abstract #455

Companion Animals

M44 Vitamin E and seminal quality in Rottweiler dogs. L. K. Hatamoto-Zervoudakis*[1], C. A. Baptista-Sobrinho[3], M. Nichi[2], A. K. S. Cavalcante[4], V. H. Barnabé[2], R. C. Barnabé[2], and C. N. M. Cortada[5], *[1]Federal University of Mato Grosso, Cuiabá, Brazil, [2]University of São Paulo, São Paulo, Brazil, [3]Brazilian Army, Osasco, São Paulo, Brazil, [4]Federal University of Bahia Reconcavo, Cruz das Almas, Brazil, [5]Tecpar, Curitiba, Brazil.*

The objective of this study was to evaluate dogs semen quality supplemented with oral vitamin E (DL-α-tocopherol). Eighteen male Rottweiler dogs were randomly divided in 2 groups: group control (without supplementation) and group treatment (with supplementation: 500 mg of DL-α-tocopherol/animal per day). The supplementation period duration was 90 d. Semen was collected by digital manipulation twice per week and ejaculate volume, sperm motility, spermatic concentration, sperm morphology (primary defects, secondary defects, and total defects) were determined. There were not found effects of treatment ($P > 0.05$) on ejaculate volume, sperm motility, semen concentration, and percentage of total defects. Supplemented animals with vitamin E presented reduction of percentage of primary defects (8.35 ± 0.65 vs. 12.29 ± 0.98; $P = 0.0006$) and increase of percentage of secondary defects (9.37 ± 0.61 vs. 7.52 ± 0.51; $P = 0.0241$) when compared with control animals. In conclusion, supplemented animals had alteration in spermatic morphology, reduced primary defects and increased secondary defects; however, supplemented animals showed no alterations in the other evaluated characteristics

Key Words: antioxidant, fertility, tocopherol

M45 Proximate analysis of commercially available whole prey for small captive exotic cats. K. R. Kerr*[1], L. M. Garner[2], and K. S. Swanson[1,2], *[1]Division of Nutritional Sciences, University of Illinois, Urbana, [2]Department of Animal Sciences, University of Illinois, Urbana.*

Small exotic cats are commonly fed whole prey to supplement traditional diets. Data regarding the composition of commercially available prey is lacking. The objective of this study was to evaluate the macronutrient composition of mammalian and avian species of different ages. Species examined included mice (1 to 2 d, 10 to 13 d, 21 to 25 d, 30 to 40 d, and 150 to 180 d); rats (1 to 4 d, 10 to 13 d, 21 to 25 d, 33 to 42 d, and >60 d); rabbits (stillborn, 30 to 45 d, and >65 d); chicken (1 to 3 d); and quail (1 to 3 d, 21 to 24 d, and ~60 d). Differences between classes were examined. Dry matter and CP concentrations were higher ($P < 0.05$) and fat concentrations were lower ($P < 0.05$) in aves versus mammals. Differences between ages were examined within species for rats, mice and quail. For rats, there was a linear increase ($P < 0.05$) in DM concentration and a linear decrease ($P < 0.05$) in CP concentration with age. Additionally, 1 to 4 d rats had higher ($P < 0.05$) fat concentration than all other ages. In mice, DM concentration was higher ($P < 0.05$) in 1 to 2 d mice than all other ages. Ten to 13 d mice were higher ($P < 0.05$) in fat and lower ($P < 0.05$) in CP than all other age groups. In quail, there was a linear increase ($P < 0.05$) in DM concentration with age. Crude protein concentration was higher ($P < 0.05$) in 21 to 24 d quail compared with all other ages. Fat concentration was higher ($P < 0.05$) in 1 to 3 d quail than all other ages, and higher ($P < 0.05$) in ~60 d quail compared with 21 to 24 d quail. Ash concentrations were not affected by age in rats, mice, or quail. Differences in composition due to age and between mammals and aves should be considered when selecting whole prey types. These data indicate that composition changes with age; however, these changes depend on species. Further research is needed to evaluate how whole prey may be used to meet the nutritional needs of small exotic cats, including micronutrient compositional analysis and bioavailability.

Key Words: whole prey, proximate composition, carcass

M46 In vitro digestion characteristics of expanded porkskin- and rawhide-based chews. S. Hooda*[1], L. G. Ferreira[1], L. L. Bauer[1], G. C. Fahey Jr.[1], M. A. Latour[2], and K. S. Swanson[1], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]Department of Animal Science, Purdue University, West Lafayette, IN.*

Chews are a major sector of the pet food industry, but their digestion characteristics are virtually unknown. Therefore, the purpose of this study was to investigate the in vitro digestion characteristics of expanded porkskin- and rawhide-based canine chews. An in vitro method that simulated gastric and small intestinal digestion was used. Chews (in triplicate) were incubated with pepsin/HCl for 6, 12, 18, and 24 h to evaluate gastric digestion. To evaluate gastric and small intestinal digestion, chews were incubated with pepsin/HCl for similar periods, followed by incubation with pancreatin for 18 h. Gastric digestibility of expanded porkskin chews was 54.7% at 6 h and 58.6% at 12 h. An increase was observed after 18 h (76.4%) and 24 h (86.4%) of gastric digestion. In contrast, low gastric digestibility was observed for rawhide chews at 6 h (7.6%) and reached a maximum of 41.6% at 18 h. Both gastric and pancreatin digestion results indicated nearly complete disappearance of expanded porkskin chews even after 6 h gastric and 18 h pancreatin digestion. Extended gastric incubations (12, 18, and 24 h) followed by pancreatin digestion (18 h) did not change expanded porkskin chews digestibility. However, rawhide chews were only 70% digested after 6 h gastric and 18 h pancreatin digestion. Gastric digestion at 12 and 18 h did not result in further improvement in rawhide chews digestibility. The 24 h gastric and 18 h pancreatin digestion led to a increase in dry matter digestibility (85%) of rawhide chews. Thus, in vitro dry matter digestibility of whole chews clearly demonstrated that expanded porkskin chews was readily digestible and took a shorter time to be completely digested. In contrast, rawhide chews were not completely digestible, even after 24 h of simulated gastric and 18 h of simulated small intestinal digestion. Sponsored by Scott Pet Inc.

Key Words: in vitro digestibility, porkskin chews, rawhide chews

Dairy Foods

M47 Use of caseinomacropeptide index as indicator of adulteration of milk powder in Brazil. M. O. Leite, M. C. P. P. Oliveira,* L. M. Fonseca, M. M. O. P. Cerqueira, M. R. Souza, C. F. A. M. Penna, and T. Rosa, *Department of Food Technology and Inspection, Veterinary School, Universidade Federal de Minas Gerais (UFMG), Belo Horizonte, Minas Gerais, Brazil.*

Brazil is one of the largest milk producer in the world, with 16.5% of the world milk powder production. Due to raw milk high prices, adulteration by cheese whey addition is a persistent practice, which has been increasingly targeted worldwide due to the potential of affecting the economical sustainability of the dairy industry, markedly in developing countries. Chromatographic determination of caseinomacropeptide (CMP) in milk is still recognized as the most suitable method to detect this adulteration. The CMP is a soluble polypeptide formed after splitting of kappa-casein by clotting enzymes during cheese making, and it will be partitioned in the whey. This work objective was to classify milk powder according to CMP levels, and evaluate legal requirements compliance. During 2009–2010, 125 samples of milk powder, from several dairies across the country were analyzed by high performance liquid chromatography (HPLC Shimadzu LC-10), and CMP levels were evaluated according to Brazilian legal requirements. The samples presented CMP levels ranging from 0 to 1,150 mg CMP/L (amount equivalent to reconstituted milk). Average concentration of CMP was 34.1 mg CMP/L, with a median of 18.3 mg CMP/L. CMP levels up to 30 mg/L were found in 73.3% of the samples, and milk with this CMP concentration is classified as high quality milk. CMP levels ranging from 30 to 75 mg/L were found in 21.8% of the samples, being suitable for milk derivatives production. However, 4.8% of the samples were found with CMP levels above 75 mg/L, being classified as poor quality milk and suspected of adulteration by cheese whey addition, not being suitable for human consumption. It is concluded that is necessary a more strict control and inspection, because 4.8% of the samples were not compliant with the legal requirements for milk destined to human consumption, due to adulteration and abnormal composition.

Key Words: caseinomacropeptide, HPLC, milk powder

M48 Effects of vacuum-deaeration on reconstituted milk flavor made from whole milk powder. H. J. Kang,* Y. K. Shin, and S. C. Baick, *Institute of Dairy Food Research, Seoul Dairy Cooperative, Ansansi, Kyunggi, South Korea.*

This study was conducted to evaluate the influence of vacuum-deaeration during the manufacturing process on flavors of reconstituted milk made from whole milk powder. As the first sample groups for pre-vacuum treatment before heating, whole milk powder solution (12%, wt/wt) was deaerated with a vacuum pump at 40°C for 10, 20 and 30 min, and then heated. On the other hands, as the second sample groups for post-vacuum treatment after heating, reconstituted milk was heated at 95°C for 10 min, and then deaerated at 40, 50 and 60°C for 10 and 20 min. Volatile sulfur compounds were analyzed with SPME and GC/PFPD, whereas ketones and aldehydes were analyzed with SPME and GC/MSD. Statistical evaluations including ANOVA and Turkey honest significant difference ($P < 0.05$) were conducted using SAS 9.0. When reconstituted milk was deaerated before heating, dimethyl sulfide and carbon disulfide were significantly reduced as compared with untreated reconstituted milk ($P < 0.05$). Dimethyl disulfide was significantly reduced in reconstituted milk deaerated at 40°C for 10 and 20 min ($P < 0.05$). Hexanal and 2-heptanone were significantly reduced in reconstituted milk deaerated at 40°C for 10 min ($P < 0.05$). In post-vacuum treatment test, hydrogen sulfide, methanethiol, and carbon disulfide in the reconstituted milk deaerated at 50°C for 20 min after heat treatment were significantly lower than untreated reconstituted milk ($P < 0.05$), whereas volatile sulfur compounds except for dimethyl disulfide in reconstituted milk deaerated at 60°C for 10 min were significantly decreased ($P < 0.05$). Hexanal and 2-heptanone of reconstituted milk deaerated at 50°C for 10 and 20 min after heat treatment were significantly decreased as compared with untreated reconstituted milk. It was concluded that vacuum-deaeration before or after heat treatment during the manufacturing process could reduce the volatile compounds developing off-flavors of reconstituted milk made with whole milk powder.

Key Words: reconstituted milk, off-flavor, volatile compound

M49 Evaluating the efficacy of a typical CIP protocol for cleaning membrane biofilms under in vitro conditions. D. Singh* and S. Anand, *Dairy Science Department, Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

This study was carried out to evaluate the effectiveness of different chemicals of an industrial CIP protocol against in vitro biofilms formed on whey RO membranes. Bacterial cells isolated from biofilm consortia of 2- to 14-mo-old membranes included species of *Bacillus, Escherichia*, *Klebsiella*, *Enterococcus*, *Streptococcus*, *Staphylococcus*, *Micrococcus*, *Aeromonas*, *Corynebacterium*, and *Pseudomonas*. The CIP protocol tested against 24-h-old single and mixed species biofilms of above microflora included 6 treatment steps based on alkali, surfactant, acid, enzyme, a second surfactant, and a sanitizer application. Experiments were conducted with individual steps of cleaning, as well as, the sequential CIP protocol under static and dynamic conditions, and the data was statistically analyzed. The results revealed a variation in resistance of single species biofilms against the 6 individual steps of cleaning. Biofilms of *Bacillus* isolates were found to be most resistant, and even the most effective step of the cleaning protocol; acid treatment reduced their counts by only 2.09 and 2.16 logs under static and dynamic conditions, respectively. Biofilms of other isolates followed a similar trend. The sequential CIP protocol using all the 6 steps resulted in a greater reduction as compared with individual steps, but presence of survivors even after sanitizer treatment under static and dynamic conditions concluded the inefficacy of CIP chemicals against *Bacillus* biofilms. Mixed species biofilms developed using 10 mo. consortium of *Bacillus*, *Staphylococcus*, and *Streptococcus* was found to be more resistant than the single species biofilms. Even the acid cleaning step resulted in lower reduction of 1.52 log counts under the dynamic conditions. Overall, the sequential CIP protocol against mixed species biofilms resulted in cumulative reductions of 4.48 and 3.56 log under static and dynamic conditions, respectively. It can be concluded that tested CIP protocol had a limited effectiveness to clean membrane biofilms formed on the whey RO membranes.

Key Words: biofilm, CIP, sequential

M50 Effect of transglutaminase treatment on the functionality of MPC and MCC: Process cheese product slice formulations.

P. Salunke,* C. Marella, and L. E. Metzger, *Dairy Science Department, Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Milk protein concentrate (MPC) is used as an ingredient in process cheese product (PCP) formulations. However, its use can result in texture defects such as soft body and restricted melting characteristics. Use of micellar casein concentrate (MCC), which has a higher level of casein and less whey protein improves the texture of PCP. Further improvement in PCP products may be possible with the use of transglutaminase (TGase), an enzyme that has the ability to crosslink proteins. The objective of this study was to determine the effect of TGase treatment of MPC and MCC retentates on the functionality of MPC and MCC when they are used in a PCP slice formulation. Three lots of MCC and MPC retentate were produced using 3 different lots of pasteurized skim milk. Each replicate of retentate was divided into 3 equal portions. One portion of the retentate was treated with TGase at 0.3 U/g of protein, one portion was treated with TGase at 3.0 U/g of protein and one had no TGase addition. All the retentates were incubated for 25 min at 50°C, heat treated at 72°C for 10 min, cooled to 10°C and then spray dried. Each MCC and MPC was then used in a PCP slice formulation that was standardized to 20.0% fat, 1.26% salt, 48.0% moisture, 17.5% protein, and 2.0% sodium citrate. In each formulation, the MPC or MCC contributed 15.7% protein to the formulation. Each formulation was manufactured in a Rapid Visco Analyzer (RVA) where it was mixed at 1000 rpm for 2 min at 95°C. Subsequently, the cheese was mixed at 160 rpm for a minute. Functional properties of PCP were analyzed using a penetration test, Dynamic stress rheology (DSR) for transition temperature (TT) and Schreiber melt test. As the TGase addition increased, there was significant ($P \leq 0.05$) increase in TT and a significant ($P \leq 0.05$) decrease in Schreiber melt area. The PCP made from MCC had higher TT and Schreiber melt area values than that made from MPC as an ingredient (TGase or no TGase). It was concluded that TGase treatment modifies the melt characteristics of MCC and MPC in PCP application.

Key Words: transglutaminase, MCC or MPC, process cheese product slice functionality

M51 Radio frequency dielectric heating treatment of NDM affects whey protein nitrogen index and solubility.

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Radio frequency dielectric heating (RFDH) provides uniform, rapid heating throughout a medium, including dry powders. Nonfat dry milk (NDM), one of the major dried milk products made in the US, can be consumed directly or used as an ingredient in foods. However, NDM can be contaminated post pasteurization or spray drying with opportunistic pathogens. While RFDH may provide additional food safety effects, it has also been reported to improve functional applications of other dried powders. Thus, the objective of the study was to determine if RFDH affects the whey protein nitrogen index (WPNI) and solubility of NDM. High heat (HH) and low heat (LH) NDM was treated using RFDH at 75, 80, 85, and 90°C and held for a range of time from 0 to 125 min. Treated powders were assessed for WPNI and solubility following standardized methods and compared with a non-treated sample. Three replications were done, ANOVAs were done to determine significant effects ($P \leq 0.05$) and significant means were differentiated by the Dunnett's test. LH-NDM treated at 75°C had similar WPNI and solubilities compared with a non-treated sample, regardless of time. However, at all other temperature/time combinations significant decreases in WPNI and solubility occurred ($P \leq 0.05$). For WPNI, decreases ranged from 10.5 to 18%, whereas for solubility decreases ranged from 3.4 to 5%. Overall, the WPNI of treated HH-NDM was not affected; however, the solubility was ($P \leq 0.05$). Solubility decreases ranged from 1.2 to 3% compared with a non-treated sample and significant decreases were observed in all but one sample. Although, some significant changes were observed in the RFDH-treated NDM, it is concluded that this technology merits further evaluation both as a post-process lethality treatment as well as its effects on other functional properties.

Key Words: nonfat dry milk, radio frequency dielectric heating, whey protein nitrogen index

M52 Effect of transglutaminase treatment on the functionality of MPC and MCC. III. Imitation mozzarella cheese formulations.

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A critical parameter in dairy based imitation mozzarella cheese (IMC) is the amount of intact casein provided by dairy ingredients in the formulation. Intact casein provides IMC with a firm unmelted texture and a stringy, elastic melted texture. From a functionality perspective, rennet casein is the preferred ingredient to provide intact casein in a formulation and is superior to milk protein concentrate (MPC) and micellar casein concentrate (MCC). The use of a cross-linking enzyme such as transglutaminase (TGase) has the potential to modify the physical properties of MPC or MCC and may improve its functionality in IMCs. The objective of this study was to determine the effect of TGase treatment of MPC and MCC retentates on the functionality of MPC and MCC when they are used in IMCs. Three lots of MCC and MPC retentate were produced using 3 different lots of pasteurized skim milk. Each replicate of retentate was divided into 3 equal portions. One portion of the retentate was treated with TGase at 0.3 units/g of protein, one portion was treated with TGase at 3.0 units/g of protein and one had no TGase addition. All the retentates were incubated for 25 min at 50°C, heat treated at 72°C for 10 min, cooled to 10°C and then spray dried. Each MCC and MPC was then used in IMC formulation that was standardized to 21.0% fat, 1.0% salt, 48.0% moisture, and 20.0% protein. In each formulation, the MPC or MCC utilized contributed all the protein. Each formulation was manufactured in a Rapid Visco Analyzer (RVA) where it was mixed at 1000 rpm for 2 min at 95°C. Subsequently the cheese was mixed at 160 rpm for a minute. The IMC formulation using either MCC or MPC treated with the highest TGase did not form an emulsion. The RVA end of manufacturing viscosity and transition temperature (TT) was significantly ($P \leq 0.05$) higher and Schreiber melt test area was significantly ($P \leq 0.05$) lower for IMC containing TGase. The IMC made from MCC (with or without TGase) had higher TT values and Schreiber melt test area as compared with that made from MPC. The study demonstrates that TGase treatment modifies the melt characteristics of MCC and MPC in IMC application.

Key Words: transglutaminase, MPC or MCC, imitation mozzarella cheese functionality

M53 Effect of transglutaminase treatment on the functionality of MPC and MCC: Process cheese product loaf formulations.

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Milk protein concentrate (MPC) is used as an ingredient in process cheese product (PCP) formulations. However, its use can result in texture defects such as soft body and restricted melting characteristics. Use of micellar casein concentrate (MCC) which has a higher level of casein and less whey protein improves the texture of PCP. Further improvement in PCP products may be possible with the use of transglutaminase (TGase), an enzyme that has the ability to crosslink proteins. The objective of this study was to determine the effect of TGase treatment of MPC and MCC retentates on the functionality of MPC and MCC when they are used in a PCP loaf formulation. Three lots of MCC and MPC retentate were produced using 3 different lots of pasteurized skim milk. Each replicate of retentate was divided into 3 equal portions. One portion of the retentate was treated with TGase at 0.3 U/g of protein, one portion was treated with TGase at 3.0 U/g of protein and one had no TGase addition. All the retentates were incubated for 25 min at 50°C, heat treated at 72°C for 10 min, cooled to 10°C and then spray dried. Each MCC and MPC was then used in a PCP loaf formulation that was standardized to 18.0% fat, 1.0% salt, 49.0% moisture, 15.0% protein, and 2.5% disodium phosphate. In each formulation the MPC or MCC contributed 12% protein to the formulation. Each formulation was manufactured in a Rapid Visco Analyzer (RVA) where it was mixed at 1000 rpm for 2 min at 95°C. Subsequently the cheese was mixed at 160 rpm for a minute. Functional properties of PCP were analyzed using a penetration test, RVA remelt test and Schreiber melt test. The PCP manufactured from the higher level of TGase had significantly ($P \leq 0.05$) higher RVA apparent viscosity after manufacture, RVA melt viscosity, penetration hardness and had significantly ($P \leq 0.05$) lower Schreiber melt area. The PCP made from MCC and MPC showed no difference in RVA viscosity; however the Schreiber melt area was significantly ($P \leq 0.05$) higher in PCP made from MCC. The study demonstrated that TGase treatment modifies the melt characteristics of the PCP made from either MCC or MPC.

Key Words: transglutaminase, MCC or MPC, process cheese product loaf functionality

M54 Influence of fat replacement by inulin on rheological properties and kinetics of milk coagulation and syneresis of milk gels.

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The objective of this study was to evaluate the effect of inulin as a fat replacer on the rheological properties, coagulation kinetics and syneresis of milk gels. A randomized factorial design, replicated 3 times, with 3 inulin concentrations (0, 3, and 6%), 2 levels of fat (<0.2 and 1.5%) and 3 coagulation temperatures (27, 32, and 37°C) was used. The coagulation process was monitored using NIR spectrometry, small amplitude oscillatory rheometry and visual coagulation indexes. The syneresis was evaluated by volumetric methods. Inulin addition significantly ($P < 0.05$) increased the rates of aggregation and curd firming reactions in the casein gels. The observed effect, which was more evident on the aggregation reaction, depended on the concentration of inulin and the coagulation temperature. Addition of 6% inulin reduced the clotting time by ~26% and the time at which the gel reached a storage modulus equal to 30 Pa by ~36%. The optical parameter *R'max* defined as the maximum value of *dR/dt*, was used to calculate an approximation of the temperature coefficients (Q_{10}) for milk coagulation. The apparent Q_{10} values obtained in milk having 0.2% fat were 3.1, 2.8 and 2.4 for samples with 0, 3 and 6% inulin, respectively. These results suggest that inulin addition attenuates the effect of temperature on the coagulation rate. Increasing fat concentration induced a consistent increase in all the optical, rheological, and visual parameters studied, although the observed trend was not statistically significant. The addition of inulin at a level of 6% produced a significant ($P < 0.05$) reduction in syneresis and significantly ($P < 0.05$) increased the curd yield by ~30%. It was concluded that the addition of inulin affects the kinetics of milk coagulation and the cutting time and therefore the use of inline sensors such as NIR may be necessary for an optimal process control.

Key Words: inulin, milk gels, NIR sensor

M55 Effects of season and locality on amino acid composition of raw milk in dairy cows.

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Raw milk is a good source of antioxidants, vitamins (including B^{12}), essential amino acids, and natural protein and fat. Favorite balance of amino acids profile in dairy foods would promote absorption in digestive tract. Amino acids composition in milk is influenced by many factors, such as feed composition and lactation stage. The objective of this study was to investigate the effects of season and locality on raw milk amino acid. Milk samples were collected from 6 cities (Beijing, Chuzhou, Harbin, Hohhot, Urumqi, and Xi'an) in spring (February, March, and April) and summer (July, August, and September), respectively. Amino acids were extracted by hydrolyzed with 7.8 mol/L HCl for 24 h, and concentrations of amino acids were determined by Hitachi L-8900 high speed amino acid analyzer. The experimental data were analyzed by SAS 8.0 with GLM procedure and expressed as absolute concentration (mg/mL). The results showed that significant variation ($P < 0.01$) of Cys, Val, Tyr, Phe were determined between spring (1.83, 206.07, 113.33, 140.98) and summer (13.08, 193.83, 101.38, 148.19). Significant difference ($P < 0.01$) of all amino acids existed among these 6 regions. Raw milk from Hohhot had highest Asp (251.37), Glu (691.21), Gly (67.59), Ala (111.38), Ile (177.40), Leu (315.03), Lys (276.34), and Pro (329.54), while Urumqi samples contained highest Ser (133.11) and Tyr (118.07). It was concluded that amino acids in raw milk were influenced by locality significantly, and some of them were also affected by season.

Key Words: season, locality, amino acid

M56 Qualitative analysis of fatty acids variation in milk of different farms in China.

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There are several factors affecting fatty acids (FA) in milk. The variation of milk FA could be defined by a reliable qualitative and quantitative analysis. Principal component analysis (PCA) convert a set of related variables into several new uncorrelated variables called principal components (PCs), using an orthogonal transformation. The number of PCs is less than or equal to the number of original variables. And first few PCs explain the majority of data variation. The objective of this study was to investigate the variation in FA composition of milk from different farms in China using PCA. During April and May, samples were collected from primiparous or multiparous cows (30–90 d in milk) screened from 3 different dairy farms, which were situated in Anhui (n

= 29), Heilongjiang (n = 21) and Xinjiang (n = 27) provinces. Samples were stored at less than −20°C and unfrozen at room temperature. Milk fat was extracted through centrifugation. The FA methyl esters (FAME) were prepared by base-catalyzed trans-esterification and measured using gas chromatography (GC). Data analysis was completed by PCA with cross validation in Unscrambler 9.8 (CAMO, Bangalore, India). The first 4 PCs explained variation of total fatty acids 99.1%. PC1 exhibited heavy loading on C14 (−0.29), C16 (−0.50), C18 (0.46) and c9C18:1 (0.64). PC2 and PC3 had opposite loading values on FA except C18 and c9C18:1. PC4 held a high loading on c9c12C18:2 (0.66) particularly. And the 3D scatter scores of the first, third, and fourth PCs could discern the 3 farms′ FA clearly. The scores and loading plots showed: milk from Anhui had higher C18 and c9C18:1, Xinjiang samples contained more c9c12C18:2, and Heilongjiang milk appeared to have more C16. It was concluded that variation of milk FA profile in these farms is attributed to the difference of some specific individual FA.

Key Words: principal component analysis, milk FA, different farms

M57 Qualitative identification of cow, buffalo, and yak milks using near infrared spectroscopy (NIRS). J. H. Yang, J. Q. Wang,* Y. X. Yang, D. P. Bu, P. Sun, L. Y. Zhou, T. J. Yuan, and J. X. Zhang, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Near infrared spectroscopy (NIRS) has been used in agricultural and food products testing extensively. Compared with many other detection methods, it has better for accuracy, in non-destructive to samples and rapid. The spectrum of dairy milk can predict major components such as protein, fat, and lactose with high precision. The objective of this study was to investigate the variations of milk spectrum between 3 dairy species, which included dairy cows (n = 27), buffaloes (n = 21) and yaks (n = 30). The milk samples were stored at below −70°C. After thawing in 37°C water, samples were shaken lightly for uniformity. Milk raw spectrums were obtained with a DA 7200 diode array Near-IR analyzer (Perten instruments AB, Huddinge, Sweden) in the spectral range 950–1650nm with 100 scans. Operation of the spectrophotometer and collection of spectra were performed using Simplicity software 4.0. Data were processed by multivariate regression software (Unscrambler, version 9.8, CAMO, Bangalore, India). After transformation of MSE/RMSE and elimination of outliers, the PCA analyst with cross validation showed: first 3 principal components (PC) explained the variation of calibration and validation set 98.8 and 98.7%, respectively. PC1 represented the variation of milk spectrum on 1382 nm, PC2 and PC3 described spectrum difference on 1454 and 1404 nm wavelength respectively, although first 3 PCs had same interpretation on 1210 nm. 3D scatter scores image showed PC1, PC2 and PC3 could distinguish between the milk spectra of the 3 species. Milk from buffaloes had its characteristic absorption peaks on 1404 nm wavelengths, while yak samples on 1382 nm, and milk spectrum from cows had a subtle trait on 1518 nm, according to the loading and scores images. It was concluded that the NIRS spectrum was able to distinguish milk from cows, buffaloes, and yaks through multivariable analysis.

Key Words: NIRS, qualitative identification, milk species

M58 Transfer of conjugated linoleic acid from milk to ice cream. G. A. Gagliostro*[1], L. E. Antonacci[1], G. Genero[1], M. R. Williner[2], and C. A. Bernal[2], [1]*INTA, Balcarce, Buenos Aires, Argentina,* [2]*UNL, Sante Fé, Argentina.*

The objective was to test the recovery rate (RR) from milk to ice cream (IC) of cis9 t11C18:2 (RA), t11 C18:1 (VA) and other fatty acids (FA). The experimental dairy cows were treated as 2 group (5 animal each): One Oralac (OR) supplemented group (0.798 kg/d), and one control (C) without supplementation. OR is a lipid supplement, which has 90% DM, 68.6% fat, and contains palmitic (11.25%), stearic (4.65%), oleic (31.7%), linoleic (44.7%), linolenic (2.45%), EPA (0.6%) and DHA (1%). After 21 d of OR feeding milk samples were analyzed for FA (GLC) and used for IC making. Differences between milk and IC FA were tested by the Student *t*-test for paired observations. OR cows produced (kg/d) more milk (32.1 vs. 26.5) and 4%FCM (25.4 vs. 22.9). Milk fat (g/kg) decreased (33.3 in C vs. 25.1 in OR, $P < 0.009$) and milk protein (35.2 vs. 31.9) and lactose (48.7 vs. 47) were not affected. Milk from OR cows showed higher contents (g/100 g) of VA (7.39 vs. 2.75) and RA (2.96 vs. 1.23) and lower C12:0 (2.23 vs. 3.35), C14:0 (8.39 vs. 9.82), and C16:0 (19.45 vs. 23.45). The atherogenicity index (IA) of milk was reduced from 1.92 (C) to 1.37 (OR). IC making showed no differences in FA composition. The RR of FA ranged from 115% for RA (1.23 in milk vs. 1.42g/100g in IC) to 82% for C18:2n-6 (2.84 in milk vs. 2.33g/100g in IC). When the high RA milk was transformed in IC, the RR of VA and RA was 97%. Composition (g/100 g) of C14:0 (8.39 vs. 7.59) and C18:2n-6 (2.25 vs. 1.95) were lower in IC and C16:0 increased (19.45 vs. 23.44). The IC elaborated with the high RA milk (IC-OR) showed a lower ($P < 0.05$) composition (g/100g) of C12:0 (1.95 vs. 3.38) and C14:0 (7.59 vs. 10.00) with a reduction in the AI (1.48 vs. 2.07) compared with the IC-Control. Values (g/100 g) for VA (7.19 vs. 2.96) and RA (2.71 vs. 1.42) resulted higher in IC- OR. Content (g/100 g) of t9 C18:1 was higher ($P < 0.0002$) in IC-OR (0.58) than in IC-Control (0.17) whereas t10 C18:1 did not differ (1.42 vs. 0.86). Saturated FA were lower ($P < 0.02$) in IC-OR (50.5 g/100 g) than IC-Control (57.4 g/100 g). Unsaturated FA (g/100 g) were higher ($P < 0.04$) in OR-IC (37.5) than IC-Control (32.9). Content of C18:2 and C18:3 were not different. It was concluded that no losses in VA or CLA concentrations were detected when milk was transformed into ice cream.

Key Words: conjugated linoleic acid, milk, ice cream

M59 Assessment of adulteration by urea addition to milk by Fourier transform infrared methodology (FTIR). M. C. P. P. Oliveira,* R. S. Conrrado, L. M. Fonseca, M. M. O. P. Cerqueira, and M. O. Leite, *Department of Food Technology and Inspection, School of Veterinary Medicine, Universidade Federal de Minas Gerais (UFMG), Belo Horizonte, Brazil.*

Urea or milk urea nitrogen (MUN) is a non-protein component of milk. Non-protein nitrogen is composed of 30 to 50% of urea nitrogen, while the remaining is composed of creatinine, uric acid, amino acids, and ammonia, among others. MUN has been used as a tool to assess the herd nutritional status, and the excretion of nitrogen to the environment. Adulteration of milk by urea has been occurring in some developing countries. This fraudulent practice seeks to increase analytical values for solid-not-fat (SNF) or protein content of milk. The objective of this study was to evaluate the CombiScope FTIR, an equipment based on Fourier transform infrared methodology (FTIR) in comparison with ChemSpec 150 Analyzer, a enzymatic method, to quantify adulteration by urea addition to milk, and to investigate its effect on protein levels. Extraneous urea was added to the raw milk, simulating a fraudulent practice, and simultaneously analyzed by CombiScope FTIR, and ChemSpec 150 Analyzer. A total of 60 raw milk samples were split into 3 subsamples each, respectively, without any urea addition, 20 mg, and 40 mg of urea addition for 100 g of milk. FTIR results for MUN in milk samples added with extraneous urea were lower than expected only at levels of 40 mg/100 g ($P < 0.05$). There was no significant difference in the levels of protein readings by FTIR equipment after urea addition to the milk. It was concluded that FTIR equipment failed to detect extraneous urea added to the milk at levels of 40 mg/100 g, and protein levels measured by FTIR were not affected by added urea, as happens with the standard nitrogen analytical methods.

Key Words: milk, FTIR, urea addition to milk

M60 Freezing point of raw milk by Fourier transform infrared methodology (FTIR).

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Milk adulteration with water addition is a worldwide problem, with prominence in developing countries. Several methods have been developed for its detection. Determination of freezing point of raw milk has been known as one of the best methods in detection of milk adulteration. Classical methods for freezing point determination have high precision and accuracy, but low output. The objective of this study was to evaluate the freezing point of milk analyzed by FTIR equipment, in comparison with a standard method (freezing point determination by thermistor cryoscope). About 220 samples of bulk tank milk were randomly chosen from 220 farms located in Minas Gerais State, Brazil, and simultaneously analyzed by a thermistor cryoscope (Laktron, LK 7000; PZL, Londrina-PR, Brazil) and a FTIR equipment (CombiScope FTIR; Advanced/Delta Instruments, Drachten, Netherlands). The chosen farms are representative of each region of the state, which is responsible for 30% (7 million metric tons) of Brazilian milk production. Each sample was added with bronopol as preservative, and final freezing point results were obtained by subtracting the effect of its soluble components. Average results for milk freezing point was −0.518°C with a standard deviation of 0.0013°C. Values of freezing point for samples obtained from herds predominantly crossbred were significantly lower when compared with pure Holstein herds. Average values for thermistor cryoscope, and FTIR were, respectively −0.520°C, and −0.518°C, with no significant difference between the 2 methods ($P > 0.05$), and Pearson correlation coefficient of 0.87. It is concluded that FTIR equipment presented a good reliability and repeatability over the range of freezing point for normal milk and for abnormal milk; that is, above −0.520°C, being an efficient screening method to detect milk adulteration by water addition to milk samples in dairy herd improvement programs and dairy industry payment systems.

Key Words: freezing point, thermistor cryoscope, FTIR cryoscope

M61 Identification of a high γ-aminobutyric acid-producing *Lactobacillus plantarum* from traditional dairy products in Inner Mongolia of China.

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γ-Aminobutyric acid (GABA) as a non-protein amino acid, is the major inhibitory neurotransmitter in the sympathetic nervous system and plays a crucial role in cardiovascular function. It is well known that GABA is widely distributed in nature and could be produced by animal brains, plant germs and microorganisms. The objective of this study is to isolate and identify high GABA-producing lactic acid bacteria from traditional dairy products in Inner Mongolia of China. Eighteen strains exhibited different GABA-producing ability in MRS broth by high performance liquid chromatography analysis. Among them the strain NDC 75017 produced the highest amount of GABA, and its yield reached to 138 mg/L. By phenotypic, physiological and biochemical methods, NDC 75017 was characterized as gram-positive, catalase-negative, facultatively anaerobic, non-spore-forming and non-motile rod, which could produce lactate from lactose and did not ferment L-arabinose and D-turanose. In addition PCR amplifications of 16S rDNA and 16S-23S rDNA intergenic spacer region (IGS) were carried out with primers P1 (AGAGTTTGATCCTGGCTCAG), P6 (GGTTACCTTGTTACGACTT) and P2 (CTTGTACACACCGCCCGTC), P7 (GGTACTTAGATGTTTCAGTTC), respectively. Based on 16S rDNA gene sequence, we found that the strain NDC 75017 shared 99.8% similarity with *Lactobacillus plantarum* WCFS1 and *L. plantarum* ST-III. Furthermore, the similarity of 16S-23S rDNA IGS gene sequence between NDC 75017 and above reference strains was 99.5%. Therefore the strain NDC 75017 was identified as *L. plantarum*. Contributed to its high GABA-producing ability, this strain can be used as a potential starter culture to produce GABA-enriched fermented dairy products in future. This work was supported by National Science and Technology Project (2011AA100902), National Natural Science Foundation of China (31171718), Program for Changjiang Scholars and Innovative Research Team in University (IRT-0959–203), and Key Project of Education Department of Heilongjiang Province (12511z005).

Key Words: identification, *Lactobacillus plantarum*, γ-aminobutyric acid

M62 Whey protein isolate affects cysteine content and gel quality of yogurt.

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Whey protein isolate (WPI) is an excellent protein source which is used in a variety of processed foods. Some people with diminished γ-cystathinase are prone to develop cataracts due to decreased glutathione in their eye tissues. For this group, dietary cysteine may be beneficial for their health. Yogurt contains a significant quantity of whey proteins, hence if supplemented with WPI, cysteine could be enhanced. The objective of this research was to increase cysteine content in yogurt while maintaining gel quality. All yogurt mixes were formulated to have a total solids of 12.5% - the control mix consisted of nonfat dry milk (NDM) and the experimental formulas contained mixtures of NDM and WPI (2.0, 2.5 and 3.5%). Mixes were heat treated at 90°C for 7 min, cooled to 43°C, inoculated and fermented at 43°C until 4.5- 4.6 pH. Yogurt samples were maintained at 4°C for 24 h and evaluated for total solids, pH, cysteine content and gel quality following published methods. Three replications were performed, and ANOVA and Dunnett's test were done to determine significant differences. All yogurts had similar total solids contents, but the experimental yogurts had significantly greater cysteine contents, which ranged from 2 to 3.8 × when compared with the control (~141 mg/1000mL). The pH of the experimental yogurt with WPI (2.0%) was similar to the control (~4.52) but the other experimental yogurts had a lower pH compared with the control. The experimental yogurts had significantly greater firmness (ranged from ~2.3 to 8.2 ×) and water-holding capacity (ranged from ~2 to 3 ×) compared with the control (~51 g and 21% wt/wt, respectively). The yogurt with WPI (2.0%) had a 2-fold increase in cysteine content but the gel firmness was ~116 g. Supplementing yogurt mixes with WPI increased the cysteine content in the yogurt without adversely affecting the yogurt quality, except for gel firmness; however, other strategies may need to be used to address the gel firmness.

Key Words: yogurt, whey protein isolate, cysteine

Forages and Pastures I

M63 Body growth and first-lactation milk production of pregnant Holstein heifers reared on pasture or conventional diets. R. R. Peters*[1], S. W. Fultz[2], J. W. Semler[3], and R. A. Erdman[1], [1]*University of Maryland, College Park,* [2]*University of Maryland Extension, Frederick,* [3]*University of Maryland Extension, Boonesboro.*

The objective was to compare body growth rates and first lactation milk production of pregnant heifers reared on intensively grazed pasture (P) to those fed conventional (C) diets in a 2-yr replicated study. Pregnant Holstein heifers based on date of pregnancy confirmation were assigned to P (yr 1, n = 15; yr 2, n = 16) or C (yr 1, n = 15; yr 2, n = 16) for study in spring to summer seasons of 2010 and 2011. Heifers fed conventional TMR included corn and rye silage, grass hay, and a monensin-supplemented grain mix. Pastured heifers were fed 0.454 kg /heifer per d of ground shelled corn with minerals and monensin. Pasture consisted primarily of endophyte-infected tall fescue. Pasture-fed heifers were rotated daily to a new paddock of 0.1 to 0.3 ha, based on available DM. Measurements included body weight (BW), wither height (WH), and hip height (HH) taken every 2 wk. Growth rates and projected first lactation 305 d actual milk, fat, protein, calving age, and somatic cell count from DHI records were analyzed using ANOVA using treatment group within year as a replicate. No differences were found in least square treatment means of any variable averaged by year when comparing pasture and conventionally raised heifers. It is concluded that pregnant heifers can be reared on pasture without detrimental effects on skeletal development, milk production, or somatic cell count.

Table 1.

Growth and lactation measure	Pasture	Conventional	SEM	*P*-value
ADG, kg/d	0.77	0.75	0.347	0.876
WH gain, cm/d	0.042	0.038	0.004	0.606
Mean HH gain, cm/d	0.028	0.034	0.004	0.724
Projected 305 d milk, kg	8558	8369	253	0.651
Projected 305 d fat, kg	341	328	6.1	0.255
Projected 305 d protein, kg	270	259	6.4	0.330
Calving age (mo)	23.0	23.0	0.24	0.926
SCC (cells/mL)	52	76	20	0.481

Key Words: pasture, body growth, milk production

M64 Antioxidant activity and blood parameters in early weaned calves fed yeasts and fermented apple pomace. C. Rodríguez-Muela,* P. Mancillas-Flores, C. Arzola, D. Díaz-Plascencia, O. Viramontes, G. Corral, A. Grado-Ahuir, and A. Ramírez-Godínez, *Universidad Autonoma de Chihuahua, Chihuahua, México.*

The objective was to evaluate the effect of a yeasts inoculate and fermented apple pomace in the diet on the antioxidant activity and blood biometric. Twenty-seven calves (BW = 126.2 kg) were randomly assigned to 3 diets. CD: 1.2 kg oat hay, 1.7 kg corn silage, and 1.2 kg DMI.d^{-1} protein and energy supplement; FD: CD + 12% of fermented apple pomace in the supplement and YD: CD + 2% of yeasts in the supplement. Animals were fed for 98 d including a 14-d adaptation period and were bled every 28 d. The variables evaluated were antioxidant activity (AA), white cells count (WBC), hemoglobin (HM), corpuscular volume (CV), corpuscular hemoglobin (CH) and plaques (PQ). The data were analyzed with PROC MIXED of the SAS program in a completely randomized design. The results are shown in Table 1. AA in the calves of the 3 diets was reduced during the study, however, AA at 84 d as well as WBC were higher ($P < 0.05$) in the calves of FD and YD than those of CD. We concluded that the addition of the fermented apple pomace and yeasts in the diet of early weaned calves increased the antioxidant activity and tended to improve the immune system.

Table 1. Means of the square minimums and standard error of antioxidant activity (AA) and blood parameters (d 56 of test) in early weaned calves

	CD	FD	YD	SE
AA d 0 (mM Fe$_2$)	15.73^{c}	15.99^{a}	15.81^{b}	±0.03
AA d 84 (mM Fe$_2$)	15.62^{b}	15.72^{a}	15.71^{a}	±0.03
WBC (10^3/µL)	0.24^{b}	0.53^{a}	0.59^{a}	±0.09
HM (g/dL)	11.45^{a}	11.33^{a}	11.71^{a}	±0.05
CV (fL)	73.78^{a}	63.51^{b}	61.53^{b}	±3.38
CH (g/dL)	31.47^{b}	33.29^{b}	37.02^{a}	±1.25
PQ (105/µL)	5.69^{a}	5.67^{a}	4.37^{b}	±0.37

Different superscripts between columns indicate statistical difference ($P < 0.05$).

Key Words: blood parameters, antioxidant activity, yeasts

M65 Use of yeasts and fermented apple pomace in the diet of early weaned calves. P. Mancillas-Flores,* C. Rodríguez-Muela, C. Arzola, D. Díaz-Plascencia, A. Grado-Ahuir, O. Viramontes, A. Flores, and A. Ramírez-Godínez, *Universidad Autonoma de Chihuahua, Chihuahua, México.*

The objective was to evaluate the effect of yeasts inoculate and fermented apple pomace on blood mineral levels of early weaned calves diets. Twenty 7 Angus calves (PV = 126.2 kg) were assigned to CD:oat hay 1.2; corn silage 1.7 and protein and energy supplement 1.2 kg DMI/d^{-1}), FD: CD+12% of fermented apple pomace in the supplement and YD: CD+2% of yeasts inoculate in the supplement. The animals were fed during 98d. The variables evaluated were DMI, ADG and Zinc (Zn), Manganese (Mn) and Copper (Cu) in the blood serum. Data were analyzed with PROC GLM of the SAS program, in a completely randomized design for DMI and AVG and PROC MIXED for minerals concentration. The results are shown in Table 1. DMI of YD calves was greater ($P < 0.05$) than those of CD and FD. There was a reduction ($P < 0.05$) of level of Zn at 84 d in calves of FD. Calves of YD showed a greater concentration of Zn at 84 d of study ($P < 0.05$) than those of CD and FD. We concluded that the yeasts inoculate in early weaned calves diets increased significantly DMI and Cu serum concentration however fermented apple pomace decreased Zn serum concentration.

Table 1. Means of the square minimums and standard error of the variables analyzed by tratment in early weaned calves

	CD	FD	YD	SE
DMI (kg/d)	4.260^b	4.114^b	4.711^a	±0.10
ADG (kg/d)	0.855^a	0.816^a	0.771^a	±0.05
Zn d 1 (ppm	0.56^a	0.57^a	0.56^a	±0.05
Zn d 84 (ppm)	0.52^a	0.40^b	0.45^a	±0.05
Mn d 1 (ppm)	0.41^a	0.38^a	0.38^a	±0.04
Mn d 84 (ppm)	0.40^a	0.43^a	0.43^a	±0.04
Cu da 1 (ppm)	0.40^a	0.44^a	0.42^a	±0.04
Cu d 84 (ppm)	0.42^b	0.38^b	0.53^a	±0.04

Different superscripts between columns indicate statistical difference ($P < 0.05$).

Key Words: early weaned, apple pomace, yeasts

M66 Performance and carcass traits of steers grazing annual ryegrass supplemented with increasing levels of flaxseed.

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This study evaluated the effects of increasing flaxseed addition to corn grain supplemented to steers grazing annual ryegrass on performance and carcass traits and whether dietary treatment effects were affected by animal live weight (LW). Forty-eight Angus steers were randomly assigned to 8 treatment combinations: 2 animal weights (LIGHT and HEAVY) and 4 dietary treatments (CNTRL = no supplement; CORN = 0.7% LW of cracked corn; LFLAX and HFLAX = CORN + 0.125% and 0.250% LW of whole flaxseed, respectively). Steers assigned to LIGHT received their dietary treatment when the average LW reached 366 ± 27.3 kg (mid winter) and those assigned to HEAVY, when they reached 458 ± 42.8 kg (mid spring). Steers were managed under a daily rotational system with no forage limitation and individually supplemented with 0.5 kg/d of wheat bran in addition to their dietary treatment. Steers were slaughtered after 70 d on trial. Data were analyzed as a complete randomized design with a 2 × 4 factorial arrangement; preplanned contrasts were used to compare CNTRL vs. supplemented treatments, and linear and quadratic flaxseed effects. No main factor interactions were found ($P > 0.10$). Average daily gain (ADG) was greater ($P < 0.01$; SEM = 0.028) in LIGHT than in HEAVY (1.43 and 0.75 kg). Final LW and HCW were greater ($P < 0.05$) in HEAVY than in LIGHT, but subcutaneous fat thickness (FT), carcass yield and ribeye area did not differ ($P > 0.05$). Supplemented steers tended ($P = 0.06$) to have greater ADG (87 ± 45 g) than CNTRL steers, but no effect was observed ($P > 0.05$) by increasing flaxseed level. Supplementation increased ($P = 0.04$) FT by 1.4 ± 0.68 mm, and each increment of flaxseed increased ($P = 0.03$) FT by 0.9 ± 0.42 mm. No dietary treatment effects ($P > 0.05$) were observed for final LW, HCW, carcass yield, or ribeye area. In conclusion: (a) the different animal weights considered in the present study did not influence supplementation response; (b) with no limiting forage availability, the main effect of energy supplementation was to increase FT; and (c) flaxseed could be supplemented up to 0.25% of LW without negative effects on animal performance or carcass traits.

Key Words: pasture, oil, corn

M67 Evaluating grazing performance and forage quality differences between AC-Saltlander green wheatgrass (*Elymus hoffmannii*) and smooth bromegrass (*Bromus inermis*).

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AC-Saltlander (ACS) green wheatgrass (*Elymus hoffmannii*) is a Canadian perennial forage cultivar that has salinity tolerance equaling that of tall wheatgrass. Study objective was to evaluate beef and forage production and forage quality differences between ACS and smooth bromegrass (SB; *Bromus inermis*). Seeding of the 6 paddocks (ea 1.2 ha in size) occurred in 2006 and each pasture treatment was replicated 3 times. Paddocks were grazed by Angus yearling steers (308 ± 10 kg) when the grasses were at the bloom to heading stage at a stocking rate of 2.0 AU ha^{-1}. Forage and gazing data were collected over 4 production years (2008 to 2011). No interactions ($P \geq 0.10$) were observed, thus only significant main effects were presented. Available biomass production at time of grazing and peak biomass production did not differ ($P \geq 0.10$) between pasture treatments. However, peak forage biomass production for ACS was numerically higher than SB in 2008, 2009 and 2010. Percent organic matter digestibility (OMD), NDF, ADF, CP, Ca and P differed ($P \leq 0.01$) among years which was expected due to changing environmental growing conditions. Percent forage OMD values (mean ± SE) were higher ($P \leq 0.01$) for SB versus ACS and were 60.8 versus 57.6 ± 0.48, respectively. Average daily gains, total livestock production and number of grazing days did not differ ($P \geq 0.10$) between ACS versus SB, and the values were 1.32 and 1.14 ± 0.12 kg d^{-1}, 87.9 and 87.8 ± 1.9 kg ha^{-1}, and 53.2 and 46.8 ± 5.8 d ha^{-1}, respectively. Beef cattle grazing performance and forage qualities were generally similar between ACS and SB. Throughout the entire study differences in overall system performance of the 2 grasses were not observed.

Key Words: AC-Saltlander green wheatgrass, smooth bromegrass, grazing

M68 Continuous versus rotational stocking of rye and ryegrass pastures at different stocking rates and forage allowance.

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Stocking strategies are implemented for cool-season annual grass pastures to enhance efficiency of gains per animal and per unit land area. A 7-year stocking study with 482 steers and heifers quantified ADG and gain/ha using stocking methods (MTH) of continuous (CONT) vs. an 8-paddock rotational (ROTN) system on Maton rye (*Secale cereale* L.) plus TAM-90 annual ryegrass (*Lolium multiflorum* Lam.) pastures at different fixed stocking rates (STK). Two replicate pastures of MTH × STK each with 6 to 8 270-kg fall-weaned calves were stocked from late Dec to mid-May each year at the Texas AgriLife Research Center at Overton. The 8-paddock ROTN system consisted of a 2 d graze and 14-d deferment cycle with forage mass measurements pre- and post-graze. The ADG ranged from 1.38 kg/d on low STK to 0.23 kg/d on high STK, and was affected ($P < 0.01$) by year, STK, year × STK, year × MTH, and at $P = 0.07$ for STK × MTH. Only at one STK in each of 3 years and when forage allowance (FORG) was <0.80 kg forage DM per kg body weight was ADG affected ($P < 0.01$) by MTH. At low STK with FORG >1.0, MTH had no affect on ADG. Gain per ha was affected ($P < 0.01$) by year, STK, and year x STK, and ranged from 1206 kg/ha for medium STK to 389 kg/ha for high STK. Gain per ha was maximum at the medium to medium-high STK. With the nutritive value of rye plus ryegrass, there were no biological nor economic advantages to using an 8-paddock ROTN system compared with CONT

stocking. Although forage DM tended to be increased on ROTN pastures due to the 14-d deferment, gains were not enhanced. Stocking rate and resultant decreased forage DM and FORG affected ADG and gain/ha each year, thus, STK should be the primary consideration for stocking strategies and management.

Key Words: stocking rate, rotational stocking, ryegrass

M69 Improving calf performance by extending the grazing season with warm season grasses and brassica forages.

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The objectives of this experiment were to determine whether grazing cow-calf pairs on warm season grasses and brassica pastures would extend the grazing season by providing high quality forage into the late summer and improve calf weaning weight. Treatments were pasture type; extended season pasture (EXT), a new planting mixture of sorghum × Sudangrass (*Sorghum bicolor* (L.) Moench) and brassica forages (*Brassica* and *Raphanus* species), and control pasture (CON), an existing field of cool season forage (*Festuca* and *Lolium* species plus *Trifolium repens* and *subterraneum*). Thirty cow-calf pairs (cows with 6 mo old steer calves) were stratified by calf weight and assigned to treatments randomly. Each pasture type was divided into 3, 2-ha paddocks (replicates of experimental unit) and grazed with 5 cow-calf pairs until late summer weaning. Data were analyzed by ANOVA as a randomized design. Cool spring weather at planting (May 14, 2010) slowed EXT establishment and growth so that grazing was delayed until mid-August, allowing for only a 14-d grazing period. Prussic acid and nitrate screening tests were conducted, and forages were determined to be safe to graze. Forage yield of EXT tended ($P = 0.06$) to be lower than that of CON (4,972 and 7,642 kg/ha, respectively; SEM ± 746.8). In contrast, CP (10.3% and 6.7%; SEM ± 0.839) and TDN (69% and 56%; SEM ± 2.86) of pasture plants sampled randomly were higher ($P < 0.04$) for EXT compared with CON, respectively. Calf weaning weights (205-d adjusted) were not different ($P = 0.21$) between EXT and CON (288.1 and 305.0 kg, respectively; SEM ± 9.36). In year 2, planting strategy for EXT was adjusted to delay seeding until soil temperature reached 16°C (June 15, 2011). However, growing conditions were again less than optimal, pasture was not sufficient for grazing, and no additional data were obtained. Early establishment of warm season forages in western Oregon can be severely affected by weather, making it difficult to graze cows with February–March born calves for the purpose of improving late summer weaning weights. Strategies that include grazing cow-calf pairs that are to be weaned in the fall may be more advantageous.

Key Words: brassica, sorghum, weaning weight

M70 Beef steer performance when grazing native warm season grasses.

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Use of native warm-season grasses (NWSG) in forage systems may maintain, or improve, animal performance while providing vital ecosystem services. The drought tolerance, low fertilizer needs, high production, and nutritive value of NWSG suggest they could provide a valuable forage base for cattle producers in the south. Also, NWSG provide superior wildlife habitat compared with non-native forages such as Bermudagrass (*Cynodon dactylon*). The objective of this study is to evaluate the productivity of forage systems for beef cattle production that integrate NWSG. Three forage treatments were evaluated: Indiangrass (*Sorghastrum nutans*) monocultures (IND); mixed specie pastures of Big Bluestem (*Andropogon gerardii*), Little Bluestem (*Schizachyrium scoparium*), and Indiangrass (MIX); and Common Bermudagrass (BG) which is a typical summer forage of the region. Site preparation began in spring 2008 and forages were planted in spring 2009. Grazing began in May 2011, with 225 British-crossbred beef steers (IBW 237 kg ± 1.5). Nine pastures were used (3 per treatment) ranging in size from 7 to 11 ha. Pastures were stocked at 2.7 steers/ha and continuously grazed. Cattle were weighed every 28 d and remained on pasture for 110 d. Selected cattle wore activity monitors (IceTag, v 2.004) to measure grazing behavior. Data were analyzed using PROC MIXED of SAS (SAS Inst., Cary, NC) and a significance level of $\alpha \leq 0.05$ was used, with trends defined at $0.10 \geq \alpha > 0.05$. Average daily gain (ADG) of steers did not differ between treatments during periods, d 1–28, 56–84, or 84–110. However, during the peak of the season (d 28–56), ADG was greater ($P < 0.02$) in IND (1.1 kg) and MIX (0.9 kg) than BG (0.64 kg). Overall season ADG tended ($P \leq 0.10$) to be greater for IND (0.6 kg) and MIX (0.6 kg) than BG (0.4 kg). Percent of the day that animals spent grazing (IND 45%, MIX 45%, BG 46%), lying down (IND 41%, MIX 40%, BG 38%), or standing still (IND 13%, MIX 13%, BG 14%) did not differ within period or overall during the season. Time spent walking did differ between treatments with IND steers walking less (1.6%, $P < 0.05$) than BG (2.3%) or MIX (2.2%) steers. These NWSG show promise for use in beef grazing systems in Mississippi.

Key Words: native warm season grass, forage systems, grazing behavior

M71 Animal performance on pastures managed at two forage heights to produce grass finished beef.

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The animal benefits of management intensive grazing (MIG) are well documented but little is known about managing pastures using the tall grass grazing (TGG) principle. The purpose of this experiment was to evaluate animal performance on pastures managed using either MIG or TGG. Sixteen Angus steers (n = 10, BW = 371 ± 15 kg) and heifers (n = 6, BW = 317 ± 15 kg) were assembled from 2 farms (8 per farm). The cattle were blocked by sex and randomly assigned to MIG or TGG (treatments) based on projected adjusted final BW (AFBW) computed from frame score. Land area required was computed based on average BW, 2 d rotation, 60 d rest period, an estimated forage yield of 183 kg/ha/rotation, and a DMI of 2.5% of BW. Before animals were rotated, forage height was measured on both paddocks. Forage was sampled to approximate the plants cattle grazed. Statistical analyses were conducted assuming farm as a random factor; treatment and sex were assumed to be fixed effects. The initial BW was used as covariate. No interactions were significant ($P > 0.10$) and were removed. Cattle were placed on MIG and TG when forage was 4.24 ± 0.08 cm and 7.43 ± 1.95 cm, respectively. There were no treatment effects ($P > 0.05$) for AFBW, initial BW, final BW, 64 d ADG or 64 to 135 d ADG. The ADG was greater ($P = 0.0067$) for MIG compared with TGG from 64 to 135 d (0.90 ± 0.09 vs. 0.54 ± 0.07 kg, respectively). Cumulative ADG (165 d) was greater ($P = 0.0197$) for MIG compared with TGG (0.95 ± 0.08 vs. 0.79 ± 0.07 kg, respectively). Body condition score was higher ($P = 0.0089$) for MIG compared with TG (7.7 ± 0.13 vs. 7.0 ± 0.21, respectively). There were no treatment effects ($P > 0.05$) for forage NDF, CP, ME or forage composition. However MIG tended ($P = 0.0632$) to produce higher proportion of grass (86.0 ± 2.2%) compared with TGG (71.0 ± 7.4%) and a lower ($P = 0.0743$) proportion of weed (8.5 ± 1.7% vs 22.5 ± 7.2%, respectively). It is likely that the MIG cattle consumed more DM compared with TGG, but the residual forage height between MIG and TGG (0.24 ± 0.11 vs. 0.49 ± 0.12 cm, respectively) was not significant ($P = 0.1778$). While TGG forage was of similar quality to MIG animal performance was reduced, perhaps due to reduced DMI.

Key Words: beef, pasture, finishing

M72 Nutritive value of plants and milk production from crossbreed cows grazing Tanzania guinea grass subjected to rotational stocking managements.

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Managements for grazing strategies can promote change in the sward structure and can affect nutritive value and animal production in grazing system. The objectives were to evaluate the crude protein (CP) and neutral detergent fiber (NDF) and milk yield from crossbred cows grazing Tanzania guinea grass (*Panicum maximum* Jacq. cv. Tanzania) and the stocking rate, subjected to rotational stocking managements. The 2 treatments were grazing when swards height was 70 cm or growing fixed period of 30 d, according to a randomized complete block design. The 16 paddocks with 4,000 m^2 were evaluated during spring, summer and fall (5 grazing cycles). The pre-grazing samples of plants and leaves were analyzed for CP and NDF. Eight cows, per treatments, were used for milk production evaluations, in a randomized complete block design. The concentrate supplementation was 4 kg/cow/day. The data were analyzed using the Proc Mixed Procedure of SAS. Interactions between treatments and grazing cycles for CP in forage mass and leaves ($P < 0.001$) were observed. The average for CP was 12.6% for grazing when swards height was 70 cm. The grazing cycles affected ($P = 0.014$) the CP for the fixed period of 30 d treatment. The average of CP was 8.6% for the 1st cycle and end 9.6% for the last cycle (fall). During the summer, the CP was 13.16% for leaves. NDF of leaves was higher ($P = 0.006$) for growing fixed period of 30 d (75.3%) compared with swards height was 70 cm (72.3%). No effect on milk yield and milk composition was found. The average were 19.83 and 18.56 kg/cow/day for 3.5% fat corrected milk, 3.19 and 3.14% of fat; 3.02 and 2.99% of protein; 4.46 and 4.37% of lactose for grazing when swards height was 70 cm or for fixed period of 30 d, respectively. The stocking rate was higher ($P = 0.0456$) for the fixed period of 30 d treatment (6.18/ha) compared with grazing when swards height was 70 cm (5.76/ha). The management based on growing fixed period of 30 d can affect the nutritive value of pasture and the stocking rate but do not affect the milk production from cows supplemented with concentrate.

Key Words: milk components, *Panicum maximum*, sward height

M73 Sward structural characteristics, herbage accumulation of Tanzania guinea grass subjected to rotational stocking managements.

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Managements for grazing strategies promote change in sward structure and can affect herbage accumulation. The objectives of this study were to evaluate the plants structural characteristics, the production and the herbage accumulation in pasture of Tanzania guinea grass (*Panicum maximum* Jacq. cv. Tanzania) subjected to rotational stocking managements. The 2 treatments were grazing when swards height was 70 cm or growing fixed period of 30 d for each grazing cycle, according to a randomized complete block design. The 16 paddocks with 4,000 m2 were evaluated during spring, summer and fall, for 5 grazing cycles. The height of plants was compared. The forage mass was evaluated before and after grazing time and the herbage accumulation. The morphological composition of plant (leaves, stem and dead material), the interception of the incident light (LI) and the leaf area index (LAI) were evaluated in pre-grazing samples. The data were analyzed using the Proc Mixed Procedure of SAS. No influence of treatments was found for post-grazing mass and herbage accumulation. The height of plants was 20% higher ($P = 0.0014$) and the forage mass was higher ($P = 0.0034$) for the fixed growing period of 30 d treatments. In pre-grazing samples, the leaves ($P = 0.00429$), stem ($P = 0.0131$), dead material ($P = 0.0106$), LI ($P = 0.0071$) and LAI ($P = 0.023$) were higher for the fixed growing period of 30 d treatment. The results for forage mass were 2508 and 3317 kg/ha; the leaves mass were 1527 and 1790 kg/ha; the stem mass were 699 and 984 kg/ha; the dead material were 282 and 472 kg/ha; the IL were 97 and 91% and the LAI were 4.5 and 5.2, for grazing when swards height was 70 cm and the growing fixed period of 30 d, respectively. The fixed period of 30 d for each grazing cycle improved the forage production and change characteristics in sward.

Key Words: grazing management, *Panicum maximum*, sward height

M74 Simulation of the effect of stocking rate on forage harvest efficiency under New Zealand intensive grazing systems.

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Long-term experiments comparing the effect of stocking rates (SR) on forage harvest efficiencies (FHE) in dairy grazing systems are costly and time consuming; however, this can be facilitated by the use of simulation models. The objective of this work was to explore the effect of SR on FHE using DairyNZ Whole Farm Model (WFM). The WFM is a farm-scale computer model that includes a mechanistic model of a dairy cow and a climate driven pasture growth model, which interact with a grazing behavior model to mechanistically and dynamically determine FHE (proportion of forage consumed [FC] by cows related to the net forage produced [NFP] by pasture). An average, pasture-based New Zealand farm (forage base: 80% *Lolium perenne* and 20% *Trifolium repens*; cow: Holstein-Friesian crossbreed, 450 kg liveweight and 270 d in milk) was simulated using 7 SR (treatments) and over 3 series of 3 different (e.g., rain, temperature, solar radiation and potential evapotranspiration) climate years (replicates). Resulting variables of the simulation, NFP (ton DM/ha/year) and FC (tonnes DM/ha/year) were analyzed by regression analysis. Then FHE was estimated as FC/NFP. Results of the simulations (Table 1) demonstrated a significantly ($P < 0.001$) positive relationship between SR and the output variables (NFP, FC and FHE), which are concomitant with experimental results (Macdonald et al., 2008 J. Dairy Sci.). Simulation modeling allows examination of costly experimental frameworks and outcomes under pastoral production systems, providing useful information for researchers and farmers in a relatively short period of time and at low cost. This study indicates that under the simulated conditions, increments in SR will lead to greater NFP and FC, and consequently a greater FHE.

Table 1. Effect of stocking rate (SR) on net forage production (NFP), forage consumed (FC), and forage harvest efficiency (FHE)

	NFP (t of DM/ha/yr)		FC (t/ha/yr)		FHE	
SR (cows/ha/yr)	Mean	SD	Mean	SD	Mean	SD
2.0	18.4	0.88	10.5	0.21	0.57	0.146
2.5	18.6	0.66	12.4	0.21	0.67	0.129
3.0	18.8	0.47	13.9	0.33	0.74	0.030
3.5	19.0	0.52	14.5	0.56	0.77	0.207
4.0	19.4	0.56	15.5	0.52	0.80	0.041
4.5	19.9	0.69	15.8	0.60	0.80	0.048
5.0	20.0	0.59	15.8	0.68	0.79	0.086
P-value	<0.001		<0.001		<0.001	
SE	547		426		0.01	
Intercept	17.2		176		0.03	
Linear coefficient	533		6.61		0.35	
Quadratic coefficient			−697		−0.04	
R^2 adjusted	0.48		0.95		0.97	

Key Words: modelling, forage produced and consumed, grazing management

M75 Nitrogen fertilizer management to improve forage production in south-central Vietnam. K. C. McRoberts[1], D. Parsons[2], J. H. Cherney[1], Q. M. Ketterings[1], and D. J. R. Cherney*[1], [1]*Cornell University, Ithaca, NY,* [2]*University of Tasmania, Hobart, Tasmania, Australia.*

The objective of this field trial was to assess the effect of nitrogen (N) fertilization from composted cattle manure and urea on forage yield in tropical sandy soils (organic matter < 1%). *Brachiaria* 'Mulato II' was established in summer 2010 on 6 farms in Binh Dinh Province of south-central Vietnam. Experimental design was a randomized complete block with 5 levels of manure N (0, 40, 80, 120, 240 kg N/ha/yr) and 3 levels of urea N (0, 60, and 120 kg N/ha/yr) applied in 6 split applications at 2 mo intervals. Canopy height, maximum height, live tiller count, and dry matter (DM) yield were measured monthly ($n = 830$). DM yield data through January 2012 were log-transformed and analyzed using a linear mixed model (REML) in JMP Pro 9.0.2. Coefficient of determination was 0.78. Fixed effects included urea ($P < 0.0001$), manure ($P = 0.8387$), and their interaction ($P = 0.0994$), as well as additional covariates (pre-experiment soil pH, month, and plant count). Random effects included block (52.4% residual variance) and block x treatment (4.1%). Mean differences were evaluated using Tukey's test. Urea levels 60 (18 mt/ha/yr; 95% CI [11.3, 28.6]) and 120 (18.5; [11.6, 29.4]) were significantly higher than level 0 (14.7; [9.2, 23.4]). In the urea × manure interaction, 120 × 240 (21; [13.2, 33.5]) and 60 × 40 (20.9; [13.1, 33.3]) treatment combinations were significantly higher than 0 × 120 (14.1; [8.8, 22.4]). Urea significantly affects yield. Manure × urea interaction plot suggests positive yield response for urea level 120 at increasing levels of manure. Yield response to urea level 60 across manure levels suggests net N immobilization when the C:N ratio is high. Yield response to manure was absent without urea. Model results for tiller count response were similar to the yield model. Preliminary results suggest that high forage yield requires sufficient inorganic N, and organic matter in composted manure may decrease N available for plant uptake. Future field trial priorities include continued field data collection and assessment of forage nutritive value and soil fertility changes over time. N fertilization recommendations will be developed and disseminated to farmers and educators in the study region.

Key Words: tropical forage yield, nitrogen, manure

M76 Anatomy and histochemistry of lignin in *Festulolium* and its progenitors. J. M. Vargas-Romero[1], H. A. Zavaleta-Mancera[2], S. S. González-Muñoz*[2], J. Burgueño-Ferreira[3], M. Meneses-Mayo[2], and B. Alarcón-Zúñiga[4], [1]*Universidad Autónoma Metropolitana-Iztapalapa, México D.F., México,* [2]*Colegio de Postgraduados, Montecillo, Estado de México, México,* [3]*CIMMYT, Estado de México, México,* [4]*Universidad Autónoma Chapingo, Chapingo, Estado de México, México.*

The objective of this study was to evaluate the lignified tissue distribution in *Festulolium* and its progenitors. *Festuca arundinacea* Schreb, *Lolium perenne* L. and *Festulolium* sp. (*F. arundinacea* × *L. perenne*) were cultivated in a greenhouse. At 22 d after sowing mature leaves from the 3 species were studied for anatomy, lignin histochemistry and NDF and ADF content by light microscopy, scanning electron microscopy, phloroglucinol staining and the Van Soest method. The cross sectional area of protoxylem and metaxylem of the central vein, number of bulliform cells, number and distance between vascular bundles, stomata and epidermal hair density were measured. The relative lignin content (%) was estimated measuring the cross sectional area or the lignified cellular components/total leaf area with the software Motic Images Plus 2.0. The data were statistically analyzed with SAS using the *genmod-zero inflated* Poisson method of the observed and residuals data. The number of vascular bundles did not show differences among species but it related significantly with the epidermal hair density. The adaxial stomata density was related inversely with the metaxylem size; in contrast the abaxial stomata density showed a positive relation with the protoxylem, but there were no differences among species. The distance between veins, associated with the photosynthetic mesophyll, was directly proportional with the NDF and inversely with ADF, behaving differentially among species. There was more lignin in *Festuca* than in the other species, particularly in the abaxial and adaxial epidermis, subepidermal fibers, vascular bundle sheath, marginal fibers, metaxylem vessels and fibers. *Lolium* showed lignin only in the metaxylem of veins. *Festulolium* inherited from *Festuca* large vascular bundles but less lignified, and from *Lolium* the absence of lignin in epidermis, margin and vascular bundle sheath. These characters confer a greater robustness to *Festulolium* in its architecture but with less lignin and greater digestibility.

Key Words: *Festulolium*, anatomy, lignin

M77 The n-alkane technique provides a reliable estimate of fescue and clover composition in mixed forages. N. Vargas Jurado,* A. E. Tanner, S. R. Blevins, H. M. McNair, and R. M. Lewis, *Virginia Polytechnic Institute and State University, Blacksburg.*

N-alkanes are saturated hydrocarbons found in the cuticular wax of plants. Because patterns of n-alkanes differ among plants, they can be used to define the dietary composition of grazing herbivores. N-alkanes are extracted by saponification, with concentrations determined by gas chromatography. Methodological differences, including operator expertise, may contribute to variability in the technique's reliability. Our objectives were to determine: (i) the reliability of estimating the composition of a 2-plant mixture using n-alkanes, and (ii) the extent within and between operator variability affects those estimates. Pure and 2-plant mixtures of red clover and fescue were prepared; the mixtures contained 10 to 90%, at 10% increments of each plant. Two operators, one experienced and one novice, performed 2 extractions of each mixture. For the 4 extractions, concentrations of C_{27}, C_{29}, C_{31} and C_{33}, as plant markers, and C_{22} and C_{34}, as internal standards, were determined. The compositions of the 9 mixtures were estimated using nonnegative least squares. Reliability was assessed by regressing actual on estimated fescue contents, testing the hypothesis that the slope equaled unity. Operator differences were tested with ANOVA.

Across extractions, mean concentrations of C_{27}, C_{29}, C_{31} and C_{33} were 28.0 ± 1.5, 116.8 ± 6.7, 168.5 ± 5.9 and 45.6 ± 1.5 mg/kg for fescue, and 19.6 ± 1.5, 284.6 ± 6.7, 35.6 ± 5.9 and 8.6 ± 1.5 mg/kg for red clover, respectively. The 3 longer chain n-alkanes provided greater discrimination between the plants. Within operator, concentrations of C_{27} and C_{29} differed between extractions ($P < 0.05$). Between operators, only concentrations of internal standards differed (C_{22}, $P = 0.02$; C_{34}, $P = 0.01$), likely due to differences in the standard solutions used. For the experienced operator, the slopes were 0.98 ± 0.03 and 0.98 ± 0.01. For the novice operator, the slopes were 0.83 ± 0.08 and 0.97 ± 0.04. None of the slopes differed from unity, although predictions based on the first extraction of the novice operator were less consistent. Clearly, with training, the n-alkane methodology provides reliable estimates of the composition of plant mixtures.

Key Words: n-alkanes, forage composition, reliable estimate

M78 Assessment of stockpiling methods to increase late summer and early fall forage biomass.

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In Virginia, tall fescue can be found on more than 4 million acres as hay and pastureland. Management programs to optimize stockpiled tall fescue can potentially increase livestock productivity in Virginia and throughout the region. Prior to making a decision on stockpiling, the producer needs to consider the need for high quality forage. This includes the time of greater forage needs, number, and production level of animals. The objective of this study was to assess the effect of summer stockpiling endophyte-infected Kentucky 31 tall fescue on biomass and nutritive value of tall fescue forage. The experiment consists of 4 treatments each replicated 6 times in a split plot design. The 4 treatments were 2 nitrogen application timing, legume inclusion, and control. Each of the 4 treatments was divided into a cut and a no cut treatment. The cutting treatment consisted of a single cutting taken in May. Nitrogen in the form of urea was applied in March (before the cutting) to one nitrogen application timing treatment and in May (after the cutting) to the other nitrogen application timing treatment at the rate of 56.04 kg/ha. The extent of clover establishment was dependent on the amount of tall fescue residue present at the time of frost seeding. Yield and nutritive value results were analyzed using the glimmix procedure in SAS statistical analysis software. Significance was determined at a level of $\alpha = 0.05$ and responses for significant effects were separated using the Tukey-Kramer grouping of least squares means. Initial results indicate no biomass yield differences between fertilization treatments ($P = 0.3556$) or cutting treatments ($P = 0.8510$). However, some differences in the nutritive value of the stockpiled fescue were observed between the cut and no cut treatments for acid detergent fiber ($P < 0.0001$), neutral detergent fiber ($P < 0.0001$), and crude protein ($P = 0.0022$). Additionally, effect of fertilization treatment on nutritive value was not evident for acid detergent fiber ($P = 0.1199$), neutral detergent fiber ($P = 0.5637$), or crude protein ($P = 0.1488$). The same experiment will be repeated during the 2012 growing season.

Key Words: tall fescue, summer stockpile, forage

M79 Soil nutrients in tall fescue (*Festuca arundinacea* L.) paddocks managed under different outdoor hog systems.

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To evaluate the effects of outdoor hog management systems (MS) on soil nutrients, nine 0.16-ha tall fescue paddocks were established at the Center for Environmental Farming System (Goldsboro, NC). The 12-wk-long experiment was conducted twice (Dec 2010 - Mar 2011, and May - Aug 2011). The stocking rate was equivalent to 49 wean-finish hogs/ha. Hogs (23.4 ± 0.6 and 84.8 ± 1.12 initial and final weight, respectively) had ad libitum access to shelter, water and a concentrated feed (16% CP). Animals were managed under 3 systems: continuous (C), rotational (R) and strip (S). In C, hogs had access to the whole paddock area. In R, the paddocks were divided into 9 sections and the central section where shelter and water were located considered a heavy use area (HUA); hogs had permanent access to the HUA and were moved weekly to one of the other 8 sections where feed was provided; after the first 8 weeks, animals had access to the HUA + 2 sections. In S, the paddocks were divided into 8 strips and shelter, water and feed were moved with the animals once a week; after the first 8 weeks, animals were moved to 2 strips on a weekly basis. Soil samples were hand probe collected on 2 dates: before (Dec 2010) and after (Aug 2011) hogs, and at 2 depths (0–15 cm; D1) and (15–30 cm; D2). Paddocks were divided into 9 sections, and 12 core samples per depth were randomly collected within each section and composited. A composite sample per paddock was analyzed for nitrate concentration. The experimental design was a randomized complete block with 3 field replicates. Data were analyzed using the PROC MIXED procedure of SAS and included MS and depth as main effects. The MS affected concentrations of P, K, Mn, Zn, Cu ($P < 0.05$) and NO_3 ($P < 0.09$). Higher ($P < 0.05$) concentrations of nutrients were observed in D1. According to the conditions of this experiment, lower soil nutrient contents were observed in the paddocks managed under the rotational compared with the continuous system.

Table 1. Soil nutrients (mg/dm^3) in tall fescue paddocks under 3 outdoor hogs managing systems (C, R, S[1]) and 2 depths (D1 and D2)

	C	R	S	D1	D2
P	49.0 ^{a}	40.2 ^{b}	39.6 ^{b}	50.4^b	35.4^b
K	97.6^a	78.7^b	78.5^b	113.3^a	56.6^b
Ca	643	650.5	655.5	654.5	644.8
Mg	151	155.9	157.9	151.8	158.1
S	14.4	14.4	13.4	15.6	12.5
Mn	47.5^a	41.0^b	46.3^a	46.4	43.5
Zn	4.2^a	3.4^b	3.8^{a,b}	4.6^a	3.0^b
Cu	1.8^a	1.6^b	1.7^{a,b}	2.0^a	1.5^b
Na	23.1	26.1	25.6	26.8^a	23.0^b
NO_3[2]	21.8^c	16.9^d	18.1^{c,d}	25.2^c	12.8^d

Means with different letters differ (a, b: $P < 0.05$; c, d: $P < 0.09$).

[1] C, R, S values averaged over depths.

[2] Composite sample/paddock.

Key Words: outdoor swine, soil nutrients, *Festuca arundinacea*

M80 Effect of outdoor swine management systems on tall fescue (*Festuca arundinacea* L.) ground cover and animal performance.

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During 2 seasons (S; December 2010-March 2011 = S1, and May–August 2011 = S2), the ground cover (GC) of tall fescue paddocks (0.16 ha) was recorded weekly for 12 wk at the Center for Environmental Farming Systems (Goldsboro, NC), to evaluate the effects of 3 outdoor hogs management systems (MS). The stocking rate (8 pigs/plot) was equivalent to 49 weaning-finishing hogs/ha. Initial and final (avg 23.3 ± 1 and 84.8 ± 1 kg, respectively) animal weights were recorded and daily weight gain (DWG) was calculated. The MS evaluated were: continuous (hogs had permanent access to the entire paddock [MS1]), rotational (hogs had permanent access to 1/9 of the area considered as a heavy use area, and were rotated to another 1/9 section on a weekly basis (wk 1–8) or to 2/9 sections (wk 8–12) [MS2]) and strip grazing (hogs had access to 1/8 of the paddock (wk 1–8) or to 2/8 sections (wk 8–12) [MS3]). Animals had ad libitum access to shelter, water and feed (16% CP). Intake averaged 1.96 kg/pig/d. A modified step point method was employed to estimate live vegetation (LV), vegetation residue (VR) and bare soil (BS). The GC was defined by GC = LV+VR. The experimental design was a randomized complete block with 3 field replicates (REP). The LV, BS and GC data were log(x+1) transformed whereas the equation $((x+1)/100)^{1/2}$ was used for VR. After pigs removal data (wk 12) were analyzed using PROC MIXED of SAS v 9.2, following a mixed linear model including MS, S and MS*S as fixed effects, and REP and REP*MS as random effects. For DWG, initial weight and sex condition (female or castrate) were used as covariates. Under the conditions of this experiment GC, its components or DWG did not differ ($P > 0.05$) among management systems. Season affected the variables under evaluation with the exception of DWG.

Table 1. Ground cover (%) of tall fescue paddocks and DWG (kg/pig) under 3 outdoor hogs managing systems (MS 1, MS2, MS3) during 2 seasons (S1 and S2)

	MS1	MS2	MS3	SE
LV	62.4	69.8	69.8	3.1
VR	4.6	2.6	4.4	1.1
BS	31.9	28.3	25.8	2.9
GC	67.5	72.4	74.3	2.5
DWG	0.7	0.8	0.7	0.02

	S1	S2	SE
LV	58.8^{b}	76^{a}	3.1
VR	6.7^{a}	1.0^{b}	1.0
BS	33.9^{a}	23.5^{b}	2.4
GC	65.5^{b}	77^{a}	2.5
DWG	0.7	0.8	0.02

a,b: Means with different letters differ ($P < 0.05$).

Key Words: outdoor swine, ground cover, *Festuca arundinacea*

M81 Effect of outdoor swine management systems on the botanical composition of tall fescue (*Festuca arundinacea*) paddocks.

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An experiment was performed at the Center for Environmental Farming Systems (Goldsboro, NC) to compare the botanical composition (BC) of tall fescue paddocks under 3 outdoor swine management systems. The systems consisted of Continuous (C; hogs had access to the entire paddock during the length of the evaluation), Rotational (R; the paddocks were divided into 9 sections with the central section used as a heavy use area [HUA]); hogs had permanent access to the HUA and were moved weekly to one of the other 8 sections), and strip grazing (S; the paddocks were divided into 8 strips, and the hogs were moved once a week with shelters, feeders and drinkers). Nine 0.16-ha tall fescue paddocks were managed with a stocking rate equivalent of 49 weaning-finishing hogs/ha for 12 weeks during 2 periods: winter 2010–2011 and summer 2011 (S2011). Hogs had ad libitum access to feed (16%CP) and water and free-choice access to shelter. One week after hog removal in S2011, the botanical composition of the paddocks (tall fescue, broadleaf weeds and other grasses) was estimated using the visual estimation (VE) and the dry weight rank (DWR) methods. Paddocks were divided into 9 sections, and 5 quadrats (0.25 m^2) were randomly thrown into each section for the DWR, and the VE of each section was also estimated. The experimental design was a complete randomized block with 3 field replicates. Data were analyzed using Proc Mixed of SAS 9.2 and repetition, treatment × repetition, method × treatment, and method × repetition were included as random effects. No statistical differences ($P > 0.05$) were observed among management systems nor methods of botanical composition estimation. Tall fescue was the main component of the pasture (64.97%), followed by other grasses (29.82%) and broadleaf weeds (4.13%). Crabgrass (*Digitaria sanguinalis*) was the most frequently observed grass, while ragweed (*Ambrosia artemisifolia*) was the most prominent broadleaf weed. The 3 management systems under evaluation had no impact on the botanical composition components of tall fescue paddocks. In addition, similar botanical composition results were obtained using the VE or the DWR methods.

Key Words: outdoor swine, botanical composition, *Festuca arundinacea*

M82 Endophyte-infected fescue seed causes constriction of the palmar and uterine arteries in pregnant mares.

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Pregnant mares grazing endophyte-infected (E+) tall fescue may incur problems in late pregnancy such as extended gestation, thickened placenta, decreased prolactin secretion and agalactia. One hallmark of E+ fescue consumption in cattle is vasoconstriction, and we previously demonstrated that it also caused a marked constriction of the palmar artery in nonpregnant horses. The purpose of this experiment was to determine if consumption of E+ tall fescue seed caused constriction of the palmar and uterine arteries in pregnant mares, and if it altered the combined uterine/placental thickness (CUPT). Pregnant mares (n = 23) at 276 + 4.79 (mean ± SE) days gestation were used in an experiment that was divided into 3 periods (P) of 1-week each. During P1, all mares received E- fescue seed, while during P2, 11 mares received E- seed and 12 mares received E+ seed. During P3, all mares once again received E- seed. Seed, averaging 6.5 ppm ergovaline + ergovalinine, was mixed with the daily grain ration in twice/day feedings such that each day mares received seed at 0.2% body weight. Three times per week during P1 and P2 the left palmar and uterine arteries of each mare were scanned via Doppler ultrasonography, and CUPT near the cervical star was measured. The same measurements were taken again on the last day of P3. Blood samples were taken 3 times per week throughout the study to measure hormone concentrations. When P2 was compared to P1, mares consuming E+ fescue seed, but not E- seed, had reduced diameters of the palmar ($P = 0.0001$) and uterine ($P < 0.0174$) arteries. However, there were no period or treatment differences in the CUPT measurements. Prolactin was lower ($P = 0.0009$) in P2 vs P1 when mares received E+ seed but there were no differences in progesterone or estradiol concentrations. In conclusion, consumption of E+ fescue seed caused constriction of both the palmar and uterine arteries but did not alter CUPT. Constriction of the palmar artery is a sensitive response variable in mares receiving E+ seed, and measuring palmar artery diameter may be a useful tool in monitoring mares' exposure to E+ tall fescue in pastures.

Key Words: horse, fescue, pregnancy

M83 Consumption of endophyte-infected tall fescue seed causes constriction of the palmar artery and vein but does not alter estradiol, progesterone, or estrous cycle length in nonpregnant mares.

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Endophyte-infected (E+) tall fescue (TF) has deleterious health effects in pregnant mares, however, effects are not well understood in nonpregnant mares. Previously, our lab has demonstrated constriction of the palmar artery of nonpregnant horses consuming E+TF seed (Moore et al., 2008). The purpose of this experiment was to determine if the consumption of E+TF seed by nonpregnant mares alters interovulatory intervals and serum hormone concentrations, and to determine if E+TF causes constriction of the palmar vein as well as the artery. Nonpregnant cycling mares (n = 12) were used in a crossover experiment consisting of 2 periods (P), where each P was the duration of 1 estrous cycle (from ovulation, d 0, to next ovulation). On d 0 of P1 mares were assigned to receive either E+ (at 6.5 ppm ergovalinine + ergovalinine) or endophyte free (E-) TF seed. All mares were placed on E- seed at the end of P1 to allow for a washout period, where Lutalyse (10 mg) was given on Day 6 to cause luteal regression. On d 0 of P2 (day of next ovulation) mares began receiving the treatment alternate from P1. Seed was mixed with the daily grain ration such that each day mares received seed at 0.2% body weight. During P1 and P2, the palmar artery and vein of each mare were scanned via Doppler ultrasonography every 2 to 3 d. Blood samples were taken every other day during P1 and P2, with more frequent ultrasound scanning and blood sampling on days immediately around ovulation. Lengths of estrous cycles and concentrations of progesterone and estrogen were not different between treatments. However, E+ seed caused constriction of the palmar artery ($P < 0.0001$) and vein ($P = 0.014$) compared with the E- seed. Measuring vasoconstriction therefore may be a useful tool in monitoring mares' exposures to E+ TF, and vasoconstriction could affect fertility and embryonic development. Future experiments will assess the effects of E+TF on the vascularity of the uterine endometrium.

Key Words: tall fescue, Doppler ultrasound

M84 Changes in bovine vascular contraction and constriction relative to time off endophyte-infected tall fescue.

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Beef cattle grazing endophyte-infected (E+; *Neotyphodium coenophialum*) tall fescue (TF; *Lolium arundinaceum*) are exposed to ergot alkaloids produced by the endophyte. Ergot alkaloids induce constriction in vascular tissue of extremities of animals grazing TF, which leads to an inability to regulate body temperature and an increased susceptibility to heat and cold stresses. To better understand consequences of alkaloid exposure, a study was conducted to evaluate changes in vascular contraction relative to time-off E+ TF pasture after an 88-d grazing period. Lateral saphenous veins were biopsied from 24 predominantly Angus steers (361 ± 4 kg) at 0-, 21-, 42-, and 63-d off of TF pasture (n = 6 per time point) and 6 control steers (370 ± 18 kg) at 0-d and 63-d off bermudagrass (BG) pasture (n = 3 per time point). Off pasture, steers were housed in a dry lot and fed a non-toxic corn silage diet. To evaluate contractile response, biopsied vessels were cleaned, incubated in a multimyograph, and exposed to increasing concentrations (1×10^{-11} to 10^{-4} M) of ergotamine. Myograph data were normalized to a reference edition of 1×10^{-4} M norepinephrine. Cross-sectional ultrasound scans of caudal artery at the fourth coccygeal vertebra were taken on d 0, 8, 15, 21, 29, 36, 42, and 45 using an Aloka 3500 Ultrasound Unit with a UST-5542 (13 MHz) linear array transducer set to 2-cm depth to determine mean artery luminal area to evaluate constriction. Data were analyzed as a CRD using mixed models in SAS with steer as experimental unit. Veins from steers of TF pasture differed over time ($P < 0.05$) and d-0 TF veins had a much lower ($P < 0.05$) contractile response to ergotamine compared with d-0 BG veins. By 63-d myograph contractile responses for TF steers were similar to those of BG steers ($P = 0.29$). Luminal areas of caudal arteries in steers grazed on E+ TF had relaxed and were similar to steers that had grazed BG by 36-d on the non-toxic diet ($P = 0.15$). Measures of contraction indicate that cattle should be removed from E+ TF pastures for a minimum of 4 weeks to obtain vascular responses similar to those of cattle grazed on non-toxic pastures.

Key Words: bovine, ergot alkaloid, tall fescue

M85 Lateral saphenous vein responses to serotonergic and α-adrenergic receptor agonists increase with time off endophyte-infected tall fescue.

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Previous research has indicated that serotonergic and α-adrenergic receptors in peripheral vasculature are affected by exposure of cattle grazing toxic endophyte-infected (E+) tall fescue (TF; *Lolium arundinaceum*). This study was conducted to investigate changes in vascular contractile response over time relative to removal from an E+ TF pasture after an 88-d grazing period. Lateral saphenous veins were biopsied from 24 Angus-cross steers (361 ± 4 kg) at 0-, 21-, 42-, and 63-d off of TF pasture (n = 6 per time point) and 6 steers (370 ± 18 kg) off of bermudagrass (BG) pasture on d-0 and d-63 (n = 3 per time point). Off pasture, steers were housed in a dry lot and fed a corn silage diet. Biopsied vessels were cleaned and incubated in a multimyograph and exposed to increasing concentrations (5×10^{-8} to 1×10^{-4} M) of TCB-2 (TCB; 5HT$_{2A}$ agonist), guanfacine (GF; α$_{2A}$-adrenergic agonist), and

(R)-(+)-m-nitrobiphenyline oxalate (NBP; α_{2C}-adrenergic agonist). Data were normalized to a reference addition of 1×10^{-4} M norepinephrine and analyzed as a CRD using mixed models of SAS for main effects of d off pasture, agonist concentration, the interaction, and comparison of TF to BG veins at d 0 and d 63 included a pasture effect. Steer was the experimental unit. Increasing concentrations of 3 agonists incubated with TF veins were significant for agonist ($P < 0.01$) and d off pasture ($P < 0.01$), but only TCB was significant for d off pasture × concentration interaction ($P < 0.01$). Vasoactivity to agonists was reduced when steers were initially removed from E+ TF pasture. Contractile response at d 63 was greatest ($P < 0.05$) for GF, NBP, and TCB and d-42 TCB response was greater ($P < 0.05$) than on d 21 or d 0 (which did not differ). Contractile responses to NBP at d 0 were greater in BG veins ($P < 0.01$) than TF and tended to be greater ($P = 0.07$) for GF and TCB, but none were different at d 63. These data demonstrate changes in peripheral vasoactivity occur beyond 1 mo off pasture and $5HT_{2A}$ receptors appear to be more dramatically affected in the lateral saphenous vein by grazing E+ TF pasture than adrenergic receptors.

Key Words: bovine, tall fescue, vasoconstriction

M86 Validation of a housekeeping gene for use in bovine vascular gene expression studies.

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Exposure of ungulate vasculature to ergot alkaloids while grazing endophyte (*Neotyphodium coenophialum*)-infected tall fescue (*Lolium arundinaceum*) affects vasoactivity and causes vasoconstriction. Bovine vascular gene expression as affected by exposure to ergot alkaloids in tall fescue is largely unstudied. The objective of this study was to investigate the suitability of β-actin (ACTB), glyceraldehyde 3-phosphate dehydrogenase (GAPD), hypoxanthine phosphoribosyl-transferase I (HPRT), succinate dehydrogenase flavoprotein subunit A (SDHA), and ubiquitin C (UBC) as potential housekeeping genes for use in bovine vascular gene expression studies that include different levels of exposure to ergot alkaloids. Lateral saphenous (SV) and right ruminal veins (RV) were selected as models for comparison of peripheral and visceral vasculature for future experiments. Veins were collected immediately after slaughter from 19 predominantly Angus steers that had grazed either a low-endophyte-infected tall fescue pasture (LE; 5.7 ha; n = 9; BW = 266 ± 6 kg) or a high-endophyte-infected tall fescue pasture (HE; 5.7 ha; n = 10; BW = 267 ± 6 kg) for 89–105 d. Isolated veins were frozen in liquid N and stored at −80°C until completion of total RNA isolation and 1st strand synthesis of cDNA. Real-time PCR was run using SYBR Green with PCR product verified by dissociation curve analysis. Relative standard curve analysis of each gene was done using separate serial dilutions of composite cDNA (10 ng/μL) from SV and RV. Transcript levels (ng/μL) for each gene were analyzed as CRD factorial for endophyte level and vein with mixed models in SAS. Endophyte level (HE vs. LE) did not affect expression of any gene, nor were any endophyte level × vein interactions detected. There was a main effect of vein for HPRT, GAPD, and SDHA ($P < 0.01$). Expression levels of HPRT, GAPD, and SDHA were all greater ($P < 0.05$) in SV than RV, whereas levels of ACTB and UBC did not differ between veins. Thus, ACTB or UBC mRNA transcripts are appropriate to use as normalizing genes when assessing the effects of grazing endophyte-infected tall fescue on gene expression by bovine RV and SV tissues.

Key Words: bovine, housekeeping gene, vein

M87 Tiller appearance in pastures of Guinea grass ‘Tanzania’ managed with different frequencies and defoliation severities.

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The experiment was conducted from November 2005 to October 2006 in Viçosa, MG, Brazil (20°45′ S; 42°51′ W; 651 m a.s.l.). Tiller appearance was evaluated in Guinea grass ‘Tanzania’ (*Panicum maximum* ‘Tanzania’) subjected to rotational stocking management characterized by 2 post-grazing heights (30 and 50 cm) and grazings carried out at the 90 and 95% canopy light interception condition. The 4 grazing management strategies (90/30, 90/50, 95/30, and 95/50) were allocated to experimental units in a completely randomized block design with 3 replications.Tiller dynamics were assessed in 3 clumps per experimental unit. This assessment made it possible to calculate the tiller appearance rate {[new tillers/total of live tillers in the previous marking) x 100]/regrowth days}. The data were grouped into 4 seasons: end of spring (November and December 2005), summer (January to March 2006), fall (April to June 2006) and winter/beginning of spring (July to October 2006). The data were submitted to variance analysis using the GLM Procedure of SAS (Statistical Analysis System) and compared by the Tukey′s test, with 10% of significance. The tiller appearance rate was influenced by the interaction post-grazing height × light interception × season of the year ($P < 0.10$). In the end of the spring, pastures managed with 90/30 and 90/50 presented higher values ($P < 0.10$) relatively to the ones managed at 95/30 and 95/50 (1.10 and 0.85 versus 0.45 and 0.45 tiller/100.tiller.day, respectively). Swards managed with 90/30 (1.92 and 1.10 tiller/100.tiller.day) and 95/30 (2.33 and 1.30 tiller/100.tiller.day) presented higher values ($P < 0.10$) in comparison to the ones managed at a 90/50 (1.66 and 1.79 tiller/100.tiller.day) and 95/50 (1.40 and 0.70 tiller/100.tiller.day) in the summer and in the fall, respectively. In the winter/beginning of the spring, pastures managed with 95/30 presented lower tiller appearance rate ($P < 0.10$) comparatively to the ones managed at 90/30, 90/50, and 95/50 (0.69 versus 1.21, 1.08 and 0.98 tiller/100.tiller.day, respectively). All the evaluated management strategies were adequate for Guinea grass.

Key Words: ecophysiology, post-grazing height, light interception

M88 Aerial tiller density in pastures *Pennisetum purpureum* submitted to different post-grazing heights.

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Elephant grass is a plant that has a high forage yield potential and is widely used in dairy farming under grazing in Brazil. With this type of management, attention should be given to the type of tiller being produced because, under grazing, Elephant grass produces a great quantity of aerial tillers. The experiment was carried out from February to May in 2009 to evaluate the aerial tiller density in Elephant grass ‘Napier’ (*Pennisetum purpureum* Schum.) submitted to different grazing severities. The study was conducted in an area cultivated with Elephant grass ‘Napier’ in Vicosa, MG, Brazil (20°45′ S; 42°51′ W; 651 m a.s.l.). Soil is classified as Inceptic Hapludults, with clay-loam texture. Treatments corresponded to 3 post-grazing conditions (residues of 30, 50 and 70 cm) associated with a pre-grazing condition of 95% sward canopy light interception during regrowth. A complete randomized block design with 3 replications was used. The monitoring of the light interception was done using the canopy analyzer (LAI 2000). The aerial tiller density was evaluated by counting the living tillers within 4 existing metal frames measuring 0.25 m × 1.00 m per experimental unit. The data were grouped by month and subjected to an ANOVA using the Mixed Procedure of SAS (Statistical Analysis System).The means were compared by the Student's *t*-test at a 5% significance level. The aerial tiller density was influenced by the post-grazing height ($P = 0.0017$) and was lower in the pastures that were managed at a post-grazing height of 30 cm (125 tillers/m^2) compared with those that were managed at 50 or 70 cm (211 and 201 tillers/m^2, respectively). These swards had also lower tiller renewal and higher quantity of weeds, suggesting the beginning of degradation process and that this post-grazing height (30 cm) should not be recommended for grazed elephant grass. The aerial tiller density was not affected by the month ($P = 0.5567$), being on average 179 tillers/m^2. The post-grazing height of 30 cm can drastically reduce the pasture accumulation rate.

Key Words: ecophysiology, grassland management, light interception

M89 Tiller density stability of Piatâ palisadegrass swards deferred with different initial heights. B. M. L. Sousa[1], D. Nascimento Júnior*[1], M. E. R. Santos[2], H. H. Vilela[1], M. C. T. Silveira[3], G. O. Rocha[1], B. D. Faria[1], and C. A. S. Freitas[1], [1]*Univsersidade Federal de Viçosa, Viçosa, MG, Brazil,* [2]*Faculdade de Medicina Veterinaria e Zootecnia, Uberlândia, MG, Brazil,* [3]*Empresa Brasileira de Pesquisa Agropecuária - Pecuária Sul, Bagé, RS, Brazil.*

The study was conducted to evaluate the stability index of the tiller density of the Piatâ palisadegrass (*Brachiaria brizantha* 'Piatâ') deferred with 3 initial heights of the sward (20, 30 and 40 cm) and 4 deferring periods (1 to 30, 31 to 60, 61 to 90, and 91 to 120 d). The experiment was carried out in the Federal University of Vicosa, in Viçosa, Minas Gerais, from March 1 to July 7, 2011. The experimental design was a complete randomized block with 3 replications in subdivided plots repeated in time. Tillering was evaluated inside of a 30 cm diameter metal ring in each experimental unit. This evaluation made it possible to calculate the stability index of the tiller density [survival rate × (1 + appearance rate)] for the basal and aerial tillers. Data were analyzed using the SAEG (Statistical Analysis System and Genetics) and the means comparisons were made by the Student-Newman-Keuls′s test at a probability of 5%. In general, the stability index values under 1.0 indicate that the survival and appearance of new tillers are not enough to compensate the death rates, and, thus, the density tends to decrease, while higher values than 1.0 suggest increase, and values near 1.0 indicate a stable tiller density, in which the number of tillers does not practically vary. The stability index of basal ($P = 0.6652$) and aerial ($P = 0.6907$) tillers was not affected by the initial deferring height, presenting, in average, 1.05 and 1.68, respectively. However, the stability index of basal ($P = 0.0007$) and aerial ($P = 0.0003$) tiller density was influenced by the deferring period. The Piatâ palisadegrass deferred from 1 to 30 d (1.62 and 4.11) presented higher value of stability index of basal and aerial tillers in relation to the ones deferred from 31 to 60 (0.89 and 0.90), 61 to 90 (0.83 and 0.94) and 91 to 120 d (0.85 and 0.79), respectively.

Key Words: *Brachiaria brizantha*, grassland management, structural characteristics

M90 Tiller density in Piatâ palisadegrass deferred in different seasons and initial heights. B. M. L. Sousa[1], D. Nascimento Júnior*[1], H. H. Vilela[1], M. E. R. Santos[2], C. Z. Assis[1], G. O. Rocha[1], and B. D. Faria[1], [1]*Univsersidade Federal de Viçosa, Viçosa, MG, Brazil,* [2]*Faculdade de Medicina Veterinaria e Zootecnia, Uberlândia, MG, Brazil.*

Deferring management strategies can affect the number of tillers of the sward, compromising the persistency, the productivity and sustainability of the grassland. Therefore, the study was conducted to evaluate the effect of the seasons and initial deferring heights on the number of tillers of the Piatâ palisadegrass (*Brachiaria brizantha* 'Piatâ'). The experiment was carried out in the Federal University of Viçosa, in Viçosa, Minas Gerais, in 3 areas deferred in March 20, April 10, and May 1, 2010, and with initial heights of 20, 30, and 40 cm. A complete randomized block design with 3 replications in a subdivided plot scheme was used. The area was deferred until 07/01 in 2010, at which time the number of tillers inside 2 square metal frames of 0.4 × 0.4 m was determined. The data were analyzed using the SAEG (Statistical Analysis System and Genetics) and compared by the Tukey test at 5% of significance. The number of tillers was influenced by the interaction between initial height and season ($P = 0.0345$). Higher number of tillers was obtained in the area deferred in May 1 in the initial heights of 20 (1,056 tillers/m^2), 30 (1,158 tillers/m^2), and 40 cm (1,113 tillers/m^2), in April 10 in the heights of 20 (1,069 tillers/m^2) and 30 cm (1,356 tillers/m^2), and in March 20 in the height of 20 cm (1,135 tillers/m^2), in relation to the ones deferred in April 10 in the height of 40 cm (704 tillers/m^2) and in March 20 in the heights of 30 (911 tillers/m^2) and 40 cm (808 tillers/m^2). Long deferring periods associated to the high initial sward heights decreases the number of tillers of deferring Piatâ palisadegrass.

Key Words: *Brachiaria brizantha*, grassland management, structural characteristics

M91 Animal productivity on brachiaria grass deferred at different heights[1]. M. C. T. Silveira[1], D. M. Fonseca[2], D. Nascimento Júnior*[2], M. E. R. Santos[3], V. M. Gomes[2], F. K. Gomes[2], V. L. N. Brandâo[2], G. O. Rocha[2], B. M. L. Sousa[2], A. Deus[2], R. L. Albino[2], L. S. Moura[2], and G. A. Borges[2], [1]*CPPSU-Embrapa Pecuária Sul, Bagé, RS, Brazil,* [2]*Universidade Federal de Viçosa, Viçosa, MG, Brazil,* [3]*Faculdade de Medicina Veterinaria e Zootecnia-UFU, Uberlândia, MG, Brazil.*

Pasture deferment consists of postponing the grazing in one area for utilization in the offseason period. Thus, the objective of this study was to evaluate the animal productivity on brachiaria grass pastures deferred at different heights. The experiment was conducted in a field of the Animal Science Department of Universidade Federal de Viçosa, Minas Gerais, Brazil. The experimental area consisted of Brachiaria decumbens Stapf. 'Basilisk' pasture subdivided in 8 paddocks (experimental units), plus a reserve area, totaling approximately 3 ha. The experiment was conducted in randomized block design with 2 replicates and 4 heights at the beginning of deferment (10, 20, 30, and 40 cm). In March 2010, pastures were managed under continuous stocking and variable stocking rate, so that the heights could be established, and the deferment was started. In June 2010, the grazing on deferred pastures began. During 115 d, pastures were managed under continuous stocking, and the initial fixed stocking rate was approximately 3.0 AU/ha. The animals were growing crossbred steers, with an average weight of 190 kg. During the grazing period, cattle consumed, in addition to deferred pasture, mineral salt ad libitum. Average daily weight gain, stocking rate and production per area were measured. Variance and regression analyses at significance level up to 10% of probability were carried out. Stocking rate and animal production per area were not affected by pasture heights ($P > 0.10$), with an average value of 3.78 AU/ha and 0.69 kg/ha.d. This result can be explained by the stocking rate, which was fixed at the beginning of the grazing period. These productivity rates are high for this period, since in Brazil the climatic conditions are not conducive to pasture growth. The average daily gain increased quadratically with pasture height at the beginning of deferment ($P < 0.10$), with maximum value of 0.134 kg/animal.d in the pasture deferred at 20 cm. Therefore, with lowering of brachiaria pastures to 20 cm at the beginning of the deferment period, it is possible to avoid weight loss in cattle kept on pasture, which is common during the fall and winter seasons (June to September).

Key Words: *Brachiaria decumbens* 'Basilisk', grazing management, stocking rate

M92 The effect of cutting at different stages of maturity on yield and quality of nine forage oat varieties in the peace region of Alberta.

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Beef cattle producers commonly use annual cereals for silage, greenfeed and swath grazing in parts of the Peace Region of Alberta. In Alberta, oats account for more than 40% of total annual greenfeed production. As with most forage crops, there is a yield and quality trade off as small grains mature from boot to dough maturity stages. Timing of the cereal forage harvest is critical to obtain the desired forage quality. The objective of this study was to examine the effects of stage of maturity at cutting on forage yield and feed value of forage oat varieties for greenfeed and swath gazing systems. Nine forage oat varieties were seeded and cut at the late milk and dough stages for yield and feed value in a split-plot experimental design. Forage dry matter (DM) yields of all oat varieties did not show any significant ($P > 0.05$) increase as cutting was delayed from the late milk stage until the dough stage. The mean forage DM yields across the 9 oat varieties ($P > 0.05$) were, respectively, 8,496 and 9,601 kg/ha for late milk and dough stages. When pooled across the 2 stages of maturity at cutting, the average forage DM yield was in the following order ($P > 0.05$): Warden > Foothills > Mustang > SO-I > Murphy > Baler > Morgan > Everleaf > Jordan. When averaged across the 9 oat varieties, mean forage crude protein (CP) was significantly ($P < 0.05$) higher at the late milk stage (9.17%) than at the dough stage (5.66%). For the late milk stage, SO-I oat had the highest CP (10.55%) and Jordan oat had the least CP with 7.24%. When harvesting was delayed till the dough stage, Everleaf significantly ($P < 0.05$) had the most CP (7.20%), while Mustang had the least CP (4.54%). Generally, for each oat variety, cutting at the late milk stage gave slightly lower total digestible nutrients (TDN) (3–8% less energy) than cutting at the dough stage. For all the forage oat varieties examined, the dough stage had significantly ($P < 0.05$) lower ADF and NDF contents than the late milk stage. In summary, the stage of maturity at cutting oat in the present preliminary study did not affect forage DM yield. However, harvesting the forage oat in the late milk stage gave better CP than at the dough stage, but higher energy harvested per acre occurred at the dough stage.

Key Words: Stages of maturity, oats, forage yield and feed value

Graduate Student Competition: ADSA Dairy Foods Division Graduate Poster Competition

M93 Structural properties of milk protein concentrate (MPC) dispersions and emulsions as influenced by presence of small molecule components. Y. Liang*[1,2], H. Patel[1], L. Matia-Merino[2], A. Ye[3], and M. Golding[2,3], *[1]Fonterra Research Centre, Palmerston North, New Zealand, [2]Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, New Zealand, [3]Riddet Institute, Massey University, Palmerston North, New Zealand.*

Heat-stable milk-protein-stabilized emulsions with desirable mouthfeel and shelf-life stability are a challenging system. The compositions (i.e., proteins, sugars, and small molecule surfactants) of various emulsion phases affect the stability and the rheological properties of this type of emulsion. This study investigated and elucidated the potential ingredient interactions (i.e., protein—sugar) in protein-based dispersions and emulsion systems. MPC-I and MPC-II were used as model proteins. They had similar protein contents of ~81% and calcium contents of 2230 and 1140 mg/100 g, respectively. They were reconstituted as 10% w/w dispersions at neutral pH and the pHs were adjusted to 6.2, 6.4, 6.6, 6.8, 7.0, 7.2, and 7.4. Model emulsions with 10% w/w protein and 10% w/w oil were prepared at pH 6.8. Sucrose was added at 0—30% w/w. Oscillatory rheology and heat coagulation time (HCT) were measured twice for each sample, and all samples were prepared in duplicate. The presence of sucrose (5—30% w/w) influenced the aggregation process of 10% w/w MPC-I dispersions during a heating and cooling cycle (25 to 90 to 25°C), as shown by an inhibition of the increase in the complex modulus during cooling. The heat stability, which would be expected to have a marked maximum at pH ~6.5 and a minimum at pH ~6.9, of the MPC dispersions was influenced by protein type, pH, and sucrose concentration. MPC-I exhibited a marked maximum at pH 7.2 in the absence of sucrose, which shifted to pH ~6.8 in the presence of 30% sucrose. The HCT of MPC-I was higher in the presence of up to 15% sucrose than in the absence of sucrose and decreased gradually with increased sucrose (>15%) to less than that in the absence of sucrose. In contrast, MPC-II dispersions exhibited a marked maximum at pH 6.4 regardless of the addition of sucrose. The emulsions stabilized by MPC-I and MPC-II, with and without sucrose, had markedly different stabilities and rheological properties. The aggregation state of casein micelles and sugar-induced calcium activity changes affected the heat stabilities and rheological properties of MPC-based dispersions and emulsions. The results help in our understanding of the behavior of milk proteins in systems with high carbohydrate content.

Key Words: milk protein concentrate, emulsion, rheology

M94 Application of bixin as an alternative colorant for Cheddar cheese. X. Li,* T. J. Smith, and M. A. Drake, *North Carolina State University, Raleigh.*

Colorless whey ingredients are desirable in food applications, therefore bleaching is necessary to remove residual annatto (norbixin) colorant from Cheddar cheese whey. Bleaching negatively affects the flavor of dried whey ingredients and new restrictions on chemical bleaching agents have increased the need for bleach or cheese color alternatives. Bixin is a nonpolar form of annatto and is not currently used in the cheese industry. However, because bixin is nonpolar, it may have an increased retention in the cheese matrix with less carryover into cheese whey. The objective of this study was to determine viability of bixin as an alternative cheese colorant and if less bixin was present in cheese whey compared with norbixin. Preliminary studies established minimal homogenization pressure to stably suspend bixin in milk. A concentration of 60 mL bixin /454 kg milk was selected for comparable concentration to norbixin incorporation concentration. Pasteurized milk was cooled to 55°C, then 60 mL bixin/454 kg milk (3.8% wt/vol bixin) was added and homogenized (single stage) at 80 bar. Milk with no colorant and milk with 15 mL/454 kg milk norbixin (3% wt/vol norbixin) were processed analogously as controls. Mass balance was determined by extraction and quantification of bixin and norbixin in milk, whey, and cheese. The experiment was replicated 3 times. Nine percent norbixin (2.1 ppm) was recovered in the unseparated cheese whey compared with 1.3% bixin (0.3 ppm; $P < 0.05$). The amounts of norbixin and bixin both decreased after fat separation of whey, but the decrease was greater for bixin than for norbixin ($P < 0.05$). Whey from cheese with bixin was visibly lighter in color concurrent with decreased b* values compared with whey from cheese with norbixin ($P < 0.05$). These results confirm that less bixin colorant was present in cheese whey compared with norbixin colorant, thus potentially circumventing the need for whey bleaching. Bixin may be a viable alternative to norbixin in the cheese and whey industry.

Key Words: bleaching, norbixin, bixin

M95 Cold enzymatic bleaching of fluid whey and retentate. R. E. Campbell* and M. A. Drake, *North Carolina State University, Raleigh*

Chemical bleaching of fluid whey and retentate with hydrogen peroxide (HP) requires high concentrations (250 to 500 ppm) and is most effective at temperatures greater than 35°C. Off flavors are generated during HP bleaching. Enzymatic bleaching of fluid whey and retentate with lactoperoxidase or Maxibright at cold temperatures (4°C) may be a viable alternative to chemical bleaching. The objective of this study was to compare enzymatic and traditional chemical HP bleaching of fluid whey and retentate at 4°C. Fluid Cheddar whey was manufactured in triplicate from pasteurized whole milk, and subsequently, 80% whey protein retentate was manufactured from the fluid whey. The optimum concentration of HP for enzymatic bleaching at 4°C (10 ppm for fluid whey and 15 ppm for retentate) was determined. In subsequent experiments, bleaching efficacy, sensory characteristics, and volatile compounds were evaluated after 1 h (retentate) or 24 h (fluid whey) bleaching. Controls with no bleaching and traditional HP bleaching (250 ppm HP) were also evaluated. Bleaching efficacy was determined by measuring norbixin destruction compared with the unbleached control, sensory profiles were evaluated by descriptive analysis, and volatiles were measured by gas chromatography mass spectrometry (GCMS). At 4°C, enzymatic bleaching of fluid whey and retentate resulted in higher bleaching efficacy than chemical bleaching with HP alone ($P < 0.05$). Due to concentrated levels of naturally present lactoperoxidase, retentate bleached to completion (>80% norbixin destruction) in less than 10 min. In fluid whey, the addition of Maxibright increased the rate of enzymatic bleaching ($P < 0.05$), from 6 to 2 h for 80% norbixin destruction. Percent norbixin destruction by HP was 11% (after 24h) and 90% (after 1h) in fluid whey and retentate, respectively. Bleached wheys and retentates had decreased sweet aromatic and cooked/milky flavors compared with unbleached controls. Wheys and retentates bleached chemically by HP displayed sulfur flavors not present in enzymatically bleached samples. Volatile compound results were consistent with sensory analysis. These results suggest that enzymatic bleaching may be a viable and desirable alternative to HP bleaching.

Key Words: bleaching, whey, lactoperoxidase

M96 The effect of milk pasteurization temperature on the bleaching of fluid whey.

E. Kang* and M. A. Drake, *North Carolina State University, Raleigh.*

Chemical bleaching is a commonly applied unit operation in whey protein processing that negatively influences whey protein flavor. Recent studies have shown that native milk lactoperoxidase (LP) is active in cheese whey and can be used to bleach annatto colored fluid whey. A low concentration of hydrogen peroxide (10–50 ppm) is required for LP activity. When excess concentrations of HP (>100 ppm) are applied, LP is inactivated and HP chemical bleaching occurs. Fluid milk can be subjected to a wide range of heat treatment before cheese manufacture and heat treatment may influence subsequent whey bleaching efficacy. The objective of this study was to investigate the effect of milk pasteurization temperature on the bleaching efficacy of fluid whey. Milk was pasteurized at 63°C for 30 min (LHT) or 79°C for 20 s (HHT) and colored Cheddar whey was produced and fat separated. LP activity (LHT) or inactivation (HHT) was determined by a colorimetric assay. Hydrogen peroxide was then added at 250 ppm (chemical bleaching) or 25 ppm (LP bleaching) at 35 or 50°C and aliquots were collected after 10, 20, or 60 min. Unbleached colored wheys was used as a control. Norbixin extraction and quantification as well as b* values were measured to determine bleaching efficacy. The norbixin content of HHT whey was 82% lower than that of LHT ($P < 0.05$), and the protein content was decreased by 22% for HHT whey compared with LHT whey. Whey from LHT had a higher bleaching efficacy ($P < 0.05$) from 25 ppm HP (80% norbixin destruction) than 250 ppm HP (10% norbixin destruction) at 35°C and 50°C, consistent with LP activity. Bleaching of whey from HHT was lower than LHT in all treatments and there were no differences ($P > 0.05$) between 25 and 250 ppm HP (1.2% norbixin destruction). Regardless of milk pasteurization temperature, greater bleaching was observed with increased time. These results demonstrate the influence of milk heat treatment on bleaching efficacy and also suggest differences in norbixin association with whey components with different milk heat treatment.

Key Words: bleaching, lactoperoxidase, pasteurization

M97 The effect of acidification of retentate on the flavor of spray-dried whey protein concentrate.

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Off-flavors in whey protein negatively influence consumer acceptance of whey ingredient applications. Clear acidic beverages are a common application of whey protein and recent studies have demonstrated that beverage processing steps, including acidification, enhance off flavor production from whey protein. The objective of this study was to determine the effect of pre-acidification of whey protein retentate before spray drying on flavor of dried whey protein concentrate (WPC). Cheddar cheese whey was manufactured, fat-separated, pasteurized, bleached (250 ppm hydrogen peroxide), and ultrafiltered (UF) to 80% protein retentate, 13% solids (wt/wt). The liquid retentate was then acidified using a blend of phosphoric and citric acids to the following pH values: no acidification (pH 6.5), pH 5.5, or pH 3.5. UF permeate was added to pH 5.5 and pH 6.5 retentates to dilute the protein to the same level as the pH 3.5 retentate (74% protein retentate, 13% solids (wt/wt)). The retentates were then spray dried. The experiment was replicated 3 times. Flavor and volatiles of the WPC74 were evaluated by sensory and instrumental analyses, respectively. Each WPC74 ($n = 9$) was rehydrated to 10% solids (wt/vol) and adjusted to each of the pH values (6.5, 5.5, or 3.5). Both main effects (pH 6.5, 5.5, and 3.5 before spray drying) and interactions between treatments and final pH when evaluated were investigated. Pre-acidification to pH 3.5 resulted in decreased cardboard flavor and aroma intensity and an increase in soapy flavor ($P < 0.05$) with decreased concentrations of lipid oxidation products hexanal, nonanal, decanal, as well as the protein degradation products dimethyl disulfide and dimethyl trisulfide ($P < 0.05$). Adjustment to pH 5.5 before spray drying increased cabbage flavor ($P < 0.05$) and increased the concentration of the protein degradation product dimethyl trisulfide ($P < 0.05$). The effects of pre-acidification were consistent regardless of the pH the solutions were adjusted to after spray drying. These results demonstrate that acidification of WPC80 retentate before spray drying decreases off flavors compared with acidification of spray dried WPC.

Key Words: whey protein, flavor, acidification

M98 Sensory properties and composition of permeate and permeate fractions.

K. Frankowski* and M. A. Drake, *North Carolina State University, Raleigh.*

One of the major contributing factors to hypertension in the US is from the amount of sodium in the American diet. Many food companies are trying to limit the amount of sodium in their products. Permeate, the liquid remaining after whey or milk is ultrafiltered, has been suggested as a salt substitute. It has not been established what component(s) of permeates contribute to sodium replacement or if permeates exhibit salty taste. The objective of this study was to determine the sensory properties of permeates and their composition with a specific focus on organic acids and mineral composition. Eighteen milk or whey permeates and permeate fractions were obtained in duplicate from commercial facilities. Proximate analyses and specific mineral contents were determined. Descriptive analysis of permeates, fractions and model solutions was conducted using a trained sensory panel. Organic acids were extracted and separated and quantified by high performance liquid chromatography (HPLC). Milk and whey permeates were characterized by cooked/milky and brothy flavors, sweet taste and low salty taste. Permeates with lactose (DLC) removed were distinctly salty. Sensory tests with sodium chloride solutions confirmed salty taste of DLC and the low salty taste of permeates were not solely due to the sodium concentration present. Lactic and citric acids and minerals were higher in DLC compared with milk or whey permeates, concurrent with increased salty taste. These results demonstrate that organic acids and minerals enhance salty taste in permeates.

Key Words: permeate, lactose, sodium reduction

M99 Effect of SO-TEC clear whey on physico-chemical characteristics of Cheddar cheese and its whey.

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Annatto is a color extract that is widely used to produce colored cheddar cheeses. Approximately 15 to 20% of the annatto added to the cheese milk partitions into the whey, which gives it an undesirable yellow color that is bleached chemically or enzymatically. However, bleaching can generate off flavors and a reduction in the nutritive and functional value of proteins. Recently, SO-TEC Natural Cheese color NCC22000, a patent-pending proprietary color formulation, was developed. This cheese color is prepared by encapsulating a blend of red and yellow fat-soluble carotenoid colors of paprika and β-carotene. This color is claimed to be selectively entrapped within the cheese curd with none of the color being carried into the whey stream. Consequently, using this color, cheddar cheese can be produced while generating an uncolored whey stream. The objective of this study was to characterize the physicochemical properties of cheddar cheese and its whey manufactured using SO-TEC cheese color. Three replicates of 3 treatments of cheddar cheese were produced in this study. The treatments were: a control with no color addition (NC); annatto color (AC) addition at 0.007% of milk weight; and SO-TEC NCC22000 color (STC) at 0.056% of the milk weight. The whey from each treatment was separated, pasteurized, and analyzed for color and compositional analyses. There were no significant differences ($P > 0.05$) in whey composition (fat, protein, total solids, and ash) or cheese composition (fat, protein, total solid, ash, and salt) among the treatments. The color of the STC cheese and AC cheese were similar. The L*, a*, and b* values were 74.27, 14.92, and 56.05, respectively, for the STC cheese and 74.34, 13.16, and 50.89, respectively, for the AC cheese. There were no significant ($P > 0.05$) differences in the color of the STC whey and the NC whey and both of these treatments had a significantly ($P < 0.05$) higher L* value and a significantly ($P < 0.05$) lower a* and b* value compared with the AC whey. The whey produced from SO-TEC Natural Cheese color NCC22000 has a color identical to uncolored cheese whey and would not need to be bleached to remove undesirable yellow/orange color.

Key Words: cheese color, no-color whey, cheddar cheese

M100 Effectiveness of ultrasonication in inactivating spores of *Bacillus* spp. in skim milk. S. Khanal*[1], S. Anand[1], and K. Muthukumarappan[2], [1]*Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings,* [2]*Agricultural and Biosystems Engineering Department, South Dakota State University, Brookings.*

Bacterial spores are resistant to pasteurization and may affect quality of milk products. They are known to form biofilms within dairy processing environments. Non-thermal processes such as high pressure, and pulse electric field have been tried to inactivate spores but with a limited success. In this investigation, effect of ultrasonication has been studied on spores of 3 *Bacillus* species, commonly isolated from thermally processed dairy products. Spores of *Bacillus coagulans* (ATCC 12245), *B. licheniformis* (ATCC 6634), and *G. stearothermophilus* (ATCC 15952) were produced by 1 to 2 wk of incubation on modified Brain Heart Infusion agar plates. Spores were harvested from plates by washing and centrifugation, followed by heating at 85°C for 10 min to inactivate the vegetative cells. Sterile skim milk samples, spiked with individual spores at an average level of log 5 cfu/mL, were subjected to ultrasonication through a 13 mm probe using a 20 KHz-VC 505 sonicator (Sonics and Material, USA), at 80 and 100% amplitude for 1, 5, and 10 min. Samples were kept in an ice bath during the treatments for temperature control. Ultrasonicated samples were batch pasteurized at 63°C for 30 min to study the combined treatment effect. Experiments with 3 replicates each were repeated twice. Spore counts were compared before and after respective treatments and were found to be significantly different ($P < 0.05$). A maximum of 35, 33, and 49% of *B. coagulans*, *B. licheniformis*, and *G. stearothermophilus* spores were inactivated respectively, by the ultrasonication treatment of 80% amplitude for 10 min. The combined ultrasonication and pasteurization resulted in 50, 40, and 65% reduction of these spores, respectively. No changes were observed in spore morphology or dimensions, as visualized under the scanning electron microscope. From this research, it is evident that the ultrasonication has the limited ability to destroy *Bacillus* spores. The inactivation percentage was increased up to 65 by combining pasteurization with ultrasonication. Among the spores studied, *B. licheniformis* and *G. stearothermophilus* were the most and least resistant, respectively

Key Words: ultrasonication, spores, amplitude

M101 Screening of different enzymes for modification of the enzyme cleaning step of an existing membrane CIP protocol. D. Singh* and S. Anand, *Dairy Science Department, Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Our previous studies revealed that the *Bacillus* species were observed to be most resistant against the cleaning protocol being followed for the entire constitutive microflora isolated from commercial whey concentration membranes. The present investigation was conducted to degrade biofilms by screening of different enzymes (protease, lipase, lactase, α-glucosidase, β-galactosidase) against 24-h-old in vitro biofilms developed by a *Bacillus* isolate using a CDC bioreactor. Data were statistically analyzed using PROC GLM of SAS program with treatment being a fixed effect. The enzyme β-galactosidase was observed to be most effective as it resulted in reductions of 1.71 logs and 0.88 logs under static and dynamic conditions, respectively. Protease and lipase were also found to be effective against embedded cells to some extent. For further evaluations, 3 different approaches were applied to modify the existing CIP protocol. Replacement of existing enzyme cleaning step with only β-galactosidase enzyme (CIP-1) as first modification, against single and mixed species biofilms did not result in any improvement in the effectiveness of the existing CIP protocol. Second approach with modified cleaning conditions (CIP-2) using a narrower range of pH for all the steps, and extended time (60 min) for the enzyme cleaning (step 4) followed by surfactant step (20 min) resulted in greater cleaning efficacy. Third approach (CIP-3) applied a combination of enzymes; protease, lipase, and β-galactosidase to replace the enzyme cleaning step along with modified cleaning conditions as given above. Results revealed increased effectiveness of CIP-3 against *Bacillus* biofilms with cumulative reductions of 3.21 logs as compared with 3.09 logs of existing CIP protocol. Similarly, treatment with CIP-3 against mixed species biofilms resulted in a reduction of 3.86 logs, as compared with the existing CIP reductions of 3.56 logs. Application of CIP-3 on other single and mixed species biofilms also showed a similar trend of effectiveness. It is concluded that the CIP-3 protocol may serve as an effective replacement for the existing CIP protocol.

Key Words: biofilms, CIP, dynamic

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

M102 Meta-analysis: Impact of corn silage harvest practices on intake, digestion, and milk production by dairy cows. L. F. Ferraretto* and R. D. Shaver, *University of Wisconsin-Madison, Madison.*

A meta-analysis was performed to determine effects of DM content, kernel processing (PROC), and theoretical length of cut (LOC) of whole-plant corn silage (WPCS) on intake, digestion, and lactation performance by dairy cows using a data set composed of 106 treatment means from 24 peer-reviewed journal articles published from 2000 to 2011. Categories for DM content at silo removal and PROC and LOC at harvest were: ≤28% (VLDM), >28% to 32% (LDM), >32% to 36% (MDM), >36% to 40% (HDM), and >40% (VHDM) DM; 1 to 3 or 4 to 8 mm roll clearance or unprocessed; 0.48 to 0.64, 0.93 to 1.11, 1.27 to 1.59, 1.90 to 1.95, 2.54 to 2.86, and ≥3.20 cm LOC. Data were analyzed using Proc Mixed in SAS with WPCS treatments as fixed effects and trial as a random effect. Milk yield was decreased ($P = 0.01$) by 2 kg/d per cow for VHDM. Fat-corrected milk yield decreased ($P = 0.01$) as DM content increased. Total-tract digestibility of dietary starch (TTSD) was reduced ($P = 0.03$) for VHDM compared with HDM and LDM. Processing (1 to 3 mm) increased ($P = 0.001$) TTSD compared with 4 to 8 mm PROC and unprocessed WPCS. Milk yield tended ($P = 0.10$) to be 1.8 kg/cow/d greater, on average, for PROC (1 to 3 mm) and unprocessed WPCS than 4 to 8 mm PROC. An observed interaction ($P = 0.01$) between DM content and kernel processing for TTSD revealed that the mechanical processing of WPCS increased ($P = 0.01$) TTSD for diets containing 32% to 40% DM WPCS but not ($P > 0.10$) VHDM. The LOC of WPCS had minimal effect on any of the parameters evaluated. However, an observed interaction ($P = 0.01$) between LOC and kernel processing for TTSD revealed that kernel processing increased diet TTSD when LOC was 0.93 to 2.86 cm ($P = 0.01$), but not ($P = 0.01$) when ≥3.20 cm LOC. Starch digestibility and lactation performance were reduced for dairy cows fed diets containing WPCS with > 40% DM or WPCS with insufficient kernel processing. Furthermore, kernel processing WPCS to improve starch digestibility is effective across a wide range of DM contents and LOC, but does not overcome adverse effects of very high DM content on TTSD and was ineffective at a very long LOC.

Key Words: corn silage, dairy cow, meta-analysis

M103 Response to different concentrations and sources of dietary protein on blood urea nitrogen concentrations and plasma amino acid utilization for milk production. I. P. Acharya,* D. J. Schingoethe, K. F. Kalscheur, and D. P. Casper, *South Dakota State University, Brookings.*

A trial was conducted to determine the response of feeding 2 different crude protein (CP) concentrations (15% and 17%) and sources [canola meal (CM) and high-protein dried distillers grain (DG)] on blood urea nitrogen (BUN) concentration and plasma amino acid (AA) utilization. Sixteen lactating Holstein cows were used in multiple 4 × 4 Latin squares having a 2 × 2 factorial arrangement of treatments. Each period was 4 wk and blood samples were collected once during wk 4 of each period from tail artery (TA) and mammary vein (MV) 3 h after feeding. Diets were formulated with 15% CP with CM (15CM), 15% CP with DG (15DG), 17% CP with CM (17CM) and 17% CP with DG (17DG). All diets contained 55% forage (50% alfalfa hay and 50% corn silage) and 45% concentrate and approximately 4.1% ether extract. Average DMI (25.2 kg/d) and milk yield (34.2 kg/d) were similar between diets. Concentration of BUN (mg/dL) from TA was higher ($P < 0.01$) for cows fed 17% CP diets than the 15% CP diets (18.1 vs. 14.3), but similar between CM and DG. Concentration of BUN from MV and artery-vein difference (AVD) were different ($P < 0.01$) between CP concentrations but similar between CP sources. Total essential amino acid (EAA) concentrations (μmol/dL) in TA plasma were higher ($P < 0.01$) for cows fed 17% CP diets compared with 15% CP diets (106.1 vs. 91.1), but similar for CM and DG. Branched chain amino acid (BCAA) concentrations (μmol/dL) in TA plasma were higher ($P < 0.01$) for cows fed 17% CP diets compared with 15% CP diets (62.9 vs. 52.0), but similar for CM and DG. Total plasma MV EAA concentrations were higher ($P < 0.01$) for 17% CP diets, but similar between sources. Total EAA AVD (μmol/dL) were higher ($P < 0.05$) for 17% CP diets than for 15% CP diets (33.6 vs. 27.8), but similar between sources. Mammary gland extraction efficiency of EAA indicated that Met was first limiting AA for CM-based diets followed by Lys, Arg, and Phe, while Lys was first limiting for DG-based diets followed by Met, Arg, Glu, and Phe. The order of limiting AA for milk production is altered by protein sources.

Key Words: crude protein, blood urea nitrogen, plasma amino acid

M104 Effects of adjustable and stationary fans with misters on core body temperature and resting behavior of lactating dairy cows in a semi-arid climate. S. D. Anderson*[1], B. J. Bradford[2], J. P. Harner[2], C. B. Tucker[3], J. D. Allen[1], L. W. Hall[1], S. Rungruang[1], E. Rajapaksha[3], R. J. Collier[1], and J. F. Smith[1], [1]*The University of Arizona, Tucson,* [2]*Kansas State University, Manhattan,* [3]*University of California, Davis.*

Cows readily seek shade to reduce solar heat load during high ambient heat. When shade structures are orientated north-south, stationary cooling systems are unable to follow shade as sun angle shifts during the day. The FlipFan Dairy Cooling System (FLFN) employs fans and misters to follow shade by rotating on a horizontal axis and compensates for wind speed. Multiparous, lactating Holstein cows (n = 144) on a commercial dairy in Arizona were cooled by either a system comprised of stationary fans and misters (CTRL) or the adjustable FLFN operated for 16.5 h/d (0830 to 0100 h). Core body temperature (CBT) of 64 cows (4 pens/treatment; 8 cows/pen; 7 d) and resting behavior of 144 cows (4 pens/treatment; 18 cows/pen; 5 d) was collected by intravaginal and leg data loggers, respectively. Cows were allotted to pens based on milk production and DIM. Pen was the experimental unit. Mean temperature-humidity index (THI) during the study was 80.2 (33.0°C and 40.3% relative humidity) and ranged from 76.3 to 84.4. Mean 24-h CBT was lower for cows cooled by FLFN than CTRL (38.9 vs. 39.1 ± 0.04°C; $P < 0.01$). A treatment × time interaction was observed in which CBT of FLFN was 0.4°C lower than CTRL ($P < 0.001$) from 0600 to 0800 h and 1500 to 1600 h. Cows cooled by FLFN spent more time lying down compared with CTRL (9.5 vs. 8.6 ± 0.13 h/d; $P < 0.001$). Cows in the FLFN treatment had more frequent lying bouts than CTRL (12.8 vs. 10.7 ± 0.10; $P < 0.001$). Lower CBT and decreased standing time are consistent with other studies in which ambient heat load was reduced. In a second experiment, isothermal maps representing the shaded area of pens at different times of day were analyzed for differences in THI provided by each cooling treatment. The FLFN provided a lower THI in the morning and evening (5.9 and 1.7%, respectively; $P < 0.001$) and tended to be lower (0.8%) in the afternoon ($P < 0.10$) compared with CTRL. Results suggest that FLFN is more effective than stationary fan systems at decreasing CBT, increasing lying time and bouts, and providing a more desirable microenvironment for cows throughout the day. The FLFN may yield similar results in different housing systems.

Key Words: adjustable fan, body temperature, resting behavior

M105 Evaluation of fc receptor gene variants in cow genomic dna. J. Williams* and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro, North Carolina.*

Genetic differences exist among cows in susceptibility to mastitis. Receptors for the Fc portion of immunoglobulin molecules (FcR) provide an important link between circulating antibody and cellular functions. Cattle possess the 3 classes of immunoglobulin G (IgG) FcR (FcγRI, -II, and -III). Further, activating (CD32a) and inhibitory (CD32b) isoforms of IgG Fcγ receptor (FcγR) II (CD32) have also been identified. Genetic variations in FcR have been identified as risk factors for chronic inflammatory conditions in man. Genetic differences in FcR may affect response to pathogens in cattle. The objective of this study was to detect FcR I, FcR II and their sub isoforms in cows. Blood was collected from 10 lactating cows (8 were 100% Holstein Friesian and 2 Holstein × Jersey). The somatic cell counts (SCC) were recorded. Genomic DNA was isolated from blood stored on FTA cards. Specific primers for FcRI (CD64), FcRII (CD32) and FcRII sub-isoforms were used to amplify Fc receptor genes. A primer for GAPDH was used as a loading control. Amplified products were separated on a 1% agarose gel and observed following staining with ethidium bromide. Genes encoding FcRI and FcRIIc were detected in all cows. The activating (FcRIIa) and inhibitory (FcRIIb) respectively were detected only in Holstein × Jersey crossbred cows regardless of SCC. Further studies are needed to evaluate the effect of FcR gene polymorphism on the cellular response in cattle.

Key Words: fc receptor, crossbreed, genetic variation

M106 Quantitative calcium determination from an ashed feed sample. D. J. LaMay,* J. L. Squire, K. D. Baldock, and D. L. Smith, *Eastern New Mexico University, Portales.*

Advances in technology have continued to improve the speed and quality of feed analyses. This protocol is a quantitative spectrophotometric method of determining calcium in an ashed feed sample. Hydrochloric acid (HCl) aids in the release of calcium bound to other molecules; while O-Cresolphthalein Complexone binds calcium ions in an alkaline medium, and 8-Hyrdroxy-quinoline binds magnesium ions to eliminate their interference. To maintain an alkaline pH, 2-amino, 2-methyl, 1-propranol (AMP) is used as a buffer. From a stock solution of calcium carbonate, dilutions (0.078, 1.56, 3.13, 6.25, 12.5, 25, and 50 mg/dL) are produced. One gram of ashed feed sample is transferred to a 50 mL conical tube. The crucible is rinsed with 10 mL of 0.1N HCl. Add 0.7 mL of 37% HCl to the tube and vortex for 5 s. Pour the solution into an acid rinsed beaker. Rinse the tube with 10 mL of distilled water into the beaker, then add 479.3 mL of distilled water. Vortex each standard for 5 s, and pipette 50 µL of each standard into 4 wells of a 96-well microplate. The 6.25 and 12.5 mg/dL standards are used as controls. Vortex each control and pipette 50 µL of each. Mix the ash solution and pipette 50 µL of the solution. All the standards, controls, and samples are run in quadruplicate. Pipette 180 µL of color reagent and AMP buffer into all wells. Incubate the plate at room temperature for 10 min on a shaker plate at 318 rpm. The test is analyzed at 630 nm with a background subtraction of 490 nm. The curve fit of the standard dilution is linear and the test samples are compared with these values. Results obtained from Cumberland Valley Analytical Services (CVA) were compared with results obtained from our laboratory (OL), replicated 6 times. Results for Feed Sample A were 0.27 versus 0.28% on a dry matter (DM) basis for CVA versus OL, respectively. Results for Feed Sample B were 3.92 versus 3.94% on a DM basis for CVA versus OL, respectively. Results for Feed Sample C were 0.79 versus 0.76% on a DM basis for CVA versus OL, respectively. These results present validation the quantitative spectrophotometric protocol is an effective and inexpensive method of calcium determination.

Key Words: calcium, ashed feed, spectrophotometric

M107 Cow comfort in dry lots: Lameness, leg injuries and lying times on dairy farms in Texas and New Mexico. 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, British Columbia, 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 dry lot dairies in Texas and New Mexico. Data were collected by the same 2 trained individuals from 35 predominantly Holstein herds. Herd size had on average (±SD) 3056 ± 1047 milking cows. One group of high production multiparous cows was monitored on each farm, with pen size averaging (±SD) 286 ± 177 cows. 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 5 (1 = healthy and 5 = evident swelling and 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 31.7 ± 7.7%; severe lameness averaged 2.0 ± 1.6%. Prevalence of swollen knees averaged 16.8 ± 10.2%. The overall prevalence of hock injuries (≥2) was 18.2 ± 11.0%; the prevalence of moderate-to-severe hock injuries (3, 4, and 5) was 4.7 ± 3.7%, with almost no presence of severe injuries (4 and 5). Lying times were similar across farms, averaging 10.2 ± 0.8h/d, but cows within farms varied from 1.9 to 17.9 h/d. To our knowledge this study is the first to describe the variation in lameness, injuries and lying times in dairy cattle housed in dry lot dairies.

Key Words: dry lot, lameness, leg injuries

M108 The effect of temperature on performance of Keto-Test strips. J. Shire*[1], J. L. Gordon[2], and E. L. Karcher[1], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada.*

Ketosis is estimated to affect 15% of early lactation dairy cows. The Keto-Test (Elanco Animal Health, Greenfield, IN) offers producers an easy test to determine the concentration of β-hydroxybutyrate (BHBA) in milk and track herd incidence of ketosis. The objective of this study was to determine the effect of altering temperature at time of test on the reliability of the Keto-Test. A total of 116 Holstein cows, ranging from 5 to 17 DIM, were selected from a commercial Holstein dairy herd in Michigan. A milk sample was collected from one quarter of each cow during the AM milking. Each sample was tested under 4 temperature treatment conditions, A: Keto-Test strips and milk at room temperature (RT, 24.0°C ± 0.1; control, manufacturer's recommendations); B: cold strips (10.8°C ± 0.9) and milk at RT; C: cold strips and fresh milk; D: strips at RT and fresh milk. Blood samples were collected immediately following milk collection and analyzed for BHBA concentration using a Precision Xtra meter (Abbott Laboratories, Abbott Park, IL). Cows with BHBA of ≥ 1400 μmol/L were considered positive for subclinical ketosis. Accuracy of the Keto-Test strips under the 4 conditions was determined by the kappa coefficient of agreement, using the result of treatment A as the control. Additionally, sensitivity and specificity were calculated using the blood BHBA concentrations and results of the treatment A. Using the Keto-Test 60.2% of cows tested negative for milk BHBA, 24.6% tested weak positive, 14.4% tested positive, and 0.8% tested highly positive. The weighted kappa coefficient of agreement between the control test (A) and tests B, C, D and 95% lower and upper confidence intervals were: test B = 0.71 (0.62, 0.80), test C = 0.69 (0.60, 0.78), and test D = 0.63 (0.54, 0.73). These results indicate good agreement between the outcome of the treatment A and tests B, C, and D. The sensitivities/specificities for A, B, C, and D are as follows: 0.70/0.81, 0.68/0.77, 0.60/0.88, and 0.58/0.87 indicating that the test in all temperature conditions had a strong ability to detect the presence of BHBA in milk. In conclusion, the reliability of the Keto-Test strips was not dependent on the temperature of the milk or the strips.

Key Words: BHBA, ketosis, Keto-Test

M109 Effects of prepartum grouping strategy on immune parameters of peripartum dairy cows.

P. R. B. Silva*[1,2], J. G. N. Moraes[1,2], L. G. D. Mendonça[1], A. A. Scanavez[1], G. Nakagawa[1], M. I. Endres[2], M. A. Ballou[3], and R. C. Chebel[1], *[1]Department of Veterinary Population Medicine, University of Minnesota, St. Paul, [2]Department of Animal Science, University of Minnesota, St. Paul, [3]Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

Objectives were to evaluate the effect of an "all-in-all-out" (AIAO) prepartum grouping strategy on immune parameters of Jersey cows. Cows (254 ± 7 d of gestation) were paired by gestation length and assigned randomly to an AIAO or control (CON) treatment. In the AIAO treatment groups of 44 cows were moved into a pen where they remained for 5 wk, whereas in the CON treatment approximately 10 cows were moved into a pen weekly to maintain stocking density (44 cows for 48 headlocks). Pens were identical in size and design and each of the pens received each treatment a total of 3 times, totaling 6 replicates and 259 and 308 cows enrolled in the AIAO and control treatments, respectively. Blood was sampled weekly from d-14 to d 14 from a subgroup of cows (n = 34/treatment) to determine neutrophil phagocytosis (PHAGO), oxidative burst (OXID), and expression of CD18 and L-selectin and for hematology. Data were analyzed by MIXED procedure with the fixed effect of treatment (AIAO vs control) and random effects of pen by replicate and cow by pen by replicate. Among the subgroup of cows evaluated for immune parameters no differences between treatments were observed in percentage of male calves ($P = 0.81$) and twins ($P = 0.57$) or incidence of retained fetal membranes ($P = 0.71$) and metritis ($P = 0.43$). Percentage of neutrophil positive for OXID ($P = 0.91$) and intensity of OXID ($P = 0.94$) were not different between treatments. Similarly, no differences were observed between treatment regarding percentage of neutrophil positive for PHAGO ($P = 0.98$) and intensity of PHAGO ($P = 0.91$). In addition, percentages of neutrophil expressing CD18 ($P = 0.17$) or L-Selectin ($P = 0.83$) were not different between treatments. Number of leukocytes ($P = 0.64$), neutrophils ($P = 0.33$), and lymphocytes ($P = 0.80$) were not affected by treatment. Cows submitted to an AIAO prepartum grouping strategy had similar innate immunity and hematological parameters compared with cows submitted to a conventional prepartum grouping strategy.

Key Words: prepartum dairy cow, grouping strategy, immune parameters

M110 Detection of clinical and subclinical mastitis using reticulorumen temperatures.

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The objective of this study, conducted at the University of Kentucky Coldstream Dairy from September 15, 2011, to February 1, 2012, was to examine the relationship between changes in reticulorumen temperature (RT) and subclinical and clinical mastitis. The DVM Systems, LLC (Boulder, CO) bolus system monitors RT using a passive RFID transponder (Phase IV Engineering, Inc., Boulder, CO) equipped with a temperature sensor queried twice daily by a panel reader placed in parlor entrances. A composite milk sample was obtained from each cow in the herd every 14 d for SCC analysis (Fossomatic FC somatic cell counter, Foss, Hillerød, Denmark). Subclinical mastitis events were established by SCC >200,000 cells/mL. Milkers recorded clinical mastitis events. Data were analyzed using SAS (Cary, NC). Reticulorumen temperatures <38.9°C were interpreted as erroneous reads, likely from water intake before entering the parlor, and were eliminated from the data set. Reticulorumen temperatures were adjusted for the change in herd RT at each milking to account for the effect of changing ambient conditions and diurnal variation. A 30-d rolling mean baseline RT was calculated along with the number of SD from which each respective RT varied from this baseline. The maximum RT and number of SD among all RT within the previous 10 d were used as a baseline to assess whether a RT alert was observed for mastitis and high SCC events. Using alert levels of >2 SD and >3 SD within 10 d of a mastitis event, alerts occurred for 47% (n = 7) and 33% (n = 5) of clinical mastitis events, respectively (n = 15). Using alert levels of >2 SD and >3 SD within 10 d of a high SCC event, alerts occurred for 23% (n = 10) and 5% (n = 2), respectively. Across all RT (n = 23,298), 11% (n = 2491) were >40°C. Using alert levels of RT >40°C, alerts occurred for 80% (n = 12) and 50% (n = 22) of clinical mastitis and high SCC events, respectively. Reticulorumen temperature may be an indication of subclinical and clinical mastitis, but natural variation may limit the utility of a RT monitoring system.

Key Words: mastitis, reticulorumen, temperature

M404 Effect of precision processing barley grain on dry matter intake, milk production, rumen pH and nutrient digestibility in lactating dairy cows.

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The objective of this study was to evaluate the effects of precision processing (processing based on kernel size and volume weight) barley grain on rumen fermentation and productivity of lactating dairy cows. Twenty multiparous lactating Holstein cows including 8 ruminally cannulated cows were used in a replicated 4 × 4 Latin square design with 21-d periods. Cows were fed diets containing light barley grain (52.8 kg/hL) processed using a narrow roller setting (LIGHT, processing index (PI) = 80.2); heavy barley grain (68.6 kg/hL) processed using a wide roller setting (HEAVY, PI = 76.4); light and heavy barley grain precision processed and mixed equal proportions (PP, PI = 76.3); or light and heavy barley grain mixed equal parts then processed at a single narrow roller setting (industry standard; CON, PI = 82.9). All diets consisted of 40%

barley grain, 40% barley silage, and 20% of a supplement premix. There were no treatment effects between LIGHT and HEAVY or PP and CON on DMI (24.0 vs. 23.9 kg/d and 24.7 vs. 23.5 kg/d, respectively), rumen pH (6.13 vs. 6.25 and 6.20 vs. 6.07, respectively), rumen metabolites or sorting index. Digestibility of DM, OM, CP, starch, and NDF were unaffected by treatment. Milk yield was not different between LIGHT and HEAVY or PP and CON (28.8 vs. 28.3 kg/d and 28.6 vs. 28.9 kg/d, respectively); nor was milk fat, protein, and lactose. MUN was higher for cows fed the PP diet compared with those fed the CON diet (11.0 vs. 10.4 mg/dL; *P* = 0.02) and for cows fed the LIGHT diet compared with those fed the HEAVY diet (11.6 vs. 10.7 mg/dL; *P* = 0.05), which can be attributed to the differences in starch availability in the rumen and amount of N captured by rumen microbes for protein synthesis. These results suggest that precision processing barley grain may not drastically affect rumen fermentation or productivity in dairy cows. Previous research on beef steers showed that precision processing barley grain improves nutrient digestibility without affecting rumen pH. Different responses between dairy and beef cattle might be explained by the difference in the level of barley grain in the diet.

Key Words: rumen acidosis, precision process, barley grain

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

M111 Effects of energy supplementation for pasture forages on in vitro ruminal fermentation in continuous cultures. C. T. Noviandi*[1], M. N. McDonald[1], D. R. ZoBell[1], J.-S. Eun[1], M. D. Peel[2], and B. L. Waldron[2], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Forage and Range Research Laboratory, USDA-ARS, Logan, UT.*

Eight dual-flow continuous culture fermentors (700 mL) were used to assess effects of energy supplementation [no concentrate, 30% ground corn, or 30% dried distilled grains with solubles (DDGS)] with 4 pasture forages [tall fescue (TF) without N fertilizer (TF-NF), TF with N fertilizer (TF+NF), TF-alfalfa mixture, and TF-birdsfoot trefoil mixture (TF+BFT)] on in vitro ruminal fermentation and N utilization. Twelve dietary treatments were tested in a completely randomized design with a 3 (energy supplements) × 4 (pasture forages) factorial arrangement. Each culture fermentor was offered a total of 15 g DM/d. Forages were supplied in 4 equal portions at 0600, 1200, 1800, and 2400 h, while energy supplements were fed in 2 equal portions at 1200 and 2400 h. Three replicated runs lasted 10 d each, with the first 7 d allowed for microbial adaptation to the diets, and 3 d for sampling. Average daily culture pH was affected by energy supplementation ($P < 0.05$), but not by forage, ranging from 5.94 to 6.44. Energy supplementation increased total VFA concentration ($P < 0.01$). Corn supplementation resulted in greater VFA concentration in the TF+NF compared with DDGS supplementation, whereas the DDGS supplementation increased VFA concentration in the TF+BFT compared with corn supplementation ($P < 0.05$), leading to an interaction between energy supplements and pasture forages ($P < 0.01$). However, corn supplementation resulted in greater total VFA concentration than DDGS (43.4 vs. 41.5 m*M*). Decreases in ruminal ammonia-N concentration, methane production, and acetate-to-propionate ratio were observed when corn or DDGS was added into diets ($P < 0.01$). These results indicate that supplementing pasture forages with corn or DDGS enhanced microbial assimilation of ammonia-N and shifted metabolic pathways of microbial fermentation. Supplementation of corn in the TF+BFT elicited a similar ammonia-N concentration as the corn supplemented in the TF+NF. Therefore, grass-legume mixtures would be a sustainable component in grass grazing systems to improve N utilization efficiency with appropriate energy supplementation.

Key Words: continuous cultures, energy supplementation, pasture forage

M112 Evaluation of feed delivery methods for prepubertal dairy heifers during the growing period. T. S. Dennis,* J. E. Tower, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

The objective of this study was to evaluate effects of feed delivery method on growth, dry matter intake (DMI), feed efficiency, and rumen fermentation characteristics of prepubertal dairy heifers during the growing period. Ninety Holstein heifers (179.1 ± 29.9 kg, 171 ± 26 d of age) were randomly assigned to 1 of 15 pens by body weight (BW). Treatment diets contained 56% forage and 44% grain mix (DM basis) and were delivered using a hay feeder and grain bunk (HF), forage and grain fed side-by-side in a bunk (SBS), or a total mixed ration (TMR) for 98 d. Heifers were weighed every 2 wk, and hip and withers heights and heart girth circumference (HGC) were measured monthly. Blood and rumen fluid were collected at the beginning, middle, and end of the study to measure plasma urea N, plasma glucose, and rumen NH_3 and volatile fatty acids (VFA). Data were analyzed as repeated measures using PROC MIXED of SAS with pen as the experimental unit. Feed delivery method affected final BW, as HF heifers were 11.1 kg and 9.7 kg heavier than SBS and TMR heifers ($P < 0.01$ and $P < 0.01$), respectively. Average daily gains were lower for SBS ($P < 0.05$) and tended to be lower for TMR ($P < 0.10$) compared with HF, averaging 0.75, 0.78, and 0.87 kg/d, respectively. Average DMI was greater for HF compared with SBS and TMR (8.2, 7.7, and 7.7 kg/d, respectively; $P < 0.01$), resulting in similar gain:feed between delivery methods overall ($P > 0.10$). Heifers fed using HF had greater HGC than SBS ($P < 0.05$) and tended to have greater HGC than TMR ($P < 0.10$); however, hip and withers heights were not affected by delivery method ($P > 0.10$). Heifers fed using SBS had increased acetate and butyrate concentrations on d 42 ($P < 0.05$), resulting in increased total VFA concentrations on d 42 ($P < 0.05$). Acetate and butyrate concentrations were similar for HF and TMR throughout the study ($P > 0.10$). Blood metabolites, rumen pH, and rumen NH_3 were not affected by delivery method ($P > 0.10$). Results from this study showed that component feeding using a hay feeder increased ADG; however, the manner of feed delivery did not affect feed efficiency or growth in prepubertal dairy heifers.

Key Words: dairy, heifer, feed delivery

M113 Prediction of pregnancy outcome using machine learning algorithms. S. Shahinfar*[1], K. Weigel[1], D. Page[2], J. Gunter[1], V. Cabrera[1], and P. Fricke[1], *[1]Department of Dairy Science, University of Wisconsin-Madison, Madison, [2]Department of Biostatistics and Medical Informatics, and Department of Computer Science, University of Wisconsin-Madison, Madison.*

On a daily basis making decisions about whether or not to breed a given cow and knowledge about expected outcome outcome of the breeding would have an economic impact on profitability of breeding program and net income of the farm. The outcome of each breeding can be affected by many management and physiological factors that vary between farms. Machine learning algorithms offer a great opportunity with regard to problems of multi co-linearity, missing values, or complex interactions among variables (Caravielo et al., 2006). The objective of this study was to develop a user friendly and intuitive on-farm tool to help farmers making decisions about breeding cows. To achieve our goal, we applied several different machine learning algorithms to predict the pregnancy status of each cow after breeding based on phenotypic and genotypic data. Data from 26 dairy farms in Alta Genetics Advantage progeny testing program were used, representing a 10-year period from 2000 to 2010. Reproduction, production, health events, and breeding values of cows and sires were extracted from an on-farm dairy management software and USDA-AIPL databases. The edited data set consisted of 195128 breeding records for multiparous lactation dairy cows, and each of record had 38 potential explanatory variables. Naïve Bayes classifier, Bayesian network, and bagging with RepTree were applied to the data. Among all of these methods, bagging had the best performance with 0.697, area under the ROC curve and 0.665 precision. Naïve Bayes and Bayesian network had 0.599 and 0.615 area under ROC curve respectively. An Information base variable selection procedure identified Mean conception rate in last 3 mo in herd, period, DIM at breeding, past times breed, current times breed and calving interval as the most effective explanatory variable in predicting pregnancy outcome.

Key Words: machine learning, bagging, fertility

M114 Genes for lysine catabolism in lactating dairy cows are responsive to postruminal lysine supply.

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Lysine supply is potentially limiting for milk protein production in dairy cows. The availability of lysine to the mammary gland and other tissues is a function of the quantity of metabolizable lysine and hepatic lysine catabolism. This experiment evaluated the effect of increased postruminal lysine supply on expression of aminoadipate semialdehyde synthase (AASS), a committing step in lysine catabolism in liver, and ornithine transcarbamoylase (OTC) and argininosuccinate synthase (ASS), key urea cycle enzymes. Eight multiparous early lactation Holstein cows were utilized in a replicated 4 × 4 Latin square. Cows were fed a lysine-limited ration and infused post-ruminally with 0, 9, 27 or 63 g/d of lysine. Periods consisted of a 10-d washout phase followed by 10 d of lysine infusion. On the last day of infusion liver samples were collected for mRNA analysis and blood samples were collected for analysis of blood urea nitrogen, amino acids, and α-aminoadipic acid. Milk protein percent was increased ($P < 0.05$) with infusion of lysine (2.53 vs. 2.68 ± 0.05% for 0 and 63g/d lysine). Blood urea nitrogen decreased ($P < 0.05$) with infusion of lysine (11.4 vs. 10.8 ± 0.4 mg/dL for 27 and 63 g/d lysine). Plasma lysine increased ($P < 0.01$) with lysine infusion (39.5, 45.8, 60.7 and 68.7 μM for 0, 9, 27, 63 g/d lysine). Plasma α-aminoadipic acid concentration increased ($P < 0.05$) with lysine infusion (2.9 vs. 4.7 ± 0.4 μM for 27 and 63 g/d lysine). Expression of OTC and ASS did not differ with increased postruminal lysine. Expression of AASS resulted in numeric differences between 0 and 63 g/d lysine (0.50 vs. 1.38 ± 0.44 arbitrary units, respectively), but were not significant ($P > 0.05$). These data indicate responsiveness of milk protein synthesis to lysine and suggests changes in amino acid and nitrogen metabolism in liver in response to postruminal lysine supply in early lactation dairy cows.

Key Words: lysine, gene expression, postruminal infusion

M115 Evaluation of rumen protected lysine supplementation to lactating dairy cows consuming increasing amounts of DDGS.

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Twenty multiparous Holstein cows were used in 4 5 × 5 Latin squares to determine the effects of feeding increasing amounts of dried distillers grains plus solubles (DDGS) in diets with or without the supplementation (60 g/d) of a rumen protected Lys (RPL) product (AminoShure-L; L-Lysine 38%) on milk yield and composition and plasma concentration of AA. Dietary treatments were (1) Control, (2) 10% DDGS (10DDGS), (3) 20% DDGS (20DDGS), (4) 10% DDGS+RPL (10DDGSRPL), and (5) 20% DDGS+RPL (20DDGSRPL). Basal diets were formulated using the CPM Dairy model (v3.0) to provide a predicted decreasing supply of Lys, 117, 99, and 91% of requirement for the Control, 10DDGS, and 20DDGS diet, respectively. Periods lasted 21 d with the last 3 d for data collection. Compared with cows fed the Control diet, cows fed diets with DDGS had a similar DMI (25.2 vs. 25.4 ± 0.04 kg/d; $P = 0.14$), milk yield (30.1 vs. 30.9 ± 0.11 kg/d; $P = 0.11$) and composition except for protein percentage which was higher (3.15 vs. 3.21 ± 0.03%; $P = 0.03$) and resulted in higher (0.94 vs. 1.00 ± 0.05 kg/d; $P = 0.04$) protein yield by cows fed diets with 20% DDGS. Supplementation of basal diets with RPL had no effect on milk production or composition. Compared with an expected DMI of 23.3 kg/d and milk yield of 38.5 kg/d, cows had a greater intake and lower milk production across diets, which resulted in diets that were predicted to supply sufficient amounts of Lys (140, 118, 104% of requirement for the Control, 10DDGS, and 20DDGS diet, respectively). Plasma concentration of Lys decreased (11.8%; $P = 0.01$) as DDGS inclusion increased and supplementation with RPL did not change Lys concentration. For other essential AA, plasma concentrations of cows fed diets with DDGS were lower ($P \leq 0.05$) for His and Val (8.62 ± 0.03 and 40.62 ± 0.01 μg/mL) and greater ($P \leq 0.01$) for Met (4.27 ± <0.01 μg/mL) compared with cows fed the Control diet (9.50 ± 0.03, 44.38 ± 0.01, 3.47 ± <0.01 μg/mL; respectively). Overall, inclusion of DDGS increased the yield of milk protein and when combined with RPL resulted in no response in milk production parameters suggesting that Lys was not the first limiting AA.

Key Words: dairy cow, dried distillers grains plus solubles, rumen-protected Lys

M116 Integrating nutritional and reproductive models to improve reproductive efficiency in dairy cattle.

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The objective was to integrate 2 existing mechanistic, dynamic models of nutritional and reproductive processes in the dairy cow. The objective of this research model is to be suitable for evaluation of data, concepts, and hypotheses regarding underlying genetic, nutritional, and physiological control of reproduction. A model of metabolism (Molly, UC Davis); which describes metabolism of glucose, amino acids, and fatty acids in tissues at an aggregated metabolic pathway level was integrated with a model of reproductive processes which describes growth and decay of the follicles and corpus luteum, gonadotropin releasing hormone, follicle stimulating hormone, luteinizing hormone, progesterone, estrogen, oxytocin, and prostaglandin F2α over time. The nutritional and reproductive processes are integrated at specific points: glucose, IGF-I, leptin and growth hormone affect rates of follicle stimulating hormone, luteinizing hormone, and follicular growth. Degradation of estrogen and progesterone is a function of metabolic clearance rate (MCR); (MCR progesterone, ng/μl = 2.6455 - 0.1606(DMI)2 - 0.5896(DMI) $r^2 = 0.9964$). Progesterone affects probability of embryo survival (% survival = 51.74 + 4.18 (ng/ml) $r^2 = 0.9943$). Pulse frequency of LH is a function of leptin (LH pulses/8h = 0.591 + 0.0015 (ng/ml)5 - 0.025(ng/ml)4 + 0.144(ng/ml)3 - 0.319(ng/ml)2 + 0.237(ng/ml) $r^2 = 0.65$). The probability of ovulation is a function of dominant follicle diameter (probability, % = 465.6 - 0.72(diam.)3 + 21.1(diam.)2- 180.0 (diam.); $r^2 = 0.99$). Probability of first service conception is a function of IGF1: (prob., % = 11.36 + 10.42(IGF1 ng/ml) $r^2 = 0.97$). Changing energy intake or milk production causes a pattern and direction of response in reproductive processes consistent with literature values. Increased metabolic rate decreases estrogen and progesterone concentration, reduces the ovulatory surge and decreases embryo survival. This research model should be useful to frame specific hypotheses on control of reproductive processes by genetic and nutritional driven mechanisms.

Key Words: systems biology, reproduction, nutrition

M117 Variation of mucosal innate immune genes expression in the gastrointestinal tract of dairy calves fed with or without calf starter during weaning transition.

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Weaning transition is considered as the most critical period in calf management, which causes significant level of stress in animals, and the dietary changes associated with weaning can cause functional and morphological changes in the gastrointestinal tract (GIT). However, how these drastic changes affect immunity of calves and what immune mechanisms help calves dealing with their stress are not fully understood. This study aimed to investigate the expression of mucosal innate immune genes (toll-like receptors and antimicrobial peptides) in the GIT of calves in weaning transition (8 weeks old). Holstein bull calves were assigned to one of 2 diets 2 weeks of age to 8 weeks of age; milk replacer only (MR, n = 4) or milk replacer plus calf starter (MR+S, n = 4), and mucosal tissue samples were collected from jejunum, ileum, cecum and colon at the end of feeding trial. Gene expression data were analyzed using MIXED procedure in SAS and statistical model includes diet and location as fixed effects. Expression of mucosal innate immune genes displayed distinct patterns between 2 feeding regimens. TLR 9 and 10 were differentially expressed among the GIT locations of claves fed MR ($P < 0.05$) whereas TLR 1, 2, 4, 7, 9 and 10 were differentially expressed among the GIT locations of calves fed MR+S ($P < 0.01$). TLR 2, 3, 5 and 6 showed a significantly higher expression in MR+S group than the calves fed MR. However, TLR 4 and 10 showed a significantly lower expression in MR+S calves. β-defensin and peptidoglycan recognition protein 1(PGLYRP1) expressions were observed in both groups of animals without any regional variation except for significantly higher expression of PGLYRP1 in the jejunum than the other GIT regions of MR+S calves (($P = 0.04$). However, β-defensin expression was lower in MR+S calves than MR calves with a significantly lower expression in the cecum, while PGLYRP1 showed a significantly higher expression in MR+S calves than MR calves in all regions except the ileum. Gene expression differences observed in the present study suggest that the consumption of solid feed may affect immune responses of calves and thus possibly determine the capability of calves to deal with stress associated with weaning.

Key Words: gastrointestinal tract, weaning transition, mucosal immunity

M118 Web forums as a method for engagement on contentious issues in dairying: Should dairy calves be separated from the cow within the first few hours after birth?

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Over the past few decades the public has become increasingly interested in the welfare of food animals. However, the food animal industries, including the dairy industry, possess few mechanisms for discussion of contentious practices. Here we present results from a web-based forum designed to promote discussion of controversial issues among stakeholders. In the present application we asked participants to respond to the question, "Should dairy calves be separated from the cow within the first few hours after birth"? A total of 163 people participated in 4 independent web forums; 33% were students/teachers, 13% animal advocates, 23% farmers, veterinarians, and industry professionals, and 31% had no involvement in the dairy industry. Overall there was little participant consensus, with 44% choosing "yes," 48% choosing "no," and 9% neutral. Responses varied with demographics, with opposition to early separation higher among females, advocates, and those with no involvement in the industry. Participants were also able to provide reasons in support of their views, with opponents and supporters often referencing similar issues in their reasoning. Opponents of early separation gave reasons such as: it is unnatural, it compromises calf and/or cow physical health, it is emotionally stressful, and the industry can and should accommodate cow-calf pairs. In contrast, supporters of early separation reasoned that it promotes calf and/or cow physical health and production, emotional distress is best minimized by separating before bonds develop, and the industry is limited in its ability to accommodate cow-calf pairs. These results illustrate the potential of web-based forums to identify areas of shared concern and disagreement among stakeholders, providing a foundation to develop practices that satisfy both producer and consumer expectations. More generally, the results suggest that web-based forums can provide a safe platform for much needed discussion on contentious issues in the dairy industry.

Key Words: public attitudes, animal welfare, maternal filial bond

M119 A cluster analysis to describe profitability on Wisconsin dairy farms.

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A survey was implemented on Wisconsin dairy farms to understand the impact of farm management on profitability. Farms were selected across 3 systems: conventional (C), grazing (G) and organic (O). The objective was to characterize main factors associated with profitability. A cluster analysis using complete linkage was conducted on 20 farms as preliminary analysis: 4 O, 4 G and 12 C. The analysis yielded 3 clusters. Cluster 1 included 1 O, 2 G and 6 C farms; cluster 2 included 4 C and 1 G farms; and cluster 3 included 3 O, 1 G and 2 C farms. Clusters 1 and 3 had the same income over feed cost (IOFC, $5.97 and $5.22/d per cow, respectively) whereas cluster 2 had an IOFC of $8.09/d per cow. Farms in cluster 2 had 71 cows and 95 ha and were managed by the youngest farmers (44 years old). They used a ration with 35% grass silage (GS), 1% hay, 18% corn silage (CS) and 46% concentrate (CC). They had the greatest milk production (10,764 kg/cow per year) and the lowest percentage of milk withheld from sale (0.49%). They produced milk with 3.55% fat, 3.03% protein and 203,000 somatic cells (SCC), but received the lowest milk price (0.348$/kg). Farms in cluster 1 had 72 cows and 115 ha and were managed by 49 years old farmers. They used 20% GS, 32% hay, 12% CS and 36% CC in the ration. They had a lower milk production (7,068 kg/cow per year) and more milk withheld (1.65%) than farms in cluster 2. Their milk had 3.78% fat and 2.99% protein with a price of 0.368$/kg. Farms in cluster 3 were the smallest farms with 48 cows and 54 ha and were managed by 49 year old farmers. They used 17% GS, 54% hay, 5% CS and 24% CC in the ration. They produced the least amount of milk (4,146kg/cow per year) and withheld 3.08% of production. They had the greatest milk fat and protein content (4.36% and 3.25%, respectively), the greatest SCC (317,167) and the greatest milk price (0.480$/kg). The 3 clusters contained farms from different systems indicating that management system was not a major descriptor of IOFC. However, this study suggested that IOFC was associated with quantity and quality of milk, percentage of milk withheld, feeding strategy and age of the farmer.

Key Words: cluster analysis, farm profitability, farm management

Growth and Development I

M120 Effect of protein supplementation in the last trimester of gestation in Nellore cows on subsequent growth of their bull calves submitted or not submitted to creep-feeding.

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The objective of this study was to evaluate the effect of supplemental protein to Nellore cows in the last trimester of gestation on subsequent growth of their calves, submitted or not to creep-feeding. Cows (n = 227) were assigned to a randomized complete block design. Blocks were balanced for BW (432 ± 50 kg) and BCS (2.85 ± 0.4; 1 to 5 scale). Treatments were arranged in a 2 × 2 factorial. Cows and bull calves were kept on pasture containing 8% crude protein (CP). The treatments were 1 and 2 - cows (n = 119) supplemented with soybean meal (0.5 kg/cow/d) and bull calves in either a creep (1, n = 114) or non-creep feeding program (2, n = 113) and; 3 and 4 - cows not supplemented (n = 108) and bull calves in either a creep (3) or non-creep (4) feeding program. Chemical composition of the creep diet was 22% CP, and 72% TDN. Data were analyzed using GLM procedure of SAS and differences among means were tested using Student's *t*-test ($P < 0.05$). At weaning time, there were no effects of cows prepartum supplementation on ADG and BW of bull calves (0.789 ± 0.16 vs. 0.777 ± 0.17 kg/d and 189.7 ± 34.0 vs. 191 ± 38.1 kg) for supplemented or not supplemented cows, respectively. Bull calves supplemented with creep feeding had greater ($P < 0.01$) ADG (0.842 ± 0.14 vs. 0.725 ± 0.16 kg/d for creep vs. non-creep feeding program, respectively) and BW at weaning (196.0 ± 30.1 vs. 184.6 ± 40.3 kg for creep vs. non-creep feeding program, respectively). In conclusion, supplementation with 0.5 kg of soybean meal in Nellore cows during the last trimester of gestation did not alter subsequent growth of their bull calves. However, the creep feeding increased ADG and BW at weaning in Nellore bull calves.

Key Words: beef cattle, fetal programming, creep diet

M121 Protein supplementation of Nellore cows in the last trimester of gestation and consequent performance of their heifer calves in creep feeding.

D. D. Nepomuceno[2], A. V. Pires[2], R. Sartori[2], F. M. da Rocha[3], M. V. Biehl*[2], I. Susin[2], E. M. Ferreira[3], M. V. C. Ferraz Junior[3], J. R. S. Goncalves[4], F. M. Abreu[1], L. H. Cruppe[1], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]University of Sao Paulo, Pirassununga, SP, Brazil, [4]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, PR, Brazil.*

The objective of this study was to evaluate the effect of supplemental protein to Nellore cows in the last trimester of gestation on subsequent growth of their heifer calves in creep feeding. Cows and their calves were managed on pasture containing 8% crude protein (CP). The cows were assigned to a complete randomized block design. Blocks were balanced for BW (431 ± 49 kg), age (8.9 ± 2.2 years), and BCS (2.8 ± 0.4; 1 to 5 scale). Treatments were arranged in a 2 × 2 factorial. The treatments were designated: 1 and 2 - cows (n = 106) supplemented with soybean meal (0.5 kg/cow/d) and heifer calves in either a creep (1, n = 106) or non-creep (2, n = 103) feeding program or; 3 and 4 - cows not supplemented (n = 103) and heifer calves in either a creep (3) or non-creep (4) feeding program. Chemical composition of the creep diet was 22% CP, and 72% TDN. Data were analyzed using GLM procedures of SAS and differences among treatments means were tested using Student's *t*-test ($P < 0.05$). At weaning time, there were no effects of cow supplementation on ADG and BW of heifer calves (0.677 ± 0.13 vs. 0.664 ± 0.126 kg/d and 168.2 ± 26.0 vs. 170.5 ± 32.8 kg) for supplemented or non-supplemented cows, respectively). Heifer calves supplemented with creep feeding showed greater ($P = 0.01$) ADG (0.708 ± 0.112 vs. 0.632 ± 0.13 kg/d) and BW at weaning (172.7 ± 26.7 vs. 165.8 ± 31.9 kg) than those not supplemented. In conclusion, supplementing 0.5 kg of soybean meal for Nellore cows in the last trimester of gestation did not alter subsequent growth of their heifer calves but ADG and BW at weaning were increased with creep feeding.

Key Words: beef cattle, growth, production systems

M122 Identification of key amino acids associated with fetal skeletal muscle growth in sheep.

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The role played by free amino acids (FAA) in the regulation of muscle growth during gestation in ruminants is poorly understood. The objective of this study was to compare maternal and fetal plasma and muscle FAA profiles between single and twins fetuses, and to examine the potential association between these profiles and muscle weight from well-fed late-gestation ewes. Single- (n = 9) and twin-bearing (n = 10) ewes, fed ad libitum on pasture were used. At d 140 of gestation ewes were euthanized, maternal and fetal plasma and fetal semitendinosus muscle (ST) collected and stored at −80°C. Reverse phase HPLC was used for FAA determination in plasma and ST muscle. Analysis of variance was used for comparisons of muscle weight and FAA concentration between single and twins and Pearson correlation analysis to estimate the relationship between ST weight and intracellular FAA. Twin fetuses had lighter ST muscles compared with singles (8.6 ± 0.3 g vs. 11.1 ± 0.9 g, $P = 0.02$). Total maternal plasma FAA was similar between single- and twin-bearing ewes ($P > 0.05$). Total fetal plasma FAA was similar between single and twin fetuses ($P > 0.05$). Twin fetuses had lower plasma concentrations ($P < 0.05$) of aspartate, glutamate, citrulline, and ornithine, and higher ($P < 0.05$) concentrations of glutamine and methionine compared with single fetuses. In muscle, lower concentrations of aspartate and threonine, and higher concentrations of citrulline and methionine were found in twins compared with singles ($P < 0.05$). Significant correlations between ST weight and intracellular arginine concentrations were found in both singles ($r = 0.62$, $P = 0.007$) and twins ($r = 0.67$, $P = 0.03$). These results indicate that restricted growth of twins compared with singles may be associated with altered placental AA transport and/or fetal AA metabolism. Observed differences between singles and twins in plasma AA and muscle FAA profiles indicate possible differences in AA transport and/or utilization in muscle. Arginine was the only FAA correlated with muscle mass in both single and twins, indicating that arginine may play an important role in the regulation of muscle growth in the ovine fetus.

Key Words: skeletal muscle, amino acids, sheep

M123 Is placental functionality different between singletons and twins in sheep? D. S. van der Linden* and S. A. McCoard, *Animal Nutrition Team, AgResearch Grasslands Limited, Palmerston North, New Zealand.*

A greater understanding of the factors that regulate placental nutrient transport will help elucidate mechanisms underlying perturbations in fetal growth. This study investigated the relationship between fetal weight and placentome type and size in placentae of singleton and twin fetuses in late pregnancy. In addition, free amino acid (AA) profiles were measured in fetal, umbilical artery and vein plasma using ion exchange chromatography and used as an indicator of placental nutrient transport. Singleton (n = 9) and twin (n = 10) placentae, from ewes offered ad libitum grazing throughout pregnancy were studied at d 140 of pregnancy. Blood samples from each fetus, umbilical vein and artery were collected before being removed from the placenta. Individual placentae per fetus were dissected and placentomes were classed per type and size and placentome number and individual weight were recorded. Data was analyzed using the PROC MIXED procedure in SAS with the fixed effects of birth rank, plasma pool type, their interactions and the random effect of ewe.Twin fetuses were 16% lighter ($P = 0.01$) than singletons, and had a smaller placenta with 28% decreased placentome weight ($P = 0.03$) and 35% fewer placentomes ($P = 0.001$). However, compared with singletons, twins tended ($P = 0.19$) to have a 17% more efficient placenta than singletons. In addition, twins showed a different distribution of placentome type and size compared with placentae of singletons, such that twins showed a greater proportion of type B and light placentomes compared with singletons. Fetal plasma of twin fetuses had 44% lower arginine ($P = 0.03$), 34% lower histidine ($P = 0.02$) and 20% lower leucine ($P = 0.04$) concentrations than singletons. In twins, fetal plasma had 55% lower asparagine ($P = 0.005$) and 47% ($P = 0.03$) higher glutamine (Glu) ($P = 0.03$) concentrations than umbilical artery plasma. No differences in AA concentrations between fetal, umbilical vein and artery plasma were observed in singletons. Glutamine is a major oxidation-energy source for the placenta and the fetal liver is the net producer of Glu. This may indicate that the functionality of the feto-placental unit is different between singletons and twins. In conclusion, individual placentae of twins may differ in functionality and nutrient transport from singletons and more research is warranted to better understand placental nutrient transport and function.

Key Words: placenta, sheep, amino acid

M124 Placental efficiency at birth has no effects on postnatal muscle development. T. A. Wilmoth*[1], C. S. Perkins[2], Z. E. Kerley[2], Z. D. Callahan[2], M. E. Wilson[1], and B. R. Wiegand[2], *[1]West Virginia University, Morgantown, [2]University of Missouri, Columbia.*

By d100 of gestation the populations of primary and secondary muscle fibers have formed. This number changes little after birth and throughout postnatal growth, however the size of these fibers can change, influencing pork quality. Placental function is an important factor in fetal and muscle development. Placental efficiency (fetal weight divided by placental weight) is often a measure of placental function and may impact muscle development during gestation and assumedly at slaughter. The objective of this work was to determine the relationship of placental efficiency to muscle development of the market weight hog. Placental efficiency was determined for each piglet at birth. At 2 mo of age, barrows (n = 19) were individually housed and fed to a final weight of 121 kg. Following a 24 h chill, a 2.5 cm^2 sample of longissimus dorsi (LD) at the 10th rib and semitendonosus (ST) from the middle of the muscle were collected and frozen. Two sections were taken of each muscle type and 2 images of each section were captured. The number and diameter of primary and secondary fiber types were determined by ATPase assay using acid preincubation. From each image 15 primary fibers and 20 secondary fibers were measured for diameter. The GLM procedures of SAS were used to determine Pearson correlation coefficients between variables. The diameter of primary and secondary muscle fibers in LD were positively related ($P < 0.0001$, r = 0.80). The diameter of primary muscle fibers was negatively correlated to the number of secondary muscle fibers in the LD ($P < 0.05$, r = −0.42). As primary fiber diameter increased in the LD, primary and secondary fiber number also increased in the ST ($P < 0.05$, r = 0.62, r = 0.56, r = 0.49, respectively). The number of secondary muscle fibers in LD were negatively correlated to the diameter of secondary muscle fibers in LD ($P < 0.05$, r = −0.40). In ST, the secondary to primary fiber ratio was found to be positively correlated to the diameter of primary fibers (r = 0.39, $P < 0.05$). Placental efficiency, determined at birth, appears to have to no effects on future muscle development of the animal.

Key Words: fiber number, postnatal growth, placental efficiency

M125 Effects of metabolizable protein supply during late gestation on ovine offspring growth and development. C. A. Schwartz*[1], K. R. Maddock-Carlin[1], C. O. Lemley[1], L. E. Camacho[1], W. L. Keller[1], J. S. Caton[1], R. D. Yunusova[1], C. S. Schauer[2], and K. A. Vonnahme[1], *[1]Department of Animal Sciences, North Dakota State University, Fargo, [2]Hettinger Research Extension Center, North Dakota State University, Hettinger.*

The objective of this study was to evaluate the effects of maternal metabolizable protein (MP) supply on fetal growth in sheep. Multiparous singleton pregnant ewes (n = 18) were randomized to receive 1 of 3 diets that were isocaloric and formulated to supply 60% (MP60), 100% (MP100), or 140% (MP140) of MP requirements during late (d 100 to 130) gestation. Metabolizable protein requirements were calculated as: MP (g/d) = (CP, g/d x (64 + (0.16 x undegraded intake protein of diet)))/100. Pregnant ewes and fetuses were euthanized and necropsied on d 130 ± 1 of gestation. Data were analyzed using PROC GLM of SAS. There was no effect ($P \geq 0.12$) of maternal MP supplementation during late gestation on fetal BW, empty BW, curved crown rump length, heart girth circumference, or adrenal, brain, heart, kidney, lung, pancreas, large intestine, spleen, and stomach weights when expressed as g or as g/g BW. Fetuses from MP140 ewes (8.8 ± 0.4) had increased ($P \leq 0.05$) small intestinal mass (g/g BW) at d 130 compared with fetuses from MP60 (7.3 ± 0.5) and MP100 (7.0 ± 0.5) and ewes. Fetuses from MP60 (21.4 ± 1.59) ewes had increased ($P \leq 0.05$) perirenal fat mass (g and g/g BW) compared with fetuses from MP100 (15.5 ± 1.5) and MP140 (17.2 ± 1.5) ewes. Although all pregnant ewes were provided adequate energy, restricting levels of maternal MP supply during the defined period of gestation increased fetal perirenal fat whereas high levels of MP supply increased fetal small intestinal mass, all while not altering fetal BW.

Key Words: fetal growth, metabolizable protein, ovine

M126 Vascularization in ovine utero-placental tissues during early pregnancy: Effects of assisted reproductive technology (ART). P. P. Borowicz,* L. P. Reynolds, D. A. Redmer, and A. T. Grazul-Bilska, *Department of Animal Sciences, and Center for Nutrition and Pregnancy, North Dakota State University, Fargo.*

Compromised pregnancies can be caused by genetic, epigenetic, environmental and/or other factors. Assisted reproductive technology (ART) has profound effects on placental and fetal development, leading eventually to compromised pregnancy. Development of an adequate blood supply to the placenta, which is regulated by numerous angiogenic factors, is critical to support normal fetal development. We hypothesized that vascular development, reflected by the number, density and size of capillaries, is altered in utero-placental tissues in compromised pregnancies due to ART. Pregnancies were achieved through natural breeding (NAT, control, n = 3), transfer of embryos generated through natural breeding (NAT-ET, n = 7), in vitro fertilization (IVF, n = 4), or in vitro activation (IVA; parthenogenetic clones, n = 4). On d 22 of pregnancy, cross sections of gravid uteri, containing utero-placenta, were collected and fixed for histochemical (hematoxylin and periodic acid Schiff staining) detection of capillaries followed by image analysis to determine the capillary area density (CAD), capillary surface density (CSD, exchange area), and capillary number density (CND) per unit of maternal placental (caruncular) tissue area, as well as area per capillary (APC; i.e., average capillary size).Data were analyzed using the general linear models (GLM) procedure of SAS with the main effect of pregnancy type. Area per capillary (APC) was less ($P < 0.05$) in IVA and IVF vs. NAT or NAT-ET groups (NAT, 203 ± 32; ET, 177 ± 21; IVF, 110 ± 27; IVA, 117 ± 27; μm^2). Capillary number density (CND), CAD and CSD were similar for all pregnancy types. Thus, in sheep, ART affects specifically capillary size, which may reflect altered vascular growth and function of utero-placental tissues. These data provide a foundation for determining the basis for altered vascularization in placental tissues in compromised pregnancies and may help to identify strategies for rescuing placental development in such pregnancies. Supported by Hatch Project ND01712; USDA 2007–01215 to LPR and ATGB, NIH HL64141 to LPR and DAR, and NSF-MRI-ARRA-0959512 to ATGB.

Key Words: sheep placenta, vascularity, early pregnancy

M127 Influence of *Bos indicus* genetics on pregnancy-associated glycoproteins (PAG) and their association with fetal development.

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Cross-breeding *Bos indicus* and *Bos taurus* genotypes improves various production traits for cattle maintained in sub-tropical or tropical climates. Pregnancy-associated glycoprotein (PAG) concentrations are influenced by various factors during gestation and recent evidence indicates that *Bos taurus* subspecies impacts concentrations of PAG and fetal size during early gestation. We determined the correlation between maternal genotype, PAG concentrations, and fetal development during early gestation in cattle with distinct subspecies genotypes. A fixed-time AI estrous synchronization protocol with semen of multiple sires within each breed was used on multiparous Angus (n = 17), Brangus (n = 25) and Braford (n = 9) cows. Transrectal ultrasonography was used to measure fetal size at 35 (crown-rump) and 62 d (nose-crown) of gestation. Blood was harvested to determine plasma concentrations of PAG and progesterone (P4). Orthogonal contrasts were used to compare outcomes for cattle containing *Bos indicus* genetics (Brangus and Braford) from those containing solely *Bos taurus* genetics (Angus). Concentrations of PAG tended to be greater ($P = 0.09$) in Angus (5.0 ± 0.5 ng/mL) than Brangus (4.3 ± 0.5 ng/mL) and Braford (3.4 ± 0.5 ng/mL) at d 35 of gestation. At d 62 of gestation, concentrations of PAG tended ($P = 0.09$) to be lower in Angus (2.0 ± 0.4 ng/mL) than Brangus (2.5 ± 0.4 ng/mL) and Braford (3.3 ± 0.4 ng/mL). Concentrations of P4 were not influenced by cow genotype. Concentrations of PAG were positively correlated ($P = 0.01$) with concentrations of P4 at d 35 but not at d 62 of gestation. Cow breed did not affect fetal size at d 35 of gestation(15.5 ± 0.4, 15.4 ± 0.4 and 14.6 ± 0.4 mm for Angus, Brangus, and Braford, respectively), but at d 62 of gestation Angus cows (29.6 ± 0.3 mm) contained larger fetuses ($P \leq 0.01$) than Brangus (28.0 ± 0.3 mm) and Braford (28.4 ± 0.3 mm) cows. No correlation between PAG and fetal size were observed at 35 or 62 d of gestation. In conclusion, cow genotype influenced fetal size on d 62 and tended to influence concentrations of PAG on d 35 and 62. Plasma PAG concentration had a correlation with cow breed and plasma P4 concentrations, indicating that maternal genotype may influence placental activity and early fetal development.

Key Words: PAG, fetal size, cow genotype

M128 Fetal size and pregnancy-associated glycoprotein concentrations are influenced by *Bos indicus* genetics during early gestation.

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Several gestational events influence newborn calf size and survivability. Subspecies genotype (*Bos taurus* vs. *Bos taurus* × *Bos indicus*) influences fetal development and uteroplacental activity during late gestation and recent evidence suggests it also may affect events of pregnancy in early gestation. The objective of this study was to examine fetal size and plasma pregnancy-associated glycoprotein (PAG) concentrations between Angus and Brangus cows in early gestation. Primiparous and multiparous Angus (n = 43) and Brangus (n = 33) cows were bred by AI to multiple sires within their respective breeds. Transrectal ultrasonography was completed by the same technician on d 33–34, 40–41, 47–48 and 54–55 post-insemination and crown rump length or nose to crown length (d 54–55 only) was recorded. Blood was collected on each occasion, plasma was harvested, and concentrations of PAGs were determined by enzyme immunoassay. Data were analyzed by ANOVA. Fetuses in Angus cows tended to be smaller at d 33–34 than fetuses in Brangus cows (1.29 vs. 1.37 cm; pooled SE: 0.03, $P = 0.06$). Fetus size was not different between genotypes on d 40–41 and 47–48 but nose to crown size was greater for fetuses in Angus than Brangus cows (2.08 vs. 1.95 cm, pooled SE: 0.03, $P = 0.001$). Breed-dependent changes in the rate of fetal growth were also detected. Specifically, the rate of change in fetus size between d 33–34 and 54–55 was greater for fetuses from Angus than Brangus cows (4.14 vs. 3.67 cm, pooled SE: 0.09, $P = 0.003$). Plasma PAG concentrations were less in Angus than Brangus cows at each time point and after averaging PAG concentrations across time points (4.9 vs. 8.2 ng/ml; pooled SE: 0.9, $P = 0.005$). In conclusion, the *Bos taurus* × *Bos indicus* (Brangus) genotype influences fetal size, rate of fetal development, and placental PAG production in the first 8 weeks of gestation in cattle. Such effects may help explain postnatal growth potential for these animals.

Key Words: fetal size, pregnancy-associated glycoprotein, early gestation

M129 Effects of nutrient restriction in beef cows during early gestation on maternal and fetal small intestinal and hepatic mass and in vitro oxygen (O_2) consumption.

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The objectives were to examine the effects of maternal nutrient restriction during early gestation on maternal and fetal small intestinal and hepatic mass and in vitro O_2 consumption. Pregnant multiparous beef cows at d 30 of gestation were randomly assigned to one of 2 treatment groups: 100% NRC (CON; n = 6) or 60% NRC (RES; n = 6) requirements. At d 85 of gestation, animals were slaughtered and fetuses were immediately removed, weighed, and liver and intestine were collected. Maternal liver and jejunal tissues were also collected, and weighed. After collection, fetal and maternal tissues were transported to the laboratory for O_2 consumption analysis. Tissue weight relative to BW (g/kg) in the cow (liver = 7.58 ± 0.7; jej = 2.4 ± 1.5) and fetus (liver = 37.2 ± 3.4; jej = 18.6 ± 1.9), and tissue weight (g) for maternal liver and jejunum (4148.3 ± 462.7; 1270.5 ± 791.5), and fetal small intestine (2.4 ± 0.4), were not influenced ($P > 0.2$) by nutrient restriction. However, fetal liver weight (CON = 4.29 ± 0.27g; RES = 5.1 ± 0.7g; $P = 0.04$) was greater for the RES group. Oxygen consumption per unit of tissue (maternal liver = 1.62 ± 0.52µl/g/hr; maternal jej = 0.87 ± 0.36µl/g/hr; fetal liver = 2.95 ± 0.85µl/g/hr; fetal jej = 0.9 ± 0.3µl/g/hr), total O_2 consumption per tissue (maternal liver = 6729.4 ± 2325.4µl/tissue/hr; maternal jej = 1098.9 ± 780.5µl/tissue/hr; fetal liver = 14.1 ± 5.4µl/tissue/hr; fetal jej = 2.2 ± 0.8µl/tissue/hr), and O_2 consumption relative to BW (maternal liver = 12.28 ± 4.05µl/BW/hr; maternal jej = 2 ± 1.4µl/BW/hr; fetal liver = 110.1 ± 30.1µl/BW/hr; fetal jej = 17.1 ± 5.7µl/BW/hr) were not influenced ($P > 0.2$) by nutrient restriction in maternal and fetal liver and intestine. These data indicate that nutrient restriction in pregnant cows during early gestation increased fetal liver mass at d 85 but did not alter maternal and fetal O_2 consumption in liver and small intestine.

Key Words: oxygen consumption, gastrointestinal tract, gestational nutrition

M130 The effects of intrauterine growth retardation (IUGR) due to poor maternal nutrition on muscle development in lambs.

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Recent research has demonstrated that poor maternal nutrition can cause a decrease in carcass quality as the resulting offspring exhibit a reduction in muscle tissue. We hypothesized that lambs experiencing intrauterine growth retardation (IUGR) due to poor maternal nutrition will have decreased muscle development and reduced expression of key genes involved in myogenesis. Ewes pregnant with twins (n = 24) were fed 100% (CON), 60% (RES) or 120% (OVER) of NRC requirements beginning at d 85 of gestation. The offspring were euthanized within 24 h of birth (d 1; n = 3/treatment) or at 3 mo of age (n = 3 to 5/treatment). Animals maintained until 3 mo of age were removed from the ewe and fed a control diet of milk replacer and 18% creep feed. Quadricep muscle was collected immediately following euthanasia for gene expression analysis using real time-reverse transcriptase (RT)-PCR. Data were analyzed using ANOVA with significance considered as $P \leq 0.05$. As reported, BW were reduced in RES lambs by 16% at d 1 and 3 mo ($P \leq 0.05$) compared with CON. There was a tendency for a 2.9 ± 0.1-fold increase in *IGF-I* mRNA expression in RES animals at d 1 ($P \leq 0.18$) but not at 3 mo ($P \geq 0.90$). A difference in *IGF-I* mRNA expression was not observed in OVER lambs at d 1 or 3 mo ($P \geq 0.76$). We did not observe an effect of poor maternal nutrition on the expression of markers of muscle development, *myogenin, myogenic regulatory factor-5* (*myf-5*) and *paired box protein-7* (*PAX7*), at either time point ($P \geq 0.32$). In addition, we did not observe an effect of treatment on genes affected by glucose availability, *glucose transporter type 4* (*GLUT4*) and *tuberous sclerosis protein 2* (*TSC2*; $P \geq 0.36$), within the muscle. In summary, although we did not observe an effect of IUGR on markers of myogenesis, *IGF-I* gene expression tended to be increased in RES lambs at d 1 but not at 3 mo. Based on the reduced size of the RES lambs and the critical role of IGF-I in muscle growth, these data suggest there may be altered sensitivity to IGF-I in the muscle of lambs suffering from IUGR at birth.

Key Words: intrauterine growth retardation, insulin-like growth factor-I, muscle

M131 Maternal diet interactions with fetal sex in beef cattle.

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Prenatal nutrition affects postnatal life in many mammals, including cattle. Our aim is to determine which physiological processes are affected, to what degree, and how we can optimize prenatal nutrition to ensure/enhance performance in economically important traits. Multiparious beef cattle (n = 46) were fed a haylage-based TMR containing 20% wheat straw at either 85% (n = 23; LOW) or 140% (n = 23; HIGH) of maintenance energy requirements (NEm). The treatment began mid-way through gestation (~150 ds), and continued for 105 ds. Diet treatment (TRT) had a significant effect upon cow ADG ($P < 0.0001$), and TRT and cow age had significant effects upon cow average end weight (AEWt) (both $P < 0.0001$). Only cow age was significant for average start weight (ASWt) ($P = 0.0001$). Least squares means AEWt for HIGH and LOW cows was 853 and 765 kg resp., therefore dietary treatment performed as expected. Birth weights of calves born from these cows were evaluated using a mixed model which included TRT and sex of calf (plus interaction), and cow age as fixed factors, with pen as random effect. Only TRT*calf sex was significant ($P = 0.038$). Cow weight measurements (ASWt, CowADG, AEWt) were tested separately as covariates in the model for calf birth weight. Both ASWt and AEWt significantly interacted with TRT, and appeared to explain some of the same variation in birth weight as fetal sex. In retrospect we included calf sex in models for ASWt, CowADG, and AEWt. We found that CowADG was significantly affected by both TRT and calf sex ($P < 0.0001$, $P = 0.013$ resp.). Cows carrying bulls as opposed to heifers gained more weight during the trial. By weaning there was no difference in cow weights for any parameters tested except cow age ($P = 0.0019$). Adjusted (205-d) weaning weights of calves, as well as average daily gain from birth to weaning, were not affected by any parameters tested. These results illustrate that maternal diet during the second trimester in beef cattle has sex-specific effects upon birth weight of calves, and that fetal sex interacts with rate of gain in pregnant cows. Translating the maternal-fetal dialog can lead to innovative management practices for the pregnant beef cow.

Key Words: fetal-programming, epigenetics, bovine

M132 Lamb growth in response to the duration of maternal undernutrition during gestation in twin sheep pregnancies.

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The experimental objective was to determine the impact of duration of maternal undernutrition during gestation in twin pregnancies on lamb growth and development. Multiparous western whiteface ewes were randomly assigned to one of 3 treatments and acclimation to individual pens (7d) began at 21 d of gestational age (dGA). Ewes were fed 100%

(Control; n = 8), or 50% of their nutrient requirements from 28 to 78 dGA and readjusted to 100% beginning at 79 dGA (50–100; n = 10), or 50% from 28 to term (50–50; n = 9). Lambs were birthed naturally and harvested at 18 wk of age. Data were analyzed by preplanned orthogonal contrasts: Control vs. 50–100 and 50–50 and 50–100 vs. 50–50. Lambs born to 50–100 ewes were heavier ($P = 0.02$; 5.41 ± 0.28 kg) than 50–50 (4.34 ± 0.29 kg) lambs. Crown-rump length (CRL) tended ($P = 0.09$) to be greater in 50–100 (17.90 ± 0.54 cm) than 50–50 (16.38 ± 0.68 cm) lambs. Body weight of 50–100 lambs was greater ($P < 0.05$) than 50–50 lambs at 2 (8.52 ± 0.51 kg vs. 4.34 ± 0.29 kg) and 3 wk (9.79 ± 0.53 kg vs. 7.94 ± 0.53 kg) and the same trend ($P = 0.07$) was observed at 4 wk (11.63 ± 0.70 kg vs. 9.51 ± 0.81 kg). At 4, 16 and 17 wk body weight tended ($P < 0.10$) to be greater in Control than 50–100 and 50–50 lambs. At 18 wk rear leg length was greater ($P = 0.03$) in 50–100 (63.92 ± 1.30 cm) and 50–50 (61.54 ± 1.26 cm). At 18 wks CRL of 50–100 (114.46 ± 2.82 cm) lambs tended ($P = 0.09$) to be greater than 50–50 (107.30 ± 3.72 cm) lambs. At 18 wk, brain weight was greater ($P = 0.03$) in 50–100 (107.98 ± 2.61 cm) than 50–50 (99.74 ± 2.47 cm) lambs. Elevated body weight and CRL of 50–100 lambs at birth may indicate a shift in fetal metabolism to compensate for nutrient restriction during early gestation. 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: maternal undernutrition, lamb growth, sheep

Lactation Biology I

M133 Nursing frequency alters circadian patterns of mammary gene expression in lactating mice. D. L. Hadsell,* W. Olea, and L. W. Rottman, *Baylor College of Medicine, Houston, TX.*

Milking frequency impacts lactation in dairy cattle and in rodent models of lactation. The role of circadian gene expression in this process is unknown. The hypothesis tested was that changing nursing frequency alters the circadian patterns of mammary gene expression. Mid-lactation CD1 mice were studied in 2 groups, for up to 54 h. Ad-libitum (AL) nursed dams were allowed AL access to their litters for the entire study. Variably nursed (VN) dams were placed on a 4-time (4X) per day (d) schedule on d1, and an AL nursing schedule on d 2 of the study. Samples were collected at 6 h intervals (n = 3 dams/ treatment-time combination). Mammary gland (MG) weight was used to indicate the combined effects of secretory activity and suckling-dependent milk removal. Total MG RNA was analyzed by real-time qRT-PCR for the expression of Bmal, Per1, Per2, Lalba, and B4galt1. On d 1, MG weight in the AL dams exhibited circadian oscillations with a peak at Zeitgeber time (ZT) 12 and a trough at ZT0. MG weight was higher ($P < 0.01$) in VN dams for the first 18 h on 4X, but then decreased. Placement of VN dams back onto AL nursing during d 2 of the study decreased ($P < 0.01$) MG weight during the subsequent 18 h. On d 1, both Bmal and Per2 mRNA levels exhibited circadian oscillations with peaks at ZT0 and 18, respectively, and troughs at ZT12 and 6, respectively. In AL dams, both Lalba and B4galt1 mRNAs also oscillated, with troughs at ZT12 and peaks at ZT18. Both Per2 and B4galt1 were affected ($P < 0.05$) by decreased nursing frequency in the VN dams on d 1. For Per2, the response was an increase in amplitude at ZT18 ($P < 0.02$) while B4galt1′s expression pattern was decreased ($P < 0.0001$). These differences resolved during d 2 when VN dams were placed on AL nursing. These results support the conclusion that decreased nursing frequency alters circadian gene expression and could influence lactose synthesis through dampening the expression of B4galt1. This project supported by National Research Initiative Competitive Grant no. 2007–35206–17831 from the USDA Cooperative State Research, Education, and Extension Service and by the USDA/ARS Cooperative Agreement #6250–51000–048.

Key Words: lactation, milking frequency, circadian

M134 Functional analysis of swine mammary gland transcriptome during late gestation using two bioinformatics approaches. W. S. Zhao*[1,2], K. Shahzad[1], D. E. Graugnard[1], J. Luo[2], J. J. Loor[1], and W. L. Hurley[1], [1]*University of Illinois, Urbana,* [2]*Northwest A & F University, YangLing, Shaanxi, China.*

As in other mammals, sow mammary glands are essential to support growth and development of neonatal piglets via the synthesis of milk. We used a newly developed dynamic impact approach (DIA) and the online bioinformatics tool DAVID to perform functional analysis of the sow mammary transcriptome during pregnancy. Mammary tissue was harvested at slaughter on d 80, 100 and 110 of gestation. A swine oligoarray (70 mer) with 13,263 inserts was used for transcriptome profiling. An ANOVA with false discovery rate (FDR < 0.15) correction resulted in 1,539 genes with a significant time effect. Bioinformatics analysis using DIA included the entire data set with Entrez gene ID, FDR, fold-change, and post-hoc P-values between time points ($P < 0.05$; d 110 vs. 80, d 110 vs. 100, d 100 vs. 80). For the DAVID analysis, a cut-off of FDR < 0.15 and P-value <0.05 was used. By implementing a criterion of mean impact +1 SD to the final results, a total of 14 highly impacted KEGG pathways were uncovered during gestation. Within the 'Metabolism' KEGG category, DIA uncovered that 'one carbon pool by folate', 'galactose metabolism', and 'fatty acid biosynthesis' were among the most-impacted pathways on d 100 and 110 vs. d 80; whereas 'linoleic acid metabolism' was inhibited overall on d 100 and 110 vs. d. 80. Within 'Genetic Information Processing' in KEGG, protein export was markedly activated at d 110 compared with d 80 and 100. Within 'Environmental Information Processing' KEGG category, 'ABC transporters' was the most-induced pathway during late gestation, while 'ECM-receptor interaction' was inhibited at d 110 vs. 80. The latter category was markedly activated at d 110 vs. 100. Within the 'Organismal Systems' KEGG category, 'intestinal immune network for IgA production' was markedly induced during d 110 and 100 vs. 80. Similar findings were obtained using DAVID approach. Overall, preliminary results from both bioinformatics approaches indicated that folate-mediated one carbon metabolism may serve an important metabolic role in preparation for copious milk synthesis. In addition, the immune system properties of the mammary gland also seem to play an important role in allowing the organ to recognize potential pathogens. Such response may be a mechanism of the mammary gland to prevent invasion of microbes during late gestation.

Key Words: systems biology, microarray, transcriptomics

M135 Changes in milk composition of Holstein dairy cows within a milking. D. E. Rico,* E. R. Marshall, and K. J. Harvatine, *Penn State University, University Park.*

The variation in milk composition within a milking was studied in high producing cows. Eight multiparous Holstein cows (54.86 ± 6.8 kg milk/d; mean ± SD) fed a 31.5% NDF and 17.0% CP diet were used in the experiment. A milk-sampling device was designed to allow collection of multiple samples during a milking without loss of vacuum or interruption of milk subsampling. The average milk yield of the previous 7 milkings was used to determine 5 equal weight sampling intervals. If milk yield exceed expected by more than 25% of the interval weight a sixth sample was collected. Milk was collected during consecutive morning and afternoon milkings for all cows and was replicated one week later. Each sample representing approximately 20% of the milking was analyzed for fat, true protein, and lactose by infrared spectroscopy. A second subsample was stored at −20°C without preservative for analysis of FA composition. Data were analyzed using the Proc Mixed procedure (SAS institute) as a random regression. The model included the random effect of cow and week and the fixed effect of milking fraction, time of milking (AM vs PM) and the interaction of milking fraction by time of milking. Denominator degrees of freedom were calculated by the Satterthwaite procedure. Milking fraction (MF) was a continuous variable calculated as the midpoint of the sampling interval. There was an effect of milking (AM vs PM) on total milk yield and milk protein, lactose, and fat concentration. There also was an interaction of milking time (AM vs PM) and milking fraction, and a quadratic effect of milking fraction on milk fat, protein and lactose concentration ($P < 0.001$). Milk fat concentration exhibited the most marked change during milking and the best fit predictions for the AM and PM milkings were $1.43 + 1.65 \times MF + 2.71 \times MF^2$ and $1.89 + 1.42 \times MF + 2.7124 \times MF^2$, respectively. Milk fat content increased quadratically over the course of milk let down in high producing dairy cows, while much smaller changes were observed in protein and lactose. This pattern is consistent with previous results in lower producing dairy cows and reflects the dynamic nature of milk fat secretion from the mammary gland.

M136 Osteopontin secretion in milk is correlated to the presence of DNA polymorphisms in the secreted phosphoprotein 1 (*SPP1*) gene.

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Osteopontin (OPN), encoded by secreted phosphoprotein 1 (SPP1) gene, is a phosphoglycoprotein that is present in various tissues and secreted into body fluids, such as bovine milk. It is recognized as an important pro-inflammatory cytokine which has numerous functions, including its role in early T-cell activation during bacterial infection. The goal of the study was to evaluate the impact of polymorphisms in the *SPP1* gene on OPN secretion in milk. In a previous study, elevated OPN expression in response to mammary gland infection has been characterized. Furthermore, several polymorphisms detected in the 5′ untranslated region of the gene (promoter) have an impact on the estimated breeding value (EBV) for somatic cell score (SCS), an indicator of udder health. Also, haplotypes were defined for low (H1 × H4) and high (H2 × H3) SCS. In dairy cows, OPN is secreted during lactation and could be involved in the mammary gland immunity. In the present study, the main objective was to determine whether polymorphisms in the *SPP1* gene are related to the presence of isoforms or the level of OPN in milk. An antibody panel was used to characterize OPN isoforms by immunoblotting and to measure the amount of OPN secreted in milk. This enabled the selection of the most suitable antibodies to develop an ELISA. The sensitivity of the ELISA was determined at 220 pg/mL with a recovery of 94 ± 5%. Variations in OPN milk concentrations were detected during lactation for cows representing haplotype H1 × H4 (n = 3) and H2 × H3 (n = 3). Elevated concentration in colostrum (678.5 ± 68.7 mg/L) drastically decreased within the first week to reach 19.3 ± 3.7 mg/L of milk, and then remained constant until d 150. From d 150 to 200, cows with haplotypes associated with a low EBV for SCS had increased OPN level in milk ($P < 0.0006$) compared with the cows with haplotype associated with high EBV. This is the first study to demonstrate that a cow′s *SPP1* genetics affects OPN concentration in milk.

Key Words: osteopontin, bovine lactation, genetic variation

M137 Growth hormone influences mTORC1 and IGF-1 signaling in the lactating bovine mammary gland.

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The objective of this study was to determine whether mTOR and IGF-1 signaling mediates the effect of growth hormone (GH) on milk protein synthesis in the bovine mammary gland. Mammary tissue was obtained post-mortem from non-pregnant second parity Jersey cows (178–200 d postpartum) 6 d after a single subcutaneous injection of either a slow-release formulation of commercially available GH (Lactatropin) 500mg; (n = 4) or saline (n = 4). Total DNA, RNA and protein were extracted using TRIzol reagent and relative ratios used to evaluate cell size, number and translational efficiency and capacity. The abundance and phosphorylation status of targets of mechanistic target of rapamycin complex 1 (mTORC1) and insulin-like growth factor-1 (IGF-1) signaling were evaluated using Western blotting. Expression of IGF-1 signaling targets was evaluated using qPCR and the data analyzed using LinRegPCR and REST software. Treatment with GH increased mammary gland weight (33%; $P = 0.03$) and total protein content (34%; $P = 0.05$) and tended ($P < 0.10$) to increase ribosome number (33%) and cell size (30%) and DNA concentration (20%), while protein synthetic efficiency, capacity and cell number were unchanged ($P > 0.10$). These results suggest that GH stimulation of global protein synthesis is mediated by an increase in ribosome number and cell size. Abundance of mTOR and mTOR-Ser2448 (1.5 fold, $P < 0.05$), eIF4E (1.8 fold, $P < 0.05$), eIF4E-Ser209 (2.6 fold, $P < 0.01$), the eIF4E-eIF4G complex (1.8 fold, $P < 0.01$) and eIF4E-4EBP1 complex (1.3 fold, $P < 0.05$), MKNK1 (1.5 fold, $P < 0.05$), phosphor-MKNK1 (2.1 fold, $P < 0.01$), RPS6KA1 (1.7, $P < 0.01$) were increased in response to GH, but 4EBP1, p70S6K1 and p85S6K1 were unchanged. Expression of IGF1BP3 (1.4 fold, $P < 0.01$) and IGF1BP5 (1.6 fold, $P < 0.01$) were increased, IGF-1 receptor (1.3 fold, $P < 0.01$) was decreased, and IGF-1 was unchanged in response to GH. Overall, these results indicate that the mTOR pathway may mediate the effect of GH on ribosome biogenesis and cell size, while GH-activation of global protein synthesis is linked to changes in the abundance, phosphorylation and association state of components of the IGF-1 signaling pathway and downstream targets of translational regulation.

Key Words: mTOR pathway, bovine, mammary gland

M138 First demonstration of decorin, an extracellular matrix molecule, in bovine mammary tissue.

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In the mammary gland, an extracellular matrix (ECM) is secreted by and surrounds cells located in both mammary parenchyma (PAR) and stroma. Decorin is an ECM proteoglycan with cell growth regulatory effects mediated by its ability to interact with growth factors or upregulation of cyclin-dependent kinases. It also serves a structural role by regulation of collagen crosslinking. Based on these known roles, we undertook a pilot scale study to examine the spatial and temporal localization of decorin in bovine mammary tissue at various physiological stages. Mammary PAR (n = 6) was obtained from female Holsteins (n = 4). Samples represented 3 prepubertal times (d40, 56 and 100 of postnatal life), 2 gestational times (d213 and 248 of gestation) and one lactating time point (d10 post calving). Slides were subjected to immunohistochemical staining for the decorin antigen. A horseradish peroxidase conjugated secondary antibody and diaminobenzidine chromagen were used for detection. The negative control for the assay was incubated with control sera instead of the decorin primary antibody; all other procedures were the same. The negative control was free of chromagen. Our analyses demonstrated that decorin is present in bovine mammary ECM. Furthermore, temporal and spatial localization changed with physiological stage. At all time points observed, except for d56, decorin was not observed immediately surrounding epithelial cells comprising ducts. Across all time points, decorin localization in the intralobular stroma was minimal. Interlobular stroma showed a temporal distribution pattern of decorin staining. At d40, the gestational time points and d10 post calving, decorin localization was intense; at the d56 and d100 prepubertal time points, comparatively less decorin was localized in the interlobular stroma. To the best of our knowledge, this report is the first demonstration of the localization of decorin in bovine mammary PAR. Given our observation that localization appears to vary with physiological state, decorin may be important in the regulation of growth, development and remodeling of bovine mammary gland.

Key Words: decorin, extracellular matrix, mammary gland

M139 MicroRNA expression patterns are affected by stage of lactation in dairy cattle mammary gland. M. Z. Wang*[1,2], S. Moisa[2], D. Bu[1], J. Wang[1], and J. J. Loor[2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]University of Illinois, Urbana.*

MicroRNA (miRNA) are small non-coding RNA which regulate gene expression post-transcriptionally and play a key role in development and specific biological processes. The human breast-specific signature is characterized by the expression of 23 miRNA and the mouse mammary-specific signature is characterized by the expression of 9 miRNA (let-7a, let-7b, let-7c, miR-26a, miR-26b, miR-24–2, miR-145, miR-30b, and miR-30d). Those data suggest that miRNA could play a role in mammary gland physiology. Knowledge of the expression patterns of miRNA in bovine mammary gland during the transition from pregnancy into lactation might provide insights into their role in regulating aspects of metabolism, differentiation and apoptosis, and immune response. The objective of this work was to determine the expression pattern of selected miRNA involved in cellular proliferation, lipid metabolism, and innate immunity in dairy cow mammary gland tissue at different stages of lactation. Cows from the University of Illinois Dairy Research farm were used in this study. The expression of miR-10a, −15b, −16, −21, −31, −33b, −145, −146b, −155, −181a, −205, −221, and −223 was studied by RT-PCR in tissue ($n = 7$/stage) harvested via repeated biopsy during the dry period (−30 d prepartum), early lactation (7 d postpartum), and peak lactation (30 d postpartum). The results showed that expression of all miRNA, except miR-31, increased markedly between the dry period and early lactation. Among those, the expression of miR-221 increased further by peak lactation potentially suggesting a role in the control of endothelial cell proliferation/angiogenesis; whereas, the expression of miR-223 decreased by peak lactation but to a level that was greater than the dry period suggesting it may play a role in the mammary response to pathogens soon after parturition. The expression of miR-31, a hormonally regulated miRNA that inhibits cyclin gene expression, was greater at peak lactation vs. the dry period. From a metabolic standpoint, the consistent upregulation of miR-33b during early lactation vs. dry period suggests that this miRNA may exert control over lipogenesis in mammary tissue as it does in rodents. Collectively, results indicated that expression of miRNA associated with regulation of transcription of genes across diverse biological functions is altered by stage of lactation. Determining the specific roles of these miRNA during lactation requires further research, including examination of the expression patterns of their target genes.

Key Words: metabolism, genomics, bioinformatics

M140 Proteomic analysis in MAC-T cells reveals proteins involved in *cis*-9, *trans*-11 CLA de novo synthesis. T. Wang,* J. J. Oh, D. C. Piao, J. H. Hwang, Y. C. Jin, S. B. Lee, K. H. Lee, J. N. Lim, H. S. Kang, and H. G. Lee, *Department of Animal Science, Pusan National University, Miryang, Gyeongnam, Korea.*

This study was conducted to explore proteins involved in *cis*-9, *trans*-11 CLA de novo synthesis through proteomic analysis in MAC-T cells. Cells were routinely cultured in DMEM growth medium at 37°C and 5% CO_2. After reaching 100% confluence, the cells underwent differentiation in lactogenic medium for 90 h. Treatments were performed in triplicate with BSA (control) or t11 C18:1 (50 μM in BSA) and samples were collected every half hour for 4 h. Lipids were extracted following the Folch method and the lipid methyl esters were quantified by GC with a SP-2560 fused silica capillary column. The expression of SCD1 protein was detected by Western blotting using a specific mouse monoclonal primary antibody to SCD. On the basis of the SCD1 expression in 2.5 h, the difference of protein expression among control and t11 C18:1 group were compared by 2-DE. The striking differently expressed spots (≥2 or ≤ 0.5) were identified using ESI-Q-TOF and a protein search engine. Results showed that t11 C18:1 continually converted into *cis*-9, *trans*-11 CLA in MAC-T cells and showed a positive correlation ($R^2 = 0.887$) during the test. The SCD1 protein expression increased more than 2-fold at 2 h and 2.5 h whereas it decreased by half at 4 h. One upregulated and 6 downregulated proteins were identified in 2.5 h. The expression pattern of the upregulated protein (RASGRP4) (0–3.5 h) was positively related ($R^2 = 0.466$) to that of SCD1, however 3 of the 6 downregulated proteins (PGAM1, ANXA3, TPMT) were negatively ($R^2 = 0.280$, $R^2 = 0.297$, $R^2 = 0.182$) related to SCD1. Our results suggest that these identified proteins may be involved in the *cis*-9, *trans*-11 CLA de novo synthesis of MAC-T cells.

Key Words: *cis*-9, *trans*-11 CLA de novo synthesis, MAC-T cells, proteomic analysis

M141 Potent growth promoting activity of prolactin and estrogen to E-cadherin/β-catenin adhesion molecules in bovine mammary gland: Modulation of Wnt signaling. J.-J. Tong, Q.-Z. Li,* X.-J. Gao, N. Zhang, and Y. Lin, *Key Lab of Dairy Science, Ministry of Education, Northeast Agriculture University, Harbin, Heilongjiang, China.*

The Wnt signaling pathway and subsequent upregulation of β-catenin driven downstream targets (e.g., cyclinD1) are associated with development of mammary gland. E-cadherin is a key molecule component of the cell-cell adhesion junctions, which plays a principal role in maintaining the morphogenesis of numerous organs including mammary gland. Therefore, the objectives of this presentation is that to fully elucidated the molecular mechanisms underlying the effects of prolactin and estrogen on E-cadherin, β-catenin and cyclinD1 in Wnt signaling pathway in bovine mammary epithelial cells (BMECs). The effect of prolactin and estrogen (5 μg/mL) treatment on expression the key elements of Wnt signaling pathway components in BMECs was analyzed at mRNA level and protein level by qRT-PCR, immunofluorescence and Western blotting. Our present findings showed that prolactin and estrogen effectively promoted the expression of E-cadherin and cyclin D1 on mRNA level ($P < 0.05$), as well as protein level ($P < 0.05$), tested by by qRT-PCR, immunofluorescence and Western blotting. The analysis of β-catenin protein showed that prolactin and estrogen can markedly reduce the nuclear β-catenin expression at protein level. Furthermore, we suggest that modulation of Wnt signaling may be one of the mechanisms implicated the effect on cell proliferation in BMECs by prolactin and estrogen. We demonstrated that prolactin and estrogen can activate cell proliferation in BMECs tested by Reagent WST-1 ($P < 0.05$). Prolactin and estrogen enhanced Wnt signaling through increasing E-cadherin on protein level by lowering the levels of intracellular β-catenin and the influence on the important component of Wnt pathway target-cyclinD1. In conclusion, we were first focused on the effect of prolactin and estrogen on modulation of key components of Wnt signaling components in BMECs. Our results also highlighted the importance of Wnt components—E-cadherin, β-catenin, cyclinD1 that may serve as future subjects in the study of development and lactation of the mammary gland in dairy cattle.

Key Words: Wnt pathway, E-cadherin, bovine mamary epithelial cells

Meat Science and Muscle Biology I

M142 Effect of power ultrasound on the physicochemical properties of beef longissimus dorsi muscle.

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High-intensity ultrasound has been used to modify the physical or chemical properties of food. Several areas have investigated the potential future development of this technique in the food industry. To determine the effect of power ultrasound on the physicochemical characteristics of beef, we excised the m. longissimus dorsi muscle from 4 Holstein cows at 48 h postmortem. Any visible fat was trimmed away and the meat was cut into 5 cm slices, before chopping into 4-cm^3 cubes. Half of the cubes from the same slice remained untreated (control samples), whereas the other half were irradiated with power ultrasound for 4 or 8 min. Ultrasound waves were applied at a frequency of 40 kHz using water as the transmission medium. We then evaluated the meat pH, color (L*, a*, and b*), water-holding capacity (WHC), drip loss (DL), and shear force (SF). The adjusted model for statistical analyses included the effects of treatment, sonication time, and the interaction of treatment x sonication time. Data were analyzed using the mixed procedure method in SAS. If the main effects or their interaction were significant ($P \leq 0.05$), the means for a given characteristic were compared among time and treatment groups using the least significant difference method. There was an effect ($P \leq 0.05$) of ultrasound on the a*, b*, pH, WHC, and DL of the meat samples. The ultrasound-treated meat had a lower redness (a*) and yellowness (b*) compared with the control samples for both ultrasound application periods. Ultrasonication of meat for 8 min produced the highest pH value and the lowest DL ($P \leq 0.05$). There was no effect ($P \geq 0.05$) of ultrasound on the L* and SF of meat. It has been reported that ultrasound alone did not change the peak force of pork, and it was only effective when combined with marination. However, the use of power ultrasound may be an alternative method for improving the physicochemical properties of beef.

Table 1. Least squares means ± standard error for physicochemical properties of beef L. dorsi muscle treated with power ultrasound

Sonication time, min	Treatment[1]	Luminosity, L*	Redness, a*	Yellowness, b*	pH	Drip loss, %	Shear force, kg/cm^2
4	C	24±1a	14±1a	12±1a	5.3±0.1a	9.2±0.4a	1.8±0.3a
4	HPU	24±1a	11±1b	11±1a	5.4±0.1a	8.3±0.4a	2.0±0.3a
8	C	23±1a	14±1a	12±1a	5.3±0.1a	9.2±0.4a	2.3±0.3a
8	HPU	22±1a	11±1b	8±1b	5.5±0.1b	7.1±0.4b	2.4±0.3a

a,bMeans in columns without common letters differ significantly (p≤0.05).
[1]C = control, HPU = high power ultrasound.

Key Words: power ultrasound, beef, quality characteristics

M143 Diffusion of sodium chloride in bovine meat treated with power ultrasound in continuous and pulse modes.

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To evaluate the effect of power ultrasound on the diffusion of sodium chloride in beef muscles, an experiment with 6 replicates was carried out using the Semitendinosus muscle of adult Holstein cows. Semitendinosus muscle was cut transversally into one -inch -thick slices and placed in an ultrasonic bath containing a salt solution that just covered the slice. The ultrasound was applied in both, pulsed and continuous modes for 6 treatment times (10, 20, 30, 40, 50 and 60 min) and in 2 salt solutions (5% and 10% sodium chloride). To assess the diffusion of salt into meat the concentration of sodium chloride was measured with a digital refractometer in 3 regions of the meat slice (external, middle and inner). The data were analyzed using PROC GLM of SAS and included the ultrasound mode, salt solution concentration, ultrasound application time, slice (external, middle and central) region and their possible interactions as fixed factors. The results showed significant differences ($P \leq 0.05$) in the diffusion of salt which depended on the salt solution concentration. There was also a significant interaction between ultrasound mode and slice region. The highest salt diffusion was observed in the 60 min continuous mode with 10% sodium chloride solution. The application of ultrasound in continuous mode resulted in the highest salt diffusion in all meat slice regions, with the external region having the highest salt concentration. The increase in salt concentration was proportional to the sonication time. It is concluded that power ultrasound may be a potential method for improving sodium chloride transfer during meat processing.

Key Words: salt diffusion, power ultrasound, beef

M144 Meat traits of steers fed with whole cottonseed.

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The objective of this study was to determine the effect of inclusion whole cottonseed in the diet on the meat characteristics of Nellore steers. Thirty-six steers (average initial body weight of 333.50 kg and aged 20 mo) were housed during 94 d in pens with 3 animals each. The animals were distributed, equally, among 4 treatments, and these corresponded to diets containing increasing amounts of whole cottonseed: without whole cottonseed, 14.35% of whole cottonseed, 27.51% of whole cottonseed and 34.09% of whole cottonseed in relation to the dry matter of the diet. The animals' final live weight average was 446.64 kg ± 27.96 kg. These animals were slaughtered and was collected from the left half carcass of each animal, it was taken off part of the sirloin steak, in the 12th thoracic vertebra - 3rd lumbar vertebra, individually wrapped in plastic bags, identified and frozen at −18oC and were sent for analysis. A completely randomized design with 4 treatments and 9 replications was used. Treatments' effects if significant ($P < 0.05$) were estimated by regression analysis. MIXED from SAS (2001) for statistical analysis. The protein values, shear force; lipid oxidation, meat and fat color were similar among the treatments. However, the addition of the whole cottonseed levels linearly reduced the intramuscular fat percentage and increased moisture content of meat. Whole cottonseed feeding reduced the fatty acids concentration of C14:1 cis 9, C16:1 cis 9, C17:0, C17:1 and C18:1 cis 9 in the meat. The fatty acids C13:0 ISO,

C13:0 ANTEISO, C14:0 ISO, C15:0 ISO, C15:0 ANTEISO, C17:0 ISO, C18:0 and C18:1 trans 10 - trans 11 content in the meat have increased by the whole cottonseed addition in the diet. Inclusion of 27.51 and 34.09% of whole cottonseed in the diet altered negatively the meat aroma and flavor, respectively. The whole cottonseed diet did not change the concentration of conjugated linoleic acid, saturated fatty acids and the total unsaturated in the meat.

Key Words: flavor, CLA, stearic acid

M145 Lipid peroxidation and color of meat from young bulls fed different levels of crude glycerin.

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The use of crude glycerin in ruminant diets has the objective of decrease the operational cost. However, its effects on the meat characteristics should be better studied. The objective was to evaluate lipid peroxidation, using thiobarbituric acid reactive substances (TBARS), and color of meat from young bulls fed different levels of crude glycerin in the diet. Forty-four Red Norte animals were slaughtered at average live weight of 519 ± 15 kg, and the levels of crude glycerin (83% glycerol) were: 0, 6, 12 and 18% DM. The experiment was conducted in a completely randomized design, with 4 treatments and 11 repetitions. The basal diet was consisted of 30% corn silage, 12% soybean meal, 56% of corn grain and 2% mineral mixture. Corn was partially replaced by glycerin, and to achieve an isonitrogenous diet, corn gluten meal (21% CP) was used. After slaughter, samples were taken from the Longissimus dorsi muscle. Then, they were vacuum packed and maintained refrigerating at 4°C for 0, 7, 14 and 21 d post mortem. The color reading was conducted on the surface, using the CIE L*a*b* system. When significant effects ($P < 0.05$), regressions analysis using PROC REG of SAS 9.1.3 were done. There was no effect of storage time on color and lipid peroxidation ($P > 0.05$). The indices of lightness (L*), red (a*), yellow (b*), saturation index (C*) and the index of hue angle (h) showed a quadratic effect ($P < 0.01$) with the inclusion of crude glycerin (Table 1). Therefore, the meat changed from a red-purple color when the animals received 6% of glycerin, for the cherry-red when 18% was used. It was observed a tendency ($P = 0{,}07$) of increase on TBARS in the muscle of animals fed crude glycerin. As a conclusion, the use of a crude glycerin provided meat with better color and better appearance to the consumer. Funded by Fapemig, CNPq, Capes and INCT-CA

Table 1. Lipid peroxidation and color characteristics of meat of young bulls fed different levels of crude glycerin

	Crude glycerin, % DM basis					
Item	0	6	12	18	SEM	*P*-value
TBARS, mg of malonaldehyde /kg of meat	0.25	0.22	0.27	0.27	0.04	0.07
L*	32.8	30.4	33.1	35.6	0.55	<0.01[1]
a*	18.0	16.1	17.4	18.1	0.31	<0.01[1]
b*	2.54	0.53	2.26	3.28	0.30	<0.01[1]
C*	18.3	16.1	17.7	18.5	0.35	<0.01[1]
h*	6.94	1.75	6.57	9.67	0.91	<0.01[1]

[1] Quadratic effect.

Key Words: beef, glycerol, TBARS

M146 The use of visible and near infrared spectroscopy for quality control of organic and conventional beef stored under protective atmospheres.

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The objective of this work was to evaluate the potential of Visible (VIS) and Near Infrared Spectroscopy (NIRS) for on-site control of beef shelf life on meat trays stored at display counters. Beef samples (steaks) were obtained from the *Longissimus dorsi* muscle of 12 young bulls managed under organic (pasture or maize silage plus organic concentrate) or conventional (finished at feedlot with concentrate meal and barley straw ad libitum) feeding. These beef samples were packed under 2 different protective atmospheres (vacuum and 80%O_2-20%CO_2) and analyzed after 1, 3, 5, 8, 12 and 15 d of storage, so the global study included a total of 144 samples (12 animals x 2 protective atmospheres x 6 storage time). Meat quality analysis included color (L*, a*, b*), microbiology (mesophilic, anaerobic, enterobacteriaceae), texture (Warner-Bratzler shear force “WBSF”) and oxidative status (TBARS index). VIS/NIRS spectra were obtained by using a portable LabSpec 5000 fitted with a fiber optic probe (ASD Inc., USA) in reflectance mode (350–2500nm). Representative spectra of each beef steak were calculated as the average of 5 scans obtained on the steak surface, with or without film interaction, that is, before and after tray wrap opening. VIS/NIRS calibrations were calculated using the software Unscrambler 9.7. The results of the calibration statistics showed good prediction for beef color (L*, a*, b*) when measured on intact (R^2 of 0.84, 0.88 and 0.73, respectively) or opened (R^2 of 0.90, 0.88 and 0.74, respectively) meat trays. However, poorer predictions were obtained for other shelf life parameters showing high stability along the storage period, like microbial spoilage (R^2 between 0.40 and 0.55), TBARS ($R^2 < 0.40$) and texture ($R^2 < 0.37$). Furthermore, VIS/NIRS spectra showed some potential for classification of beef samples into shelf-life quality grades.

Key Words: beef, NIRS, shelf life

M147 Fatty acid composition of cattle fattened with tropical forage at rainy and drought season.

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The objective of this study was to quantify intramuscular fat and fatty acid composition of meat from cattle fattened on tropical forages (*L. leucocephala*, *P. maximum* and *C. plectostachyus*) under the intensive Silvopastoril System (SSPi) at 2 seasons (rainy n = 12 and drought n = 10). Intramuscular fat of *L. dorsi* (Ld) and *Semimembranosus* (Sm) muscles was extracted and fatty acids (myristic, mirystoleic, palmitic, palmitoleic, stearic, oleic, linoleic, eicosanoic, arachidonic acid (ARA) and docosahexaenoic (DHA) acids) were quantified. The effect of season was analyzed with a linear model. The intramuscular fat was higher ($P \leq 0.05$) in rainy (3.530 ± 0.22%) vs. drought (2.47 ± 0.21%) season and myristic, mirystoleic, palmitic, palmitoleic and stearic acid were not different ($P \geq 0.05$) between seasons. Oleic acid had higher concentration ($P \leq 0.05$) in the rainy (40.69 ± 3.15%) vs. drought (27.52

± 3.46%), while linoleic, linolenic and eicosanoic acid concentration were lower ($P \leq 0.05$) in rainy season. For the essential fatty acids, ARA concentration was lower ($P \leq 0.05$) in rainy (0.08 ± 0.10%) vs. drought (0.48 ± 0.11%) season and DHA had similar concentration ($P \geq 0.05$) along year seasons. It is concluded that beef fattened with tropical forages yield leaner meat in both seasons and its fatty acid compositions is maintained during the year. The SSPi is another alternative toward more sustainable meat production and promising source of dietary fat for human nutrition.

Table 1. Least squares means ±SE of intramuscular fat composition (% of fatty acids) of cattle fattened with tropical forages at two season

Variable	Rainy	Drought
Total fat	3.53±0.22^{a}	2.47±0.21^{b}
Oleic	40.69.±3.15^{a}	27.52±3.46^{b}
Linoleic	0.11±0.88^{b}	3.11±0.97^{a}
Linolenic	1.67±0.51^{b}	6.10±0.56^{a}
Eicosanoic	0.11±0.18^{b}	0.93±0.20^{a}
Arachidonic acid (ARA)	0.08±0.10^{b}	0.49±0.11^{a}

^{ab}Superscripts different between columns denote significant difference between season ($P \leq 0.05$).

Key Words: Silvopastoril System, meat, fatty acids

M148 Genetic parameters for fat thickness measured in different anatomical points of *Longissimus* muscle in Nellore cattle. M. N. Bonin*[1], F. J. Novais[1], S. L. Silva[1], R. C. Gomes[2], A. S. Figueiredo[1], P. F. Torralvo[1], L. G. Figueiredo[1], P. A. B. McLean[1], V. N. Barbosa[1], J. H. A. Campo[1], T. V. Solpelsa[1], M. H. A. Santana[1], F. M. Rezende[1], and J. B. S. Ferraz[1], *[1]College of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, Brazil, [2]State University of Londrina, Londrina, Brazil.*

Carcass backfat thickness (FT) is usually measured between the 12th and 13th ribs, however, in Brazil, the forequarter is not separated from the hindquarter at this section to preserve the loin integrity. Therefore, investigating alternative anatomical points to measure carcass traits in the Brazilian industry is needed. The purpose of this work was to evaluate the genetic correlation between fat thickness measured in different anatomical points of the *Longissimus* muscle (LM). Nellore bulls with 30 mo of age were evaluated for fat thickness between the 12th and 13th ribs by ultrasound (FTU, n = 2,028) using an equipment Aloka SSD500 micrus and a linear 17.2 cm probe and directly in the carcass, at the same site, after slaughter (FTC, n = 610). The other anatomical point was the section between the last lumbar and first sacral vertebra, that is the site where the loin is separated from the carcass hindquarter in Brazilian industries (FTLS, n = 1,072). For the estimation of genetic parameters a pedigree matrix with 14,722 animals was used and multi-traits analyses were carried out including the fixed effects of age at ultrasound evaluations and at slaughter, using the software VCE 6.0 (Groeneveld et al., 2008). The range for FT was 0.00 to 9.00 mm for FTU, 0.5 to 13.00 mm for FTC and 0.5 to 6.00 mm to FTLS. The FTU presented high genetic correlation with FTC (0.90 ± 0.05) and FTLS (0.80 ± 0.14). These correlations suggest that ultrasound is a good predictor of FT in the carcass and is highly correlated with the fat deposition in the loin since that the measures were collected in different anatomic points of the LM. FTC presented a moderate genetic correlation with FTLS (0.52 ± 0.14). The traits heritability values were moderate to low, but similar among each other, with values of 0.14 (0.04), 0.17 (0.07) and 0.13 (0.04) for FTU, FTC and FTLS, respectively. These results suggest that there is a genetic control of the FT deposition in the loin of Nellore bulls and that the FTLS may be a useful tool for genetic evaluation programs for carcass traits in Brazilian industries.

Key Words: *Bos indicus*, Brazilian cuts, ultrasound

M149 Comparative effects of two beta adrenergic agonists on Warner-Bratzler and slice shear force of USDA Choice strip steaks from calf-fed Holsteins. A. J. Garmyn*[1], J. N. Martin[1], J. C. Brooks[1], R. J. Rathmann[1], J. M. Hodgen[2], K. D. Pfieffer[2], C. L. Armstrong[2], D. A. Yates[2], J. P. Hutcheson[2], and M. F. Miller[1], *[1]Texas Tech University, Lubbock, [2]Merck Animal Health, DeSoto, KS.*

Our objectives were to determine the effects of zilpaterol hydrochloride (ZH), ractopamine hydrochloride (RH), or no β-adrenergic agonist (β-AA) on Warner-Bratzler shear force (WBSF) and slice shear force (SSF) of USDA Choice strip steaks in response to 2 postmortem aging periods (14 or 21 d). Calf-fed Holstein steers (n = 565) were assigned to one of 3 treatments: ZH (8.3 mg/kg of DM for 20 d; Merck Animal Health, DeSoto, KS), RH (300 mg/kg/d for 28 d; Elanco Animal Health, Greenfield, IN), or no β-AA (CON). Strip loins (n = 315) were obtained and portioned into 2.5-cm steaks using a Marel Portioning Machine (IPM-3, Marel Townsend, Des Moines, IA). Interactions between treatment and aging were not detected ($P > 0.10$) for any response variables. Supplementation with β-AA resulted in greater WBSF and SSF ($P < 0.01$). Control steaks (3.25 kg) had a lower average WBSF value than steaks from steers fed ZH (3.68 kg) and RH (3.67 kg), which did not differ. Similarly, CON steaks (14.13 kg) had a lower average SSF value than steaks from steers fed ZH (16.11 kg) and RH (16.00 kg). Aging for 21 d resulted in lower ($P < 0.01$) WBSF (3.43 vs. 3.64 kg) and SSF (16.36 vs. 14.46 kg) values compared with steaks aged 14 d. The percentage of steaks with WBSF values <4.4 kg were affected ($P < 0.01$) by treatment, but postmortem aging had no effect ($P = 0.13$). Ninety percent of CON steaks would be considered tender (4.4 kg) based on ASTM guidelines, but β-AA supplementation resulted in a lower percentage of tender steaks for ZH (79.2%) and RH (77.3%). Feeding β-AA ($P < 0.01$) and postmortem aging period ($P = 0.02$) affected the percentage of steaks measuring <3.9 kg of shear force. The percentage of very tender steaks was 84.0, 66.5, and 66.8% for CON, ZH, and RH, respectively. In conclusion, feeding β-AA to calf-fed Holsteins increased shear force values of USDA Choice strip steaks, regardless of postmortem aging period. Although, feeding β-AA reduced the percentage of tender steaks, no differences in shear force were observed between ZH and RH at these inclusion levels.

Key Words: beta agonist, dairy beef, shear force

M150 Carcass characteristics of Nellore steers receiving protected linseed oil during different periods of feedlot. T. M. Pivaro*[1], W. Henrique[2], A. A. M. Sampaio[1], J. L. V. Coutinho Filho[2], E. A. Oliveira[1], B. L. Rosa[1], and V. G. Carvalho[1], *[1]FCAV/Unesp, Jaboticabal, SP, Brazil, [2]APTA, São José do Rio Preto, SP, Brazil.*

The objective was to assess the supply of linseed oil or linseed oil protected from ruminal degradation during different periods of feedlot feeding on carcass characteristics of 35 Nellore steers. The animals were housed in individual pens for 105 d at Sao Paulo Agency for Agribusiness Technology, in Sao Jose do Rio Preto, Brazil, and received one of the following diets: control (without oil), with linseed oil during all the confinement (LO), or protected linseed oil during all the feedlot (OLiP 3), in the last 70 d (OLiP 2) or the last 35 d (OLiP 1). The corn silage was used as the exclusive roughage in the proportion of 40% in DM of diet. All diets were isonitrogenous and those with addition of oil were isoenergetic. The experimental design was a randomized block, balanced by animal weight, and the means were compared by Student's *t*-test at 5% probability. After slaughter, weight (HCW), dressing percentage (HCY), length (LC) and depth (DC) of hot carcass were determined. The longissimus muscle area (LMA) and the backfat thickness (BFT) between the 12th and 13th ribs were measured 24h after cooling, and the longissimus muscle area per 100 kg of carcass (LMAC) calculated. There were no differences among the variables assessed in this study (Table 1). Therefore, there was no benefit related to the addition of linseed oil, protected or not, to the diet or to the proposed durations for the supply of protected linseed oil during feedlot feeding over the carcass characteristics of Nellore cattle.

Table 1. Carcass characteristics of Nellore steers, finished in feedlot

Treatment	HCW (kg)	HCY (%)	LC (cm)	DC (cm)	LMA (cm^2)	LMAC (cm^2/100 kg)	BFT (mm)
Control	289.14	55.84	129.85	67.64	75.57	26.11	6.88
OLiP 1	287.78	55.45	129.07	67.21	74.14	25.83	7.56
OLiP 2	293.71	56.76	129.57	67.50	74.57	25.45	5.96
OLiP 3	298.92	56.35	128.28	65.50	80.14	26.85	6.66
LO	295.14	55.77	128.57	65.42	77.28	26.25	7.44
P[1]	0.4983	0.4527	0.8436	0.2754	0.3684	0.8443	0.7726
CV (%)[2]	4.40	2.51	2.29	3.73	10.64	8.96	36.88

[1] P = probability.

[2] CV = coefficient of variation.

Key Words: backfat thickness, longissimus muscle area, weight

M151 Meat fatty acids profile of Nellore steers receiving protected linseed oil during different periods of feedlot.

T. M. Pivaro*[1], W. Henrique[2], E. A. Oliveira[1], A. A. M. Sampaio[1], B. L. Rosa[1], J. L.V. Coutinho Filho[2], and V. G. Carvalho[1], [1]*FCAV/Unesp, Jaboticabal, SP, Brazil,* [2]*APTA, São José do Rio Preto, SP, Brazil.*

The objective was to assess the fatty acid profiles in the meat of 35 Nellore steers fed linseed oil or linseed oil protected from ruminal degradation (OLiP) during different periods of feedlot. The animals were housed in individual pens for 105 d at Sao Paulo Agency for Agribusiness Technology, in Sao Jose do Rio Preto, Brazil. The treatments were: control diet (CD), linseed oil during all the confinement (LO), or OLiP fed during the last 35 d (OLiP 1), last 70 d (OLiP 2) or all the confinement (OLiP 3). Corn silage was the exclusive roughage at the rate of 40% in DM of diet. The experimental design was a randomized block, balanced by animal weight, and means were compared by Student's *t*-test at 5% probability. The animals were slaughtered at an average weight of 522.71 ± 27.99 kg and samples were taken from the Longissimus between the 12th and 13th ribs and lyophilized after 24 h of carcass cooling. The fatty acids were quantified by gas chromatography. The ratio unsaturated:saturated was different among CD, OLiP 2 and OLiP 3 treatments (1.37, 1.16 and 1.16, respectively) while OLiP 1 (1.29) and LO (1.30) did not differ from any of the treatments. A similar result was observed for monounsaturated:saturated. However, OLiP 1 and LO differed in n-3 fatty acids (0.47 and 0.72%, respectively), and both did not differ from the other treatments (0.50% for CD, and 0.64% for OLiP 2 and OLiP 3). No difference was detected in the ratio of n-6:n-3 between treatments OLiP 2 and OLiP 3 (7.32 and 6.52, respectively), but both differed from OLiP 1 (9.12), DC (10.91) and LO (4.77), which differed from each other. Increasing the supply of protected linseed oil provides improvement in the amount of n-3 and, the ratio n-6:n-3 became closer to the ideal for a more balanced diet.

Key Words: Longissimus, meat quality, unsaturated

M152 Meat quality of crossbred cattle finished at feedlot and fed increasing levels of linseed oil.

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The aim was to assess the effects of increasing linseed oil supplementations (1, 3.8 and 5.2% in diet DM) and sex on meat quality of crossbred cattle Nellore × Canchim. Fifteen steers (427.80 ± 42.01 kg and 24 ± 2 mo old) and 14 heifers (400.57 ± 33.79 kg and 24 ± 2 mo old) were housed in individual pens and fed diets with 80% concentrate in DM and sugarcane IAC 86–2480 as the exclusive roughage source at Sao Paulo State University in Jaboticabal, Brazil. The experiment was a randomized block design, arranged in a 3 × 2 factorial scheme (oil ratios × sex) and means were compared by Student′s *t*-test at 5% probability. After fattening period, the animals were slaughtered by blocks. After 24 h of cooling carcasses, samples of *Longissimus* muscle between the 12th and 13th ribs were taken and analyses were conducted (meat and fat color characteristics (L*, a*, b*), water holding capacity (WHC), cook loss (CL), shear force (SF) and pH)). Oil levels, sex, and the interaction between these factors did not show differences for meat and fat color characteristics L*, a*, b* (38.63, 7.65 and 18.75; 72.90, 7.65 and 18.75, respectively), WHC (66.93%), SF (5.04 kgF) and pH (5.71). The interaction was significant for the CL variable, and heifers fed 1% oil showed the highest value (37.44%) compared with those fed 3.8 and 5.2% of oil (32.34 and 29.41%, respectively). Thus, higher levels of linseed oil supplementation for heifers decreased CL, which can improve beef organoleptic aspects such as juiciness. Steers showed no difference among oil levels, with an average of 36.14%. Analyzing each linseed oil level, only 5.2% on diet showed higher values for steers compared with heifers (36.26 and 29.41%, respectively). The use of increasing levels of linseed oil in cattle diet, from 1 to 5.2% in DM, did not improve qualitative aspects of the meat, such as tenderness and color (characteristics related to the presentation to the customer). Steers and heifers fed increasing linseed oil supplementations produce meat with similar qualitative characteristics except for CL.

Key Words: cook loss, meat color, shear force

M153 A study of the variance in tenderness and carcass traits of pasture and feedlot finished beef cattle.

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Tenderness is an important beef quality trait and consumers judge the overall acceptability based primarily on tenderness, flavor, color and texture. The objectives of this study were to compare the variance (based on a variance ratio) in Warner-Bratzler (WB) tenderness and selected carcass traits in pasture (P, n = 47) and feedlot (F, n = 48) finished steers. The 7 dietary treatments making up P and F were: 1) steers on pasture only throughout (n = 12), 2) steers on pasture supplemented with cracked barley grain throughout (n = 12), 3) steers on pasture supplemented with whole sunflower seed (WSS) throughout (n = 23), 4) steers with no supplement on pasture and feedlot (n = 12), 5) steers supplemented with WSS on pasture and no supplement in the feedlot (n = 12), 6) steers with no supplement on pasture but supplemented with WSS in the feedlot (n = 12) and 7) steers supplemented with WSS on pasture and the feedlot (n = 12). Steers in treatments 1–3 were harvested directly off pasture and steers in treatments 4–7 were finished in the feedlot. The variation in WB tenderness in steaks taken from the M. longissimus thoracis from P steers (3.92 kg) was higher ($P < 0.01$) than in F steers (1.89 kg). The highest variance was in P finished steers fed cracked barley supplement (6.33 kg) and this was higher ($P < 0.01$) than steers given no supplement on pasture but supplemented with WSS in the feedlot (1.19 kg) and steers supplemented with WSS on pasture and in the feedlot (1.82 kg). Steaks from pasture finished steers are expected to be more variable in tenderness, less tender and have consistently less trimable subcutaneous fat compared with steaks from feedlot finished steers.

Key Words: toughness, pasture, Warner-Bratzler

M154 Partitioning of Energy into Muscle and Fat in Relation to Beef Composite Type and Age at Harvest. N. P. Y. Welegedara*[1], E. K. Okine[1], J. A. Basarab[2], Z. Wang[1], C. Li[3], H. Bruce[1], S. Markus[2], J. Stewart-Smith[4], and L. A. Goonewardene[1,2], [1]*University of Alberta, Edmonton, Alberta, Canada,* [2]*Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada,* [3]*Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, Alberta, Canada,* [4]*BeefBooster Inc., Calgary, Alberta, Canada.*

Beef composite types (CT) have combined favorable traits of pure breeds. The objective was to compare energy required to grow muscle (M) and fat (F) in the carcass tissues of 5 BeefBooster composites (M1, M2, M3, M4 and TX) serially slaughtered at 6 harvest ages (HA) from 274 to 456 d in 2 years. The foundation breed for the M1 was Angus, M2 was Hereford, M3 was various small breeds, M4 was Gelbvieh or Limousin and TX was Charolais. The energy requirement for M (EM) and F (EF) deposition, the ratio of EF:EM and the proportion (%) of energy required to produce M and F without accounting for turnover, were analyzed by GLM of SAS with CT, HA, interaction of CT and HA and year as main effects. EM, EF, EF: EM ratio and proportions of energy required to produce M and F were different ($P < 0.01$) for CT and HA. EF was dependent on both CT and HA due to interaction ($P = 0.03$). EF was 1158.7, 1121.6, 1013.3, 1012.3, 1052.5 Mcal, EP was 384.6, 412.7, 330.3, 410.9, 428.9 Mcal and EF: EM was 2.95, 2.61, 2.97, 2.38 and 2.40 for M1, M2, M3, M4 and TX respectively. EF was 423.7, 831.3, 1058.8, 1213.1, 1394.3 and 1508.8 Mcal, EP was 275.1, 362.3, 412.8, 416.4, 441.6 and 453.0 Mcal and EF: EM was 1.54, 2.33, 2.60, 2.95, 3.19 and 3.38 for harvest ages at 274, 347, 372, 399, 427 and 456 d respectively. The proportion of energy required to produce F increased from 60.2% at 274 d to 76.8% at 456 d ($P < 0.01$) and the proportion of energy required to produce M decreased from 39.8% at 274 d to 23.2% at 456 d ($P < 0.01$). Based on energy partitioning and energetic efficiency of producing M and F, M1 and M3 can be harvested before 456 d and TX harvested after 456 d to avoid the production of excessively fat carcasses.

Key Words: energy partitioning, fat, muscle

Nonruminant Nutrition: Amino Acids and Energy

M155 Influence of energy concentration of the diet and terminal sire line on growth performance and carcass and meat quality of pigs slaughtered at 115 kg of BW. G. Coca[1], M. P. Serrano[1], L. Cámara[1], P. Guzmán[1], J. D. Berrocoso[1], J. Coma[2], and G. G. Mateos*[1], *[1]Animal Science Department, Universidad Politécnica de Madrid, Madrid, Spain, [2]Vall Company, Lleida, Spain.*

In total, 480 pigs (48 ± 5.15 kg BW) were used to investigate the effects of net energy (NE) concentration of the diet (2,350, 2,400, 2,450, and 2,500 kcal/kg) and terminal sire line (PIC L62 vs. Pietrain) on growth performance and carcass and meat quality of gilts and boars slaughtered at 115 kg BW. Pigs were fed according to a 2-phase feeding program using diets based on cereals, rapeseed meal, and soybean meal. Within each feeding period the lys:NE (g/Mcal) ratio was the same for all diets (3.8 vs. 3.5 respectively). Cumulatively, feed intake was reduced ($P < 0.001$) and G:F was improved ($P < 0.001$) as the level of NE of the diet increased but ADG and carcass and meat quality traits were not affected by diet. Crossbreds from PIC L62 sire line had higher ADFI and ADG ($P < 0.001$) than crossbreds from Pietrain sire line but G:F was not affected. Carcasses from Pietrain crossbreds were leaner ($P < 0.001$) and tended to have higher shoulder ($P < 0.08$) yield and less intramuscular fat ($P < 0.05$) than carcasses from PIC L62 crossbreds. Fat at m. gluteus medius was higher ($P < 0.001$) for PIC L62 crossbreds than for Pietrain crossbreds. Boars had better ADG ($P < 0.01$) and G:F ($P < 0.001$) and higher shoulder yield ($P < 0.001$) and less carcass yield ($P < 0.001$) and fat at m. gluteus medius ($P < 0.01$) than gilts. Also, boars tended to have less intramuscular fat ($P < 0.08$) in m. longissimus dorsi than gilts. In conclusion, an increase in NE concentration of the diet did not affect ADG or carcass quality of pigs. Therefore, an increase in energy content of the diet might not be justified under most economic circumstances. PIC L62 crossbreds had better growth performance but fatter carcasses than Pietrain crossbreds and gilts had higher carcass yield than boars. Consequently, gilts from PIC L62 crossbreds are preferred when carcasses are destined to the dry-cured industry.

Key Words: carcass quality and growth performance, sex and sire line, net energy concentration

M156 The utilization of energy by pigs differing in estimated growth potential. A. D. Beaulieu*[1], D. A. Gillis[1], J. N. Shea[1], J. P. Marriott[1], and J. F. Patience[2], *[1]Prairie Swine Centre Inc., Saskatoon, SK, Canada, [2]Iowa State University, Ames.*

A significant challenge in pork production is managing the variability within a cohort of pigs. Our objective was to compare the utilization of dietary energy for growth and protein deposition among pigs selected at nursery exit based on growth potential (GP). Treatments, arranged as a 3 × 2 × 2 factorial were 3 GPs, 2 dietary energy concentrations (NE; 2.18 or 2.40 Mcal NE/kg) and 2 intake levels (IN; 100 or 85% of ad libitum). Dietary energy was increased with canola oil and substituting wheat for barley. Each wk for 8 wks, 15 barrows were selected at nursery exit (about 62 d of age, DOA) from 3 litters and divided into a fast (0.46 ± 0.04), average (0.40 ± 0.04) or slow (0.34 ± 0.04 kg/DOA ± SD) GP group. Within GP, pigs were randomly allocated to 1 of the 4 NE by IN treatments or to an initial slaughter group (ISG). Dietary treatments began at 90 kg BW. Pigs were slaughtered at 90 (ISG) or 120 kg BW. Growth rate between 90 and 120 kg BW was unaffected by GP or NE ($P > 0.10$) and decreased by lower IN (0.86 vs. 1.01 kg/d; $P < 0.01$). GP did not affect feed intake ($P > 0.10$) which was increased when pigs were fed 2.18 vs. 2.40 Mcal NE/kg or 100% IN ($P < 0.05$). Feed efficiency was similar among treatments ($P > 0.10$). Efficiency of energy utilized for BW gain (Mcal NE/kg) was unaffected by GP and NE but tended to be higher at the 85 vs. 100% IN ($P = 0.06$). The efficiency of energy utilized for protein deposition (g CP/Mcal NE) was increased or tended to be increased by low NE ($P < 0.05$) or low IN ($P = 0.09$). The rate of protein deposition was increased at low NE (161 vs. 137 g/d; $P < 0.05$), tended to be increased by higher IN ($P = 0.09$) and was unaffected by GP ($P > 0.10$). Pigs fed 100% IN or 2.40 NE had an increased rate of lipid deposition ($P < 0.05$) which was unaffected by GP ($P > 0.10$). The rate and efficiency of protein deposition from 90 to 120 kg BW were increased by a lower NE. Pigs selected for GP at nursery exit, however, were similar during finishing with respect to rate and efficiency of growth and protein deposition. Separating pigs into GP classes at nursery exit will not aid management of variability in the finishing barn.

Key Words: swine, variability, dietary energy

M157 Effect of starch level in pig diets on digestible energy value of crude glycerin using the mobile nylon bag technique. C. A. Ordoñez-Gomez*[1,2], C. Ariza-Nieto[1], and G. Afanador-Tellez[2], *[1]CORPOICA, Bogota, Colombia, [2]Universidad Nacional de Colombia, Bogota, Colombia.*

In recent years, crude glycerin production has increased exponentially, which has led to a reduction of its price, making it possible for this co-product to reduce feed production costs in the pig industry. The aim of this study was to evaluate the effect of starch level on the digestible energy (DE) value of crude glycerin. Eight barrows (46 kg initial body weight and fitted with a duodenal T-cannula) were used to estimate DE of crude glycerin derived from diets containing 2 starch levels (10 and 12%) and 5 crude glycerin levels (0, 2.5, 5.0, 7.5, 10%). Therefore, 10 mixed diets were formulated and evaluated by the mobile nylon bag technique. A total of 320 nylon bags were used for DE value determination (32 per diet). In vitro digestion of the bags was carried out in pepsin-HCl solution with 450 IU pepsin/L at pH 2.0 and 37°C for 4 h. In the in vivo phase, 8 nylon bags were inserted into the duodenal cannula of each pig daily, during feeding times (800, 1030, 1300, and 1530 h). The nylon bags used in the study were excreted within 24 h of insertion and were carefully isolated from feces with a dry paper towel, then were frozen (−20°C) and freeze-dried for gross energy determination. The amount of material remaining in the nylon bag after passage through the digestive tract was used to calculate energy digestibility. The DE value of each bag was corrected for the DE of corn starch. Data were analyzed by a multiple linear regression model using PROC REG of SAS (v9.0). The slope of the regression line indicated the DE for crude glycerin, while the regression intercept indicated the effect of starch level. Results showed no interaction between the level of starch in the basal diet and the digestible energy value of crude glycerin ($P = 0.239$). The apparent DE of crude glycerin fed to pigs was 3251 kcal/kg DM ($R^2 = 0.578$; $P < 0.001$). According to the results of this study, the level of starch in pig diets does not affect the digestible energy value of crude glycerin.

Key Words: digestible energy, crude glycerin, pig

M158 Dynamic changes in blood flow, oxygen consumption and metabolite responses to acute arginine supplementation in growing-finishing pigs. B. E. Tan[1], Y. L. Yin*[1], X. F. Kong[1], and G. Y. Wu[1,2], [1]*Institute of Subtropical Agriculture, The Chinese Academy of Sciences, Chansha, Hunan, China,* [2]*Department of Animal Science, Texas A&M University, College Station.*

Arginine plays an important role in regulating nutrient metabolism. This study was conducted to determine the dynamic changes in blood metabolite responses to acute arginine supplementation in growing-finishing pigs using a blood catheter technique. Eight barrows (Duroc × Large White × Landrace) with an average initial BW of 70 kg were surgically fitted with chronic catheters in the portal vein, ileal vein and carotid artery and were randomly allocated to 2 groups to receive alanine (103 mg/kg body wt, isonitrogenous control) or L-arginine-HCl (61 mg/kg body wt) by the portal vein. Blood flows were measured with infusion of p-aminohippuric acid (PAH) into the ileal vein, and blood samples were obtained every 0.5 h for 4 h to determine oxygen consumption by portal vein-drained organs (PVDO) and concentrations of blood metabolites. Compared with alanine treatment, arginine infusion increased portal vein blood flow at 30, 60 and 90 min after infusion, but decreased ($P < 0.05$) PVDO at 60, 90, 120 and 150 min after infusion. Plasma concentrations of glutamate (at infusion times of 180 and 240 min) and arginine (at infusion times of 60, 120, 180 and 240 min) in arginine-infused pigs were higher ($P < 0.05$) than those of alanine-infused pigs at the same infusion time. However, arginine infusion decreased ($P < 0.05$) plasma cystine concentrations at infusion times of 60, 120, 180 and 240 min and valine at infusion times of 60 and 120 min compared with alanine treatment. Plasma concentrations of insulin and glucagon at infusion times of 30, 60 and 90 min were higher, and free fatty acids at infusion times of 60, 90 and 120 min were lower, compared with pigs both in alanine treatment at the same infusion time and at the pre-infusion (baseline) time ($P < 0.05$). These results suggest that acute arginine supplementation improves blood flow and reduces PVDO oxygen consumption, thereby enhancing amino acid availability for utilization. Insulin and glucagon may also play important roles with arginine infusion by transiently regulating nutrient metabolism.

Key Words: pig, nutrition, amino acids

M159 Dietary valine:lysine ratios of 0.80 and 0.85 did not differ performance of primiparous sow and nursing large litters. S. M. Hong,* P. Y. Zhao, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choongnam, South Korea.*

An experiment using 18 primiparous sows (Landrace × Yorkshire) to determine the effect of dietary valine:lysine ratios on performance in primiparous sows and litter. Sows were randomly assigned to 1 of 2 experimental diets (9 replicate pens per treatment and 1 sow per pen) containing different valine:lysine ratios of 0.80 or 0.85. Corn-soybean-wheat based diets were formulated to achieve the dietary treatments (0.86% SID lysine, and 0.69% or 0.73% SID valine). All diets were formulated to have 3.45 Mcal ME/kg and contained vitamins and minerals that exceeded NRC (1998) recommendations. The experiment lasted for 21 d. On d 107 of gestation, sows were moved into farrowing crates in an environmentally regulated farrowing house. Farrowing crates (2.1 × 0.6 m) contained an area (2.1 × 0.6 m) for newborn pigs on each side, and the temperature in the farrowing house was maintained at a minimum of 20°C. After farrowing, daily feed allowance increased gradually, and sows had ad libitum access to feed by wk 2. Overall, body weight loss (41.8 vs. 37.7 kg), backfat loss (5.5 vs. 7.9 mm), and ADFI (5.39 vs. 5.72 kg) of sows were not affected ($P > 0.05$) by different dietary valine:lysine ratios. No difference ($P > 0.05$) was noted in estrus interval (5.5 vs. 5.8 d). There was no difference ($P > 0.05$) in average body weight of piglets on the day of birth (1.39 vs. 1.26 kg) and d 21 (7.14 vs. 6.99 kg) between treatments. The numbers of weaned piglets (11.75 vs. 11.67), piglet survival rate (97.03 vs. 98.15%), weaning litter weight (83.60 vs. 81.49 kg), litter weight gain (67.25 vs. 66.76 kg), piglet gain (5.75 vs. 5.73 kg) and piglet daily gain (240 vs. 239 g) were not affected ($P > 0.05$) by dietary treatments. In conclusion, dietary valine:lysine ratios of 0.80 and 0.85 had no effects on lactation performance of primiparous sow and their offspring.

Key Words: lactation performance, primiparous sows, valine:lysine ratio

M160 Sequence of apparent ileal digestible lysine for growing-finishing gilts. G. C. Rocha*[1], F. C. O. Silva[2], R. F. M. Oliveira[1], L. Alebrante[1], A. Saraiva[1], and J. L. Donzele[1], [1]*Federal University of Viçosa, Viçosa, MG, Brazil,* [2]*EPAMIG, Viçosa, MG, Brazil.*

This study was conducted to evaluate sequences of apparent ileal digestible lysine (AIDL) for gilts from 63 to 153 d of age. Eighty gilts (AGPIC 425 x Camborough 25), were used in a randomized complete block design to evaluate 5 AIDL level treatments with 3 phase-feeding per treatments (9–8-7; 10–9-8; 11–10–9; 12–11–10 and 13–12–11 g/kg from 63 to 103, 103 to 133 and 133 to 153 d of age, respectively). Each treatment was replicated with 8 pens (1.87m^2/pig) with 2 pigs each. The basal diet for each phase contained corn, soybean meal and no supplemental industrial amino acids. Four additional diets (each phase) were formulated by adding L-lysine HCl 78% and when necessary DL-methionine 99%, L-threonine 98%, L-tryptophan 98%, L-valine 96.5% and L-isoleucine 99% replacing the starch. At the beginning and the end of each phase, pigs and feeders were weighed to assess ADG, ADFI, final BW and feed to gain ratio (F:G). From 63 to 103 d the AIDL levels (9, 10, 11, 12 and 13 g/kg) influenced linearly ($P<0.05$) the ADG (945, 956, 965, 981 and 1004 g) of the pigs, while the F:G (2.12, 2.00, 2.00, 1.97 and 1.99) was improved ($P<0.05$) quadratically to 1.97 at a level of 11.8 AIDL g/kg, and with no effects ($P>0.05$) on the ADFI and the final BW. There was no effect ($P>0.05$) of the sequences of AIDL on the gilts growth performance between 63 to 133 d, and 63 to 153 d. Sequences of diets containing 9-8-7 of AIDL g/kg fed from 63 to 103, 103 to 133 and 133 to 153 d, respectively, meet the AIDL requirements of growing-finishing gilts from 63 to 153 d of age.

Table 1. Growth performance of gilts from 63 to 153 days

	Apparent ileal digestible lysine, g/kg					
Item	9-8-7	10-9-8	11-10-9	12-11-10	13-12-11	SEM
Initial BW, kg	24.4	24.5	24.2	24.2	24.3	0.54
Final BW, kg	114.1	113.2	112.6	114.4	114.2	1.86
ADFI, g	2311	2267	2279	2322	2331	44.38
ADG, g	996	988	978	1004	997	17.14
F:G, g/g	2.32	2.29	2.33	2.31	2.34	0.02

Key Words: amino acids, performance, requirements

M161 Feed efficiency and carcass grade can be improved in finishing pigs by increasing the standardized ileal digestible lysine to metabolizable energy ratio. J. A. Jendza* and S. K. Baidoo, *University of Minnesota, Waseca.*

Two trials were conducted to evaluate the effect of increased standardized ileal digestible (SID) lysine to ME ratio on growth performance and carcass characteristics in finishing pigs. Trial 1 fed 256 mixed sex pigs with an initial BW of 99.2 kg (SD = 8.9 kg) for 4 wk. Pigs were housed 8 to a pen in a completely randomized design with 8 pens per treatment. Treatments consisted of a 72.8% corn/22% soy basal diet containing 7.5 g SID lysine and 3,401 kcal ME/kg of feed supplemented with 0, 1.2, 2.4, and 3.6 g lysine HCl/kg for treatments 1 to 4, respectively. At the end of 4 wk, pigs were individually identified and carcass characteristics recorded. Carcass grade was a composite measure of hot carcass weight and percent lean. Grading scores ranged from −7.5 to +10, with lighter and fatter pigs receiving lower scores than heavier and leaner pigs. With pen as the experimental unit, dietary treatments had no effect on any measure of growth performance or carcass quality. Trial 2 used 317 pigs, housed by sex 7 or 8 to a pen, with an initial BW of 90.4 kg (SD = 6.5 kg) for 4 wk. Treatments were based on a 72.9% corn/ 22% soy basal diet containing 7.85 g SID lysine and 3,404 kcal/kg of feed. This basal was then supplemented with lysine HCl to achieve SID lysine to ME ratios of 2.3, 2.6, 2.9, and 3.2 g SID lysine/Mcal ME. Crystalline DL-methionine, L-threonine and L-tryptophan were also added to maintain their respective ratios to lysine in the basal diet. Growth performance and carcass characteristics were recorded at the end of 4 wk. Average daily gain and ADFI were not affected by dietary treatment, nor were most carcass characteristics. However, linear improvements were detected in feed efficiency and carcass grade ($P < 0.05$). Feed efficiency increased from a low of 0.313 to a high of 0.329. Carcass grade increased from a low of 6.2 to a high of 6.86. There was also a trend to increase hot carcass weight ($P < 0.10$). In summary, carcass grade and feed efficiency of finishing pigs can be improved by feeding a higher SID lysine to ME ratio as long as care is taken to maintain adequate concentration of the other essential amino acids to lysine.

Key Words: swine, standardized digestible lysine, carcass characteristics

M162 Chemical composition of dietary fat affects fat and energy digestibility when supplemented to lactating sows.

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Levels of free fatty acids (FFA) and saturation of supplemental fat affects fat digestibility, which may be particularly important in lactating sows which require high amounts of nutrients. This hypothesis was tested using 85 mature sows assigned randomly to a 4 × 5 factorial arrangement of treatments and a control diet with no added fat. Factors included: 1) FFA level: 0, 18, 36 and 54% and 2) Iodine value (IV): 77, 88, 100, 112 and 124. Diets were corn-soybean meal based, and contained 3.42 g standardized ileal digestible lysine/Mcal ME. Dietary fat was supplemented at 6% and different FFA and IV levels were obtained by blending 4 fat sources: choice white grease (FFA = 0.3%, IV = 74.8, GE = 9469 cal/g), choice white acid grease (FFA = 57.8, IV = 79, GE = 8266), soybean-cotton seed oil (FFA = 0.1, IV = 67.5, GE = 9442) and soybean acid oil (FFA = 67.5, IV = 112.9, GE = 9196). Titanium dioxide was added to diets (0.5%) and used as a marker to determine digestibility of fat and energy. After 6 d of adaptation to treatment diets, fecal grab samples were collected from sows during the following 4 d (d 10 to 13 of lactation), twice per day. Digestibility of fat from ingredients in the control diet was 31.5%. Digestibility of the supplemented fat increased with levels of IV (quadratic, $P < 0.001$; 74.4, 84.5, 85.2, 82.9 and 73.53 for IV of 76, 88, 100, 112 and 124, respectively), and decreased with increasing levels of FFA (linear, $P < 0.001$; 87.4, 81.6, 74.0 and 77.3% for 0, 18, 36 and 54%). Apparent digestible energy content of the diet decreased with higher levels of FFA (quadratic, $P = 0.007$; 88.8, 88.2, 87.4 and 88.6%) and increased with increasing levels of IV (quadratic, $P = 0.017$; 87.6, 87.5, 88.9, 89.2 and 88.2%). Digestibility of supplemental fat was described by: Fat digestibility $= -78.45 - 1.59 \times \text{FFA} + 3.75 \times \text{IV} + 0.007 \times \text{FFA}^2 - 0.02 \times \text{IV}^2 + 0.01 \times \text{FFA} \times \text{IV}$, $r^2 = 0.47$. Digestibility of energy content of the diet was described by: Digestible energy $= 73.48 - 0.12 \times \text{FFA} + 0.31 \times \text{IV} + 0.001 \times \text{FFA}^2 - 0.001 \times \text{IV}^2$, $r^2 = 0.19$. In conclusion, higher levels of FFA negatively affected fat and energy digestibility. Also, saturation of the fat affected digestibility in a quadratic manner when fed to lactating sows.

Key Words: lactating sows, free fatty acids, saturation

M163 Feeding phytonutrients to chickens: The relationship between energy availability and growth performance.

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A total of 400 male day-old Ross 308 chicks were used in a floor pen study to investigate the effects of dietary supplementation of a mixture of carvacrol, cinnamaldehyde and capsaicin (XT, Pancosma S.A.) on dietary apparent metabolizable (AME), dietary net energy for production (NEp), and bird growth performance. Four diets (maize- or wheat-soybean based and with or without XT in a 2 × 2 factorial arrangement) were offered to the birds from 0 to 21 d of age. The diets were formulated to be adequate in protein (215 g/kg diet) but marginal in AME (2890 kcal/kg), and slightly higher in non-starch polysaccharides than recommended in the control diets supplemented with XT (100 g/t). The diets were provided in mash form ad libitum throughout the experiment. The treatments were allocated in a randomized complete block design with each treatment having 10 replicate floor pens with 10 birds per pen. The pens were bedded with used litter. Feeding wheat-based diets resulted in lower AME ($P < 0.05$) but higher NEp ($P < 0.05$), and feed efficiency ($P < 0.05$). Irrespective of cereal type, XT supplementation improved AME, NEp and feed efficiency ($P < 0.05$). There was a lack ($P > 0.05$) of cereal source by XT interaction suggesting that similar responses may be expected when XT is added to both, maize or wheat-based diets. Linear regression analysis was used to assess the relationship between determined dietary energy and bird growth performance. Dietary NEp was more highly correlated with performance criteria than dietary AME and seems to be a more sensitive way to evaluate broiler response to phytonutrients supplementation.

Key Words: phytonutrients, broiler, energy availability

M164 An evaluation of glutamine feed supplementation on the immune response, intestinal morphology, and growth performance of broilers at various stages of development.

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Banned antibiotic feed additives classed as growth promoters in poultry feed, have resulted in increased incidence of disease and depressed growth performance. Glutamine (Gln) may be an alternative feed additive to resolve these problems, since many beneficial effects of it have been reported in animals. Gln is the principle metabolic fuel for small intestine enterocytes, lymphocytes, macrophages and fibroblasts and is considered an essential amino acid in some species under inflammatory conditions. In a previous study we found that the addition of 1% Gln provided the highest efficacy without any negative effects on dry matter, organic matter and ash digestibility and nitrogen retention. Therefore, the purpose of this study was to evaluate the effect of glutamine supplementation at various stages of development on the immune response, intestinal morphology and growth performance of broilers. Three hundred, day-old male chicks were randomly assigned in a completely randomized design into 5 treatments with 3 replicates of 20 birds per treatment. Dietary treatment groups consisted of a control and the control supplemented 1% Gln that was fed to broilers for 7, 14, 21 or 28 d of age. The birds were raised through 42 d of age. Feed and water were provided ad libitum throughout the experimental period. Significant differences among treatment were assessed by Duncan′s new multiple range-test at $P < 0.05$. Orthogonal contrasts were used to evaluate treatment effects of control vs. mean of glutamine supplementation period. The addition of Gln at a level of 1% provided no significant benefits in most parameters studied, including growth performance, and immunoglobulin measured in serum and small intestinal tissue samples ($P > 0.05$). However, chicks receiving 1% Gln for 7 and 14 d had significantly wider villi in the duodenum compared with chicks fed the control diet ($P < 0.05$). In which the mean value of villus wide in chicks fed Gln for 7 and 14 d of age compared with control were 24 vs 55 and 35 vs 63.5 µm, respectively. Thus, it was concluded that the most advantageous time to add Gln to the diet of newborn chicks is from 0 to 14 d of age, beyond which point 1% added dietary Gln has little to no effect.

Key Words: broiler chicken, glutamine, intestinal morphology

M165 Velocity of L-methionine incorporation into the blood plasma of broiler chickens at the first week of age. A. C. Stradiotti*[1,4], C. Ducatti[2], J. R. Sartori[1], J. A. Bendassolli[3], V. C. Pelícia[1], P. C. Araujo[1], M. K. Maruno[1], L. V. C. Girão[1], F. G. Luiggi[1], R. Fasanaro[1], M. M. P. Sartori[2], J. C. Denadai[2], E. T. Silva[2], C. R. Souza-Kruliski[2], and A. C. Pezzato[1], *[1]São Paulo State University, Faculty of Veterinary Medicine and Animal Science, Botucatu Campus, Botucatu, Brazil, [2]São Paulo State University, Institute of Bioscience, Botucatu Campus, Botucatu, Brazil, [3]University of São Paulo, Center of Nuclear Energy in Agriculture, "Luiz de Queiroz" Campus, Piracicaba, Brazil, and [4]FAPESP.*

Studying the metabolic pathway of methionine using a carbon-13 enrichment protocol to measure kinetics of this amino acid in various tissues of birds may provide a greater understanding of methyl group metabolism. The aim of this study was to use stable isotope methodology to assess the rate of incorporation of labeled methionine in blood plasma of broilers aged 1–7 d old. A total of 51 one-d-old male Cobb chicks were housed (density = 12 birds/m^2) and selected with an initial BW of 45 ± 1.125 g. The diet was formulated based on corn and soybean meal and supplied ad libitum. To promote tissue enrichment, we used a dosage of 29 µmol of L-[$^{13}C_1$]methionine/kg BW/h, administered orally within 6 h (99 atom% ^{13}C; Cambridge Isotope Laboratories, Inc.). At the times 0 (control), 0.5, 1, 2, 3, 4, 5, 6, 8, 10, 12, 16, 20, 24, 48, 72 and 96 h after initial dosing, 3 birds per time point were slaughtered for sampling of blood plasma for carbon isotope ratio analysis using a mass spectrometer. The isotope ratios obtained were analyzed by a first-order exponential equation expressed as: $\delta^{13}C(t) = \delta^{13}C(f) + [\delta^{13}C(i) - \delta^{13}C(f)]\, e^{-kt}$, which enables calculation of the half-life of carbon-13 ($t = \ln 2/k$), obtained using a software package (OriginPro 8 Professional). Maximum enrichment occurred 8 h after oral administration of enriched solution. The results of $\delta^{13}C$ blood plasma to the maximum enrichment resulted in the following equation: $\delta^{13}C = -15.60 - 3.24\, e^{-0.2291t}$, with a carbon half-life calculated as 3.03 h and $R^2 = 0.93$, representing the velocity of incorporation of methionine into embedded tissue. Thus, the time required for 50% of orally-administered methionine to be metabolized is approximately 3 h at this dose and age of bird.

Key Words: labeled carbon, methyl-13C, turnover

Nonruminant Nutrition: Enzymes

M166 Influence of dietary Quantum phytase on bone strength and bone phosphorus contents of weaned pigs. S. K. Baidoo*[1], Q. Yang[1], G. He[1], T. D. Crenshaw[2], C. L. Wyatt[3], and J. A. Jendza[1], *[1]University of Minnesota, SROC, Waseca, [2]Department of Animal Science, University of Wisconsin, Madison, [3]AB Vista Feed Ingredient, Stillwell, KS.*

A total of 180, 18-d crossbred pigs (GAP English Belle × Duroc) with BW of 7.0 ± 1.1 kg were randomly allotted to 6 treatments with 5 replicate pens/treatment for 3 phases with 11, 11 and 12 d in each feeding phase, respectively. Six corn-soybean meal mash diets were formulated: a positive control (PC) diet (0.32% available P (aP); met NRC, 1998 recommendations), a negative control (NC) diet with approximately 10% reduction of aP (0.28% aP), NC + 200 FTU/kg Quantum (QP: *E. coli* phytase expressed in *Pichia pastoris*), NC + 500 FTU/kg QP, NC + 1,250 FTU/kg QP, and NC + 500 FTU/kg Natuphos (NP; fungal phytase expressed in *Aspergillus niger*). On d 42, 9 pigs from each treatment were randomly selected and euthanized for metatarsal collection to measure breaking strength and to determine ash and P content. Ash and P content of the metatarsal bone was not different among the dietary treatments. However, sex influenced ($P < 0.01$) metatarsal ash, and P content. In general, the average ash and P content of both fresh and dry metatarsal bone in female pigs was higher ($P < 0.05$) than in male pigs. There were no differences ($P > 0.05$) for the P content per unit of ash among the dietary treatments or between sexes. The metatarsal bone breaking strength was reduced ($P < 0.05$) in pigs fed the NC diet compared with pigs fed the PC diet or pigs fed the NC + 1,250 FTU/kg QP or NC + 500 FTU/kg NP. There were no other differences in bone breaking strength between the dietary treatments. In conclusion, Quantum supplementation at 1,250 FTU/kg and Natuphos at 500 FTU/kg improved the bioavailability of P. In addition, metatarsal P content was higher in female pigs than male pigs.

Key Words: piglet, phytase, bone strength

M167 Dietary effects of Quantum phytase on performance and phosphorus utilization of weaned pigs. S. K. Baidoo*[1], Q. Yang[1], G. He[1], C. L. Wyatt[2], and J. A. Jendza[1], *[1]University of Minnesota, SROC, Waseca, [2]AB Vista Feed Ingredients, Stillwell, KS.*

A total of 180, 18-d old crossbred pigs (GAP English belle × Duroc) with BW of 7.0 ± 1.1 kg were divided into 6 treatments with 5 replicates pens/treatment for 3 phases with 11, 11 and 12 d in each phase, respectively. Corn-soybean meal mash diets were formulated with a positive control (PC) diet (NRC, 1998 requirement), a negative control (NC) diet with approximately 10% reduction of available phosphorus (aP), NC + 200 FTU/kg Quantum (QP; *E. coli* phytase expressed in *Pichia pastoris*), NC + 500 FTU/kg QP, NC + 1,250 FTU/kg QP, and NC + 500 FTU/kg Natuphos (NP; *Aspergillus niger* phytase). Growth performance was not influenced ($P > 0.05$) by diet during phase 1 or phase 3. However, in phase 2, ADG of pigs fed the NC diet was reduced ($P < 0.05$) compared with pigs fed the PC, NC + 1,250 FTU/kg QP, or NC + 500 FTU/kg NP. Quantum supplementation to the NC at 200 or 500 FTU/kg improved ADG comparable to the PC diet, but not different than the NC diet. Overall, ADG was reduced ($P < 0.05$) in pigs fed the NC diet compared with pigs fed the NC + 1,250 FTU/kg Quantum. Phosphorus digestibility was reduced ($P < 0.05$) in pigs fed the PC diet compared with all other diets. Quantum supplementation to the NC diet at 1,250 FTU/kg improved ($P < 0.05$) P digestibility compared with pigs fed the PC or NC diet. Crude protein (CP) digestibility was reduced ($P < 0.05$) in pigs fed the PC diet, but this was not different than pigs fed the NC diet. Quantum supplementation to the NC diet at 200 or 500 FTU/kg improved ($P < 0.05$) CP digestibility compared with the PC, but not different than the NC diet. Quantum supplementation at 1,250 FTU/kg or NP at 500 FTU/kg improved ($P < 0.05$) CP digestibility compared with all other diets. In conclusion, phytase supplementation improved ADG and digestibility of P and CP in diets for early-weaned pigs fed reduced P diets.

Key Words: piglet, phytase, phosphorus digestibility

M168 Evaluation of phytase with different calcium and phosphorous density diet on the growth performance, nutrient digestibility, blood characteristics, and fecal noxious gas emission in growing pigs. L. Yan*[1], S. Zhang[1], D. S. Nam[2], and I. H. Kim[1], *[1]Department of Animal Resource and Science, Dankook University, Cheonan, Choongnam, South Korea, [2]Nonghyup Feed Co. Ltd., Seoul, South Korea.*

A 6-week trial with 96 growing pigs [(Landrace × Yorkshire) × Duroc, BW = 22.49 ± 1.38 kg] were conducted to investigate the effects of phytase with different calcium and phosphorous density diet on the growth performance, nutrient digestibility, blood characteristics, and fecal noxious gas emission in growing pigs. Pigs were assigned to 1 of 4 treatments in a randomized complete block design according to their sex and BW. Each treatment contained 6 replication pens with 4 pigs (2 gilts and 2 barrows) per pen. Treatments included: 1) T1, CON, basal diet (0.70% Ca, 0.65% P); 2) T2, CON + 0.01% phytase (0.65% Ca, 0.60% P); 3) T3, CON + 0.015% phytase (0.60% Ca, 0.55% P); 4) T4 + 0.02% phytase (0.55% Ca, 0.50% P). Pigs were housed in an environmentally controlled, slatted-floor facility in 24 adjacent pens and were allowed ad libitum access to feed and water through a self-feeder and nipple drinker throughout the experimental period. No differences were observed in growth performance and nutrient digestibility throughout the experimental period. Pigs fed CON diet had a lower ($P < 0.05$) red blood cell concentration than other treatments. Pigs fed T2 and T4 had an increased ($P < 0.05$) serum calcium concentration compared with those fed T3. Pigs fed T1 had higher ($P < 0.05$) ammonia and acetic acid emissions compared with pigs fed T3 and T4 on d 7. Higher ($P < 0.05$) total mercaptan emission was also observed in the CON group compared with T4 and the other treatments on d1 and d7, respectively. Pigs fed T1 also had higher ($P < 0.05$) H_2S and acetic acid emissions compared with those fed T3 and T4 during 3–5 d of the study. In conclusion, our results indicate that dietary phytase supplementation with lower calcium and phosphorous density could reduce the fecal noxious gas emission without any negative effects on the growth performance and digestibility in growing pigs.

Key Words: growing pigs, phosphorous, phytase

M169 Nutritional balance of broilers at starter and grower phase fed diets containing multienzyme complex and lipid sources.

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The aim of this paper was to evaluate the nutritional balance of broilers fed diets containing multienzyme complex (MeC) and different lipid sources during starter (16 to 21 d-old) and grower (30 to 35 d-old) phases. A total of 150 1-d-old male Cobb chicks were allotted in a completely randomized design featuring a 2x2+2 factorial arrangement of soybean oil or poultry fat added at 2 or 4% to diets supplemented with MeC. Two control diets without added lipids were without or with added MeC. There were 5 replications with 5 birds per experimental unit. The diets were corn and soybean meal-based and had similar energy and amino acid levels within each phase. The MeC contained enzymatic activities of pectinase, protease, phytase, β-glucanase, xylanase, cellulase and amylase. Water and feed were supplied ad libitum. There was no interaction ($P > 0.05$) between lipid source and inclusion level for the metabolizability coefficient of dry matter (MCDM), nitrogen (MCN), fat (MCF) and energy (MCE). Lipid sources did not influence ($P > 0.05$) the nutritional balance, 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 a good alternative to soybean oil. In the starter phase, higher levels of lipid reduced the MCDM ($P < 0.01$); however, this seems to be related to the greater amount of content of inert material added to keep diets isocaloric. Birds fed diets containing lipids showed greater MCF ($P < 0.01$) in both periods compared with birds fed lipid-free diets, and this was also observed when comparing the diets with 4% and 2% added lipids ($P < 0.01$). Addition of MeC to diets without lipid resulted in greater MCF ($P < 0.01$) at starter and grower phase. Treatments did not affect MCN and MCE ($P > 0.05$). In conclusion, the increasing levels of lipid in feed increase the MCF in broilers at starter and grower phases, regardless of lipid source. Addition of a multienzyme complex shows better MCF in diets without lipid inclusion in both phases.

Key Words: poultry fat, soybean oil

M170 Performance of 1- to 42-day-old broilers fed diets supplemented with multienzyme complexes.

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The aim of this work was to evaluate the effect of 2 multienzyme complexes (MeC) on the performance of broilers from 1 to 42 d old. A total of 868 Cobb chicks were allotted into 7 treatments, distributed in a completely randomized design with 4 replications. Diets and water were provided ad libitum according to the following treatments: T1 = basal diet; T2 = basal diet with MeC-A (SSF Allzyme); T3 = replacement of MeC-A by inert material; T4 = basal diet with MeC-B (Vegpro Allzyme); T5 = replacement MeC-B by inert material; T6 = basal diet with MeC-A and MeC-B; T7 = replacement MeC-A and MeC-B by inert material. MeC inclusions were made considering nutritional value of the enzyme as follows: MeC-A provided in the diet 75 kcal/kg ME, 0.20% CP, 0.029% Lys, 0.02 Met+Cys, 0.014% Thr, 0.004% Trp and 0.1% of P and Ca; MeC-B provided 7 kcal/kg ME, 7% CP and 7% in amino acid values of soybean meal. Treatments T3, T5, and T7 differed from T1 in nutrient content due to substitution of an inert material (kaolin) for the MeCs. The MeCs were composed by pectinase, protease, phytase, β-glucanase, xylanase, cellulase and amylase (MeC-A) and protease and cellulase (MeC-B). All experimental diets were formulated based on corn and soybean meal. The BW and ADG of broilers fed with multienzyme complexes were lower ($P < 0.05$) than those fed basal diets. However, AFI was not affected by the treatments ($P > 0.05$). The G:F ratio was worse in diets with MeC-A and with MeC-A + MeC-B supplementation compared with the basal diet ($P < 0.05$). The comparison between diet with MeC-A supplementation (T2) and diet without MeC-A (T3) indicated that the inclusion of MeC-A is not effective to improve G:F ratio of broilers, except in the diet containing both MeCs (A+B) which presented better results comparing to the T7 ($P < 0.05$). These results suggest that the supplementation with MeCs in diets with reduced nutrients is not effective to improve BW and ADG, and only MeC-B provides the same G:F ratio as basal diets to broilers from 1 to 42 d-old.

Key Words: enzymes, nutritional value, poultry

M171 Effects of Crina Poultry Plus and Ronozyme ProAct supplementation on growth performance, nutrient digestibility, relative organ weight, blood profiles, fecal microflora, and fecal noxious gas emission in broilers.

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A total of 720 1-d-old male ROSS 308 (BW = 39.8 ± 1.8 g) broilers were randomly allotted to 1 of 8 treatments (15 birds/pen, 6 pens/treatment) to evaluate the effects of Crina Poultry Plus (Crina) and Ronozyme ProAct (Ronozyme) in different nutrient density diets on growth performance, apparent total tract digestibility (ATTD), relative organ weight, blood profiles, fecal microflora, and fecal noxious gas emission. Dietary treatments were: PC, basal diet; PCR, PC + 0.02% Ronozyme; PCC, PC + 0.03% Crina; PCRC, PC + 0.02% Ronozyme + 0.03% Crina; NC, 4% CP and AA lower than PC; NCR, NC + 0.02% Ronozyme; NCC, NC + 0.03% Crina; and NCRC, NC + 0.02% Ronozyme + 0.03% Crina. Crina contains an ultra-pure grade of benzoic acid and essential oils (thymol, eugenol and piperine), and Ronozyme is a preparation of serine protease produced by *Bacillus licheniformis*. During d 8–21, NCC treatment increased ($P < 0.05$) BWG compared with NC treatment. During d 22–35, BWG was higher ($P < 0.05$) in PCRC treatment than that in NC treatment. Overall, chicks in PCR, PCC, PCRC, and NCRC groups had greater BWG ($P < 0.05$) than those in NC group. The ATTD of DM, N, and energy were improved ($P < 0.05$) in PCR, PCC, PCRC, and NCC treatments compared with PC and NC treatments at 5 week. The relative weights of liver and breast muscle were heavier ($P < 0.05$) in PCC treatment than those in PC and NCC treatments. The gizzard relative weight was increased ($P < 0.05$) in PCRC and NCRC groups compared with PC group. NCRC treatment increased ($P < 0.05$) the fecal *Lactobacillus* population compared with NC treatment. Fecal H_2S, NH_3, and total mercaptans emission was decreased ($P < 0.05$) in NCR treatment compared with PC treatment. In conclusion, application of 0.02% Crina + 0.03% Ronozyme in low nutrient density diet could improve growth performance, and increase the fecal *Lactobacillus* population in broilers.

Key Words: Crina Poultry Plus, Ronozyme ProAct, broilers

Nonruminant Nutrition: Weanling Pig

M172 Effects of freeze-dried *Lactobacillus reuteri* on growth performance, serum indices, and intestinal microflora of weaned pigs. D. Y. Zhang, H. F. Ji,* J. Wang, S. X. Wang, H. Liu, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China.*

The objective of this study was to evaluate the effect of supplementation of freeze-dried *Lactobacillus reuteri* on growth performance, serum indices, and intestinal microflora of weaned piglets compared with antibiotic. The strain was isolated from the cecum mucosa of healthy weanling pigs in our laboratory. Sixty 4 crossbred (Duroc × Landrace × Large White) weaned pigs with (9.02 ± 1.01 kg BW) were randomly distributed to 4 groups comprised of an antibiotic-containing control (Zinc Bacitracin; 1 g/kg) and 3 dietary inclusion levels of *L. reuteri* (5.6×10^6, 2.4×10^7 and 1.5×10^8 cfu/g of diet). The experiment lasted 30 d. Live weight gain and feed consumption of the weaned pigs were recorded weekly. Blood and fecal samples were collected at the end of the experiment. Viable bacterial counts were estimated by a standard plate counting method. *L. reuteri* supplementation had the same effect on ADG, ADFI, and FCR compared with the antibiotic control. Supplementation of *L. reuteri* decreased ($P < 0.05$) the serum urea nitrogen concentration and increased ($P < 0.01$) the IFN-γ concentration compared with the antibiotic control. Overall, supplementation with 2.4×10^7 cfu of *L. reuteri*/g produced the greatest improvements ($P < 0.05$) in serum indices among the 3 different probiotic levels. The number of *Lactobacilli* in the feces was increased ($P < 0.01$) by the supplementation of *L. reuteri* compared with control (2.74×10^8, 3.00×10^8, 5.35×10^8 vs. 1.25×10^8 cfu/g). The 2.4×10^7 and 1.5×10^8 cfu/g *L. reuteri* supplementation showed lower ($P < 0.01$) *Escherichia coli* in the feces compared with control group (4.65×10^6, 6.75×10^6 vs. 4.35×10^7 cfu/g), and 2.4×10^7 cfu/g supplementation had lower ($P < 0.01$) *Escherichia coli* than 1.5×10^8 cfu/g. This experiment indicated that *L. reuteri* at 2.4×10^7 cfu/g may be the most appropriate and feasible level with regard to enhance the growth performance, promote the serum indices, and improve the intestinal bacteria of weaned pigs.

Key Words: *Lactobacillus reuteri*, weaned pigs

M173 Effects of two kinds of lactic acid bacteria on productive performance and intestinal microflora of weaned piglets. H. Liu, H. F. Ji,* S. X. Wang, J. Wang, D. Y. Zhang, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China.*

The objective of this study was to evaluate the effects of 2 kinds of lactic acid bacteria (*Lactobacillus plantarum* and *Enterococcus faecalis*, isolated from small intestinal mucosa of healthy piglets) on the productive performance and intestinal microflora of weaned piglets. Ninety weaned piglets (Duroc × Large Yorkshire × Landrace) at 35 ± 2 d were randomly assigned to 3 groups and each group had 3 replicates with 10 piglets per replicates on the basis of body weights. Group A was fed basal diet, group B was fed basal diet with *Lactobacillus plantarum* (1.0×10^7 cfu/g diet), and group C was fed basal diet with *Enterococcus faecalis* (3.6×10^6 cfu/g diet). The concentrations of 2 bacterium were based on the previously study in our lab and were the optimal additional level. The experiment lasted 30 d. All piglets were free access to feed and water. The liveweight gains and feed consumption of the piglets were recorded weekly and fecal samples were collected at the end of the experiment. Data were analyzed using the ANOVA procedures of SPSS 18.0. Supplementation of *Lactobacillus plantarum* and *Enterococcus faecalis* significantly improved ADG (by 7.37% and 8.79% respectively; $P < 0.05$) and FCR (by 7.28% and 8.05% respectively; $P < 0.05$) compared with control group. Pigs supplemented with *Lactobacillus plantarum* and *Enterococcus faecalis* had lower diarrhea incidence compared with pigs fed basal diet (1.44%, 1.33%, vs. 2.56%, $P < 0.05$). The result also showed that, compared with basal diet group, there was increase in lactobacillus counts (by 4.18% and 3.96%, $P < 0.05$) and decrease in *E. coli* counts (by 9.31% and 10.08%, $P > 0.05$) in the fecal samples of weaned pigs fed *Lactobacillus plantarum* and *Enterococcus faecalis*. There was no significant difference between group B and C on ADG, FCR, diarrhea incidence, and fecal bacterium. This experiment indicated that supplying 2 kinds of lactic acid bacteria had the same beneficial effect on enhancing growth performance, reducing diarrhea incidence, and improving the intestinal health of weaned piglets.

Key Words: lactic acid bacteria, weaned piglet, intestinal microflora

M174 Assessment of probiotic properties of *Enterococcus faecalis* isolated from gastrointestinal tract of piglet and its effect on growth performance of weaned pigs. J. Wang, H. F. Ji,* F. M. Wang, S. X. Wang, D. Y. Zhang, H. Liu, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China.*

The objective of this study was to evaluate the probiotic characteristics of *Enterococcus faecalis* isolated from gastrointestinal tract of healthy piglet and its effects on growth performance of weaned pigs. Acid tolerance of *Enterococcus faecalis* was estimated by the survival rate when it cultured in simulated gastric fluid with pH of 2.0 and 3.0 after 2 h. Bile salt resistance of this strain was examined in MRS broth containing pig bile salt concentration from 0.1% to 0.3%. The sizes of the inhibitory zone of *Enterococcus faecalis* against *S.* aureus, *E. coli*, and *S. choleraesuis* were also determined to estimate the inhibition of this strain on pathogenic bacteria. Sixty-four piglets weaned at 28 d of age (8.05 ± 0.47 kg BW), were divided into 4 groups comprising of control with zinc bacitracin at 60 mg/kg, 3 treatments of different *Enterococcus faecalis* concentration (1.8×10^6,6.2×10^7,3.1×10^8 cfu/g diet). The experiment lasted 4 weeks. Data were analyzed using the ANOVA procedures of SAS. The results showed that *Enterococcus faecalis* had high tolerance to simulated gastric fluid at pH 2.0 and 3.0 with survival rates were 86.1% and 91.3%, respectively. The viable count of *Enterococcus faecalis* achieved 10^7 cfu/mL when it cultured in 0.2% pig bile salt medium of MRS 6 h, while the viable count achieved 10^6 cfu/mL cultured in 0.3% medium. Furthermore, *Enterococcus faecalis* performed well in inhibitory activity to 3 selected pathogens. The feeding trial results exhibited that *Enterococcus faecalis* supplementation enhanced average daily gain (490, 508, 471 vs. 466 g/d; $P < 0.05$) and feed conversation ratio (1.59, 1.60, 1,65 vs. 1.76; $P < 0.05$) in weaned pigs compared with control. The incidence of diarrhea was significantly decreased along with the increase of *Enterococcus faecalis* concentration in the diet compared with antibiotic control (13.1, 10.4, 9.0 vs. 15.2). It was also showed that there was increase in *Lactobacillus* counts and a numerical decrease in *E. coli* counts in the fecal samples of weaned pigs fed *Enterococcus faecalis*, especially with 6.2×10^7 cfu/g of feed. It was concluded from this study that the strain *Enterococcus faecalis* could be considered as a potential probiotic for weaned pigs.

Key Words: *Enterococcus faecalis*, probiotic, growth performance

M175 Digestibility of feed containing energy and protein ingredients to substitute dried whey and lactose for weanling pigs. L. V. C. Girão*[1], F. G. Luiggi[1], G. Mello[1], A. C. Stradiotti[1], C. C. E. J. Villela[1], N. B. Athayde[1], V. S. Cantarelli[2], R. Fasanaro[1], and D. A. Berto[1], *[1]São Paulo State University, Faculty of Veterinary Medicine and Animal Science, Botucatu Campus, Botucatu, SP, Brazil, [2]University Federal of Lavras, Lavras, MG, Brazil.*

This experiment was carried out with the aim of evaluating apparent digestibility of pre-initial (PI) and initial (I) diets for weanling pigs containing a combination of energetic and protein ingredients to substitute dried whey and lactose. A total of 108 crossbred pigs (Landrace × Large White) weaned at 21 ± 2 d of age with an average of 6.02 kg BW were used in a 4-wk experiment. Piglets were blocked by weight and distributed in a randomized complete block design of 4 treatments and 3 animals per pen: 1) control with dried whey and lactose; 2) whey protein concentrate, maltodextrin and an energetic blend containing maltodextrin and corn oil; 3) gluten meal 60% CP, maltodextrin and energetic blend containing maltodextrin and corn oil; and 4) protein energetic blend containing maltodextrin, corn steep liquor and corn oil. The blends used were obtained by spray dryer. Two digestibility trials were performed with diets containing 0.1% chromium (III) oxide as a digestibility marker starting on the 7th and 19th day of the experiment. Pooled fecal samples were collected from an experimental unit (3 animals per pen) during the 2 periods (12th to 17th and 24th and 29th day post-weaning), and digestibility parameters evaluated included: dry matter (DCDM), ether extract (DCEE), crude protein (DCCP), and gross energy (DCGE); digestible values for dry matter (DMD), protein (PD), ether extract (EED), and energy (ED). Data was statistically analyzed using the GLM models of SAS. Differences were found just for I diet in DCEE was higher ($P = 0.007$) for piglets fed diets 3) and 4) (71.19 and 69.38%, respectively), PD was higher ($P = 0.002$) for piglets fed diets 1) and 4) (12.35 and 12.03%, respectively), and EED was higher ($P < 0.001$) for piglets fed diet 3) (4.27%). The ingredient blends tested in this experiment, whether associated or not with vegetable or animal protein sources, were feasible substitutes for dried whey and lactose in PI and I diets. They did not interfere in the digestibility coefficient of dry matter, crude protein and gross energy of weanling pigs aged from 21 to 50 d old.

Key Words: blend, maltodextrin, microencapsulated

M176 Dietary clay does not negatively affect growth performance, nitrogen and iron status, or diarrhea score of weanling pigs. M. Song*[1], B. G. Kim[2], O. Osuna[3], and H. H. Stein[1], *[1]University of Illinois, Urbana, [2]Konkuk University, Seoul, Korea, [3]Milwhite Inc., Brownsville, TX.*

Clay may be included in diets fed to weanling pigs as mycotoxin binders, but it has been speculated that dietary clay may bind nutrients in the intestinal tract of pigs and increase diarrhea among pigs. The objective of this experiment was, therefore, to test the hypothesis that dietary clay does not negatively influence growth performance, serum nitrogen, serum iron parameters, and diarrhea score (DS) of weanling pigs. A total of 256 weanling pigs (initial BW: 6.49 ± 0.97 kg) were randomly allotted to 8 diets, 8 replicate pens per diet, and 4 pigs per pen in a randomized complete block design. A conventional control diet was formulated. Seven additional diets that were similar to the control diet with the exception that 0.3% clay was added to each diet were also formulated. The 7 clay treatments included 0.3% smectite (SM), 0.3% kaolinite (KL), 0.3% zeolite (ZL), 0.15% SM + 0.15% KL, 0.15% SM + 0.15% ZL, 0.15% KL + 0.15% ZL, and 0.10% SM + 0.10% KL + 0.10% ZL. No antibiotics were included in the diets. Pigs were allowed ad libitum intake of the diets throughout the 29 d experiment, and blood was collected from 2 pigs per pen on the last day of the experiment. For the overall experimental period, no differences in ADG, ADFI, or G:F were observed among treatments (Table 1). Serum urea nitrogen (SUN), red blood cells (RBC), hemoglobin (HGB), hematocrit (HCT), and DS were also not different among treatments indicating that dietary clay did not impair N and Fe absorption. In conclusion, dietary clay does not negatively affect growth performance, nitrogen and iron status, serum values measured, or diarrhea score of weanling pigs.

Table 1. Effects of dietary clay on growth performance and N and Fe status of weanling pigs[1]

Item	Control	SM	KL	ZL	SM + KL	SM + ZL	KL + ZL	SM + KL + ZL	SEM
ADG, g/d	247	276	261	264	267	245	249	276	10
ADFI, g/d	382	413	403	407	392	377	381	411	15
G:F, g/kg	649	672	650	649	679	653	657	671	15
SUN, mg/dL	10.4	10.0	10.0	9.0	9.3	10.1	9.7	9.9	0.5
RBC, M/μL	5.9	5.8	5.9	5.9	5.8	5.9	5.9	5.9	0.1
HGB, g/dL	10.6	10.7	10.6	10.6	10.5	10.7	10.5	11.1	0.2
HCT, %	31.2	32.0	31.6	31.4	31.6	31.8	31.5	33.0	0.5
DS	1.5	1.6	1.5	1.5	1.4	1.5	1.5	1.6	0.1

[1]SM = smectite; KL = kaolinite; ZL = zeolite.

Key Words: clay, growth performance, weanling pigs

M177 Effects of dry matter content of milk replacer on intake and growth in suckling pigs. S. M. Mendoza*[1], E. van Heugten[1], P. Hock[2], D. McKilligan[3], and R. D. Boyd[2], *[1]Department of Animal Science, North Carolina State University, Raleigh, [2]Hanor Company Inc., Franklin, KY, [3]TechMix Inc., Stewart, MN.*

This study was designed to determine the effect of dry matter (DM) content of milk replacer (MR) on intake and growth in suckling pigs. Data were collected from one hundred litters in a 2,600-sow commercial research unit. Litters (10 ± 1.0 pigs) were randomly assigned to treatments consisting of a control without MR and supplementation with MR having 15, 20, 25, 30, 35, or 40% DM. Litters were adapted from d 10 to 12 of age to MR with a 20% DM content. At d 13, litters were weighed (43.8 ± 0.8 kg) and fresh MR was provided in enclosed, gravity dispensed containers on a daily basis according to disappearance. Milk consumption was measured daily by the difference of MR addition minus refusal. At weaning (20.3 ± 2.0 d) litter weights (63.8 ± 1.2 kg) were recorded. Milk replacer linearly increased ($P = 0.007$) total litter gain (19.5, 18.5, 20.1, 20.4, 23.7, and 21.9 kg for 15, 20, 25, 30, 35, and 40% DM, respectively) and tended ($P < 0.10$) to increase gain per pig (2.03, 1.81, 1.95, 2.00, 2.16, and 2.08 kg), and ADG (244, 231, 239, 256, 279, and 263 g/d) with increasing DM. Supplementation with MR tended to improve ($P = 0.06$) gain per pig compared with non-supplemented pigs (2.00 vs. 1.86 kg). Litter gain (23.7 vs. 19.6 kg) and gain per pig (2.16 vs. 1.86 kg) were greater for litters receiving MR having 35% DM compared with non-supplemented control pigs. Milk consumption was similar, regardless of DM content (140 g/pig/d; $P = 0.70$). Consequently, DM intake increased linearly ($P < 0.001$) with increasing DM content (20, 30, 34, 49, 46, and 50 g/pig/d). Conversion efficiency of DM (gain:DM intake) improved linearly ($P = 0.009$) with increasing DM (16.4, 10.7, 9.1, 6.9, 8.8, 5.9). These results demonstrate that nutrient intake in nursing pigs can be greatly increased by increasing the DM content of milk above that typical for sow milk, and that litter growth was moderately improved. Additional studies may help us understand how to take advantage of the increase in nutrient intake to promote growth recovery, especially in litters composed of small pigs, the target of this technology.

Key Words: milk replacer, litter, growth

M178 The protein-to-energy ratio is a main driver of growth performance in piglets. S. A. Guzmán-Pino, D. Solà-Oriol, J. Figueroa,* and J. F. Pérez, *Universitat Autònoma de Barcelona, Bellaterra, Spain.*

It is well accepted that there is an optimal dietary protein-to-energy ratio for young pigs. However, there is not a final recommendation and doubts may arise about how to reach this ratio through changes on the dietary levels. The aim of the present study was to determine how a difference in the dietary protein or energy content and their corresponding protein-to-energy ratio affect growth performance in post-weaned piglets. A total of 480 weanling piglets (28d-old, initial BW 7.17 ± 0.01 kg) were distributed according to their BW into 48 pens (10 pigs/pen), and were randomly allotted to 1 of 4 experimental diets formulated to have different protein-to-energy ratios: a high protein (HP, 204 g CP/kg as-fed) and a low protein diet (LP, 142 g CP/kg) with similar DE content (3.60 Mcal/kg), and a low energy (LE, 3.35 Mcal DE/kg) and high energy diet (HE, 3.90 Mcal DE/kg) with similar CP content (190 g/kg). The protein-to-energy ratios were 56.6 and 56.7 g CP/Mcal DE for HP and LE, and 39.4 and 48.7 g CP/Mcal DE for LP and HE. Performance was measured on d 8 and 18 post-weaning. Up to d 8, HP diet promoted a higher ADFI than LP and HE diets ($P < 0.05$), and a higher ADG and BW than LP, HE and LE diets ($P < 0.01$). Feed:gain ratio also was more efficient for HP piglets in this period. On d 18, LE diet promoted the highest ADFI and ADG during period 8–18d ($P < 0.001$). Piglets fed the LE diet had a statistical approach to the highest piglet BW in comparison with piglets fed the HP diet (11.89 vs. 11.42 kg; $P = 0.09$), however, both treatments were higher than piglets fed the HE diet (10.84 ± 0.13 kg) and piglets fed the LP diet (9.16 ± 0.13 kg), that were the lightest ($P < 0.05$). Feed:gain ratio of latter piglets was higher than the rest of the experimental diets for this period. Growth results are in accordance with dietary protein-to-energy ratio offered. It is concluded that independently of the nature of the nutrient promoting imbalance, dietary protein-to-energy ratio may determine post-weaning piglet performance.

Key Words: protein-to-energy ratio, protein, energy

M179 Nucleotides in weanling pig diets. C. Andrade*[1], V. V. Almeida[1], M. Sbardella[1], D. P. Perina[1], F. L. Silva[1], P. L. Y. C. Chang[2], B. Berenchtein[3], L. B. Costa[4], and V. S. Miyada[1], *[1]USP/ESALQ, Piracicaba, SP, Brazil, [2]University of North Carolina, Raleigh, [3]USP/CENA, Piracicaba, SP, Brazil, [4]UESC, Ilhéus, BA, Brazil.*

Nucleotides have been supplemented in weanling pig diets due to their beneficial effects on maintenance of animal health, performance, immune response and on intestinal histology. The purpose of this study was to evaluate the effects of dietary nucleotide levels on performance, diarrhea occurrence, and intestinal histology of weanling pigs fed complex diet based on corn, soybean, dried milk and dried plasma. One hundred and 60 weaned pigs, averaging 6.43 ± 0.71 kg initial BW, were used in a randomized complete block design experiment with 5 treatments, 8 replications per treatment and 4 animals per pen (experimental unit). The treatments were: basal diet with 120 ppm of chloro-hydroxyquinoline (antimicrobial treatment) and basal diet with 0 (control), 100, 150 and 200 ppm of nucleotides. At the end of the experimental period (34th d), an animal per experimental unit was slaughtered for analysis of intestinal histology (villus height and crypt depth) of the duodenum and jejunum. Data were analyzed using the GLM procedure of SAS. For 1–14 d of the experimental period, performance was not affected ($P > 0.05$) by treatments. For the total experimental period (1–34 d), linear effects of dietary levels of nucleotides on final BW ($P = 0.005$; 23.08, 24.13, 24.18 and 24.23 kg) and on ADG ($P = 0.008$; 0.491, 0.520, 0.523 and 0.523 kg) were observed, but not ($P > 0.05$) on ADFI and G:F. Pigs fed nucleotides had higher ($P = 0.0002$) diarrhea occurrence (0.89, 1.78, 1.78, 3.57 and 5.36%) from 1 to 14 d than those of control and antimicrobial treatments. However, for the total experimental period (1–34 d), dietary nucleotide levels did not affect ($P > 0.05$) diarrhea occurrence and intestinal histology. Therefore, added nucleotides up to 200 ppm in weanling pig complex diets showed beneficial effect on growth performance, but not on intestinal histology and diarrhea occurrence.

Key Words: feed additives, growth promoter, swine

M180 Time-related changes of serum amino acids in weanling piglets. Y. Xiao,* T. Wu, A. Chen, L. Yang, and C. Yang, *College of Animal Sciences, Zhejiang University, Hangzhou, Zhejiang, China.*

The time-course of serum amino acids following response to early weaning was investigated over a 30 d period in weanling piglets using amino acid analyzer. Eight healthy piglets were selected from 4 litters (one male and one female per litter). The piglets were weaned at 21 d of age and their blood samples were collected on d 0, 1, 3, 5, 7, 10, 15, and 30 post-weaning. Serum concentrations of arginine and its immediate precursors (citrulline and ornithine) decreased ($P < 0.05$) from d 0 to 5 post-weaning, and increased from d 7 to 30 post-weaning. Serum concentrations of leucine, proline, tyrosine, and taurine decreased ($P < 0.05$) on d 1 and 3 post-weaning, and increased to the level of d 0 post-weaning on d 30. Serum concentrations of isoleucine, lysine, glycine, and serine were lowest on d 5 post-weaning; histidine, phenyalaine, valine, aspartic acid, and serine were lowest on d 10 post-weaning, which then increased thereafter. Methionine concentration changed slightly ($P > 0.05$) from d 0 to 3 post-weaning, while it increased by 43.51% ($P < 0.05$) and 41.11% ($P < 0.05$) on d 5 compared with that on d 1 and 3 post-weaning, and kept constant thereafter. Serum concentration of threonine increased by 31.67% ($P < 0.05$) and 79.06% ($P < 0.05$) on d 3 post-weaning compared with that on d 0 and 1, and then decreased on d 15 and 30 post-weaning. Serum concentration of glutamic acid was relatively higher ($P < 0.05$) from d 3 to 30 than that on d 0 and 1 post-weaning. These findings indicate that the serum levels of amino acids are robustly altered in weanling piglets and the critical phase are from d 3 to 10 post-weaning.

Key Words: amino acids, weaning, piglets

M181 Comparing different copper sources at pharmacological levels in nursery pigs. J. Zhao*[1], G. Allee[2], M. Vazquez-Anon[1], and R. J. Harrell[1], *[1]Novus International Inc., St. Charles, MO, [2]University of Missouri, Columbia.*

Pharmaceutical $CuSO_4$ is widely used in nursery pigs to promote growth when included beyond Cu requirements as defined by NRC (1998). However, high dietary Cu antagonizes other minerals (Zn and Fe) and nutrient utilization in monogastric animals. The objective of this research was to compare different Cu sources at pharmacological levels in nursery pigs. A total of 616 crossbreed piglets (PIC, 20 d of age, 5.0 ± 0.3 kg) were randomly allocated to one of 4 treatments with 7 replicates per treatment and 22 piglets per pen. The treatments included an inorganic negative control ($CuSO_4$) at NRC level (6 mg/kg), and a pharmaceutical level (150 mg/kg) of Cu supplemented using $CuSO_4$, tribasic copper chloride ($Cu_2[OH]_3Cl$), or $Cu(HMTBa)_2$. The $Cu(HMTBa)_2$ (Mintrex, Novus International Inc., St. Charles, MO) is a chelate of one Cu molecule with 2 molecules of 2-hydroxy-4-methylthio butanoic acid (HMTBa). Pigs were fed typical commercial nursery diets for 21 d. At the completion of 21 d, one median pig per pen was harvested for liver mineral analyses. Pigs fed $CuSO_4$ and $Cu(HMTBa)_2$ exhibited 8% and 10% improvements ($P = 0.02$) in feed efficiency, respectively, compared with pigs fed the negative control. Weight gain tended to be improved by both $CuSO_4$ and $Cu(HMTBa)_2$ ($P = 0.07$). Pigs fed $Cu_2[OH]_3Cl$ were intermediate but were not differ from the negative control. No ADFI differences were observed among treatments ($P = 0.75$). For liver mineral concentration (dry weight basis), pigs fed $Cu(HMTBa)_2$ had the highest liver Cu concentration, which was significantly higher than pigs fed ($Cu_2[OH]_3Cl$) and the negative control (71% improvement, $P = 0.02$). Pigs fed $CuSO_4$ were intermediate with 39.8, 48.8, 52.1, and 68.2 mg liver Cu per kg dry weight for the negative control, $Cu_2[OH]_3Cl$, $CuSO_4$, and $Cu(HMTBa)_2$, respectively. No differences were observed for liver Fe, Mn, or Zn concentration ($P > 0.28$). In conclusion, pigs fed $Cu(HMTBa)_2$ at a pharmacological levels performed the best based on feed efficiency and liver copper concentrations, followed by $CuSO_4$. No benefits of $Cu_2[OH]_3Cl$ was observed on performance or liver Cu concentration in this trial.

Key Words: Mintrex, copper, swine

M182 Effects of steam-processed rice, natural vitamin E, and glutamine in diets for weaning piglets. G. J. M. M. Lima*[1], M. Kutschenko[2], and E. T. Nogueira[2], [1]*Embrapa, Concordia, SC, Brazil,* [2]*Ajinomoto, Sao Paulo, SP, Brazil.*

Expanded rice (R) obtained by heat steam processing, glutamine (Gln) and natural vitamin E sources (E) improve performance of young piglets. An experiment was conducted to compare these 3 ingredients using 400 barrows and gilts from the same genotype. Pigs were weaned at 21 d of age (6.90 ± 0.35 kg average initial BW) and allotted to 5 treatments according to a randomized block design, with 8 replicates/treatment and 10 pigs/pen (5 per sex). A 3-phase feeding program was used with free access to feed and water until the end of the trial (63 d of age). Treatments were: T1- control diet (corn, SBM, lactose sources, fish meal, soybean oil, amino acids, minerals, vitamins and a growth promoter); T2 – similar to T1, with the inclusion of 20% ground R in partial replacement of corn; T3 – similar to T1, with the addition of 0.8% and 0.6% of AminoGut (Gln source) in dietary phases 1 and 2, respectively, and no supplementation in phase 3; T4 – similar to T1, with the inclusion of 3% mechanically extracted rice oil (166.79 mg total E/100 g and 37.47 mg α-tocopherol/100 g) in replacement of soybean oil; T5 – similar to T2, with Gln and E addition at the same levels used in T3 and T4. Treatment diets had the same nutrient levels in each phase. Diarrhea occurrence throughout the trial did not differ among treatments (X^2 test, $P > 0.05$). Pigs fed control diet (T1) showed lower average final wt ($P < 0.06$) and daily gain (ADG, $P < 0.05$) compared with all treatments, except T4 ($P = 0.70$). There were no differences in average daily feed consumption ($P = 0.28$) or feed:gain ratio ($P = 0.40$) among treatments. Expanded rice (T2) or Gln (T3) supplementation alone or in combination (T5) improved pig BW gain, but no additive effects were observed. In conclusion, partial replacement of corn by expanded rice and Gln supplementation improved piglet performance in the nursery phase.

Table 1. Effects of expanded rice, glutamine, and natural vitamin E in diets for weaning pigs

Variable	T1	T2	T3	T4	T5	SEM	*P*-value
Final wt, kg	27.60^b	28.51^a	28.80^a	27.77^b	28.76^a	0.39	0.02
ADG, g/d	493^b	514^a	521^a	497^b	521^a	9	0.02
ADFC, g/d	712	746	745	723	711	18	0.28
Feed:gain	1.45	1.46	1.43	1.46	1.37	0.03	0.40

^{a,b}Means with different letters in the same line differ ($P < 0.05$).

Key Words: AminoGut, rice oil, swine

Physiology and Endocrinology I

M183 Cortisol levels during roping acclimation in rodeo calves. K. Comeaux, B. Pousson, A. Greathouse, D. Terro, J. Browning, and C. E. Ferguson,* *McNeese State University, Lake Charles, LA.*

Roping calves (n = 10) were evaluated for chute behavior and cortisol concentration for the first 9 weeks of being roped. These calves were between 90 to 120 d of age and weighed between 93 to 120 kg at the beginning of the study. Each Monday (haul), calves were penned via horseback, placed in a chute, and given a chute score from 1 (calm) to 5 (frantic). Calves were then weighed, a jugular blood sample was collected, and they were loaded onto a stock trailer and transported ~10 min to the rodeo area. At the rodeo arena, calves were left in a pen for 3 h. They then received a chute score, second blood sample (collected at arena), and returned to the pen. On Tuesday, calves were roped twice and on Wednesday (rope) received a chute score, and a blood sample was collected twice, once before roping. Within 30 min of second roping, a second chute score was given and blood sample was collected. Following this, calves were returned to the farm for the remainder of the week. This routine was repeated for 9 weeks and at the end of the 9-week period blood samples were analyzed for plasma cortisol via radioimmunoassay. Statistical differences among chute scores and plasma cortisol concentrations (µg/dL) pre-event, post-event, the change in cortisol (post-event – pre-event), and weight gain were analyzed using SAS Proc GLM with repeated measures. The change in cortisol decreased following roping ($P < 0.05$) compared with hauling during wk 3, −1.04 ± 0.50 (rope) vs. 2.40 ± 0.46 (haul) and wk 4, −3.08 ± 0.56 (rope) vs. 0.03 ± 0.77 (haul). There was no difference in the change of cortisol for wk 5 and 6. However, roping during wk 7 differed ($P < 0.05$) from hauling; −4.62 ± 0.92 (rope) vs. −1.54 ± 89 (haul). There was no difference in the chute score for pre-event, but chute score decreased ($P < 0.05$) post-hauling after wk 3 and remained lower compared with wk 1 and 2. The chute score was lower ($P < 0.05$) after roping compared with after hauling during first 3 weeks but did not differ afterward. Additionally, weight gain in calves significantly increased after the third week. From these results it can be concluded that although after 3 weeks calves begin to acclimate to hauling and roping they acclimate more quickly to roping than hauling ~10 min.

Key Words: rodeo, cortisol, roping calf

M184 Improving reproductive performance of Ossimi ewes using hormonal and enzymatic treatments. E. B. Abdalla*[1], A. Q. Al-Momani[2], F. A. Khalil[1], H. M. Gado[1], and F. S. Al-Barakeh[3], *[1]Ain Shams University, Cairo,Egypt, [2]Ministry of Agriculture, Amman, Jordan, [3]National Center for Agricultural Research and Extension, Al-Baq'a, Al-Balqa, Jordan.*

The current experiment was conducted to evaluate the effect of dietary supplementation of melatonin, Zado (patent product contains cellulases, xylanases, protease and α amylase) and their combination on the reproductive performance of Ossimi ewes. Fifty-seven, multiparous, adult Ossimi ewes were randomly assigned to 4 groups, each group was fed ration supplemented with one of the following components: melatonin (G1; n = 14), Zado (G2; n = 14), melatonin and Zado (G3; n = 15) and ration with no additives (G4; control, n = 14). All ewes were fed maintenance ration for one month (during June) followed by flushing ration for 5 weeks (2 weeks before and 3 weeks after ram introduction). Melatonin (3mg/h/d) and Zado (15g/h/d) started to be added with maintenance and flushing rations, respectively. Fertile rams were introduced to ewes for 2 successive estrous cycles. General Linear Model (GLM) procedure of SAS, ANOVA and Duncan's multiple range test were used for statistical analysis. Percentage of ewes expressed estrus was significantly different ($P < 0.05$) among the treated groups. All ewes expressed estrus in G1, while the lowest percentage (71%) was detected in G4. The interval from ram introduction to the onset of estrus differed ($P < 0.01$) among the treated groups. Ewes received melatonin in G1 and G3 expressed estrus earlier than ewes didnâ€t receive melatonin in G2 and G4. Neither body weight nor body condition score was different at the first estrus following ram introduction, while average daily gain was slightly promoted by treatments particularly with melatonin. Melatonin treated groups (G1 and G3) had significantly higher ($P < 0.01$) progesterone concentration than that in G2 and G4. Lambed ewes as percentage of total ewes were similar in G3 and G4 (50%), while they increased in G1 and G2 (57 and 67%, respectively). Prolificacy was greater in G1 and G3 than that in G2 and G4. Maximum prolificacy was detected in G3 while the minimum was observed in G4 ($P < 0.01$). Fecundity was lower ($P < 0.01$) in G4 (control group) than all the treated groups (G1, G2 and G3).Results of the present study indicated that melatonin could increase the estrus expression of ewes and decrease the interval to estrus after ram introduction. Thus, treatment with melatonin alone, or in combination with Zado, may provide a viable means to improve the fecundity and prolificacy of Ossimi ewes.

Key Words: Zado, melatonin, estrus

M185 Prostaglandin-$F_{2\alpha}$ may not be necessary in short-term progesterone-based estrous synchronization protocols in cyclic ewes. K. N. D'Souza,* S. L. Rastle-Simpson, Q. S. Baptiste, and M. Knights, *West Virginia University, Morgantown.*

Two experiments were conducted to determine the requirement for prostaglandin F2α to achieve ample synchrony of fertile estrus in short-term progesterone-based (STPB) estrous synchronization protocols in cyclic ewes. In Exp. 1, ewes (n = 175) were randomly assigned to receive 0, 1 or 2 CIDR inserts for 7 d before introduction of rams. At insert removal, approximately half of the ewes in each group were injected with 20mg lutalyse (dinoprost; PGF) or received no further treatment. In Exp. 2, crossbred Katahdin ewes (n = 83) were randomly assigned to receive a CIDR for 5 or 7 d before the introduction of rams, with or without PGF at insert removal. The effects of treatments on reproductive performance were analyzed using logistic regression and ANOVA for categorical and continuous variables, respectively. In Exp. 1, the use of CIDR inserts tended to increase the proportion of ewes lambing to the first service period ($P = 0.08$) and reduced the mean lambing day ($P = 0.1$) by 13 percentage points and 1.7 d, respectively. Ewes treated with 1 CIDR device were more prolific ($P < 0.001$; 1.7 ± 0.07 vs 1.4 ± 0.07), lambed earlier ($P < 0.05$; 6.4 ± 0.8 vs 9.2 ± 0.8), and a greater portion tended to lamb to the first service period ($P = 0.1$; 88 vs 74%) than ewes treated with 2 CIDR devices. There was no significant effect of PGF on any of the reproductive performance variables. In Exp. 2, neither the length of treatment with CIDR device nor the use of PGF affected estrous response. Ewes treated with CIDR for 5-d tended to have higher conception rates ($P = 0.07$; 81.3%) and pregnancy rates ($P = 0.1$; 66.7%) compared with ewes treated for 7-d (61.8 and 51.2%, respectively). Injection with PGF decreased ($P < 0.01$) both conception and pregnancy rates (53.6 and 42.9% and 84.2 and 71.1%, for PGF and non- PGF treated ewes, respectively). The effect of PGF was not altered by the duration of CIDR treatment. The results of the current study indicate that there are no beneficial effects of increasing the duration of treatment from 5 to 7 d, or using an additional CIDR device when using a STPB estrous synchronization protocol in cyclic ewes. Treatment with a CIDR device for 5-d alone is sufficient to induce fertile estrus and synchronize lambing.

Key Words: fertility, prostaglandin, synchronization

M186 Is a CIDR as effective as a sponge in a novel follicle wave emergence and estrus synchronization protocol in anestrous ewes? M. B. Gordon[1], M. Bidarimath[1], M. Moggy[1], M. Camara[1], J. A. Small[3], P. M. Bartlewski[2], and D. M. W. Barrett*[1], *[1]Department of Plant & Animal Science, Nova Scotia Agricultural College, Truro, NS, Canada, [2]Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [3]Atlantic Food & Horticulture Research Centre, Agriculture & Agri-Food Canada, Truro, NS, Canada.*

The characteristics of ovulating follicles and the timing of ovulation can be very inconsistent when estrus is synchronized in anestrous ewes. Moreover, the well-utilized MAP sponge, containing synthetic progesterone (P_4), was discontinued and replaced by the controlled internal drug releasing device (CIDR), containing natural P_4. The objectives of this study were to compare the patterns of follicular and luteal development of seasonally anestrous ewes treated with CIDR-estradiol-eCG or MAP-estradiol-eCG. During seasonal anestrus, Texel ewes were randomly assigned to receive MAP sponges (60 mg MAP; Veramix; n = 7) or CIDRs (0.33 g P_4; Eazi-Breed CIDR; n = 7) for 12 d. An intramuscular injection of estradiol-17β (350 µg) was given 6 d before intravaginal device removal and an intramuscular injection of eCG (500 IU; Folligon) at intravaginal device removal. Daily ovarian ultrasonography was performed on the day of intravaginal device insertion and continued until ovulation and corpora lutea were confirmed. Blood for P_4 analysis was collected from 5 to 15 d after device removal. To determine the exact timing of ovulation, ovarian ultrasonography was done twice daily from eCG treatment until ovulation was detected. There were no differences in the interval from eCG treatment to ovulation (4.1 ± 0.2 d; $P = 0.67$), number of follicles that ovulated (1.4 ± 0.2; $P = 0.69$), or number of corpora lutea that developed (0.9 ± 0.2; $P = 0.44$) between the sponge and CIDR treatments. There were also no differences between the sponge and CIDR treatments for P_4 concentrations from 5 (0.2 ± 0.06 ng/mL) to 15 (1.2 ± 0.3 ng/mL) d after eCG treatment ($P = 0.92$). This study demonstrates that the CIDR-estradiol-eCG treatment may be as efficacious as the MAP-estradiol-eCG treatment. Further research is required to examine the affects of the CIDR-estradiol-eCG treatment on other critical criteria of ewe reproductive performance, such as pregnancy and lambing rates.

Key Words: anestrous ewes, CIDR, synchronization

M187 Effects of parity and litter size on body reserves dynamics across a complete physiological year in Romane ewes reared under extensive grazing conditions. E. González-García*[1], V. Gozzo de Figuereido[2], D. Foulquie[3], E. Jousserand[3], A. Tessniere[1], F. Bocquier[1], and M. Jouven[1], *[1]INRA UMR868 Systèmes d'Èlevage Méditerranéens et Tropicaux (SELMET), 34060 Montpellier, France, [2]Escola Superior de Agricultura, São Paulo, Brazil, [3]INRA UE0321, Domaine de La Fage, 12250 Roquefort-sur-Soulzon, France.*

How adaptation mechanisms interact across functional levels to control the adaptability of an individual during its own lifetime and also across generations is a core complex question of contemporary research. This work belongs to a series of first efforts in our team looking for gaining insights in identifying and understanding the adaptation mechanisms of ruminants through decrypting functional levels effects in a series of environmental and physiological conditions changes. We consider the evolution of energy body reserves (BR) mobilization or accretion process as an indicator of adaptability while evidencing individual differences responsive of internally or environmentally driven changes in grazing ruminants. Forty-one Romane ewes reared in a natural extensive rangeland of Center France were allocated in homogeneous groups according to body weight (BW) and body condition score (BCS), and distributed by parity [multiparous (MULT), n = 20; primiparous (PRIM), n = 21] and litter size (LSi) [having singletons (SING), n = 21 or TWIN, n = 20]. Feeding was restricted to grazing and other fibrous sources (hay), thus avoiding luxury energy intake and enhancing BR mobilization in function of requirements. Individual BW, BCS (1 to 5 scale), plasma NEFA and glucose (GLU) were monitored across a complete physiological year at –44, 0, 24, 61, 88, 119, 168, 207, 227, 257 and 312 d relatives to lambing (DIM). Blood sampling were performed early morning before the first meal. Data were analyzed by mixed procedure of SAS (2003), considering parity, litter size and its interactions as fixed effects. MULT (59.8 ± 1.21 kg) were systematically heavier ($P < 0.0001$) than PRIM (51.7 ± 1.18 kg). Beginning of lambing, LSi affected ($P < 0.05$) BW in MULT [where ewes with SING (46.5 ± 0.95 kg) were heavier than TWIN (43.3 ± 0.92 kg)] but not in PRIM. BCS was not affected by parity but, from lambing and throughout the experiment, MULT with SING (2.8 ± 0.06) expressed consistent higher ($P < 0.0001$) BCS than those MULT with TWIN (2.5 ± 0.06). NEFA was higher for ewes having more than 1 fetus (TWIN; 0.61 ± 0.040 vs. 0.49 ± 0.041 mmol.L^{-1}) just 1.5 mo before lambing, afterward this difference disappeared probably because of a lack of sensitiveness of this parameter for the fluctuating feeding regimens in extensive grazing conditions. This was coherent with the higher concentration of GLU at lambing in MULT with one fetus (SING; 0.83 ± 0.047 vs. 0.68 ± 0.043 g.L^{-1}, $P < 0.0385$) but not in PRIM. Results indicates that MULT are able to mobilize BR easier than PRIM in situations of negative energy balance (e.g., TWINS vs. SING; peri-lambing days), confirming that flexibility in BR utilization comes with experience, as evidence of an environmentally driven character. Trying to unravel how interactions between heritable and environment-dependent differences between individuals lead to interindividual differences in BR dynamics is our main research goal in the next future.

Key Words: body reserves, extensive grazing, adaptive capacity

M188 Pregnancy per AI (P/AI) after presynchronizing estrous cycles with Presynch-10 or PG-3-G before Ovsynch-56 in four dairy herds. J. S. Stevenson* and S. L. Pulley, *Kansas State University, Manhattan.*

Our objective was to monitor P/AI at first service in 3,005 lactating dairy cows located in 4 herds in northeast Kansas. Cows with eartags ending with odd digits at calving were enrolled in Presynch-10 (Pre-10): 2 25-mg injections of $PGF_{2\alpha}$ (i.e., PG-1 and PG-2) 14 d apart. Cows with eartags ending with even digits were enrolled in PG-3-G: one 25-mg injection of PG (PrePG) 3 d before 100 µg GnRH (Pre-GnRH), with the PrePG injection administered at the same time as PG-2 in the Pre-10 treatment. Cows were enrolled in a timed AI protocol (Ovsynch-56; 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 PG-2 or PrePG injections. Median DIM at scheduled timed AI was 74 d. The study began in September 2009 and was completed in September 2011. Cows detected in estrus before the scheduled timed AI were inseminated (early bred; EB). Pregnancy was diagnosed at d 32–39 and at d 60–67 after timed AI by transrectal ultrasound or palpation. Data were analyzed using procedure GLIMMIX, with herd as a random effect and with fixed effects of treatment (EB, Pre-10, PG-3-G), lactation number (1 vs. 2+), season (hot [June through September] vs. cool-cold [October through May]), DIM, estrus at timed AI (0 vs. 1), and all 2-way interactions with treatment. The P/AI at d 32–39 for EB (n = 472), Pre-10 (n = 1,247), and PG-3-G (n = 1,286) was: 31.4, 35.0, and 41.2% ($P = 0.071$); P/AI at d 60–67 was: 29.8, 32.2, and 37.3% ($P = 0.107$); and pregnancy loss: 5.1, 7.0, and 9.2% ($P = 0.523$), respectively. Season ($P < 0.001$) influenced P/AI at d 32–39 and d 60–67, but a treatment x season interaction was not detected (d 32–39: $P = 0.468$; d 60–67: $P = 0.195$). The P/AI for PG-3-G and Pre-10 treatments did not differ during cool weather (d 32–39: 46.8 vs. 44.3%; d 60–67: 41.6 vs. 41.1%), respectively, but during hot weather, P/AI in PG-3-G was greater than in Pre-10 (d 32–39: 35.9 vs. 26.7% [$P = 0.001$] or d 60–67: 33.2 vs. 24.4% [$P = 0.009$]), respectively. We concluded that presynchronizing estrous cycles with PG-3-G produced more P/AI than Pre-10 during hot weather.

Key Words: Presynch-10, PG-3-G, pregnancy per AI

M189 Effect of bovine somatotropin (bST) injected at fixed-timed insemination of Holstein cows exposed to an ovsynch protocol. A. Reyes-Gomez, C. F. Arechiga,* M. A. Lopez-Carlos, J. I. Aguilera, R. R. Lozano, R. M. Rincon, F. De la Colina, and F. J. Escobar, *Autonomous University of Zacatecas, Zacatecas, Mexico.*

Objective of present work was to determine the effect of growth hormone (GH), or bovine somatotropin (BST; Lactotropin, Elanco, Mexico), injected at fixed-timed insemination in Holstein cows exposed to an Ovsynch protocol. Holstein cows (n = 849) from Las Palomas Dairy at Aguascalientes, Mexico, were included in the study and randomly alloted into 4 experimental groups: Control (n = 244), Ovsynch (n = 225), Ovsynch+CIDR (n = 241) and Ovsynch+BST (n = 139). Cows received 2 prostaglandin injections (i.e., 26–32 d PP and 40–46 d PP, respectively). By 52–58 d PP cows were included into treatment: 1) Control (d 0, PGF2α; d 3–7 estrus detection and insemination). 2) Ovsynch (d 0, GnRH; d 7, PGFα; d 9, GnRH; d 10, Timed A.I.). 3) Ovsynch/CIDR (d 0, GnRH + CIDR; d 7, CIDR removal + PGF2α; d 9, GnRH; d 10, timed A.I.). 4) Ovsynch/BST (d 0, GnRH; d 7, PGF2α; d 9, GnRH; d 10, timed A.I. + BST). Data was analyzed by PROC FREQ of SAS using X-square and Fisher test. Ovsynch with or without CIDR or BST, increased estrus response and estrus detection (i.e., 97% vs. 68%; total average of 89%). BST at fixed-timed insemination (i.e., d 10, of Ovsynch protocol), increased pregnancy rates determined at 62 + 3 d postpartum by rectal palpation). (30.9% Ovsynch + BST vs. 24.4%, without BST), vs. 21.7% with conventional management or 19.1% using Ovsynch + CIDR. There were differences on estrus response ($P < 0.001$), pregnancy rates to first service and/or treatment and by 160 d PP ($P < 0.02$) and differences in PR disappear by 360 d PP ($P > 0.05$). BST administration at fixed- timed insemination during Ovsynch decreased the number of services per conception (NSC = 2.12 vs. 2.44 SC) compared with Ovsynch without BST; or to Control group (2.45). Contrarily, CIDR insertion increased the number of SC (2.58 SC; $P < 0.05$). In conclusion, a BST-injection at the time of insemination increased pregnancy rates and reduced services per conception in cows exposed to ovsynch.

Key Words: dairy cows, somatotropin, fixed-insemination

M190 Effect of adding a GnRH or PGF$_{2\alpha}$ between the Presynch and Ovsynch program for first AI in lactating dairy cows. R. G. S. Bruno*[1,2], A. M. Farias[1], J. A. Hernández-Rivera[1], A. E. Navarrette[1], D. E. Hawkins[2], and T. R. Bilby[1], *[1]Texas A&M University, College Station, [2]West Texas A&M University, Canyon.*

The objective was to evaluate the effect of 3 reproductive programs for first AI on fertility in lactating dairy cows. Lactating cows (n = 1521) from a dairy in Texas were presynchronized (PS) with 2 injections of prostaglandin (PG) given at 36 and 50 ± 3 DIM. At 50 ± 3 DIM, 915 multiparous and 606 primiparous cows were blocked by parity and assigned to 1 of 3 programs: GPG (n = 552) which initiated the Ovsynch protocol 14 d after PS, GGPG (n = 402) in which a GnRH injection was given 7 d after PS followed by the Ovsynch protocol 7 d later and PG7-GPG (n = 567) in which a PG injection was given 7 d after PS followed by the Ovsynch protocol 7 d later. Cows were AI based on signs of estrus (ED) beginning after the PS and, if AI, cows were removed from subsequent injections. Ovaries were examined and blood was sampled for progesterone levels on day of first GnRH and PG of Ovsynch. Pregnancy per AI (P/AI) was diagnosed at 36 and 66 d after AI. Overall 52.3% of cows were AI based on ED with the GGPG program having the least ($P < 0.01$) number of cows being identified in estrus (GGPG = 46.8 vs. GPG = 50.7 and PG7-GPG = 57.7%). Reproductive program did not affect ($P > 0.33$) overall P/AI at 33 and 66 d after AI (36d GPG = 34.1, PG7-GPG = 34.6 and GGPG = 31.3%; 66d GPG = 32.3, PG7-GPG = 31.9 and GGPG = 28.1%) or pregnancy loss ($P = 0.68$) between 36 and 66 d after AI. Cows AI upon ED had higher P/AI than TAI (ED = 37.9 vs. TAI = 28.8%, $P < 0.01$). However, treatment did not affect ($P > 0.61$) P/AI for cows AI upon ED or TAI (36d, GGPG = 34.1, PG7-GPG = 34.6 and GGPG = 31.3%; 66d GPG = 32.3, PG7-GPG = 31.9 and GGPG = 28.1%). Reproductive program affected ($P < 0.01$) the median DIM at first service (PG7-GPG = 59 vs. GPG = 68 and GGPG = 68 d). At beginning of Ovsynch, more GGPG cows had CL (GGPG = 72.7 vs. GPG = 54.4 and PG7-GPG = 46.4%, $P < 0.01$). However, treatment did not affect ($P = 0.26$) ovulation to first GnRH of Ovsynch. In conclusion, adding a GnRH injection 7 d after presynchronization reduced number of cows AI upon ED. Pregnancy per AI was not affected by reproductive program but adding a PG injection 7 d after PS decreased the median DIM at first AI.

Key Words: dairy cows, fertility, synchronization

M191 Application of progesterone insert for the induction of lactation in nonpregnant dairy cows or heifers. F. Rivera-Acuña*[1], R. C. Fierros[1], E. M. Prado[1], P. Luna-Nevarez[1], J. G. Aceves[1], L. R. Avendaño[2], and A. C. Correa[2], *[1]Instituto Tecnológico de Sonora, Ciudad Obregón, México, [2]Universida Autónoma de Baja California, Mexicali, México.*

The induced lactation of cows or heifers can be an alternative to reduce the rate of culling and to increase the economic benefits in a dairy operation. The objective of this study consisted of evaluating the effectiveness of replacing the traditional progesterone (P4) source with injections in programs of induced lactation by means of 2 P4 vaginal inserts containing 0.186 g each. During the study 15 animals, dairy cows and heifers were blocked by days dry and parity and were assigned at random to one of 3 treatments. Natural lactation (LN, n = 5) 2 P4 inserts (CRONI2, n = 5) injections only (INY, n = 5). The LN group initiated their lactation at the time of the calving date and was handled like dairy fresh cows. Treated groups during the first 7 d received P4 of different forms, one by means of daily i.m. injections 0.25 mg/kg/d and another one with 2 P4 vaginal inserts. Additionally blood was sampled during the same period to determine P4 levels. Furthermore during the first 14 d both groups received estradiol-17Î^{2} 0.1 mg/kg/d i.m. In addition 3 bST applications at intervals of 10 or 14 d during the study and lactation respectively and dexamethasone 10 mg/cow i.m. during the d 17, 18 and 19 and the lactation beginning to the 21 d. All the cows were submitted to the Co-Synch timed artificial insemination protocol (TAI) at 60 d in milk (DM) and were inseminated at 70 DM. The data was analyzed in random blocks with replications through the commands Repeated and Random Mixed procedure of SAS. The P4 levels during the first 7 d of treatment had a similar behavior ($P = 0.9$), the milk yield at 112 DM was highly significant ($P = 0.0001$) for LN and INY groups, the milk yield to the tip result ($P = 0.001$) in LN and INY groups. On the other hand there were no differences ($P = 0.59$) between the interval of beginning of the lactation to the tip of lactation either on days of persistence period. Milk yield during the persistence period result significant ($P = 0.0004$) for LN and INY groups. Finally the 305 d adjusted milk yield also were significant ($P = 0.0001$) for LN and INY groups. The BCS at TAI tended ($P = 0.08$) to be better for CRONI2 in relation to the other groups. The pregnancy per AI was better ($P = 0.71$) in the LN group (40%) compared other 2 (20%) each. Change P4 source by means of vaginal inserts during induced lactation programs did not improved lactation performance nevertheless the application of P4 by i.m. injections can show very similar results to natural lactation cows.

Key Words: induced lactation, progesterone, milk yield

M192 Enhancing endogenous progesterone during growth of the ovulatory follicle is positively associated with fertility in dairy cows treated with Presynch-11/Ovsynch, Double Ovsynch, and G6G/Ovsynch. F. Jiminez-Krassel,* J. P. Martins, B. S. Raghavendra, M. Kron, and J. R. Pursley, *Michigan State University, East Lansing.*

Presynchronization strategies that enhance ovulation to first GnRH of Ovsynch have a greater chance of enhancing progesterone during ovulatory follicle growth. The objectives of this study were to 1) determine the effect of 3 presynchronization strategies on pregnancy/AI (PAI) of lactating dairy cows, 2) determine the relationship between P4 at PG of Ovsynch on PAI, and 3) determine if decreasing time from follicular wave induction to luteolysis during Ovsynch enhances fertility. Cows (n = 2453) were assigned to 4 treatments by parity to receive Presynch-11 (P11), G6G/Ovsynch (G6G), and Double Ovsynch 7 or 5 d between G and PG of Ovsynch (DO7, DO5) beginning 39 to 51 DIM. Cows received final GnRH of Ovsynch 72 h after PG and AI 16 h later. Ovulation was diagnosed with ultrasound. Serum was collected at strategic intervals to assay P4. Pregnancy was diagnosed with ultrasound 32 d post-AI. Percent cows with P4 > 1 ng/mL were different between treatments at final PG of the Presynch program (65, 56, 78, 77%; $P < 0.01$, n = 2451), at first GnRH of Ovsynch (67, 76, 87, 87%; $P < 0.001$, n = 2453), and at PG of Ovsynch (84, 86, 93, 93%; $P < 0.001$, n = 2451) for P11, G6G, DO7 and DO5. Ovulation rate in response to the first GnRH of Ovsynch (80, 85, 89, and 86%; $P < 0.05$, n = 1878), percent cows with luteolysis after final PG of Ovsynch (96, 92, 93, and 43%; $P < 0.001$, n = 2223) were different for P11, G6G, DO7 and DO5. PAI in cows (n = 1802) that ovulated to first GnRH of Ovsynch and had P4 > 1ng/mL at PG and decreased to <0.3 ng/mL P4 72h later were 52, 50, 49, and 48% ($P = 0.7$) for P11, G6G, DO7 and DO5. Concentrations of P4 at time of PG injection was positively associated with pregnancy outcome: 33, 43, 44, 50, 51 and 57% PAI for P4 ranges of 1–2 (n = 171), 2–3 (n = 136), 3–4 (n = 201), 4–5 (n = 308), 5–6 (n = 327) and > 6 (n = 659) ng/mL P4 ($P < 0.05$ for P4 < 4ng/mL vs. P4 > 4 ng/mL). Enhancing progesterone during growth of the ovulatory follicle is associated with enhanced PAI of lactating dairy cows. Decreasing time from wave induction to luteolysis did not increase fertility.

Key Words: Ovsynch, progesterone, fertility

M193 Effect of progesterone (P4) supplementation after AI on circulating P4 and development of the corpus luteum (CL) in dairy cattle. P. L. J. Monteiro Jr.*[1], F. L. M. Silva[1], M. Borsato[1], G. P. Nogueira[2], G. B. Mourão[1], L. D. Silva[1], M. C. Wiltbank[1], and R. Sartori[1], *[1]University of São Paulo, Piracicaba, SP, Brazil, [2]São Paulo State University, Araçatuba, SP, Brazil, [3]University of Wisconsin-Madison, Madison, WI.*

Supplementation with P4 at 3 d after AI may improve fertility of lactating dairy cows, however, concerns have been expressed that early P4 supplementation may inhibit normal CL development or lead to early CL regression. The objective of this study was to evaluate CL development, by transrectal ultrasonography, and circulating P4, as measured by radioimmunoassay. Lactating dairy cows were synchronized (2 mg estradiol benzoate + CIDR on d 0 with prostaglandin F2α on d 7 and CIDR removal and 1 mg estradiol cypionate on d 8) and received timed AI (TAI). All cows that demonstrated synchronized ovulation (ovulated 1.5 to 3.5 d after CIDR removal; n = 42) were randomized to 1 of 2 treatments: No treatment (Control; n = 21) or CIDR supplementation starting on d 3 until d 20 after TAI (CIDR-treated; n = 21). Ultrasound was performed 2, 3, and 4 d after CIDR removal to confirm ovulation. Luteal volume was measured on d 4, 7, 11, 14, and 20 after TAI and circulating P4 concentrations on day of TAI and d 3, 4, 7, 11, 14, 17, 20, and 21. The procedure GLIMMIX of SAS was utilized for statistical analysis. The circulating P4 concentration demonstrated a tendency for an effect of P4 supplementation ($P = 0.07$) and an effect of day ($P = 0.001$) and an interaction of day by P4 supplementation ($P = 0.01$). This interaction was related to the largest difference due to CIDR-treatment during the earliest stages of supplementation (d 4: 0.9 ± 0.2 vs 2.2 ± 0.2 ng/mL and d 7: 2.7 ± 0.2 vs 3.6 ± 0.2 ng/mL). In contrast, the CL volume demonstrated an effect of day ($P < 0.001$) but there was no effect of P4 supplementation ($P = 0.921$) and no interaction of P4 supplementation by day ($P = 0.352$). For example, CL volumes on d 7 were 9,030.1 ± 126.4 vs 9,021.4 ± 129.1 mm^{3} for Control and CIDR-supplemented cows, respectively. Thus, P4 supplementation 3 d after TAI induced an early increase in circulating P4, but did not compromise CL development in lactating dairy cows. Acknowledgments: Pfizer, FAPESP and CNPq of Brazil.

Key Words: progesterone supplementation, corpus luteum, dairy cow

M194 Reproductive performance of lactating dairy cows managed for first service using timed artificial insemination with or without detection of estrus using an accelerometer system. P. M. Fricke,* A. Valenza, J. O. Giordano, M. C. Amundson, and G. Lopes Jr., *University of Wisconsin, Madison.*

Lactating dairy cows (n = 564) on a commercial dairy farm were fitted with accelerometers (Heatime, SCR Engineers Ltd., Netanya, Israel) at 21 DIM and were randomly assigned to one of 3 treatments: 1) Heatime + Ovsynch (HOv): cows received AI to detected estrus from the end of the VWP (50 DIM) until initiation of Ovsynch (GnRH-7d-PGF-56h-GnRH; cows initiated Ovsynch at 65 ± 3 DIM if not detected in estrus from 21 to 65 DIM, whereas cows initiated Ovsynch at 79 ± 3 DIM if detected in estrus from 21 to 50 DIM but not from 51 to 79 DIM); 2) Presynch-Ovsynch (PGF-14d-PGF-12d-GnRH-7d-PGF-56h-GnRH) + Heatime (PSOvH): cows received AI to estrus detected after the second PGF injection of Presynch at 50 DIM, and cows not detected in estrus initiated Ovsynch at 65 ± 3 DIM; and 3) Presynch-Ovsynch (PSOv): cows were monitored for estrus after the second PGF injection of Presynch, but all cows received TAI at 75 ± 3 DIM. Pregnancy outcomes were determined by the herd veterinarian using transrectal ultrasonography 39 ± 3 d after AI. Average days to first service (DFS) differed ($P < 0.0001$) among treatments with PSOvH cows having the fewest ($P < 0.0001$) DFS (62.4 ± 8.3 d), followed by HOv cows (67.4 ± 10.7 d) and finally PSOv cows (74.7 ± 2.1 d). Overall, pregnancies per AI (P/AI) did not differ ($P = 0.58$) among treatments for HOv cows (33%; 64/194), PSOvH cows (29%; 57/194), or PSOv cows (34%; 60/176). For HOv cows, 57% were detected in estrus (P/AI = 33%), whereas 43% received TAI (P/AI = 33%). For PSOvH cows, 71% were detected in estrus (P/AI = 26%), whereas 29% received TAI and had P/AI of 36.8% (21/57). For PSOv cows, 76% showed estrus after PGF but completed the protocol and received TAI (P/AI = 35%), whereas 24% did not show estrus and received TAI (P/AI = 30%). Based on these preliminary results, the fewest DFS occurred when cows were submitted to a Presynch-Ovsynch protocol combined with detection of estrus using the Heatime system, whereas no overall differences in P/AI were observed among the 3 management strategies for submitting cows to first service.

Key Words: Heatime, Presynch-Ovsynch, timed AI

M195 Accuracy of pregnancy diagnosis outcomes using transrectal ultrasonography 29 days after artificial insemination in lactating dairy cows.

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Our objective was to assess the effect of different criteria to determine pregnancy status on the accuracy of transrectal ultrasound (TU) 29 d after a timed AI in lactating dairy cows in a commercial setting. Pregnancy status was determined 29 d after timed AI (TAI) using transrectal ultrasonography (TU; Easi-scan, BCF Technology Ltd.) based on the following criteria: presence or absence of a corpus luteum (CL), presence, absence, volume and appearance of uterine fluid (UF) typical for a 29 d conceptus, presence or absence of an embryo with a heartbeat. Cows were classified as 1) non-pregnant (NP): presence or absence of a CL, absence of UF, or insufficient UF, and absence of an embryo; 2) pregnant (P): CL present, normal UF, and no embryo; 3) pregnant embryo (PE): CL present, normal UF, and at least one embryo visualized; and 4) questionable pregnant (QP): CL present, and one or more of the following: UF, insufficient UF, and either no embryo or a non-viable embryo. At 39 and 74 d after TAI, pregnancy status was determined using transrectal palpation (TP). Overall, 802 cows were classified as NP 29 d after TAI, whereas 799 cows were classified as NP 39 d after TAI resulting in misdiagnosis rate of 0.5% (4/802) for TU 29 d after TAI. At 29 d after TAI, 1,116 cows were classified as either P (28.9%; n = 322), PE (67.9%; n = 758), or QP (3.2%; n = 36). Among QP cows, 69.4% (25/36) were classified as NP 39 d after TAI, and an additional 45.5% (5/11) of the cows were classified as NP 74 d after TAI. For cows classified as P and PE using TU 29 d after TAI, more ($P < 0.0001$) P (17.7%) than PE (4.0%) cows were classified as NP using TP 39 d after TAI. Similarly, more ($P = 0.0004$) P (12.1%) than PE (5.4%) cows diagnosed at 39 d after TAI using TP were classified as NP 74 d after TAI. From the initial pregnancy exam at 29 d to the last exam at 74 d after TAI, more ($P < 0.0001$) P (27.6%) than PE (9.1%) cows were diagnosed as NP. Cows classified as P using TU 29 d after TAI were 3.8 (95% CI = 2.7 to 5.4) times more likely to be classified as NP than PE cows 74 d after TAI. We conclude that the accuracy of TU outcomes are increased when an embryo is visualized compared with TU outcomes based only on the presence of a CL and the volume of uterine fluid. Supported by Hatch project WIS01171.

Key Words: transrectal ultrasonography, pregnancy diagnosis, dairy cattle

M196 Early detection of pregnancy-specific protein B (PSPB) following conception in Holstein heifers.

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Pregnancy-specific protein B (PSPB) is produced by ruminant placentae during pregnancy, and can be detected in maternal blood by a specific ELISA. The objective of this study was to determine the earliest appearance of PSPB after AI and when it can reliably be utilized to determine pregnancy status in Holstein Heifers as compared with the standard ultrasonography method. One hundred twenty-one Holstein replacement heifers were synchronized and subsequently submitted to timed-AI. Blood samples from all heifers were obtained at initiation of the experiment (at the time of AI, d 0), and again on d 18, d 25 and d 32 after AI for PSPB concentration. Pregnancy status was then determined by ultrasonography on d 32 after AI. The results of the PSPB data were then categorized into non-pregnant and pregnant animals based on ultrasonography results. Data were analyzed using a mixed model ANOVA for repeated measures. There was an effect of pregnancy status and pregnancy status × time ($P < 0.01$) on PSPB. Mean PSPB concentrations, expressed as optical density (OD), did not differ between pregnant and non-pregnant heifers on d 0 or d 18. However, PSPB concentrations increased by 1.7 fold, and were greater ($P < 0.01$) in pregnant compared with non-pregnant heifers on d 25 (0.083 ± 0.002 vs. 0.138 ± 0.003; $P < 0.01$) and d 32 (0.079 ± 0.002 vs. 0.296 ± 0.003; $P < 0.01$). Similarly, PSPB levels expressed as ng/mL did not differ on d 0 or d 18, but were greater ($P < 0.01$) in pregnant compared with non-pregnant heifers on d 25 (0.006 ± 0.031 vs. 0.290 ± 0.038; $P < 0.01$) and d 32 (0.026 ± 0.030 vs. 1.124 ± 0.037; $P < 0.01$). These results indicate that PSPB increases overtime and can be detected as early as d 25 after breeding and potentially used to identify non-pregnant heifers.

Key Words: PSPB, pregancy detection, heifers

M197 Possible associations between ova-embryos characteristics in early lactating cows and subsequent reproductive performance.

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Ova-embryos (348) from 321 single ovulating Holstein cows were recovered 6 d after AI. Objectives were to determine if previously collected ova-embryo influences future reproductive outcome. Cows were enrolled in a presynchronized Ovsynch program starting at 30 ± 3 DIM and only cows that responded to the first GnRH of the Ovsynch were included. The BCS was measured at enrollment; cyclicity was monitored by ultrasonography. After ova-embryos collection, cows were subjected to a timed AI protocol. Cows were then re-inseminated if in estrus or resynchronized after diagnosed non-pregnant. Pregnancy at first AI, pregnancy loss at first AI, proportion of pregnant cows at 300 DIM, number of AI and interval to pregnancy were analyzed according to grade of ova-embryos collected from the same cows. Ova-embryos were classified based on fertilization and grade quality (IETS). The following combinations of fertilization and embryo grade quality were used to predict fertility responses of dairy cows: fertilized vs. unfertilized; grade 1 vs. remaining; grades 1 and 2 vs. remaining; grades 1 to 3 vs.

remaining. Data were analyzed using GLM, LOGISTIC, and LIFETEST procedure of SAS. Cows that yielded grades 1–3 embryos had a greater number of AI to become pregnant (3.2 ± 0.2 vs. 2.3 ± 0.3), had more median days open (117 vs. 90 d) compared with other structures, but proportion of cows pregnant at 300 DIM was unaltered (90.4 vs 97.9%). Conversely, cows that yielded fertilized ova compared with unfertilized ones required fewer AI (3.0 ± 0.1 vs. 3.8 ± 0.3) and had fewer median days open (109 vs. 122 d) and greater proportion of pregnant cows at 300 DIM (91.8 vs 81.2%). No other combinations of fertilization and embryo quality were associated with number of AI, days open or conception rate at first AI or at 300 DIM. In conclusion, embryo quality in early lactation does not seem to be related to subsequent reproductive performance, but fertilization was associated with reduced subsequent days open and greater conception rate. The genetic potential to produce fertilized ova, but not necessarily good quality embryos, seems to influence reproductive performance.

Key Words: embryo, fertilization, genetic potential

M198 Effects of induced clinical and subclinical mastitis on oocyte developmental competence in bovine. S. Asaf[1], O. Furman[1], G. Leitner[2], D. Wolfenson[1], and Z. Roth*[1], *[1]The Robert H. Smith Faculty of Agriculture, Food and Environment, the Hebrew University, Rehovot, Israel, [2]The Veterinary Institute, Bet Dagan, Israel.*

Clinical and subclinical mastitis can lead to decreased fertility in cows. We examined the effects of gram-positive exosecretions (G+; *S. aureus* ex.) or gram-negative (G-; *E. coli* LPS) toxin induced mastitis on oocyte developmental competence. Two models were established to simulate short-term, acute, clinical mastitis and long-term, subclinical mastitis. Holstein cows were synchronized with GnRH and $PGF_{2\alpha}$ to induce development of a preovulatory follicle. Follicular fluid (FF) was aspirated by transvaginal probe from (1) uninfected cows, (2) cows with clinical mastitis induced by G+ or G-, and (3) cows with subclinical mastitis induced by G+ or G-. FFs were used as maturation medium for IVF procedures. Oocytes were matured (FF, 22 h, 5% CO_2, 38.5°C), fertilized (18 h, 38.5°C, 5% CO_2), and cultured for 8 d (KSOM, 5% CO_2, 5% O_2, 38.5°C). Cleavage rate and proportion of oocytes developed to the blastocyst stage were recorded 44 h and 7 to 8 d post-fertilization. Apoptotic index for blastocysts was determined by TUNEL assay. Total RNA and poly(A) mRNA were isolated from mature oocytes and 4-cell-stage embryos and subjected to real-time PCR for *COX2*, *POU5F1*, *GLUT1*, *HSF1* and *GDF9* genes. Maturation in FF aspirated from clinical- or subclinical-mastitic cows reduced ($P < 0.05$) the cleavage rate and the proportion of developing embryos and increased ($P < 0.05$) the proportion of apoptotic cells in blastocysts. Alterations in gene expression were evident in embryos developed from oocytes matured in FF obtained from mastitic cows, with the most prominent impairments being in *COX2* expression. While clinical G- mastitis decreased *COX2* expression in MII-stage oocytes ($P < 0.05$), both clinical G- and G+ mastitis and subclinical G- and G+ mastitis increased *COX2* expression in 4-cell-stage embryos ($P < 0.05$). In addition, both clinical G+ and subclinical G+ mastitis reduced *OCT4* expression in 4-cell-stage embryos ($P < 0.05$). The findings indicate a deleterious effect of FF obtained from both clinical- and subclinical-mastitic cows on oocyte developmental competence. The disruptive mechanism seems to be associated with alteration in embryonic gene expression.

Key Words: mastitis, oocyte, developmental competence

M199 Assessing the relationships of prostaglandin E2 in uterine flush fluid, peripheral blood prostaglandin E2 and progesterone with pregnancy outcome in dairy cattle. J. L. Fain*[1], M. W. Overton[2], D. J. Hurley[2], and G. P. Birrenkott[1], *[1]Clemson University, Clemson, SC, [2]University of Georgia, Athens.*

Uterine inflammation can negatively affect animal welfare, milk production and rebreeding capacity in dairy cattle. The objectives of the current work were to investigate the relationship between prostaglandin E2 (PGE) found in uterine flush fluid to that found in peripheral blood and their potential effect on reproductive success in postpartum dairy cows. Animals (n = 34) were enrolled in a presynch program beginning at 35 ± 3 d postpartum with a $PGF_{2\alpha}$ injection followed by a second at d 49. Cows then received the Ovsynch protocol (100µg GnRH d 60, 25mg $PGF_{2\alpha}$ d 67, 100µg GnRH d 69 with TAI 16–18 h later on d 70). Uterine flush samples of both horns were collected from animals before the $PGF_{2\alpha}$ injection of the Ovsynch protocol. All animals received 100µg of GnRH on d 28 post TAI for the resynchronization program. Any animals open to the first TAI as determined by transrectal ultrasonography on d 35 had a second flush sample collected from the uterine body while receiving 25mg $PGF_{2\alpha}$ with an injection 100 µg GnRH following on d 37 and TAI 16–18 h later on d 38. Cows were then monitored for and bred off standing estrus with any animals not seen in estrus having pregnancy confirmed. If open to a third breeding, a third and final flush sample was collected. Blood samples were collected at d 35, 49, 60 and 67 post-parturition and d 14, 18, 22, 25, 28, 32 and 35 post TAI for P4 and PGE analysis. Additional blood samples were collected before each flush for testing by BioPRYN and for PGE. Blood and uterine PGE values shared no relationship with P4 concentrations. Significantly higher P4 values were found on d 18 post TAI in animals that were pregnant ($P < 0.05$). Though numerically there was evidence that reduced PGE value increased the likelihood of pregnancy, neither the PGE values in uterine flush fluid nor blood were significant predictors of pregnancy success at the 1st, 2nd or 3rd breeding or the likelihood of securing pregnancy after 3 breedings ($P > 0.05$). There was a high correlation between uterine PGE values and BioPRYN optical density readings ($P < 0.05$). Though the second flush showed a strong correlation between blood PGE and uterine flush PGE when SCC was added as a covariate ($P < 0.05$), this was not consistent across flushes ($P > 0.05$). Correlation potentials with BioPRYN as well as blood PGE would lend a less complicated method for detection of uterine inflammation as assessed by PGE.

Key Words: prostaglandin E2, dairy, uterine inflammation

M200 Effect of oral or subcutaneous administration of vitamin E and selenium on milk quality and reproductive function of Holstein cows. C. Garcia-Barrios, M. Rodriguez-Loera, C. F. Arechiga, M. A. Lopez-Carlos, J. I. Aguilera, R. M. Rincon, H. Rodriguez-Frausto, D. Rodriguez-Tenorio, and Z. Cortes,* *Universidad Autonoma de Zacatecas, Zacatecas, Mexico.*

Aim of this study was to determine factors affecting milk quality and reproductive efficiency of Holstein dairy cows in response to subcutaneous or oral administration of vitamin E and selenium. Cows (n = 159) were randomly allotted into 3 groups: 1) Control cows (n = 53; non-injected or supplemented cows); 2) Cows (n = 53), injected subcutaneously with 10 mL of vitamin E and selenium at days −45, −22, 0, before parturition and d 15 and 30 after parturition, (each injection contained 600 mg of vitamin E and 109.5 mg of selenium (BeefSe, Aranda

Labs., Queretaro,Mexico) 3) Cows (n = 53), were supplemented orally with 20 g of Selenio E (Ripoll, Mexico, D.F.), containing 2,500 mg of vitamin E/cow/d, and 3 mg of selenium/cow/d) from days −45 before parturition through d 30 after parturition. Milk quality and reproductive efficiency of cows was evaluated. Data obtained include determination of fat, protein, lactose, total solids (TS), non-fat solids (NFS) using a Milkoscan equipment (Foss, Hillerød, Denmark). Reproductive data were obtained and analyzed using PROC MIXED of SAS. The model includes the effects of season, lactation, treatment and treatment by season, a REML and PPDIFF methods were utilized considering days as repeated measurements. In conclusion, milk components were reduced during autumn ($P < 0.05$). However, antioxidant administration during the peripartum period, by subcutaneous injection of vitamin E and selenium were effective preventing milk protein reduction during autumn. Moreover, oral supplemented administration of vitamin E and selenium did not prevented seasonal reductions of milk components. Whereas, reproductive function was improved during autumn

Key Words: dairy cow, milk components, reproduction

M201 Effects of supplementation with different PUFA during the postpartum periods of early lactating dairy cows, estradiol concentration and luteal function.

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Ninety high-yielding multiparous Holstein dairy cows with no over clinical illnesses were blocked according to calving date and parity. Cows were assigned randomly to be fed either 1-soybean whole roast (S, n = 30), or 2-linseed (L, n = 30), or 3-palm oil as a source of saturated fatty acid (C, n = 30) from calving until d 60 postpartum (dpp). There was no difference between groups (mean ± SEM) in parity (3.0 ± 1.90) or BCS at calving (3.2 ± 0.07). Beginning at 30 DIM, cows were induced into a synchronized ovulatory cycle with 2 injections of PGF2α 14 d apart. Blood was collected daily; from the day that second PGF2α inject until the day of next estrous. Ovarian follicular development was monitored daily by transrectal ultrasonography with a real-time linear scanning ultrasound diagnostic system (B mode; Piemedical, Falco 100; 8 MHz transducer). Ultrasonography was performed once daily from the day that second PGF2α inject until the day of next estrous. Data were analyzed with PROC MIXED of SAS. Cows offered diet S and L had a greater size of corpus luteum than cows offered Diet C. There were no significant differences between groups L and S in size of corpus luteum (17.70 ± 0.86 and 18.30 ± 0.86 mm respectively; $P < 0.05$). Although mean serum progesterone concentrations on d 17 of synchronized cycle were higher in cows fed S (8.40 ± 0.10 ng/ml) or L (9.10 ± 0.20 ng/ml) than cows fed palm oil (6.30 ± 0.15 ng/ml, $P < 0.01$), there were no significant differences between groups L and S groups. Mean estradiol concentration was higher at the time of estrus in cows fed S or L compared with those fed palm respectively (12.60 ± 0.016, 13.00 ± 0.08 vs. 10.10 ± 0.09 pg/mL; $P < 0.05$) in the cows.

Key Words: dairy cows, n-3 and n-6 fatty acid, luteal function

M202 Hepatic patatin-like phospholipase domain-containing protein 3 mRNA expression is increased during feed restriction and in transition dairy cows.

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Patatin-like phospholipase domain-containing protein 3 (PNPLA3), commonly known as adiponutrin, is part of a novel subfamily of triglyceride lipase enzymes with potential effects on triglyceride metabolism in adipose and hepatic tissues. In rodents and humans, PNPLA3 mRNA expression is suppressed during fasting and is increased by subsequent refeeding. The bovine predicted PNPLA3 sequence has been identified; however, expression of this gene has not yet been examined. The objectives of this study were to verify expression of the bovine predicted PNPLA3 gene and to determine response to whole-animal energy balance. Genomic DNA was isolated from liver biopsy samples collected from cows at +28 d relative to calving (DRTC) and the predicted PNPLA3 region was amplified via PCR and visualized to confirm expression. To determine if energy balance alters expression of PNPLA3, RNA was isolated and quantified in liver samples from mid-lactation cows (n = 5) after a 5-d ad libitum period and after a subsequent 5-d 50% feed restriction period, to determine if energy balance altered expression. Expression of hepatic PNPLA3 was decreased ($P < 0.05$) after a period of feed restriction (8.14 vs. 1.08 ± 2.17, arbitrary units, ad libitum vs. fasted). Dairy cows commonly experience negative energy balance during the transition to lactation; therefore, PNPLA3 expression was also examined in liver biopsy samples cows (n = 16) at −14, +1, +14, and +28 DRTC. Expression was decreased ($P < 0.05$) at +1 and +14 DRTC compared with −14 DRTC (23.35, 7.28, 10.17, and 14.5 ± 4.9, arbitrary units, −14, +1, +14, and +28 DRTC, respectively). The data indicate increased hepatic PNPLA3 expression that is part of the adaptive response to the transition to lactation and suggests a link to negative energy status associated with this interval.

Key Words: patatin-like phospholipase domain-containing 3, adiponutrin, energy balance

M203 Changes of the serum and milk proteome in lactating dairy cows duodenal infused with α-linolenic acid.

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This study investigated the effect of a duodenal infusion of a C18:3 free fatty acid on the serum and milk proteome of lactating dairy cows. Four primiparous Holstein cows were fitted with duodenal cannulas and received 0, 100, 200, 300, and 400 g/d of α-linolenic acid (LNA) in a 2-treatment crossover design. Blood and milk were collected for determination of protein composition by 2-dimensional gel electrophoresis. Quantitative analysis of protein dyeing density were prosessed by Quantity One 4.6. Alteration of protein spots were detected and identified using matrix-assisted laser desorption/ionization time-of-flight/time-of-flight tandem mass spectrometry (MALDI-TOF-TOF MS). Data were analyzed by SPSS 16.0. Serum haptoglobin levels, and milk β-casein A2, αs1-casein variant, and albumin, did not differ in cows after infusion of 0, 100, 200 and 300 g/d of LNA, but were increased after the cows received duodenal infusion of 400 g/d of LNA. Western blot analysis of haptoglobin expression in the serum confirmed the alterations in protein expression seen using mass spectrometry. This study demonstrated that infusion of high doses of LNA by duodenal cannula can result in metabolic stress to the cows and changes in milk composition.

Key Words: linolenic acid, proteome, dairy cow

M204 Investigation of the relationship between resumption of ovarian cyclicity and plasma nutritional markers in lactating dairy cows.

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Previous reports have shown the association between metabolic hormones, ovulation intervals and reproductive performance. The objective of this study was to investigate the relationship between the resumption of ovarian activity and plasma nutritional markers including glucose, NEFA, plasma urea nitrogen (PUN), cholesterol and β-hydroxybutyrate (BHBA). Forty-three lactating Holstein cows, housed in a free stall barn, were randomly selected from a commercial herd. From wk 2 to wk 7 postpartum, weekly ultrasonography and blood sampling was performed to characterize ovarian status, plasma metabolites, and blood progesterone. The occurrence of the first postpartum ovulation was determined by the analysis of plasma progesterone and confirmation of ovulation using visualization of a corpus luteum by ultrasonography. Based on plasma progesterone concentration and ovarian status, cows were divided into 2 treatment groups, cows that ovulated ≤25 DIM were designated early ovulators (EO) and cows that ovulated >25 DIM were considered late ovulators (LO). Data were analyzed using mixed model ANOVA for repeated measures. The mean interval to 1st ovulation for EO was 16.7 d, and for LO was 34.7d. Mean BCS was greater ($P < 0.05$) for EO than LO and (3.3 ± 0.1 vs 2.9 ± 0.1). There were effects of week ($P < 0.01$) and week by group interaction ($P < 0.05$) on blood cholesterol. Mean blood cholesterol increased over time for both EO and LO, however, mean cholesterol concentrations between wk 2 and 3 were less ($P < 0.05$) for EO compared with LO. Across all weeks, the mean glucose concentrations tended to be greater ($P = 0.06$) in EO than LO. There was no effect of group, week, or their interaction on blood BHBA. Blood NEFA did not differ between EO and LO, however, the mean concentration of NEFA decreased over time ($P < 0.01$) for both groups. Mean PUN was not different between EO and LO throughout the experiment. These results provide evidence that the 1st postpartum ovulation may be associated with blood glucose and cholesterol during the early postpartum period and may be indicative of the resumption of reproductive function in lactating dairy cows.

Key Words: blood metabolites, ovulation, dairy cows

M205 Insulin responses in dairy cows with different fat mobilization during early lactation.

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Dairy cows differ in fat mobilization around calving. Insulin has antilipolytic effects and may antagonize body fat mobilization, but insulin action is probably impaired in cows early postpartum (pp). The objective of the present study was to compare insulin responses ante partum (ap) and pp in cows differing in fat mobilization. German Holstein cows (>10,000 kg milk/305 d; ≥ 2nd lactation) were classified by liver fat concentration (LFC) pp in low (L; < 240 mg total fat/g DM; n = 9) and high (H; > 240 mg total fat/g DM; n = 10). Cows were studied from dry off up to 30 DIM and were fed TMR ad libitum. DMI and milk yield were recorded daily. Liver biopsies were taken on d 3, 18, and 30 pp to measure LFC. Hyperglycemic (HGC) and euglycemic-hyperinsulinemic clamps (EGHIC) were performed in wk 5 ap and wk 3 pp to measure pancreatic and peripheral insulin responses. In HGC glucose was infused to reach plasma concentrations 50% higher than basal glucose concentrations. In EGHIC insulin (6 mU/kg BW × min) was infused for 6 h and plasma glucose was kept constant according to pre-clamp concentrations. Blood samples were taken to measure plasma glucose and insulin and glucose infusion rates (GIR) were determined during steady-state conditions. Before and during the EGHIC pp [U-^{13}C]-glucose (prime: 5.4 μmol/kg BW; infusion: 7.5 μmol/[kg BW × h] for 9 h) was infused to measure of endogenous glucose production (eGP), glucose turnover (GT), and oxidation (GOx). Data were analyzed by Mixed Model of SAS with LFC and time as fixed effects. LFC differed between groups ($P < 0.01$) (H: 306 ± 0.2 mg/g; L: 195 ± 0.1 mg/g). Basal glucose and insulin concentrations were higher ($P < 0.05$) ap than pp. In HGC GIR was higher ($P < 0.001$) and insulin release was lower ($P < 0.01$) pp than ap. In EGHIC GIR tended to be higher ($P < 0.1$) in H than L. During insulin infusion pp eGP decreased to 19% of pre-clamp eGP. GT was higher ($P < 0.05$), but GOx relative to glucose turnover tended to be lower ($P < 0.1$) in H than L. Insulin action was not affected by elevated fat mobilization pp but stimulation of insulin secretion was impaired pp. Supported by DFG, Germany.

Key Words: dairy cow, glucose, insulin response

M206 Effects of heat stress and plane of nutrition on adipose tissue metabolism-related gene expression in lactating Holstein cows.

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During heat-stress (HS) in lactating dairy cows, adipose tissue appears to become refractory to lipolytic signals whereas pair-fed cows employ mechanisms allowing lipid mobilization to spare glucose utilization in peripheral tissues. Despite this, little is known regarding the effects of HS on metabolic gene expression in adipose tissue. Multiparous cows (n = 12; parity = 2, 305 ± 33 DIM; 665 ± 18 kg BW) housed in climate chambers were fed a TMR consisting primarily of alfalfa hay and steam-flaked corn and subjected to 2 experimental periods (P): 1) thermoneutral (TN) conditions (18°C, 20% humidity) with ad libitum intake for 9d and 2) either HS conditions (cyclical temperature 31–40°C, 20% humidity: min THI = 73, max THI = 86) fed for ad libitum intake (n = 6), or TN conditions, pair-fed (PF in TN conditions, n = 6) for 9d. Rectal temperature (Tre) and respiration rate (RR) were measured thrice daily at 0600, 1400 and 1800h. To evaluate adipose tissue gene expression, biopsies were obtained from the tail-head region at the end of each period and total RNA isolated for real-time PCR analyses. Data was normalized using β-actin as a control gene and analyzed by the Proc Mixed procedure in SAS. During P2, HS cows had a 1.8°C increase in Tre and a 3-fold increase in RR compared with TN cows ($P < 0.01$). Pair feeding did not alter Tre or RR. Heat stress reduced ($P < 0.01$) DMI by 20% and by design PF cows had similar intake reductions. Milk yield was decreased 12% during HS and 8% in PF cows. Adipose triglyceride lipase (ATGL), lipoprotein lipase (LPL), and pyruvate carboxylase (PC) significantly decreased ($P < 0.05$) during HS compared with TN, but was unaffected by PF. Fatty acid synthase (FAS) mRNA abundance decreased during PF ($P < 0.05$) but was unchanged by HS. In contrast, gene expression of β1 adrenergic receptor (AR) and perilipin (PLIN) tended to increase ($P = 0.10$) while β2 AR and the truncated leptin receptor (ObRa) increased significantly during PF ($P < 0.05$) but not HS. These results indicate that HS directly alters adipose tissue metabolism-related gene expression independently of reduced plane of nutrition. This project was supported by NRI Competitive Grant no. 2008-35206-18817 and AFRI Competitive Grant no. 2010-65206-20644 from the USDA NIFA.

Key Words: heat stress, adipose, metabolism

M207 Relevance of mineralocorticoid receptors in different fat depots of dairy cows supplemented with CLA.

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Adipose tissue (AT) consists of different cell types, among those preadipocytes, marked by preadipocyte factor-1 (Pref-1), are crucial for differentiation into mature adipocytes. This process is induced by glucocorticoids mediating their effects through the glucocorticoid (GR) and mineralocorticoid receptor (MR). Whether bovine adipocytes differentiate through GR or MR activation is not known. To investigate the main pathway of adipocyte differentiation, 25 primiparous Holstein cows were divided into control (CON, n = 15) and CLA group (n = 10), slaughtered on 1, 42 and 105 DIM. CLA cows received 100 g/d of a CLA-mixture (Lutrell BASF) from 1 DIM until slaughter. CON cows were fed with 100 g/d of a fatty acid mixture (Silafat BASF) without CLA. Samples from 3 visceral (vc) and 3 subcutaneous (sc) AT depots were obtained. MR and Pref-1 were localized on paraffin embedded sections by immunohistochemistry. Data are given as percentage of positive cells per total cell number (mean ± SEM) and were correlated by Pearson correlation (SPSS 19). Both MR and Pref-1 were detected exclusively in the stromal vascular cell fraction (SVF) of all fat depots, while GR was detected solely in adipocytes. The mean values were 1.05 ± 0.1% and 2.99 ± 0.2% for Pref-1 and MR, respectively. Significant correlation coefficients between MR and Pref-1 are given in the table ($P \leq 0.05$). We assume that bovine adipocyte differentiation is mediated through MR, for MR and Pref-1 are allocated to the SVF. In vc AT lipolysis in early lactation might be compensated by preadipocyte differentiation and seems to vary between different AT depots.

Table 1. Correlation coefficients (r) between mineralocorticoid receptor (MR) and Pref-1 (only significant data are shown; $P \leq 0.05$)

	CON	CON	CLA	CON	CLA
DIM:	1	42	42	105	105
vc mesenteric	0.916	—	—	0.914	—
vc retroperitoneal	0.905	—	—	—	—
vc omental	—	0.883	—	—	0.885
sc tailhead	—	0.917	—	—	—
sc withers	—	0.897	—	—	—
sc sternum	—	0.896	—	—	—

Key Words: preadipocyte, mineralocorticoid receptor, dairy cow

M208 The effects of a soybean and canola diet during pre-pubertal growth on dairy heifer fertility.

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Dietary phytoestrogens (such as those in soybean) can have detrimental influences on the rate of sexual maturation and reproductive physiology of animals; however, the precise effect of phytoestrogens on reproductive function in dairy cattle has not been fully elucidated. This study examined the effects of feeding a soybean (SOY) and canola (CAN) calf starter diet during pre-pubertal development on the fertility of Holstein dairy heifers. At 8 wk of age calves (n = 24) were randomly assigned to receive CAN or SOY until 24 wk of age. Calves were fed approximately 1.5 kg/calf/day and ad libitum hay and water. At 24 wk of age heifers were group housed and fed a TMR of grass and corn silage and hay. At approximately 60 wk of age heifers were synchronized for AI using Double Ovsynch (GnRH–$PGF_{2\alpha}$, 7 d–GnRH, 3 d followed 7 d later by GnRH–$PGF_{2\alpha}$, 7 d–GnRH 48 h–AI 16 to 20 h). Blood samples were collected on d −3, 0 (AI), 7, and 14 for progesterone (P_4) analysis. Transrectal ultrasonography was performed twice daily for 3 d, starting 24 h before AI, to determine timing of ovulation and ovulatory follicle size and on d 42 for pregnancy diagnosis. Ovarian and hormone data were analyzed using ANOVA; pregnancy rate (PR) was analyzed using logistic regression. The timing of ovulation following the last GnRH injection was not different (35.9 ± 2.6 h; $P = 0.39$). However, 1 CAN and 2 SOY heifers did not ovulate. The maximum ovulatory follicle diameter was similar (15.3 ± 0.5 mm; $P = 0.58$). The CAN treatment had greater P_4 concentrations than the SOY on d −3 (4.9 ± 0.5 ng/mL vs. 2.7 ± 0.5 ng/mL; $P = 0.003$). There were no differences in P_4 concentrations on d 7 (2.3 ± 0.2 ng/mL $P = 0.42$) or 14 (2.6 ± 0.3 ng/mL; $P = 0.20$). Pregnancy rates were 66.7% vs. 41.7% ($P = 0.62$) for CAN and SOY, respectively. Concentrations of P_4 on d −3 ($P = 0.10$) and 7 ($P = 0.09$) tended to influence PR. In summary, there were no differences between treatments for the timing of ovulation, ovulatory follicle size, and post-AI P_4 concentrations. However, P_4 concentrations on the day of $PGF_{2\alpha}$ treatment of Ovsynch TAI tended to influence PR and on this day CAN treatment had higher P_4 concentrations.

Key Words: phytoestrogens, dairy heifers, fertility

M209 Reproduction in grazing dairy cows treated with 14-d CIDR for presynchronization before a timed AI (TAI) compared with AI after observed estrus.

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Progesterone-releasing devices (CIDR; Pfizer, New York, NY) inserted for 14 d are used to presynchronize the estrous cycle for TAI in beef heifers (14-d CIDR-PG program). The objective was to test a similar program in dairy cows by measuring first service conception rates (FSCR), pregnancy rates, and time to pregnancy compared with a control (AI after observed estrus). Postpartum cows (Holstein, Jersey or crossbred; n = 1363) from 4 grazing dairy farms were assigned to one of 2 programs: 14dCIDR_TAI [TRT; CIDR in, 14 d, CIDR out, 19 d, $PGF_{2\alpha}$ (5 mL Lutalyse, Pfizer), 56 h, GnRH (2 mL Factrel, Pfizer), and then 16 h, TAI; n = 737] or control [AI after observed estrus; reproductive program with $PGF_{2\alpha}$ (cycling cows) and CIDR (non-cycling cows) to synchronize estrus with the start of the breeding season; n = 626]. Body condition (BCS; 1 to 5; thin to fat) was scored at trial start. The interval from the start of breeding to first AI was shorter for TRT vs control (3.0 ± 0.2 vs 5.3 ± 0.2 d; $P < 0.001$) but TRT cows had lesser FSCR than control (48 vs 61%; $P < 0.05$). Farm affected ($P < 0.002$) FSCR (69, 50, 58, and 51% for farms 1 to 4) but there was no treatment by farm interaction ($P > 0.10$). BCS affected FSCR (50, 55, and 62%; 2, 2.5, and 3; $P < 0.05$). Cows that either calved the year before (carry-over) or that calved early in the calving season had greater FSCR than cows that calved later in the calving season (55, 61, and 42%, respectively; $P < 0.001$). The percentage of cows pregnant to AI (6 wk breeding season) was similar for TRT and control (65 vs 70%; $P > 0.10$) but farm (81, 66, 69, and 62; $P < 0.01$) and time of calving (70, 76, and 56%; carry-over, early, and late; $P < 0.001$) affected the percentage. Survival analyses showed an initial advantage for TRT [more cows inseminated ($P < 0.001$) and more pregnancies achieved ($P < 0.07$) early in the breeding season] that was not maintained over time. Conclusions were that the 14dCIDR_TAI program achieved acceptable FSCR (48%) and overall 6 wk pregnancy rates (65%) for a TAI but did not surpass a control program that employed AI after observed estrus (61 and 70%; respectively).

Key Words: dairy, cow, timed AI

M210 Hormonal therapies on repeat breeder cows of a dairy production unit of central Mexico (Aguascalientes State).

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The aim of this study was to determine the factors that influence the reproductive efficiency of Holstein repeat-breeder cows (n = 320) in response to 5 different protocols or treatments used in an intensive dairy production unit at Aguascalientes State. Hormonal therapies were: 1) control; 2) GnRH at d 5 post-AI; 3) hCG at d 5 post-AI; 4) GnRH at d 5 post AI + CIDR; 5) GnRH at d 11 post-AI. Data was recorded from February to September 2011. Information obtained was analyzed by Chi-squared using the SAS statistical package (SAS, 2006). Subsequently, orthogonal contrasts were performed (control vs. hCG vs. GnRH). A high incidence of repeat-breeder cows showed reduced conception rates, which, in turn, compromise general reproductive performance of the herd and it has economic and managemental implications such as the genetc progress and replacement programs of the herd. Only 17% of repeat breeder cows were diagnosed pregnant whereas 83% were non-pregnant. Responses to all 5 hormonal therapies implemented were considerably low. However, a GnRH injection 11 d post-insemination presented higher pregnancy rates compared with the control group (31 vs. 21%), or to other GnRH (15.7%) or hCG treatments (0%). In conclusion, a GnRH injection 11 d post-insemination could be effective increasing fertility of repeat breeder cows.

Key Words: dairy cows, reproduction, repeat breeder

M211 Effects of month of breeding on reproductive efficiency of dairy cows inseminated with sexed or nonsexed semen in a hot arid environment.

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The objective of this study was to assess the effect of month of breeding on reproduction performance of Holstein cows treated with rbST throughout lactation and inseminated with sexed or nonsexed semen in a hot arid environment. Pregnancy per artificial insemination (P/AI; 62666 services over a 5-year period) both in nulliparous heifers (n = 20313) and cows (42353) from a large dairy herd in northern Mexico (26° N) were evaluated with respect to month of AI. The GENMOD procedure of SAS was implemented to assess the effect of month of breeding on P/AI. Overall, P/AI with sex-sorted semen was greater ($P < 0.01$) in heifers (41.6%) than cows (17.3%). P/AI for cows serviced with conventional semen was 10 percent points higher ($P < 0.01$) in January and December (31 vs 21) than cows serviced with sex-sorted semen. While there was no difference in P/AI between the sex-sorted sperm, and conventional semen in cows inseminated in June, P/AI plummeted for both groups of cows at this time of the year (16 and 18%, respectively). What was observed in cows, P/AI was not different between heifers serviced with sex-sorted or conventional semen during the hottest months of the year (July to October). However, during the coldest months of the year (January and February), P/AI was 10 percentage points greater ($P < 0.01$) in heifers serviced with conventional semen than heifers serviced with sex-sorted semen. It was concluded that in this hot-arid climate of northern Mexico breeding cows and heifers during summer compromise the breeding success. This data also show that the use of nonsexed semen resulted in meaningful advantages in terms P/AI compared with sexed semen, however, this advantage was reduced during extreme heat loads.

Key Words: nulliparous, sex-sorted, conventional

M212 Effects of follicular wave and progesterone concentration during follicle growth on conceptus global gene expression in dairy cows.

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Effects of wave of the ovulatory follicle and progesterone (P4) concentration during follicle growth on subsequent conceptus gene expression were evaluated. Nonlactating Holstein cows received a timed artificial insemination (AI) protocol (d-9 GnRH, d-2 and d-1 $PGF_{2\alpha}$, d0 GnRH and AI, d1 AI) initiating either during proestrus or early diestrus. The rationale was to induce ovulation of either a first (FW, n = 13) or second wave follicle (SW, n = 12) at AI, respectively. To evaluate the effects of P4 during follicle development, a third group of cows induced to ovulate first wave follicles received 3 intra-vaginal inserts containing P4 inserted sequentially at 12, 24 and 48 h after the initial GnRH (FWP4, n = 8). All inserts were removed on d-2. Cows were killed on d17 after d0 AI and uteri were flushed with PBS solution. Recovered concepti mRNA was extracted and global gene expression was evaluated using Affymetrix GeneChip Bovine Genome arrays. Data analyzed using the MIXED procedure of JMP-Genomics/SAS. Orthogonal contrasts were performed to determine the effects of P4 (FW vs. FWP4) and follicle wave (FW+FWP4 vs. SW). Differentially expressed genes were selected if $P < 0.05$ and fold-difference >1.5. Analyses identified 155 upregulated and 478 downregulated genes in response to the ovulation of a FW compared with a SW follicle. Upregulated genes were associated with 18 pathways from the Kyoto Encyclopedia of Genes and Genomes (KEGG). Downregulated genes are involved with a greater variety of biological processes (50 pathways), including several of those encompassing the upregulated transcripts. Progesterone supplementation during growth of the FW follicle induced upregulation of 73 genes from 13 pathways, including MAPK (hsa04010) and Wnt signaling pathways (hsa04310), focal adhesion (hsa04510) and regulation of cytoskeleton (hsa04810). Interestingly, P4 induced upregulation of TCF7 and EGFR in concepti. These genes have been associated with endometrial cell proliferation and cancer in humans; therefore, are potential candidates to mediate P4 maternal-conceptus communication.

Key Words: embryo gene expression, progesterone, dairy cow

M213 Expression of CYP11A1, CYP17, and CYP19A1 in granulosa cells, and determination of hormone levels in follicular fluid from dominant follicles and follicular cysts in Holstein cows.

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Follicular cysts are a major cause of infertility in dairy cattle. The objective was to assess the expression of genes coding for CYP11A1, CYP17, and CYP19A1 in granulosa cells, and to measure the level of IGF-1, 17-β estradiol (E_2), and progesterone (P_4) in follicular fluid of dominant follicles and follicular cysts. We analyzed 17 dominant follicles and 16 follicular cysts obtained from dairy cows slaughtered in Chihuahua, México. Gene expression relative to GAPDH was measured by real-time PCR using the comparative threshold cycle method. The concentration of IGF-1, E_2 and P_4 was measured by enzyme immunoassay. The experiment was conducted using a completely randomized design, with the fixed effect of follicle (cystic or dominant). We also studied the correlation among gene expression, follicle diameter and hormone levels. There were no differences ($P > 0.05$) between follicular cysts and dominant follicles for the expression of CYP11A1 (3.51 ± 0.25 vs 3.42 ± 0.26), CYP17 (1.88 ± 0.26 vs 1.84 ± 0.29), CYP19A1 (4.07 ± 0.36 vs 3.37 ± 0.42), and the concentration of E_2 and P_4 (1142.00 ± 1.82 vs 1384.65 ± 1.82, and 23.40 ± 1.45 vs 13.10 ± 1.45 ng/mL, respectively). The concentration of IGF-1 was higher ($P < 0.05$) in follicular cysts compared with dominant follicles (132.78 ± 1.88 vs 78.21 ± 1.88 ng/mL). We found significant correlations ($P < 0.05$) between the expression level of CYP11A1 with CYP17 and CYP19A1 (0.57 and 0.73, respectively) in dominant follicles. There was a negative correlation ($P < 0.05$) between IGF-1 and CYP11A1 expression (−0.69), and CYP11A1 and follicle diameter (−0.60) in follicular cysts. Level of expression for CYP19A1 was positively correlated to E_2 concentration in both follicular cysts and dominant follicles (0.93 and 0.88 respectively). Cystic follicles show greater concentration of IGF-1, which is negatively related to CYP11A1.

Key Words: follicular cyst, gene expression, IGF-1

M214 Comparison of dry matter intake and somatotropic axis components of Holstein and crossbred dairy cows.

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Objectives of the study were to compare dry matter intake (DMI), somatotropic axis components, plasma cortisol (COR), and leptin (LEP) concentrations of Holstein (HO) and Montbéliarde sired crossbred (MS) cows. Cows were enrolled in the study 45 d before calving (d −45) and followed until d 90. Daily DMI was measured from d −45 to 45. Liver was biopsied on d −14, 7, 14, and 28 to determine mRNA expression of growth hormone receptor (GHR) 1A, insulin-like growth factor-I (L-IGF1), and insulin receptor b (IRB). Plasma concentrations of growth hormone (GH), insulin-like growth factor-I (IGF1), insulin (INS), and LEP were determined on d −7, 1, 7, 14, 21, 42, and 56 and that of COR was determined on d −14, −7, 1, 7, 14, 21, and 42. Data were analyzed by ANOVA for repeated measures. Breed tended ($P = 0.08$) to be associated with DMI from d −45 to 45 (HO = 16.5 ± 0.7kg/d vs MS = 14.9 ± 0.6kg/d) and DMI expressed as percentage of body weight (DMIBW) tended ($P = 0.10$) to be affected by the interaction between breed and day because among HO cows DMIBW on d −15 and −1 were 1.89 ± 0.12% and 1.43 ± 0.14%, respectively, and among MS cows DMIBW on d −15 and −1 were 1.51 ± 0.10% and 1.41 ± 0.11%, respectively. There were no associations between breed and expression of GHR1A ($P = 0.83$), L-IGF1 ($P = 0.70$), and IRB ($P = 0.68$) mRNA. The interaction between breed and day was ($P = 0.02$) associated with expression of IRB mRNA because among HO cows IRB expression was ($P < 0.05$) greater on d 7 compared with d 28 and on d 14 compared with d −14 and 28 but no changes in IRB expression were observed among MS cows. There were no associations between breed and concentrations of IGF1 (55.4 ± 1.7ng/mL; $P = 0.81$), INS (65.2 ± 0.7ng/mL; $P = 0.69$) and LEP (2.8 ± 0.2ng/mL; $P = 0.30$), but HO cows had ($P < 0.01$) greater concentrations of GH (7.4 ± 0.4 vs 5.1 ± 0.4 ng/mL) and cortisol (9.4 ± 0.8 vs 7.1 ± 0.8ng/mL) than MS cows. The greater decrease in prepartum DMI for HO cows may have caused the increased levels of GH and COR. The similar IGF1 concentration among HO and MS cows, despite HO cows having greater GH concentration and similar expression of GH1RA mRNA to MS cows, may suggest a more pronounced decoupling of the somatotropic axis in purebred HO cows.

Key Words: transition cow, somatotropic axis, crossbreeding

M215 Effect of subclinical mastitis and postpartum uterine disease on expression of estrous behavior in cows.

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The objective of this study was to determine the effect of mammary and uterine diseases on manifestation of estrus in cows. Cows (n = 1247) from 50 to 130 d of lactation, in the summer and winter, were synchronized with 2 $PGF_{2\alpha}$ injections administered 14 d apart (before 1st AI); 36 h after the 2nd injection, cows were checked for estrus 4 times daily for 6 d. Uterine diseases were recorded during the first week postpartum. Cows were sorted to uninfected control or chronic (most likely subclinical) mastitic cows by somatic cell count in the monthly milk samples taken before and after 2nd $PGF_{2\alpha}$ injection. Body condition score difference (BCS-diff) between calving and 2nd $PGF_{2\alpha}$ injection, and milk yield were recorded. Factors relevant to manifestation of estrus were selected by stepwise logistic regression. As some interactions were detected, separate logistic regressions were performed by season and parity. In the winter, the percentage of cows not expressing estrus increased, compared with controls (26.6 vs. 12.6%; odds ratio [OR] 2.4, $P < 0.002$), in multiparous cows with uterine diseases. Similarly, a high BCS-diff tended to increase the rate of cows not expressing estrus (21.3 vs. 12.1%; OR 1.93, $P < 0.06$). In primiparous cows, subclinical mastitis as well as high milk yield increased the percentage of cows not expressing estrus (34.7 vs.14.3%; OR 3.4, $P < 0.02$, and 24.1 vs. 9.4%; OR 3.2, $P < 0.03$, respectively). In the summer, an increased percentage of cows not expressing estrus (24.2 vs. 16.9%; OR 1.7, $P < 0.05$) was recorded in multiparous cows with high BCS-diff. In primiparous cows, a subclinical mastitis by uterine disease interaction was detected, showing a higher rate of cows not expressing estrus (41.4 vs. 17.2%; OR 3.9, $P < 0.05$). Results indicate a higher risk for not expressing estrus, which is parity- and season-dependent, in cows with subclinical mastitis and postpartum uterine diseases. The above findings could result in increased days open in dairy herds, and could be associated with disease induction of anestrus, or with disruption of the endocrine process associated with expression of estrous behavior.

Key Words: estrus, mastitis, cows

M216 Dietary protein:carbohydrate ratio affects glucose tolerance and oxidation in pregnant gilts. C. C. Metges,* S. Görs, I. Lang, K.-P. Brüssow, C. Rehfeldt, and W. Otten, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Low as well as high dietary protein:carbohydrate ratios during pregnancy cause changes of maternal metabolism and body composition, and intrauterine growth restriction (IUGR) in the pig (Rehfeldt et al., J Anim Sci 2011,189:329–341; Metges et al., PLoS ONE 2012, in press). We performed intravenous glucose tolerance tests (IVGTT) with labeled glucose to further characterize maternal constraints of glucose metabolism in late pregnant gilts. Twenty-seven German Landrace gilts were fed diets with low (6.5%, L), adequate (12%, A), or high (30%, H) protein levels (n = 9/group) made isoenergetic by adjusted carbohydrate content throughout pregnancy. Gilts were fitted with jugular catheters and an IVGTT was performed on d 90 of pregnancy. After overnight fast 0.5 g/kg BW glucose and 0.5 mg/kg U^{13}C-glucose were administered i.v. Blood samples were analyzed for plasma glucose (GLC), insulin (INS), glucagon (GCG) concentrations, and U^{13}C-glucose and blood $^{13}CO_2$ enrichments by mass spectrometry. Areas under curve (AUC) and cumulative $^{13}CO_2$ appearance in blood ($^{13}CO_2$cum) were calculated. Diet effects were evaluated by PROC MIXED of SAS. L gilts had a lower BW as well as a lesser basal INS concentration and INS-AUC than controls, whereas H gilts showed a higher basal GCG level and GLC-AUC (Table 1). In H gilts lower $^{13}CO_2$cum suggested a lower GLC oxidation (Table 1). Apparently higher and lower INS sensitivity in L and H, respectively, might be explained by lower pancreatic INS secretion caused by protein deficiency, and reduced GLC oxidation due to GLC sparing, respectively. Thus, L and H diets might cause altered feto-maternal glucose interaction possibly associated to the observed offspring IUGR in these groups. Supported by Deutsche Forschungsgemeinschaft ME1420/8–1.

Table 1. Body weight and glucose metabolism analyzed by IVGTT in pregnant gilts fed L, A, or H diet throughout pregnancy

	Diet			
Item	L	A	H	*P*-value
BW, kg	174^{a}	196^{b}	197^{b}	0.017
GLC$_{basal}$, mmol/L	5	5	5	0.970
INS$_{basal}$, μU/mL	7^{a}	11^{b}	9^{a,b}	0.077
GCG$_{basal}$, ng/L	44^{a}	46^{a}	65^{b}	0.013
GLC-AUC, mmol/L × min	134^{a}	136^{a}	167^{b}	0.001
INS-AUC, μU/mL × min	724^{a}	1336^{b}	1035^{a,b}	0.021
$^{13}CO_2$cum, APE × min	0.176^{a}	0.165^{a}	0.128^{a}	0.012

Key Words: high protein, glucose, pregnancy

Production, Management and the Environment: Dairy I

M217 Measuring dry matter of corn silage, haylage, and TMR samples with a food dehydrator. R. J. Norell*[1], C. M. Matuk[2], S. Hines[2], M. Chahine[2], M. de Haro Marti[3], and S. C. Parkinson[4], [1]*University of Idaho, Idaho Falls,* [2]*University of Idaho, Twin Falls,* [3]*University of Idaho, Gooding,* [4]*University of Idaho, Preston.*

Quality control procedures for TMR feeding require on-farm measurement of dry matter for ensiled forages and prepared TMRs. Current on-farm tests require operator attentiveness during the drying process and moderate laboratory skills. In this study, we compared dry matter determinations with a food dehydrator (DEHY) against a laboratory oven (OVEN). The dehydrators were 500 Watt, Nesco brand, FD-60 with 4 trays and each tray had a fruit roll-up sheet. Temperature settings were 68 C for DEHY and 55 C for OVEN. In part 1, 4 dehydrators with 4 trays each were utilized. Single corn silage, haylage, and TMR samples were split into 16 subsamples for dry matter determination. Each feedstuff was run separately with 100g of each subsample placed on an individual tray. Tray weights were collected at 0, 2, 4, 6, and 8 h. Sample weights were stabilized at the 4 or 6 h weighing period. Data were analyzed as a randomized block design with repeated measures on the tray position. Dry matter did not differ between tray position for corn silage ($P = 0.15$), haylage ($P = 0.52$), and TMR ($P = 0.07$). In part 2, unique lots of corn silage, haylage, and TMR (12 each) were collected and split into 4 subsamples. Dry matter determinations were made in groups of 4 lots for each feedstuff and each lot was replicated 4 times (once in each dehydrator and once within each tray position). Dehydrator tray weights were collected at 0, 2, 4, 6, and 8 h. Oven dry matter determinations were collected after 24 h. Means were calculated from the 4 replicates and then used to compare OVEN versus DEHY measurements at 8 h with paired *t*-tests. Mean difference (OVEN-DEHY), SE_{diff}, and significance were: +1.11 ± 0.16%, $P < 0.001$; +0.84 ± 0.30%, $P = 0.02$; +0.65 ± 0.16%, $P < 0.001$ for corn silage, haylage, and TMR, respectively. OVEN dry matter contents were slightly higher than DEHY, possibly due to greater volatilization of VFA's or other compounds with the dehydrators. Sample dry matters were mostly stable after a 4 h drying time. We conclude that food dehydrators with fruit roll-up trays are an effective, reliable tool for on-farm determination of dry matter.

Key Words: on-farm testing, food dehydrator, dry matter

M218 Determining surface area of exposed silage on California dairy farms. D. Meyer[1], P. H. Robinson[1], P. L. Price[1], R. Rauch[1], and J. M. Heguy*[2], [1]*University of California, Davis,* [2]*University of California Cooperative Extension, Modesto.*

Ensiled forages (i.e., silage) are a key ingredient in California dairy rations, but they are also emitters of volatile organic compounds (VOC). Our objective was to evaluate silage structures (pile, bunker, drive-over) on California dairy farms to determine the number of structures simultaneously utilized per farm, as well as the exposed silage surface area of each structure. The San Joaquin Valley Air Pollution Control District (SJVAPCD) had proposed a VOC emission mitigation to restrict exposed surface area of silages to 199.7 m^2 if only one structure was open, or 399.5 m^2 if more than one structure was open, per dairy farm. Forages preserved in plastic bags were not examined because they are exempt from the SJVAPCD calculation of surface area exposure. Silage structures on 20 dairy farms were evaluated. Exposed silage surface area was determined by identifying geometric features, making appropriate measurements and calculating surface area. Number of cattle in each age group was obtained for most farms. An animal feed unit equivalent (AFU) calculation assumed coefficients for each animal group as: 1.0, lactating cows; 0.9, dry cows; 0.7, heifers 15 to 24 mo of age; 0.5, heifers 7 to 14 mo of age; and 0.2, heifers 4 to 6 mo of age. The silage structures consisted of winter cereal, corn and alfalfa. The number of structures open per farm was 2.2 (SD = 0.9) with a maximum of 4. All farms with only 1 silage surface exposed (n = 4) met the SJVAPCD surface area requirement, but 5 of 16 farms which had more than one exposed silage surface did not. Exposed silage surface area per farm was 27.7 to 738.2 m^2. Exposed surface area (m^2)/AFU was 0.01 to 0.28 with 4 of 16 farms having values > 0.10. Total AFU and exposed silage surface areas within farm did not correlate with exposed silage surface area ($r^2 = 0.32$), suggesting that AFU is not a substantive factor in the amount of exposed silage surface area needed at silage feedout. The variation in exposed surface area (m^2)/AFU among farms suggests opportunities to develop and implement management practices to reduce exposed silage surface area on commercial California dairy farms.

Key Words: silage, volatile organic compounds , regulations

M219 Comparison of two methods of collecting calf birthweights (BW) in dairy calves. N. M. Long* and J. F. Smith, *Department of Animal Sciences, University of Arizona, Tucson.*

The collection of calf BW in dairies in the US is not a common practice. Calf BW was collected on 3 dairies (2 Holstein and 1 Jersey herd) over a 6 week period. All calves BW were collected less than 2 h after birth. A total of 872 calves were weighed by both a spring scale (SP; Rubbermade Co., Huntersville, NC) and also a hooftape (HT, Calfscale BW Tape, Nasco, Fort Atkinson, WI) with both weights and sex recorded. The Proc GLM (SAS Institute Inc., Cary, NC) was used to estimate LS means for SP BW with sex of calf and also dairy. Calf SP vs HT BW was compared using the Proc Reg of SAS. Calf BW was also broken down into increments and SP vs HT BW were compared utilizing *t*-test. Bull calves had a heavier ($P < 0.001$) BW (kg) compared with heifer calves (36.7 ± 0.4, n = 450 vs 34.6 ± 0.4, n = 422, respectively). Dairy in which calves were born had a significant effect ($P < 0.001$) on calf BW (kg) (Dairy 1: 36.8 ± 0.4, n = 204; Dairy 2: 39.5 ± 0.2, n = 463; Dairy 3: 25.9 ± 0.4, n = 205). When SP calf BW was linearly regressed by HT BW there was a significant relationship ($P < 0.01$) with a R2 value of 0.91. The breakdown of calf BW and comparison of SP and HT BW are shown in Table 1. For calves less than 31.3 kg, the HF overestimated ($P < 0.001$) calf BW compared with SP. However, for calves that weighted between 31.3 to 44.9 kg there was no difference ($P \geq 0.104$) between SP and HT BW. For calves heavier than 44.9 kg, HT underestimated ($P = 0.022$) BW compared with SP. Collection of calf BW by SP or HF appears to be comparable for most calves, since most calves weigh between 31 to 45 kg, but caution should be utilized for light or heavy BW calves.

Table 1. Comparison of spring scale and hoof tape on birthweight determination (mean ± SEM)

BW, kg	n	Scale	Tape	*P*-value
<27.2	148	23.2 ± 0.2	24.6 ± 0.3	<0.001
27.2-31.3	95	28.9 ± 0.2	29.7 ± 0.2	<0.001
31.3-35.8	135	33.8 ± 0.1	34.0 ± 0.1	0.217
35.8-40.4	242	38.0 ± 0.1	37.8 ± 0.1	0.133
40.4-44.9	165	42.4 ± 0.1	42.2 ± 0.2	0.104
> 44.9	87	47.4 ± 0.3	46.5 ± 0.4	0.022

Key Words: dairy calves, birthweight, hoof circumference tape

M220 Assessing among-farm variability in heifer body weights.

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Raising healthy young stock to be productive cows is crucial to a dairy farm, but indicators of successful heifer rearing, including weight gains, are rarely measured. Our aim was to describe the variation in growth of Holstein heifers reared on dairy farms in the lower Fraser Valley region of British Columbia. Data were collected by the same individual on 33 farms, all using the Dairy Herd Improvement (DHI) recording system and with a minimum milking herd of 100 cows. Farms were visited between June 2010 and October 2010. Heart girth circumference was measured for all heifers aged 12 to 17 mo (n = 560) and these values were converted to estimate body weight (BW). Birth dates were also recorded. Data were analyzed through a simple linear regression analysis resulting in a line equation of BW (kg) = 112.9 + 5.1* (age in weeks) ($R^2 = 0.35$). Residuals derived from this regression were averaged across heifers within each farm; these farm averages ranged from −53.8 to 71.5 kg. We tested the effects of a range of farm level descriptors (including weaning method, time between weaning and moving to a new pen, size of the heifer group, frequency of regrouping heifers, times per day heifers were provided fresh feed) but only one variable was able to account for among-farm variation in residual weights; average weight gain during the pre-weaning phase (i.e., calves 0 to 2 mo of age; residual gains measured as described above for heifers). Residual weights of heifers increased with gains of the pre-weaned calves (line equation: Residual Heifer BW (kg) = −1.50 + 2.99* Residual Calf BW (kg); $R^2 = 0.39$). These results show considerable among-farm variation in heifer weight gains, indicating that some farms are doing well while others could improve performance. Farms able to rear faster growing heifers were also rearing faster growing calves, suggesting that management of milk-fed calves is especially important.

Key Words: calf growth, milk feeding, welfare

M221 The effects of increased space allowance on dairy calf performance, behavior, and respiratory antibody production.

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California dairy calves are typically raised individually in wooden hutches with a space allowance of 1.23 m^2/head. Because management and housing of livestock continues to be an important issue to both consumers and producers, the objective of the following research was to modify current calf housing systems to investigate the possible benefits of increasing space allowance. The 3 housing treatments were: 1) conventional housing (SML; 1.23 m^2/head; n = 18), 2) 1.5 x SML (MED; 1.85 m^2/head; n = 19), or 3) 3 x SML (LRG; 3.71 m^2/head; n = 20). Milk and starter intake were recorded daily and BW were measured on d 0, 20, 45, 73, and 87. Visual health assessment scores were recorded daily and behavior loggers were utilized on 21–31, 46–56, and 74–84 d to assess the effects of treatments on health and resting behavior over the 87 d study period. In a sub-experiment, healthy calves from each treatment (n = 6, SML; n = 8, MED; n = 7, LRG) were sensitized (subQ) and challenged (aerosolized) with Ovalbumin (OVA) at age 76 ± 0.5 d. Broncho-alveolar lavage fluid (BALF) was collected at age 80 ± 0.5 d and was analyzed for OVA-specific IgG, IgG1, IgA, and IgE. Calves in MED and LRG had greater body weights and average daily gains by 45 d of age ($P < 0.05$). A greater percentage of days with clean hide scores were observed in LRG calves ($P < 0.05$). Although there were no differences across treatments in clinical symptoms of respiratory illness, MED calves had less BALF OVA-IgE compared with SML and LRG ($P < 0.05$). As SML and MED calves grew, they spent less time in the standing-position ($P < 0.05$), but LRG calf standing time stayed the same ($P > 0.10$). Early in life (age 21–23 d), all calves spent 16.6 ± 0.31 h/d in resting-position ($P > 0.10$). Calves in SML and MED hutches increased resting time as they aged (47–49, 74–76 d; $P < 0.05$), but LRG calf resting time did not change over time. Although maximizing space allowance in wooden hutches provides more room for calves, a moderate increase in space allowance may be more beneficial to calf performance, resting time, and respiratory antibodies.

Key Words: bovine, performance, behavior

M222 Growth measurements of organically raised dairy steers compared with conventionally raised dairy steers.

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Bull calves (n = 50) were used to compare growth measurements of conventional and organic dairy steers. Calves were assigned to one of 3 groups at birth: conventional (CONV, n = 16), organic (ORG, n = 17), and organic-grass only (GRASS, n = 17), and were born at the University of Minnesota West Central Research and Outreach Center, Morris from March to May 2011. Breed groups of calves were: Holstein (n = 10), Holsteins (n = 11) maintained at 1964 breed average level, and crossbreds (n = 29) comprised of Holstein, Swedish Red, Montbéliarde, and Jersey. The CONV steers were fed a diet of 80% concentrate and 20% roughage and received steroidal implants. The ORG steers were fed a diet of organic corn, organic corn silage, and at least 30% of their diet consisted of organic pasture during the grazing season. The GRASS steers grazed pasture during the grazing season and were fed high quality hay or hay silage during the non-grazing season. Diets fed were recorded daily with herd management software. Body weight was recorded at birth, weaning, and monthly. Hip height, heart girth and body condition score were measured at weaning and monthly thereafter. Analysis was with PROC GLM of SAS, and independent variables for statistical analysis were the fixed effects of steer group and breed group. For the first 9 mo of age, steer performance was: total gain (kg), CONV (324), ORG (227), GRASS (146), ($P < 0.01$), and average daily gain (kg/d); CONV (1.12), ORG (0.79), and GRASS (0.51), ($P < 0.01$). From weaning (90 d) to 9 mo of age, performance was: total gain (kg) CONV (255), ORG (157), and GRASS (89) ($P < 0.01$), and average daily gain (kg/d), CONV (1.31), ORG (0.81), and GRASS (0.46), ($P < 0.01$). Hip height gain (cm) (CONV, 21.8; ORG, 15.1; GRASS, 6.7) and heart girth gain (cm) (CONV, 39.0; ORG, 21.5; GRASS, 14.2) from weaning was different ($P < 0.01$) for all steer groups. Furthermore, body condition score was different ($P < 0.01$) for all steer groups (CONV, 3.96; ORG, 3.40; GRASS, 3.01). No significant differences were found for breed groups for growth measurements.

Key Words: organic, grass-fed, dairy steers

M223 Associations between herd-level feeding management practices, feed sorting, and milk production in freestall dairy farms. A. D. Sova*[1], S. J. LeBlanc[2], B. W. McBride[3], and T. J. DeVries[1], [1]*Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada,* [2]*Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada,* [3]*Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Challenges associated with group housed dairy cows include within-herd variability in nutrient consumption and milk production, which may be related to feeding management. The objective of this study was to examine the association of herd-level feeding management factors, feed sorting, and milk production. Ten free-stall herds, with average lactating herd size of 106 ± 26 cows, feeding TMR were studied for 7 consecutive days. Milk production parameters, including yield, fat, and protein, were recorded through a DHI test occurring ± 3 d of the study. A survey of feeding management practices and barn characteristics was administered on each farm. Amount of feed offered and refused was recorded and sampled daily to assess DM and particle size distribution. 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 summarized across each 7-d period for each farm and analyzed in multivariable mixed-effect regression models. Categorical variables included in the models were milking frequency (MF; 0 = 2x/d; 1 = 3x/d) and feeding frequency (FF; 0 = 1x/d; 1 = ≥ 2x/d). Greater milk yield was associated ($P < 0.04$) with herds of lower average DIM, which milked 3x/d and fed ≥ 2x/d; milk yield (kg/d) = −0.06(SE = 0.02) × DIM + 3.5(SE = 1.2) × MF + 3.0(SE = 1.1) × FF + 40.8(SE = 3.2). Greater DMI was associated ($P < 0.02$) with herds of greater average parity, which fed ≥ 2x/d; DMI (kg/d) = 6.5(SE = 1.9) × parity + 4.1(SE = 1.1) × FF + 7.4(SE = 4.4). Higher milk fat % and less sorting against long ration particles were associated ($P < 0.03$) with herds of greater average DIM, which fed ≥ 2x/d; milk fat (%) = 0.005(SE = 0.001) × DIM + 0.3(SE = 0.1) × FF + 2.6(SE = 0.3); sorting of long particles (%) = 0.07(SE = 0.02) × DIM + 4.7(SE = 1.3) × FF + 81.0(SE = 3.0). The results suggest that herd-level feeding management practices to promote feed access, such as increased feeding frequency, may be used to improve DMI, reduce sorting, and improve milk yield and fat percentage.

Key Words: feeding management, sorting, milk production

M224 Comparison of the effects of conductive cooling to fan cooling on lactating dairy cattle. R. B. Thornton*[1], W. A. Greene[1], J. Bruer[2], and T. Steele[2], [1]*The Ohio State University, Wooster,* [2]*Conco Technologies, Chandler, AZ.*

The objective of this study was to compare physiological effects of conductive cooling (COND) to fan cooling (FANS) on lactating dairy cattle for 12 wk during the summer (June–August) of 2011 in northwest Ohio. Cows, milked 3x/day, were housed in a sand-bedded 6-row barn configuration with 122 cm fans at 12.2 m intervals over the feed aisle and free-stalls, programmed to operate at temperatures above 15.6°C. Seventy cows were paired for parity, DIM, and milk yield. Thirty-five cattle were housed in one section of the barn where fans were disabled and heat exchangers were buried 30.5 cm below the bed in the 33 freestalls (COND). Well water (12.5 to 18.1°C) was pumped through the heat exchangers. The other (paired) 35 cows were a part of an 114-cow group that had 107 freestalls with operating fans (FANS). Milk weights, milk components, and SCC were recorded for the paired cows. At the start of the trial, COND and FANS cows had similar ($P > 0.05$) least squares means (LSM) for average daily energy-corrected milk (ECM) weights (43.0 ± 1.5 vs. 42.8 ± 1.5 kg) and SCC (28,030 ± 4,416 vs. 23,969 ± 4,485 cells/mL). The percent of cows resting in each group was observed weekly at approximately 1100. Midday rectal temperatures and respiratory rates were randomly measured weekly on 15 cows in each housing group. Hourly ambient temperature and humidity measurements were recorded and thermal-humidity indexes (THI) were calculated throughout the trial. Daily average THI ranged from 62.4 to 81.7. COND and FANS cows had similar ($P > 0.05$) LSM for average daily ECM (37.8 ± 0.8 vs. 37.7 ± 0.8 kg) and SCC (36,626 ± 23,244 vs. 87,772 ± 23,191 cells/mL) during the 12 wk trial, although SCC tended to be higher for the FANS group from wk 8 to 12. There was no difference ($P > 0.05$) in LSM for average percent of cows observed resting between the COND (50.3) and FANS (50.6) groups. COND and FANS cows had similar ($P > 0.05$) LSM for average rectal temperatures (38.7 vs. 38.6°C) and respiratory rates (67.8 vs. 67.6/min). In general, there were no differences observed between the 2 methods of cooling lactating dairy cattle.

Key Words: cow cooling, heat stress

M225 Effect of FlipFan cooling system on lactating dairy cattle performance in an open dry-lot commercial dairy in a sub-tropical environment in central Texas. J. A. Hernandez-Rivera*[2], F. D. Alvarez-Valenzuela[2], U. Macias-Cruz[2], L. Avendano-Reyes[2], and T. R. Bilby[1], [1]*Texas AgriLife Research and Extension Service, Texas A&M System, Stephenville,* [2]*Instituto de Ciencias Agricolas, Universidad Autonoma de Baja California, Ejido Nuevo Leon, Valle de Mexicali, Mexico.*

Heat stress negatively affects dairy cattle performance, thus adequate cooling strategies are needed. Objective of the current study was to evaluate the effect of a new cooling system on production and physiological parameters during a 4 d period in summer. Twenty-four multiparous cows balanced for DIM, parity, and daily milk production were assigned to 1 of 3 treatments: H (control Holstein group with shade only; n = 8); FF-H (Holstein cows cooled with Flip Fan cooling system plus shade; n = 8), and JxH (control Jersey x Holstein crossbred group with shade only; n = 8). All groups were cooled before milking at 1100 and 2300 h with sprinklers and fans in the holding pen. The cooling system (Schaefer FlipFan) was placed on the south edge under the shade approximately 4 m from the ground, and consisted of 33 fans, that could rotate 180° and high pressure misters fixed to the front of the fans which followed the movement of the shade. The FlipFan system ran continuously throughout the duration of the study. Skin temperatures (ST) of the hip region (30.2 vs. 32.0 and 33.1°C), right flank (30.6 vs. 32.6 and 33.1°C), udder (31.3 vs. 32.7 and 33.4°C) and head (28.5 vs. 30.2 and 31.9°C) in the morning were lower ($P < 0.05$) in FF-H versus H and JxH cows, respectively. During the afternoon, ST of the hip, right flank, udder, and head were lower ($P < 0.05$) in FF-H cows (34.9, 34.7, 35.1 and 33.6°C, respectively) compared with H (38.5, 38.3, 38.8 and 39.3°C, respectively) and JxH (37.2, 37.2, 37.9 and 38.2°C, respectively). During the morning and afternoon, the respiration rate per minute (rpm) in H (74 and 111 rpm) and JxH (84 and 112 rpm) groups were greater ($P < 0.05$) than in FF-H (61 and 88 rpm) group. In addition, H group core body temperature peaked at 40.9°C, whereas both JxH and FF-H groups were lower and peaked at 40.5 and 40.0°C, respectively. The FlipFan cooling system reduced heat stress effects by reducing ST, respiration rate and core body temperature in lactating Holstein dairy cattle.

Key Words: dairy cow, heat stress, cooling

M226 Correlation between invasive methods for recording physiological parameters and infrared thermography in calves. P. A. B. Mac-Lean[1], H. Savastano Junior[1], L. C. Roma Junior*[2], S. Correa[1], C. N. Barra[1], C. G. Titto[1], and C. E. L. Oliveira[1], [1]*University of Sao Paulo, Pirassununga, Sao Paulo State, Brazil,* [2]*APTA Centro Leste, Ribeirao Preto, Sao Paulo State, Brazil.*

Evaluation of physiological parameters such as temperature have been used as indicators of heat stress. Human intervention and proper restraint are usually necessary to measure these physiological parameters; therefore, the development of a tool that avoids interference would be desirable. The objective of this study was to compare measurement of physiological parameters (traditional method) with infrared thermography (non-invasive method). Twenty Jersey and crossbred suckling calves were used in the study for a period of 5 d with an interval of 6 h between each measurement, totaling 400 measurements per variable. Variables analyzed were rectal temperature, ear temperature, coat surface temperature, in addition to infrared thermography (IRT) of auricular, dorsal and caudal regions. A randomized block design balanced for sex and breed was used. Data were analyzed using the Proc GLM, Proc Corr and Proc Reg of SAS. The correlations between IRT and coat surface temperature, ear temperature and caudal region temperature were 0.88, 0.86 and 0.75, respectively. Ear temperature by IRT showed the best correlation with traditional method for rectal temperature (0.69; $P < 0.001$). Thus, the regression for other physiological parameters used ear temperature recorded by IRT as the dependent variable. The coefficients of determination provided with regression were 0.53, 0.73, 0.62 and 0.47 for coat surface temperature, ear temperature, caudal region temperature and rectal temperature, respectively. It appears from these results that infrared thermography could be used to estimate physiological indicators of heat stress with minimal interference. Financial support by FAPESP, process 10/07978-8.

Key Words: physiological variables, thermoregulation, thermal imaging

M227 Agreement between reticular and vaginal measurement of core temperature in dairy cattle. J. A. Small[1,2], R. Hayman[2], T. Rudderham[2], A. Fredeen[2], and W. Webster*[3], [1]*Agriculture and Agri-Food Canada, Truro, NS, Canada,* [2]*Nova Scotia Agricultural College, Truro, NS, Canada,* [3]*DVM Systems LLC, Denver, CO.*

Agreement between reticular and vaginal measurements of core temperature (Tc) in dairy cattle was determined using fistulated lactating dairy cattle (n = 4) in good body condition (BCS 2.5 to 3.0) A prototype hand-held reader was used to capture reticulo-rumen temperatures (Trr) from passive transponder boluses containing thermistors that were placed in the reticulum (DVM Systems, LLC, Denver CO). A digital thermometer was used to determine vaginal temperatures (Tv). Cattle were offered 68 L of either warm (39°C) or cold (12°C) fresh drinking water at 0600 and 1700, in a crossover design. Starting at 0420 and 1517, Tc were taken at intervals relative to free water intake (FWI) −105, −90 (before milking) −60, −45 (milking), −30, −15 (after milking), 05, 10 (FWI) and 15, 30, 45, 60, 75, 90 min (post-FWI). Cattle were housed in tie-stalls exposed to barn lights from 0400 to 1800 and natural light, full-fed a total mixed ration (33% dry matter) offered at 0530, 0830, 1030, 1400, and moved to an exercise yard from 0730 to 0830. The barn temperature-humidity index ranged from 45 to 51. To determine agreement between Tv and Trr the average of the 3 previous Tc were deemed the baseline to calculate the deviation of the current value from baseline. Agreement between Trr and Tv was fair overall observations (kappa = 0.23; $P < 0.01$; n = 333), moderate before FWI (kappa = 0.57; $P < 0.01$; n = 96), and substantial when measurements were taken before FWI in the morning (kappa = 0.71; $P < 0.01$ n = 56) and fair (0.37; $P = 0.02$) in the afternoon. The predicted change in Trr at each time after FWI was dependent upon FWI temperature and volume. Predicted Trr decreased −4 to −9°C at 10 min after drinking 2 to 70 L of cold water and regardless of volume remained 3°C below baseline after 60 min. The predicted change in Tv at each time after drinking water was dependent upon the temperature and volume of FWI until 60 min after drinking. However, in contrast to Trr, small volumes of cold water caused a transient decrease in Tv and larger volumes increased Tv 0.2°C. In dairy cattle FWI influenced Trr and Tv, and the most accurate measurements were obtained in the morning before milking and FWI.

Key Words: reticular temperature, drinking water, dairy cattle

M228 Warm drinking water lowers core temperature in dairy cattle. J. A. Small[1,2], T. Rudderham[2], R. Hayman[2], A. Fredeen*[2], and W. Webster[3], [1]*Agriculture and Agri-Food Canada, Truro, NS, Canada,* [2]*Nova Scotia Agricultural College, Truro, NS, Canada,* [3]*DVM Systems LLC, Denver, CO.*

Fistulated lactating dairy cattle (n = 4) in good body condition (BCS 2.5 to 3.0) were used in a crossover design to determine the effects of warm free water intake (FWI) on core temperature. Cattle were offered 68 L of either warm (W; 39°C) or control (C; 12°C) drinking water twice daily at 0600 and 1700. Each period consisted of 7 d adaptation to treatment followed by 2 consecutive days of data collection. A prototype hand-held reader was used to capture reticulo-rumen temperature (Trr) from passive transponder boluses containing thermistors that were placed in the reticulum (DVM Systems LLC, Denver CO). A digital thermometer was used to determine vaginal temperature (Tv). Core temperatures taken at intervals starting at 0420 and 1517 were deemed pre-milking (−105, −90 min); milking (−60 and −45 min), post-milking (−30 and −15 min), FWI (05 and 10 min) and post-FWI (15, 30, 45, 60, 75, 90 min). Cattle were housed in tie-stalls exposed to barn lights from 0400 to 1800 and natural light, full-fed a total mixed ration (33% dry matter) offered at 0530, 0830, 1030, 1400, and moved to an exercise yard from 0730 to 0830. The barn temperature-humidity index ranged from 45 to 51. Data were subjected to Proc Mixed procedures for a cross over design with repeated measures (morning and afternoon). Mean milk yields were greater ($P < 0.05$) and mean FWI were less ($P = 0.10$) for morning than afternoon, and did not differ ($P > 0.20$) between W and C (41.9, 50.0 and 39.5, 48.1 ± 8.4 L FWI, respectively). Pre-milking, morning and afternoon Trr and Tv means for W and C were 38.7, 38.7 and 38.8, 38.9 ± 0.24°C, and 38.5, 38.6 and 38.5, 38.8 ± 0.07°C, respectively. Post-milking, morning and afternoon Trr and Tv means were 0.2, 0.4°C and 0.1, 0.3°C lower ($P < 0.05$) for W than C, respectively. After FWI, morning and afternoon Trr means were higher ($P < 0.05$) and Tv similar ($P > 0.29$) for W than C (38.7, 38.2, and 31.9, 30.6 ± 0.24°C, and 38.5, 38.7 and 38.4, 38.7 ± 0.07°C), and 90 min later were 1.4, 0.9°C and 0.1, 0.3°C higher for W than C, respectively. In conclusion, warm FWI caused a transient increase in core temperature, but had the net effect of lowering basal core temperature especially in the afternoon.

Key Words: reticular temperature, drinking water, dairy cattle

M229 Influence of time of day, breed, and season on reticulorumen temperature in lactating dairy cows. D. Liang,* D. L. Ray, J. D. Clark, and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this research was to characterize the influence of time of day, breed, and season on reticulorumen temperatures in lactating dairy cows. Reticulorumen temperatures (RT) were recorded every 15 min using SmartBolus transponders (TenXsys Inc., Eagle, ID) for 103 cows (68 Holstein, 25 crossbred and 10 Jersey) at the University of Kentucky Coldstream Dairy from November 06, 2009 to July 24, 2011. Air temperatures (AT) were collected every 15 min on location with a SmartBolus transponder. Raw RT (n = 1,646,145) were edited to remove erroneous reads and temperatures potentially influenced by water intake by removing any RT lower than 38.33°C. The mean (±SD) RT among the remaining 927,048 temperatures was 40.16 ± 0.52°C. Peak and nadir mean RT occurred at 23:45 (40.26°C) and 10:00 (39.92°C), respectively. Mean (±SD) AT was 14.75 ± 10.55°C. The MIXED procedure of SAS (Cary, NC) was used to assess the impact of breed and season on RT. The CORR procedure of SAS was used to calculate correlation coefficients between RT and AT. The reticulorumen temperature was lowly correlated with AT ($r = 0.28$, $P < 0.01$). Least squares means (LSM) Holstein RT (40.16 ± 0.01°C) were higher ($P < 0.01$) than crossbred RT (40.07 ± 0.01°C) while Jersey RT (40.09 ± 0.03°C) were not significantly different from Holstein RT or crossbred RT. Summer RT (40.24 ± 0.02°C) were higher than spring RT (40.08 ± 0.01°C), fall RT (40.09 ± 0.03°C) and winter RT (40.03 ± 0.02°C) ($P < 0.01$). In the spring, Holstein RT were higher than Jersey RT ($P < 0.01$) and crossbred RT ($P < 0.01$), with no significant differences observed between Jersey RT and crossbred RT. In the summer, Holstein RT were higher than crossbred RT ($P < 0.01$) and crossbred RT and Holstein RT were higher than Jersey RT ($P < 0.01$). In the fall, crossbred RT were higher than Holstein RT ($P < 0.01$) with no other significant differences among breeds observed. In the winter, Jersey RT were higher than Holstein RT ($P < 0.01$) and crossbred RT ($P = 0.02$) and Holstein RT were higher than crossbred RT ($P = 0.02$). These results may be useful in interpreting differences in RT obtained across varying seasons and breeds.

Key Words: reticulorumen temperature, season, breed

M230 Udder skin temperature of dairy cows under heat stress and physiological parameters tested by infrared thermography in two cooling system conditions.

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Obtaining internal temperature is difficult under practical farm management conditions and requires animal restraint. An alternative might be to directly measure animals′ surface temperature. In this study infrared thermography was used to measure udder skin temperature. Thermal stress can adversely affect milk yield and milk composition. Our primary objective was to examine how udder temperature, as a measure of core body temperature, is affected by environmental conditions; moreover we aimed to assess the effects of test day, stage of lactation and 2 different cooling systems, Sprinkler system (SP) and Shower system (SH), on physiological parameters. Twenty Holstein cows were split into 2 treatment groups, SH and SP and within each treatment had additional ventilation. Cows were assigned to 2 treatments of 10 animals with similar average days in milk (DIM), milk production and milk composition. Respiration rates (RR), rectal temperature (RT) and udder skin temperature (UST) were measured, each time, between 3 and 5:30 p.m. Individual milk samples were measured 6 times, with 15-d intervals, beginning at the end of June and analyzed for fat, protein and lactose content. At each test day, ambient temperature, relative humidity and THI were calculated. THI values at test d 1 through 6 were 73.3, 79.7, 77.8, 74.1 and 72.3, respectively. Udder skin temperature was significantly affected by test day ($P \leq 0.001$). Measured RT and RR (LSMeans ± SE) in SH were 39.3 ± 0.1 and 61.2 ± 1.6, respectively and in SP were 38.9 ± 0.1 and 53.9 ± 1.6, respectively. Udder skin temperature, milk yield, fat protein and lactose (%) were not different between treatments ($P \geq 0.05$). These parameters were only affected by test day ($P \leq 0.001$). Relative humidity with SH might be higher compared with SP and might have increased heat stress of dairy cows. In conclusion, RT and RR were more sensitive than the udder skin temperature, measured by infrared, to detect core body temperature during heat stress. More work, on different milk parameters, would be necessary to better understand the infrared application in measuring udder surface temperature.

Key Words: infrared thermography, udder skin, cooling system

M231 Establishing the summer:winter ratio to evaluate the effects of heat stress on conception rates in US commercial dairies.

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Objective was to utilize conception rates (CR) to establish a summer:winter ratio (S:W) to determine the severity of heat stress on US dairies. Records for 684 dairies totaling 767,768 lactating cows were collected from Dairy Herd Improvement Association and Reproductive Program Management software (Genex Cooperative Inc.). The average CR for 3 summer months (Jul.-Sep. 2010) was divided by the average CR of 3 winter months (Jan.-Mar. 2011) to obtain the S:W ratio. Effects of herd size (small < 500 cows, medium 500–1000 cows, large > 1000 cows), facility type (drylot vs. freestall), US region (north vs. south), and breed (Holstein vs. crossbred and Jersey) on the S:W ratio were analyzed. There was no difference between breeds (Holstein; 0.69 vs. crossbred and Jersey; 0.70). A main effect ($P < 0.05$) of US region (north: 0.89 vs. south: 0.51 ± 0.02), facility (drylot: 0.73 vs. freestall: 0.66 ± 0.25), and dairy size (small: 0.64 vs. medium: 0.71 and large: 0.74 ± 0.03) was observed. However, there was an interaction ($P < 0.01$) between US region and dairy size with small and medium-sized dairies in the north having an increased S:W ratio vs. large dairies (0.88, 0.93 vs. 0.84 ± 0.03), whereas in the south, small and medium-sized dairies had a smaller S:W ratio than larger dairies (0.40, 0.48, vs. 0.64 ± 0.02). Herds were further separated into the top and bottom 10% for S:W ratio by US region. The top herds in the north (n = 42) and south (n = 18) had a S:W ratio of 1.12 and 0.97 ± 0.01, respectively. The bottom herds in the north (n = 42) and south (n = 18) had a S:W ratio of 0.56 and 0.25 ± 0.01, respectively. An interaction ($P < 0.01$) between US region and herd ranking was observed with dairies in the north having smaller difference in S:W ratio between top and bottom herds compared with dairies in the south (1.12, 0.56 vs. 0.97, 0.25 ± 0.01). There was no effect of breed. Our results indicate that facility type, dairy size and US region can affect S:W ratio. In addition, top dairy herds have almost eliminated the summer decline in CR whereas bottom herds have a 44 - 75% reduction in CR due to heat stress.

Key Words: heat stress, dairy, summer:winter ratio

M232 Utilizing production parameters to establish the summer:winter ratio to evaluate the effects of heat stress on commercial dairies in the southwest.

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Objective was to utilize pregnancy rate, conception rate, and standardized 150 d milk production (STMLK) to establish a summer:winter ratio (S:W) for evaluating the severity of heat stress on dairies in the southwest. Records for 124 dairies totaling 192,765 lactating cows were collected from Dairy Herd Improvement Association and Reproductive Program Management software (Genex Cooperative, Inc.). The average conception rate, pregnancy rate and STMLK for 3 summer months (Jul.-Sep. 2010) were divided by the average of 3 winter months (Jan.-Mar. 2011) to obtain a S:W ratio for each. Effects of herd size (small < 700 cows vs. large > 700 cows), facility type (drylot vs. freestall), SW region (central, east, south and west), breed (Holstein vs. crossbred and Jersey) and reproductive management (bull vs. AI) on each S:W ratio were analyzed. There was no effect of any variables analyzed on S:W ratios for STMLK and conception rate. There was an effect of herd size ($P < 0.01$) and region ($P < 0.01$) with small herds having a lower S:W pregnancy rate ratio compared with large herds (0.42 vs. 0.62 ± 0.07) and herds in the west having a greater S:W pregnancy rate ratio compared with central, east and south (1.0 vs. 0.45, 0.42, 0.20 ± 0.1, respectively). Herds were further separated into the top and bottom 20% for both STMLK (1.08 and 0.86 ± 0.01) and pregnancy rate (0.71 and 0.23 ± 0.05) S:W ratio. The top 20% of the herds (n = 19) for STMLK S:W ratio also had a greater S:W pregnancy rate ratio compared with bottom herds (n = 18; 0.68 vs. 0.24 ± 0.08). In addition, the top S:W pregnancy rate ratio herds had an increased ($P < 0.01$) S:W STMLK ratio compared with bottom herds (1.02 vs. 0.96 ± 0.02). In conclusion, STMLK is reduced 22% and pregnancy rate 48% from the top versus bottom ranking herds. Also, herds which maintained an increased STMLK during summer also maintained a greater reproductive performance during summer. The top ranked herds evaluated still lost 29% of their pregnancy rate during summer whereas bottom herds lost 77%.

Key Words: heat stress, dairy, summer:winter ratio

M233 Heat stress effects on milk production and udder health in Holstein and Jersey cows. D. L. Smith, S. H. Ward,* T. Smith, and B. J. Rude, *Department of Animal and Dairy Sciences, Mississippi State University, Mississippi State.*

The objectives of this study were to: 1) investigate effects of heat stress and breed on milk and component yield for Holstein and Jersey cows on the same farm and 2) determine the effects of breed on udder health as measured by somatic cell count during times of heat stress. Data were collected from DHIA records from the Bearden Dairy Research Center at Mississippi State. After the removal of duplicates, 16,429 individual monthly records from 1997 to 2010 pertaining to Holstein and Jersey cows were used. Measures taken from the monthly records were: yield, milk fat percentage, milk protein percentage, and SCC. Milk yield (MY) and milk fat percentage were used to calculate 4% fat corrected milk (FCM). Climatological data were obtained from the National Weather service station located at the Golden Triangle Regional Airport (GTR) and the weather station operated by the Department of Geosciences on the campus of Mississippi State University (MSU). The weather measurements included, maximum and minimum temperature, along with maximum and minimum relative humidity. Any missing weather measurements were obtained from the National Weather Service station located at the Columbus Air Force base near Columbus, Mississippi. Maximum and minimum ambient temperature and relative humidity were determined from hourly data for each 24-h period and were used to calculate THI. Effects of THI, breed, and the interaction were analyzed using PROC MIXED (SAS Institute, 2009). The dependent variables were test day milk yield and milk components, SCC, and FCM. The model included fixed effects for combined THI (t), breed (b), and breed x THI, with DIM (d) as a covariate. All main effects were tested along with all interactions. Milk yield and FCM decreased during heat stress in Holsteins (34.2 vs. 32.9 kg/d, $P < 0.01$) and was not different in Jerseys (24.7 vs. 25.8 kg/d, $P < 0.20$). Heat stress affected somatic cell count although effects varied by intensity of heat stress. Breed did not have an effect on somatic cell count. Milk fat and protein percentages declined for both breeds in heat stress conditions. Milk fat but not milk protein of Jersey cows increased as stress increased from mild to severe. During heat stress and cool conditions Holstein cows had reduced FCM from 35.7 kg to 33.6 kg ($P < 0.05$) while Jersey did not differ. From mild heat stress to moderate Jersey FCM did not differ from 27.1 kg/d to 25.7 kg/d, respectively ($P > 0.05$) but was reduced to 23.7 kg/d when THI exceeded 90. FCM in Holsteins decreased during mild, moderate and severe heat stress from 34.8 kg/d to 32.8 kg/d and 30.9 kg/d, respectively. During heat stress, total MY in Holstein cows remained greater than in Jerseys, however, MY in Jersey cows was not affected by increased THI.

Key Words: dairy cows, heat stress, milk production

M234 Impact of season on the metabolic profile in transition Holstein dairy cows in summer and winter. K. J. Lager*[1,2], E. R. Jordan[1], R. G. S. Bruno[1,2], J. A. H. Rivera[3], R. Sprowls[4], and D. R. Topliff[2], [1]*Texas AgriLife Extension Service, Texas A&M System, College Station,* [2]*West Texas A&M University, Canyon,* [3]*Texas AgriLife Research, Stephenville,* [4]*Texas Veterinary Medical Diagnostic Laboratory, Amarillo.*

The objective of this study was to determine differences on an extensive metabolic profile between seasons of transition Holstein dairy cows with current genetics and dairy management strategies. Blood samples were collected in summer (n = 1787) and winter (n = 1871) from Holstein cows within the transition period via coccygeal vessel venipuncture in nonheparinized vacuum blood tubes at morning feeding on 8 commercial dairies. One day per dairy was utilized to collect blood samples for cows within the transition period and the same dairies were sampled for both time periods. 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. Weather data was collected for the 2-week period before sample collection. Herd records were reviewed to identify data points from cows experiencing dystocia, retained placenta, displaced abomasum, twin births, stillbirths and cows being dry <30d or >80d and data were analyzed using multiple regression in SAS. Seasonal effects were shown ($P < 0.05$) for all parameters exclusive of Na. Designating 3 d before 3 d post calving as week zero with 7 d intervals radiating from zero, analysis revealed that week relative to calving had an effect ($P < 0.05$) on serum P, Mg, glucose, cholesterol, NEFA, Na, K, and Cl levels. However, the effects of health parameters were limited to Ca, Cl, and albumin. Dry period length was also shown to affect ($P < 0.05$) profile parameters including P, albumin, glucose, cholesterol, NEFA, and K. Based upon these results reference values utilized for metabolic profile analysis may benefit by taking into account seasonal variation.

Key Words: dairy cow, metabolic profile, transition period

M235 Abundance of antibiotic resistance genes in the gut and feces of ionophore-fed lactating cows. T. Galligan,* P. P. Ray, A. Pruden, and K. F. Knowlton, *Virginia Polytechnic Institute and State University, Blacksburg.*

The contribution of dairy cattle to the global pool of antibiotic resistance genes (ARG) is a growing concern. The use of ionophores or subtherapeutic doses of other antimicrobials may select for antibiotic-resistant bacteria, contributing to the ARG reservoir in the cow gut. Improved knowledge of the establishment of ARG in the gut and feces would support assessment of the contribution of dairy cattle to the environmental pool of ARG. The objective was to evaluate the effect of ionophores on the abundance of ARG in ruminal fluid, ileal digesta, and feces of lactating cows. Five lactating dairy cows were examined in a crossover design over 2, 30-d periods. Cows were fed diets with and without the ionophore monensin (320 mg/d). Cows in the study were exposed to oxytetracycline in milk replacer as calves but had no history of exposure to sulfonomides or erythromycin. On d 30 of each period, ruminal, ileal, and fecal samples were collected and subjected to DNA extraction. Six common ARG were subsequently analyzed by quantitative polymerase chain reaction: *tet*W, *tet*G, *tet*X, *tet*O, *sul*1, and *erm*F, encoding resistance to tetracyclines, sulfonomides and erythromycin, respectively. The effects of site (rumen, ileum, feces) and ionophore feeding on absolute and relative abundance of the ARG were analyzed using PROC GLIMMIX procedure in SAS. All 6 ARG were detected in all samples. *Tet*W was the most abundant ARG in all sample types, followed by *tet*O. Absolute abundance (log gene copies/g wet sample) of each ARG was similar in rumen and ileal samples but lower ($P < 0.10$) in fresh feces. Relative abundance (gene copies/16s rRNA) was similar among the rumen, ileum, and feces. Monensin did not affect absolute or relative abundance of any ARG at any sampling site. The ARG were present in the digestive tract before the cows were exposed to monensin, suggesting that monensin is not a driver of the cow gut ARG reservoir. Therefore, simply removing these antibiotics from the diet will not reduce the global ARG pool. Other management strategies must be evaluated to reduce ARG contribution from dairy cattle.

Key Words: antibiotic resistance gene, ionophore, dairy cow

M236 Production and management consequences of abortion in dairy herds of central Mexico.

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The objective of this study was to evaluate annual abortion rate and consequences of abortion on dairy management, milk production and herd growth of intensive dairies in central Mexico. Abortions, as well as productive and reproductive events after abortion, were recorded for 2 consecutive years. Records included abortion-conception interval, days in milk, days to culling of cows post-abortion and days of gestation when abortion occurred. Annual rate of abortion, as well as percentage of pregnant cows and percentage of culled cows were calculated. Productive and reproductive events were analyzed using an ANOVA where parity and the reproductive state post-abortion were considered as main effects, and the herd as a block. Proportional variables were analyzed by multiple logistic regressions. Annual rate of abortion was variable between herds with a range of 13.3 to 19.9% ($P < 0.01$). Days of gestation at the time of abortion in multiparous cows with a parity greater than 3 (182.9 ± 3.6 d) was higher ($P < 0.05$) than in primiparous cows (165.7 ± 5.3 d). Stage of gestation (thirds) at the time of abortion and parity were not important on the percentage of pregnant cows after abortion ($P > 0.05$). Days in milk (274 ± 155.2 d) and abortion-conception interval (124.2 ± 96.4 d) were similar for parity ($P > 0.05$). Pregnant cows after abortion had more days in milk (307.6 ± 9.2 d) than non-pregnant cows (175.4 ± 11.7; $P < 0.01$). It was found that 36% of the cows that aborted were eliminated or culled by 223.1 ± 177.4 d post-abortion whereas only 19.5% of cows pregnant were culled ($P < 0.01$). Elevated abortion rates negatively compromised cow replacements, production and management of dairy farms located in central Mexico.

Key Words: dairy cow, abortion, Mexico

M237 Prevalence of dairy cattle diseases and abortion in central Mexico.

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Objective of this study was to describe prevalences, risk populations, and in some cases risk factors for diseases such as Leucosis, Paratuberculosis and Brucellosis in dairy cattle of Aguascalientes state in Central Mexico. Serum samples were collected to analyze for Leucosis (n = 340), Paratuberculosis (n = 422), and Brucellosis (n = 445) and it was found that the prevalence for those diseases was 51.6%, 16.3% and 20.3%, respectively. There was an association ($P = 0.01$) between cows having abortion 15 d before the blood sampling and Brucellosis. Abortion prevalence was also evaluated in milking herds at highlands of Central Mexico (Aguascalientes and Jalisco states). Four dairy herds that had similar management (i.e., related to preventive medicine, health and sanitary conditions, production, nutrition, and reproduction) were evaluated. Abortion cases were reported (n = 810), with 183.4 ± 58.0 d of gestation at abortion, average days in milk at abortion of 328.7 ± 130.9 d, interval from abortion to new pregnancy of 355.9 ± 197.7 d, and 73.9% of cows calving after abortion. Culling of cows as a consequence of abortion was reported as 36.0% with an average days in milk of 223.1 ± 177.4 d. It was also observed that 35.3% of cows had abortions during the dry period. This study provided some descriptive information related to disease and abortion prevalences in Central Mexico's dairy herds.

Key Words: dairy cows, brucellosis, Mexico

M238 Analysis of factors affecting heifer fertility traits in Chinese Holstein.

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The improvement of fertility in heifers plays a key role in improving longevity and lifetime production in dairy farm. However, there were only few studies analyzing fertility traits in Chinese Holstein. The objective of current study was to identify factors affecting fertility traits in heifers and to provide a theoretical basis for improving dairy cattle production efficiency in Chinese Holstein. Data of fertility traits from 22 dairy farms (2000 to 2010) were collected from Beijing Sanyuan Lvhe Dairy Cattle Centre, including interval from first service to conception (FSTC) and conception rate for first insemination (CR) in heifers. The final data set included 23,035 heifers, daughters of 119 bulls. Fixed effects of herd, birth year, birth season, year of first mating, season of first mating, and sire were considered in the model, and SAS 9.1 was used to run the analysis. The simple statistics for FSTC and CR were 13.59 ± 30.82 d and 74.4% ± 43.7%, respectively. All factors studied had significant association with FSTC and CR ($P < 0.05$ or $P < 0.01$) except birth season. For FSTC and CR, the largest differences among farms were 14.28 d and 26.0%, respectively. For heifers born in year 2000, average FSTC and CR were 0.34 d and 99.7%, respectively; thereafter there was a declined trend for reproductive efficiency, e.g., average FSTC increased about 3 d per year while CR decreased 6.0% per year from birth year 2000 to birth year 2006. Birth year 2006 became a turning point, since then both FSTC and CR started to be improved. Year of first mating showed exactly the same trend as birth year did. Therefore further analysis of fertility traits can drop birth season and either of the 2-year factors. The heifers first mated in colder seasons (autumn and winter) had lower CR (2.9%) and longer FSTC (1.29 d) than those mated in warmer seasons (spring and summer). The effect of sire was significant, which means genetic selection could improve heifer fertility performance. In conclusion, heifer reproductive performance was influenced by multiple factors, and could be improved by better on-farm management and selection of a fertile sire.

Key Words: fertility traits, heifer, Chinese Holstein

M239 Characterization of certified organic Wisconsin dairy farms: Management practices, feeding regimens, and milk production. C. A. Hardie*[1], V. E. Cabrera[1], M. Dutreuil[1], R. Gildersleeve[2], and M. Wattiaux[1], *[1]University of Wisconsin-Madison, Madison, [2]University of Wisconsin Extension, Dodgeville.*

The purpose of this project was to characterize certified organic Wisconsin dairy farms and evaluate their feeding regimens during the course of 2010. Farms were identified by cross listing 2 separate directories: the Wisconsin Active Dairy Producers and the Wisconsin Certified Organic Producers. All resulting organic dairy herds from these lists were invited to participate (n = 565) in this study. An on-site survey containing sections on farm demographics; feeding, pasturing, cropping and nutrient management practices; sources of income; and farm satisfaction was conducted on 54 farms throughout the state between March 2011 and January 2012. Forty-six percent of the farms relied entirely on family labor to complete farm chores. Total area operated ranged from 17.8 to 775.6 ha, with a mean (±SD) of 123.4 (±133.4). Hectares of pasture ranged from 6.1 to 145.8, with a mean (±SD) of 40.9 (±30.84). Herd size ranged from 12 to 650 cows, with a mean (±SD) of 71.3 (±92.2). The predominant breed varied on the farms, too, with 51.9, 27.8, 9.3, and 11.1% of the herds having Holstein, crossbred, Jersey, and other, respectively as their major breed. Milk rolling herd averages varied from 2,356 to 10,274 kg/cow per year, with a mean (±SD) of 6,182 (±1,846). Total dry matter intake (DMI) for lactating cows ranged from 11.8 to 25.6 kg/cow per day, with a mean (±SD) of 19.8 (±3.4). Peak pasture intake during the grazing season ranged from 1 to 100 percent of total DMI, with a mean (±SD) of 69.1 (±25.5). The farms' grazing seasons in 2010 ranged from 122 to 244 d, with a mean (±SD) of 182.0 (±28.7). During the grazing season, 79.6, 13.0, and 31.5% of the herds supplemented grain, protein, and corn silage, respectively. As indicated by the ranges and SD presented here, certified organic Wisconsin dairy farms varied widely in farm characteristics, feeding regimens, and animal production. Awareness of these extreme variations should help design extension programs and agricultural publications better suited to meet the educational needs of this growing dairy sector. Supported by AFRI Competitive Grant no. 2010–51300–20534.

Key Words: organic, grazing, supplementation

M240 Impact of dairy herd reproductive performance on predicted economic performance, enteric CH$_4$ emission and excretion of N and P using a Markov-chain model. M. J. Aguerre,* J. O. Giordano, A. S. Kalantari, M. A. Wattiaux, P. M. Fricke, and V. E. Cabrera, *University of Wisconsin-Madison, Madison.*

Our objective was to estimate the effect of reproductive performance on predicted enteric CH$_4$ emission, and N and P excretion of lactating and dry cows in a dairy herd. A Markov chain model was used to simulate herd dynamics based on productive and reproductive input parameters. Different herd structures were obtained after simulation of herds with 12 (Low) vs. 22% (High) 21d-pregnancy rate. Lactation curves from a commercial farm were used to simulate milk production whereas DMI was calculated based on NRC 2001 empirical equation. Diets for cows in early (0 to 150 DIM) or late (>150 DIM) lactation contained 16.7 vs. 15.4% CP, 44.2 vs. 41.4% NFC, 10.4 vs. 11.2% hemicellulose (HC), 16.7 vs. 23.0% cellulose (CEL) and 0.38 vs. 0.34% P, respectively. Dry cows diet was formulated to contain 13.2% CP, 34.8% NFC, 14.3% HC, 24.8% CEL and 0.27% P. Enteric CH$_4$ emission was predicted by an empirical equation (CH$_4$ g/d = [(0.814 + 0.122 x intake NFC kg + 0.415 x intake HC kg + 0.633 x intake CEL kg)/0.05565]. Manure N and P excretion (g/d) was predicted by difference between intake and milk secretion for each element. Net value ($/cow per yr) for High and Low pregnancy rate were calculated by summation of income over feed cost, replacement cost, reproductive program cost, and calf value. Compared with Low, High program resulted in higher milk production per lactating cow (40.3 vs. 41.8 kg/d), lower percentage of lactating cows (90.6 vs. 88.8%), lower average DIM (188 vs. 176), and higher income over feed cost (7.76 vs. 7.84 $/cow per d). In addition, High outperformed Low by $69.4/cow/yr. Predicted CH$_4$ and CH$_4$/milk were 425 g/d and 11.64 g/kg for Low and 419 g/d and 11.37 g/kg for High which represented a 1.4 and 2.3% reduction. Relative to Low, with the High program N and P excretion were reduced by 1.1% (373 vs. 369 g/d) and 1.3% (45.0 vs. 44.4 g/d), respectively. Under the simulation conditions of this study, changes in herd structure associated with improved reproductive performance reduced predicted environmental impact while improving profitability.

Key Words: reproductive performance, methane, nitrogen and phosphorus

M241 Reproductive indicators of dairy enterprises in north and west Mexico. H. Estrella-Quintero,* D. V. Mariscal-Aguayo, R. Núñez-Domínguez, and G. Maldonado-García, *Universidad Autónoma Chapingo, Chapingo, Estado de México, México.*

The purpose of this study was to evaluate the reproductive performance of family-based dairy enterprises in transition and business considering their technological level. Transition enterprises are those moving from subsistence to business, the latter being the ones that market all their products. The information used was registered in the AGROPEC Star software of 12 farms in transition level and 7 in business level located in northern and western Mexico, with a total of 3,935 Holstein cows and for a period from 1996 to 2011. The variables evaluated were: services per conception (SPC), calving interval (CI), calving to first estrus interval (CFEI) and interval from calving to first service (CFSI). A mixed model was used that included fixed effects of technological level, and number, year and season of birth, and significant 2-way interactions between these effects, and as random effects, the enterprise nested in the technological level and cow within enterprise. The technological level had an effect ($P < 0.05$) in SPC and CI; the interaction of technological level by year of birth had an effect ($P < 0.05$) in all the variables. The transition technological level had 1.8 ± 0.05 SPC and 403.4 ± 4.9 d of CI lower ($P < 0.05$) than the business technological level which averaged 2.08 ± 0.09 and 426.7 ± 8.1 d, respectively. No significant differences were found between technological levels for CFEI and CFSI. In conclusion, enterprises in transition had better reproductive performance than business enterprises.

Key Words: enterprises, cows, Holstein

M242 Seasonal variation on milk components and relation to quality payment program. L. C. Roma Junior*[1], A. C. S. Gonçalves[1], and P. F. Machado[2], *[1]APTA Centro Leste, Ribeirao Preto, Sao Paulo State, Brazil, [2]Clínica do Leite, ESALQ/USP, Piracicaba, Sao Paulo State, Brazil.*

The existence of a wide variation in milk quality in subtropical regions due to season of the year has been reported previously. However, participation in a payment program based on milk quality can generate profits or losses to the producer due to this variation. The main objective of this study was to quantify the effect of milk price variation, recognizing significant causes of it and possible parameters that need more attention. For one year, 250 dairy farms in the Southeast region of Brazil were inspected for the following milk parameters: fat, protein, non-fat solids, somatic cell count and total bacterial count. At the same time, monthly climate data were collected in the region to observe climate variability and allow investigation correlating those data with the outcomes. The randomized design was used, with season as a factor (summer, autumn, winter and spring). The means were evaluated using Proc GLM, by Tukey test with a significance level of 5%. It was observed that there was a significant effect between variation on milk quality and final price of the marketed milk. The bonus variation ranged from 2.34% (spring) to 7.87% (autumn), and the only season that showed a significant variation in the milk price was autumn ($P < 0.05$). One of the factors that influenced the bonus the most was somatic cell count, contributing with a year average penalty of 1.89%, followed by bacterial count, with a penalty of 0.24%. On the other hand, milk protein was the component responsible for providing most of the bonus, averaging 3.77%. In conclusion, there was an effect of season on bonus/penalty for the producer; somatic cell count was the variable that penalized price the most. Knowledge on the effect of season in payment amount for quality can inform the producer, who should act to prevent and control quality of milk produced. In some cases, the producer would be able to concentrate milk production increases and calving at a season when best bonuses are offered, aiming to achieve greater production profitability. Financial support by FAPESP, process 05/51369-8.

Key Words: environmental effects, payment for milk quality, seasonability

M243 Effects of temporary calf removal (CR) prior to fixed-time AI (TAI) on pregnancy rates and subsequent calf performance in suckled beef cows.

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Two experiments were conducted to determine the effect of calf removal (CR) on pregnancy rate and calf performance in suckled beef cows. Cows were synchronized with the 7-d CO-Synch + CIDR protocol (100 µg injection of GnRH at CIDR insertion [d −7] with 25 mg injection of $PGF_{2\alpha}$ at CIDR removal [d 0], followed by injection of GnRH and TAI on d 3). Cows were stratified by d postpartum, BCS, and parity and assigned to one of 2 treatments in Exp. 1: CON (control; n = 156) and CR72 (calves were separated from their dams for 72 h from d 0 and 3; n = 168); and one of 4 treatments in Exp. 2; CON (n = 105), CR72 (n = 107), CR48A (CR for 48 h from d 0 to d 2; n = 99), and CR48B (CR from d 1 to d 3; n = 53). Follicle dynamics and CL development were assessed on d 0, 3, and 10 and pregnancy status determined on d 30. Blood was collected on d −14, −7, 0, 3, and 10 to determine P4 and E2. Overall pregnancy rates did not differ among treatments (Exp. 1, 50.3%, $P = 0.58$; Exp. 2, 49.1%, $P = 0.15$). In Exp.1, CR72 (0.42 ± 0.15 mm/d) had increased follicle growth rate ($P < 0.01$) from d 0 to 3 compared with CON (0.02 ± 0.15 mm/d), but there were no differences in follicle diameter on d 0 or 3 ($P > 0.1$). In Exp. 2, E2 concentrations were greater ($P < 0.01$) in the CR72 treatment at 24 h after $PGF_{2\alpha}$ compared with other treatments (7.4 ± 1.4, 14.6 ± 1.6, 8.4 ± 1.6, and 7.7 ± 1.6 pg/mL for CON, CR72, CR48A, and CR48B, respectively). Young (25 to 59 d of age) and old (>80 d of age) calves lost a greater ($P < 0.05$) percent of body weight (PBW) during CR than medium (60 to 79 d of age) aged calves exposed to CR72 (−4.7 ± 0.4%, −1.9 ± 0.4%, and −2.5 ± 0.5% PBW change for young, medium, and old, respectively) and to CR48 (−4.8 ± 0.5%, −2.1 ± 0.6%, and −2.6 ± 0.8% PBW change for young, medium, and old, respectively), whereas CON calves gained weight during CR (3.7 ± 0.4%, 1.7 ± 0.5%, and 2.1 ± 0.5% PBW change for young, medium, and old, respectively). We conclude that CR was not able to improve pregnancy rates but did increase follicle growth rate before TAI. Subsequent calf performance was affected by 72 or 48 h calf removal.

Key Words: calf removal, artificial insemination, beef cows

M244 Effect of cattle processing and handling on changes in measures of temperament during a 70-d feed efficiency test.

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We determined the effect of animal handling and processing over a 70-d feed efficiency test (FET) on changes in temperament in beef cattle. Over a 3-yr period (2009 to 2011) 8 separate groups of bulls (n = 526), steers (n = 182), and heifers (n = 133) comprising *Bos taurus*, *Bos indicus*, or *Bos taurus* × *Bos indicus* genetics were processed through the University of Florida Feed Efficiency Facility using a GrowSafe feed intake system (GrowSafe Systems Ltd., Alberta, Canada) for a FET. Animal was the experimental unit. Cattle were exposed to a 14 d acclimation period before initiation of a 70 d FET. Cattle were processed every 14 d (d0, d14, d28, d42, d56, and d70) for collection of BW and temperament data. Temperament data consisted of chute score (CS) and exit velocity (EV). Chute score, the subjective measurement of the behavioral response to restraint in the squeeze chute, was assigned on a 1 to 5 scale (1 = calm and docile; 2 = restless; 3 = nervous; 4 = excited and flighty; 5 = aggressive) and EV was the speed (m/s) at which each animal exited the squeeze chute and passed by infrared sensors placed 1.83 m apart. Chute score ($r = -0.199$) and EV ($r = -0.254$) were correlated with BW ($P < 0.001$) and EV was correlated with CS ($P < 0.001$; $r = 0.273$). For repeated measures analysis on CS and EV, BW was used as a covariate and day as the repeated variable. There was no effect of sex ($P = 0.119$) on CS. However, CS was affected by breed ($P = 0.002$) with 50% Angus-50% Brahman (50/50) crossbred cattle having greater CS than Ultra Black (UB; 75% Angus, 25% Brahman) cattle ($P = 0.04$). In addition, Brangus (BN; $P < 0.001$) and Brahman cross (BX; $P = 0.003$) cattle had greater CS than Angus (AN) cattle, with BN having greater CS than UB ($P = 0.02$). For EV, a breed × sex interaction existed ($P = 0.047$) indicating that EV for heifers of BN origin was greater ($P < 0.01$) than for bulls of BN origin. Exit velocity did not differ ($P < 0.01$) between sexes among all other breeds. There was a group × day interaction ($P < 0.001$) for CS and EV, with cattle from differing FET groups having differences in CS and EV as d on test progressed. In conclusion, handling and processing during a FET did not improve animal temperament, and changes in CS and EV during a FET appear to be associated with previous management and herd genetics, as evidenced by the group × day interaction. However, breed influenced CS and EV during a 70-d FET.

Key Words: temperament, beef cattle, animal handling

M245 Culling reasons and the association of herd size and milk yield with culling rates in dairy herds in southern Brazil. R. Almeida*[1], D. F. F. Silva[1], L. Alegransi[1], R. B. Navarro[2], A. A. Valloto[3], and J. A. Horst[3], [1]*Universidade Federal do Paraná, Curitiba, PR, Brazil,* [2]*Capal Cooperativa Agroindustrial, Arapoti, PR, Brazil,* [3]*Associação Paranaense de Criadores de Bovinos da Raça Holandesa, Curitiba, PR, Brazil.*

The objective of this study was to identify reasons for culling lactating dairy cows in herds located in Arapoti county, Paraná State, southern Brazil. In addition, the association of culling rate with milk yield and herd size was also investigated. Statistical analyses were performed using CORR and GLM procedures (SAS), and herd within year was the experimental unit. A multivariate regression model was developed, where culling rate was the dependent variable, and year, herd size, and herd milk yield categories were the independent variables. Data set included 21 herds and data were collected from January 2007 to December 2010. A total of 3,961 cows were culled or died in these herds during the study period. The most important reasons for culling were reproductive disorders (33.5%), clinical mastitis and high somatic cell count (22.2%), and feet and leg problems (18.5%). The first 3 mo of lactation were critical; 28.1% of deaths and culls were observed during this period. Approximately one-fifth (19.8%) of culled cows were first-parity females. Culling rates were lower ($P < 0.05$) in the first 2 years (21.9% in 2007 and 24.2% in 2008) than in the last 2 years (26.2% in 2009 and 26.4% in 2010) of the study. The observed culling rates were lower than the 30% culling rate typically found in confined herds in Brazil, suggesting that the current milk prices encouraged dairy farmers to keep cows in their herds longer. Small herds (less than 150 cows) had lower culling rates ($P < 0.05$) than medium (150 to 250 cows) and large herds (more than 250 cows). The correlation between culling rate and herd size was moderately positive ($r = 0.25$; $P < 0.05$), suggesting that small herds kept cows for more lactations. There was a difference in culling rates between high- and low- milk yield herds and the correlation between these 2 variables was significant ($r = 0.26$; $P < 0.05$). Larger and higher-producing dairy farms had higher culling rates in the subtropical south of Brazil and these farms should carefully investigate culling reasons in their herds to identify areas for improvement.

Key Words: culling rate, reproduction, herd size

M246 Nitrogen utilization efficiency in specialized dairy herds in southern Brazil. D. Jerszurki[1], L. Jerszurki[2], R. B. Navarro[3], A. Ostrensky[4], G. T. Santos[5], and R. Almeida*[1], [1]*Universidade Federal do Paraná, Curitiba, PR, Brazil,* [2]*Universidade Tecnológica Federal do Paraná, Curitiba, PR, Brazil,* [3]*Capal Cooperativa Agroindustrial, Arapoti, PR, Brazil,* [4]*Pontifícia Universidade Católica do Paraná, Curitiba, PR, Brazil,* [5]*Universidade Estadual de Maringá, Maringá, PR, Brazil.*

The objective of this study was to determine current nitrogen utilization efficiency (NUE) of dairy herds in Arapoti county, Paraná State, southern Brazil, as well as to evaluate possible effects of dietary crude protein (CP) levels and milk yield on NUE. Twenty-eight commercial herds mostly containing Holstein cows and producing 29.0 ± 3.9 kg/cow/d were studied in a 5-year period (from January 2007 to December 2011). Each herd was monitored on average 4x per year, totaling 547 visits in the evaluation period. For validation purposes, on-site collection of TMR, milk, feces, and urine samples was conducted in 6 participating herds on February 2011. Freshly deposited feces were sampled just after being excreted by 60 lactating cows, randomly selected within herd. Urine samples from another 60 cows also randomly chosen were collected by a noninvasive method and mixed to make a composite urine sample with H_2SO_4 solution. Daily fecal and urinary volume excretions were estimated by the equations from the American Society of Agricultural and Biological Engineers Standards (ASAE, 2005). Statistical analyses were carried out with GLM procedure of SAS, and each farm visit was considered as an experimental unit. A multivariate regression was developed with NUE as the dependent variable, herd, year, and season as fixed effects, and milk yield as covariate. Estimated variables with their respective means and standard deviations were: 523 ± 49 g/d N intake (15.6 ± 0.7 dietary CP), 143 ± 19 g/d milk N (3.14 ± 0.11 milk protein %), 202 ± 16 g/d fecal N, 194 ± 20 g/d urinary N, and 27.31 ± 2.82% of NUE. N efficiency increased ($P < 0.01$) over the years: 25.2% in 2007, 27.0% in 2008, 27.3% in 2009, 28.0% in 2010, and 28.4% in 2011. Season was a significant effect ($P < 0.01$) only when the model did not include the covariate milk production, indicating that dairy cows had higher N balance in the winter season only because they produce more milk during cooler months. Correlations between NUE and milk yield ($r = 0.64$; $P < 0.01$) and between NUE and dietary CP ($r = -0.27$; $P < 0.01$) indicated that high-producing dairy herds that adopt conservative dietary CP levels had higher N efficiency.

Key Words: dietary protein, dairy cows

Ruminant Nutrition: Beef I

M247 Carcass primary cuts proportions of Nellore bulls stratified for residual feed intake. F. L. Araujo*[1], R. H. Branco[2], C. D. A. Batalha[1], S. F. M. Bonilha[2], A. C. Queiroz[1], and W. P. Costa[1], *[1]Departmento de Zootecnia, Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho, SP, Brazil.*

The study was conducted to evaluate proportion of primary cuts in carcass of Nellore bulls stratified for residual feed intake (RFI). Thirty animals with 414 ± 35.68 kg BW and 18 ± 1.11 mo of age, were evaluated in 2 experiments. The bulls were stratified in low RFI (<mean - 0.5 SD; n = 14) and high RFI (>mean + 0.5 SD, n = 16), and 2 feeding levels: ad libitum and restricted (65 g DM / kg BW0, 75). After slaughter and carcasses chilling period (24h), the right half-carcasses were divided in hindquarter, forequarter and spare ribs, which were weighed and had their ratio calculated based on cold half-carcass weight. Edible primary cuts were determined based on the relationship between the sum of cuts weights and the respective carcass primary cut weight; bones proportion was determined based on the relationship between the sum of bones weight and the respective primary cuts weight; shavings proportion was determined based on the relationship between the sum of shavings weight and the respective primary cut weight. Statistical analyzes were performed according to a 2x2x2 factorial scheme (2 RFI groups, 2 feeding levels and 2 experiments) in a completely randomized design, assuming $\alpha = 0.05$. There were no effect of different RFI levels in hindquarter weight (60.93 kg and 63.33 kg, respectively for low and high RFI; $P = 0.2549$), forequarter weight (51.39 kg and 54.82 kg, respectively for low and high RFI; $P = 0.1123$), spare ribs weight (17.95 kg and 19.01 kg, respectively low and high RFI; $P = 0.2112$), hindquarter edible portion (71.44% and 71.02%, respectively for low and high RFI; $P = 0.4621$), forequarter edible portion (64.25% and 65.60%, respectively for low and high RFI; $P = 0.1473$), spare ribs edible portion (43.26% and 45.27%, respectively for low and high RFI; $P = 0.3233$), hindquarter bones proportion (20.73% and 20.78%, respectively for low and high RFI; $P = 0.9167$), forequarter bones proportion (22.33% and 21.77%, respectively for low and high RFI; $P = 0.4982$), spare ribs bones proportion (14.37% and 14.91%, respectively for low and high RFI; $P = 0.4240$), hindquarter shavings proportion (10.14% and 10.64%, respectively for low and high RFI; $P = 0.3221$), forequarter shavings proportion (13.19% and 12.58%, respectively for low and high RFI; $P = 0.5399$) and spare ribs shavings proportion (16.64% and 16.21%, respectively for low and high RFI; $P = 0.7414$), showing that more efficient bulls (low RFI) had a lower dry matter intake ($P = 0.0003$) and had similar carcass traits ($P > 0.05$) when compared with less efficient animals (high RFI). RFI can be used to increase efficiency and reduce costs of production systems without resulting in damage to the carcasses of Nellore bulls.

Key Words: edible portion, Nellore, RFI

M248 Creatinine excretion and metabolizable protein requirements for maintenance of Red Norte young bulls. T. R. Amorim, M. M. Ladeira,* M. L. Chizzotti, J. R. R. Carvalho, A. R. V. Lima, N. L. Magalhães, and P. D. Teixeira, *Federal University of Lavras, Lavras, MG, Brazil.*

Protein is an expensive nutrient in beef cattle diets, and its correct balance is important to achieve high performance of the animals. In addition, an excess of dietary protein can increase nitrous oxide emissions. Therefore, the objective of this trial was to investigate the creatinine excretion and metabolizable protein requirements for maintenance of Red Norte young bulls. The experiment was conducted in a completely randomized design, with 5 treatments and 7 repetitions. Thirty-five animals, with an average live weight of 280 ± 4 kg, were allocated to individual pens, and received the following CP levels in the diets: 8, 10, 12, 14 and 16%. After 9 d for diet adaptation, total urine and feces collections were performed for 5 d. Metabolic fecal nitrogen, urinary endogenous losses and total endogenous losses were all estimated by regression approach. Creatinine concentration in urine was analyzed using colorimetric method. Protein levels did not influence ($P > 0.05$) creatinine excretion. The net protein requirements for maintenance were obtained as the intercept of the regression of retained nitrogen on nitrogen intake ($0.441 \times 6.25 = 2.75$ g/EBW$^{0.75}$; $P = 0{,}006$), with a partial efficiency of use of metabolizable protein to net protein for maintenance of 0.68 ($P < 0{,}001$). This efficiency is very similar of the values reported by NRC (1985) and BR-Corte (2010): 0.67, and 0.667, respectively. Using this efficiency and assuming the net protein requirement of 2.75 g of net protein/EBW$^{0.75}$ for maintenance, the daily metabolizable protein requirement was calculated as 4.05 g/EBW$^{0.75}$. According to this result, protein requirements for maintenance of Red Norte young bulls was higher than the value described by the NRC (1996) (3.8 g/EBW$^{0.75}$), and very close to the requirement recommended by BR-Corte (2010) (4.03 g/EBW$^{0.75}$).

Key Words: crude protein, nitrogen, requirement systems

M249 Measurement of purine derivatives and creatinine excretion in steers fed fescue seed. J. H. Eisemann,* G. B. Huntington, and A. E. Lamb, *North Carolina State University, Raleigh.*

The objectives were to measure urinary excretion of purine derivatives (PD) and creatinine (CRT) in steers in response to dietary ergot alkaloids, and to compare total daily and spot collections. Angus steers (n = 8) were fed a concentrate mix: switchgrass hay (40:60) diet containing endophyte-free (E-) or endophyte-infected (E+; 2.7 mg/d total ergot alkaloids, 9.6 ug/kg BW) fescue seed. Steers were housed indoors in individual pens with daily temperature ranging from 23.5 to 32.1°C. The design was a single reversal with 14-d treatment periods and 21 d between periods. Steers were fitted with a harness for total collection of urine on d 12 and 13 of each period. Urine was collected at 6-h intervals beginning at 1200 h on d 13. Aliquots from each interval collection within days were combined to form a daily collection. A spot urine sample was collected at 0800 and 1400 h. Urine PD and CRT were analyzed by HPLC. Data ANOVA included effects of treatment, day, and period. Steers' BW and DMI did not differ ($P = 0.20$) for E- (290 kg, 5.49 kg/d) and E+ (289 kg, 5.38kg/d). In total daily collections, urinary CRT excretion was lesser ($P < 0.05$) for E- than E+. Means were 1.13 and 1.21 mmol CRT per kg BW$^{0.75}$, respectively. The PDC ratio (PD/CRT, 1.21 and 1.08) and PDC index (PDC ratio x BW$^{0.75}$, 85.0 and 75.0) were greater ($P < 0.01$) for E- than E+. Total PD excretion (mmol/d) did not differ ($P < 0.15$) for E- (95.8) and E+ (91.0). Estimated microbial N production was not affected by E+ and was 58.8 and 54.8 g N/d for E- and E+, respectively. In spot collections, PDC (1.21 and 1.10) and PDC index (84.9 and 76.5) were greater ($P < 0.01$) for E- than E+. Calculated PD excretion (mmol/d) from spot collections was greater ($P < 0.01$) for E- (99.3) than E+ (89.5). Treatment responses were similar for PDC and PDC index in total daily and spot collections; however, treatment responses differed for total daily PD excretion and calculated daily PD excretion from spot samples. Treatment responses indicate urinary CRT excretion per kg BW$^{0.75}$ is not a constant for calculating PD excretion and microbial N production.

Key Words: purine derivatives, creatinine, steers

M250 Feedlot performance and carcass characteristics of limit-fed steers. K. Thompson*[1], P. Gunn[2], R. Lemenager[2], M. Claeys[2], T. Nennich[2], and S. Lake[1], [1]*University of Wyoming, Laramie,* [2]*Purdue University, West Lafayette, IN.*

The objectives of this study were to evaluate limit-fed feedlot steers on performance and carcass characteristics. Angus crossed steers (n = 168) were randomly blocked into one of 24 pens (6 pens/treatment; 7 steers/pen) and assigned to one of 4 dietary treatments: 1) 85% ad libitum intake 2) 90% ad libitum intake 3) 95% ad libitum intake; or 4) 100% ad libitum intake. Diets consisted of a corn-based finishing ration and the percentage of intake was calculated from the 100% ad libitum treatment on a weekly basis. All animals were harvested when their respective 12th rib fat depth reached 0.4 tenths. Data were analyzed using the MIXED procedure of SAS with preplanned orthogonal contrasts between the 4 dietary treatments. As expected, steers on the 100% ad libitum diet had greater DMI ($P < 0.001$) compared with all other treatments. Steers on the 95% ad libitum diet had greater DMI ($P < 0.001$) compared with the 85 and 90% ad lib diets, however, there was no difference ($P = 0.26$) between the 85 and 90% ad libitum treatments. Total ADG over the course of the study was greater ($P = 0.002$) for steers on the 100% ad libitum treatment; however, there were no differences ($P \leq 0.36$) between the other treatments. Steers on the 90% ad lib diets had a greater G:F ($P = 0.01$) compared with steers on the 95% ad lib treatment, while the 85 and 100% ad lib treatments were intermediate. Days on feed were greater ($P = 0.003$) for steers on the 85 ad libitum treatment when compared with the 95 and 100% ad libitum intake treatment; however, there was no difference ($P = 0.29$) between the 95 and 100% ad libitum treatments. Total feed costs did not differ ($P = 0.47$) between treatments. Steers on the 85% ad lib treatment group had less ($P = 0.01$) KPH fat compared with all other treatments; however, no differences ($P \geq 0.17$) were detected in HCW, 12th rib fat, REA, yield grade, or quality grade. Limit-feeding steers decreased DMI without sacrificing carcass quality; however, because days on feed were increased, there appears to be no economic advantage to limit-feeding feedlot steers.

Key Words: limit-fed, feedlot, steers

M251 Ergovaline disappearance from a ruminally incubated buffer. A. P. Foote*[1], N. B. Kristensen[2], J. L. Klotz[3], K. R. Brown[3], J. R. Strickland[3], D. H. Kim[1], A. F. Koontz[1], K. R. McLeod[1], L. P. Bush[1], and D. L. Harmon[1], [1]*University of Kentucky, Lexington,* [2]*Syddansk Kvæg, Vojens, Denmark,* [3]*USDA-ARS, FAPRU, Lexington, KY.*

Ergovaline (ERV) is an alkaloid present in endophyte-infected tall fescue (*Lolium arundinaceum*) that contributes to fescue toxicosis in cattle. To determine disappearance of ERV in the washed reticulorumen, steers (n = 8) were pair-fed alfalfa cubes at $1.5 \times NE_m$ and dosed with ground endophyte-infected tall fescue seed (E+) or endophyte-free tall fescue seed (E-) via rumen cannula 2 × daily for 7 d at thermoneutral (TN; 21°C) and heat stress (HS; 32°C) conditions. On d 8, the rumen was emptied and rinsed. Buffer containing VFA was incubated with 0.015 mg ERV/kg BW (1 × EXT) followed by an incubation with 0.045 mg ERV/kg BW (3 × EXT). The ERV in the buffer was supplied as a seed extract. For each buffer treatment there were 2 consecutive 30-min incubations where the first 30 min buffer incubation was not sampled. Following removal of the buffer an identical sampling buffer was incubated with the addition of Cr-EDTA. Buffer was sampled at 5, 15, and 30 min. Analysis of buffer samples for ERV was conducted using an Acquity UPLC with a TQ detector. Disappearance of ERV was calculated by changes in the pool size in the buffer corrected for dilution by physiological water and passage out of the rumen. In this model, ERV disappearance is the sum of absorption into blood, adsorption to the rumen wall or residual digesta particles, and metabolism. Treatment of steers with E+ seed had no effect on ERV disappearance ($P = 0.64$). ERV disappearance rate was higher with the 3 × EXT than 1 × EXT ($P = 0.02$). The interaction of temperature and buffer ($P = 0.08$) indicated that ERV disappearance increased 6.5-fold with increasing ERV during HS, but only increased 2-fold during TN. These data indicates that increasing the ruminal ERV dose increases ERV disappearance in steers at high ambient temperatures which could be caused by increased absorption rate, metabolism, or binding of ERV.

Key Words: washed reticulorumen, fescue toxicosis

M252 Body condition score and heart girth change between 7 and 18 months of age to estimate pregnancy probability of Hereford heifers mated at 18 months of age. J. B. G. Costa Junior*[1], J. O. J. Barcellos[1], J. C. Whittier[2], I. D. P. S. Diaz[3], L. Canellas[1], V. Peripolli[1], J. K. Ahola[2], and R. K. Peel[2], [1]*Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil,* [2]*Colorado State University, Fort Collins,* [3]*Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

Our objective was to use body condition score (BCS) and heart grith (HG) to estimate pregnancy probability (OR, odds ratio) in Hereford heifers at 18 mo of age originated from a commercial cattle herd at a facility in the state of Rio Grande do Sul, Brazil. Heifers were developed at 3 different levels of average daily gain - (ADG) (high - H, moderate - M and low - L) with 3 different combinations (LHM; HLL; MMH). These ADG levels were applied between 7 to 12 mo (P12); 12 to 15 mo (P15) and 15 to 18 mo of age (P18). Used to the LHM, MMH, and HLL treatments 65, 58, and 60 heifers respectively. This was done by OR, being adjusted within a complete model involving the treatment classifing variables and all the continuous variables (body weight - BW, hip's height - HH, heart girth - HG, body weight:height ratio - WH) at the age of 7, 12, 15, and 18 mo. The variables selected for this study were the BCS at 12 mo (BCS12) and HG at 18 mo (HG18), within the effect of treatment ($y = -30.6165 + 1.5294\ BCS12 + 0.1701\ HG11 + Treat$ (HLL = 0.0; LHM = 1.1699 and MMH = 2.2996); H&L = 0.30). The HLL treatment was taken as reference once it was determined to result in the lowest percentage of pregnancy. The heifers receiving the LHM treatment had 3.2 times more chances to conceive, while heifers in the MMH treatment presented a ratio 9.9 times higher than the ones of the HLL treatment. The variable HG18 effect showed higher significance ($P < 0.05$) in the pregnancy probability model than the BCS12. We conclude that high HG18, even when combined with low BCS12, produces high pregnancy probability estimates, however, the opposite does not happen. The measure of heart girth at the beginning of the mating is a good reference for the estimation of the pregnancy rate.

Key Words: average daily gain, body weight, logistic model

M253 Use of body weight gain at different ages to evaluate the pregnancy probability and the change in the pregnancy chance of Hereford heifers mated at 18 months of age. J. B. G. Costa Junior*[1], J. O. J. Barcellos[1], J. C. Whittier[2], I. D. P. S. Diaz[3], L. Canellas[1], V. Peripolli[1], J. K. Ahola[2], and R. K. Peel[2], [1]*Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil,* [2]*Colorado State University, Fort Collins,* [3]*Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

The objective of this study was to evaluate the estimated pregnancy probability and the change in the pregnancy chance (odds, ratio - OR) using variable body weight (BW) in Hereford heifers at 18 mo of age originated from a commercial cattle herd at a facility in the state of Rio Grande do

Sul, Brazil. Three different levels of average daily gain - ADG (high - H, moderate - M and low - L) with 3 different combinations (LHM; HLL; MMH) were considered. These ADG levels were applied between 7 to 12 mo (P12); 12 to 15 mo (P15) and 15 to 18 mo of age (P18). Used to the LHM, MMH, and HLL treatments 65, 58, and 60 heifers respectively. To determine these effect OR was adjusted within a complete model involving the treatment classification variables and all the continuous variables of body weight (BW), hip height (HH), heart girth (HG), body weight:height ratio (WH) at the age of 7, 12, 15, and 18 mo. This study used only the variable BW gain from 7 to 12 mo of age (BWG12), from 12 to 15 (BWG15), and from 15 to 18 mo of age (BWG18), 30 d before and during the mating time. The last 2 variables (30 d before and during the mating time) did not enter into the model and therefore were excluded from further consideration ($P > 0.3$) ($y = -3.6131 + 0.0431\,BWG12 + 0.0432\,BWG15 + 0.0302\,BWG18$; H&L = 0.77). There was a similar change in the OR as to an increase of 10 kg of BW in the P12 and P15 periods. However, at the age of 18 mo, showed a 54% increase in the changing rate. During P18, before the mating time, an increase of 35% in the pregnancy chance for every 10 kg of BW gained was observed. According to the average BW in each treatment at the end of each period, an increase of 10 kg represents 5% of the BW at the age of 12 mo, 3.7% of the BW at the age of 15 mo, and 3.2% of the BW at the age of 18 mo. We conclude that using the pregnancy probability described in this study will provide a useful tool for decisions related to heifer development for heifers mated at 18 mo of age.

Key Words: average daily gain, logistic model, mating time

M254 Use of a fescue seed model to study effects of ergot alkaloids on temperature regulation in steers.

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The objective was to measure changes in surface temperature (ST) of the left ribs, rectal temperature (RT), blood pressure (BP), heart rate (HR), and respiration rate (RR) in steers fed diets containing either endophyte-free (E-) or toxic endophyte-infected (E+) fescue seed under conditions where the temperature was above the thermoneutral zone. Angus steers (n = 8) were housed indoors in individual pens and adapted to a concentrate mix:switchgrass hay (40:60) diet. Seed replaced soy hulls in the basal diet for E- and E+ (2.7 mg/d total ergot alkaloids; 9.6 ug/kg BW). Design was a single reversal with 14-d periods and 21 d between periods. Baseline measurements were taken 2 d before the start of each period. Measurements were taken at 0730, 1230, and 1530 h on d 4, 8, and 14 of each period. Digital infrared thermographic imaging was used to measure ST. Data analysis included effects of treatment, day, and period with baseline data used as covariates. Mean (SD) daily temperature ranged from 23.5°C (1.3) to 32.1°C (1.6). Steers' BW and DMI did not differ ($P = 0.20$) for E- and E+ and were 285 and 288 kg (SE 4.3) and 5.49 and 5.38 kg/d (SE 0.09), respectively. Steers' RT, ST, and RR were greater ($P < 0.05$) with E+ and increased ($P < 0.01$) with time of day. Means for RT (°C) for E- and E+ at 0730, 1230, and 1530 h were 38.1, 38.3, and 38.5; and 38.2, 38.6, and 38.9, respectively. Steers' ST (°C) for E- and E+ at 0730, 1230, and 1530 h was 36.6, 37.9, and 38.4; and 37.1, 38.2, and 38.9, respectively. Steers' RR (breaths/min) for E- and E+ at 0730, 1230, and 1530 h was 27, 33, and 35; and 29, 41, and 44, respectively. Steers' HR decreased ($P < 0.01$) when fed E+ but increased ($P < 0.01$) with time of day. Systolic BP did not respond to E+ but diastolic BP increased ($P < 0.05$) with E+. Means for HR (beats/min) were 62 and 57, and for diastolic BP (mm Hg) were 48 and 51 for E- and E+, respectively. Greater surface temperature in response to E+ was not sufficient to prevent increased rectal temperature. Decreased heart rate in response to E+ may explain the impairment of thermoregulation.

Key Words: steers, tall fescue, thermoregulation

M255 Deposition of muscular and subcutaneous fat tissues of Nellore steers fed pasture with crude glycerin.

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The aim of this work was to evaluate the deposition of muscular and subcutaneous fat tissues of steers fed crude glycerin (CG) on pasture. The rib eye area (REA), the rib fat thickness between the 12th and 13th ribs (RFT) and the subcutaneous fat thickness in the region P8 (P8) of growing Nellore steers under grazing in the dry season were evaluated, supplemented with different levels of crude glycerin. The CG used was derived from soybean biodiesel production (80% glycerol). Fifty Nellore steers with initial shrunk body weight of 279.52 ± 16.31 kg were used, distributed in 5 treatments in a completely randomized design. The animals were distributed in 10 paddocks, with 1.8 ha each (2 paddocks per treatment), of *Brachiaria brizantha* 'Xaraés'. Treatments were constituted by 5 levels of CG inclusion in the supplement: (0, 7, 14, 21 and 28% of CG based on dry matter) as a substitute to the corn grain. The animals were supplemented daily in a proportion of 0.7% of body weight, and it contained 40% of crude protein based on dry matter. The supplement was constituted of corn grain, soybean meal, urea, gluten meal and mineralized salt. The experiment was executed in 136 d. The measurements were done in the beginning of the experiment and in each 28 d, through the use of ultrasound, to evaluate the deposition of muscular and subcutaneous fat tissues. Data was analyzed using the MIXED procedure of SAS program. There was no statistical significance ($P > 0.05$) among the treatments, and the final observed average values were: 61.5 cm^2 to REA, 2.4 mm to P8 and 2.0 mm to RFT. The gain observed in the variables (initial value – final value) AOL, P8 and SFT were of 18.2 cm^2, 0.57 mm and 0.47 mm, respectively. Crude glycerin can be a substitute to corn grain up to 28% in supplements to growing Nellore steers on pasture, without affecting animals' muscular and subcutaneous fat tissues growth.

Key Words: growth, forage, ultrasound

M256 Differences in residual feed intake are largely associated with changes in body weight gain composition.

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Residual feed intake (RFI) is defined as the difference between observed and predicted intake (predicted from the average weight and daily gain). RFI has been proposed as an index for genetic selection, however differences in body composition were pointed as a limiting factor in genetic selection based on RFI. The objective of this work was to study the relationship between RFI and gain composition in Nellore steers. Two hundred and 81 Nellore steers, progeny of 30 2 bulls, were individually fed for a minimum period of 70 d. The diet contained 2.8 Mcal ME/kg DM and 13.5% crude protein and was supplied twice a day for ad libitum intake. The animals were classified in low, medium and high RFI (mean ± 0.5SD) and then extreme classes were compared. Results are presented on the table below. The high RFI animals retained 0.7 Mcal/day more energy than the low RFI animals ($P < 0.05$). Therefore the change in estimated body weight composition explained 37.4% of the 1.54 kg/d difference in feed intake between high and low RFI classes. This effect is far greater than the 5% suggested in the literature by different authors based on regression analysis.

Table 1.

	Low RFI	High RFI	Mean ± SD
RFI, kg/d	0.79^{a}	-0.78^{b}	−0.06 ± 0.04
Gain, kg/d	1.35	1.37	1.33 ± 0.02
DMI, kg/d	9.16^{a}	7.64^{b}	8.22 ± 0.07
Initial ribeye,[1] cm^2	45.2	45.7	44.6 ± 0.4
Final ribeye,[1] cm^2	56.4	56.6	56.9 ± 0.4
Initial fat thickness,[1] mm	2.71	2.71	2.64 ± 0.07
Final fat thickness,[1] mm	5.63^{a}	5.05^{b}	5.00 ± 0.10
Retained energy,[2] Mcal/d	4.36^{a}	3.66^{b}	3.98 ± 0.08
% fat[3]	28.3^{a}	22.1^{b}	25.9 ± 0.8
% Intramuscular fat	2.70^{a}	2.30^{b}	2.62 ± 0.06

[ab] $P < 0.05$ (CONTRAST/SAS).

[1] Ultrasound.

[2] EBWEnergy = −126.7+10.9*ribeye+70*fat thickness;R^2=0.73.

[3] In the gain.

Key Words: beef cattle, body composition, fat thickness

M257 Effects of trehalose on performance and morbidity of newly received beef steers. E. M. Domby,* C. H. Ponce, J. S. Schutz, and M. L. Galyean, *Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

Trehalose is a disaccharide that has been previously associated with decreased oxidative stress in dairy cattle. The use of trehalose as a dietary supplement for newly received beef steers has not been investigated. Our objective was to evaluate the effects of trehalose concentration in the diet on performance and morbidity from bovine respiratory disease (BRD). One hundred and 24 steers (average initial BW = 182.1 kg ± 3.69 kg) purchased from auction markets in southwest Missouri were received, routinely processed (vaccinations, deworming, and metaphylactic antibiotic treatment), housed in 12 pens (10 to 11 steers/pen), and fed a 65% concentrate, steam-flaked corn-based receiving diet during a 28-d receiving period. Treatments were 0 (Control), 1, or 2% trehalose (% of dietary DM; Cargill Health and Nutrition, Minneapolis, MN). Initial BW did not differ ($P = 0.605$) among treatments. Similarly, final (d 28) BW was not affected by treatments ($P = 0.779$), and there were no differences ($P > 0.420$) among treatments for ADG, DMI, or G:F for d 0 to 14 or for the overall 28-d period. Only 7 steers were treated for BRD (5.6% total morbidity; 2, 1, and 4 steers from the Control, 1, and 2% trehalose treatments, respectively). Because of the low numbers of morbid steers, morbidity data were not analyzed statistically. Results from this experiment suggest neither positive nor negative effects on short-term receiving period performance or BRD morbidity with dietary supplementation of 1 or 2% (DM basis) trehalose in a steam-flaked corn-based receiving diet.

Key Words: newly received beef cattle, trehalose, bovine respiratory disease

M258 Performance of fattening steers on Marandu pasture supplemented with levels of total digestible nutrient in the water season. J. F. W. Koscheck[1],* J. T. Zervoudakis[1], L. K. Hatamoto-Zervoudakis[1], L. S. Cabral[1], A. A. Oliveira[1], J. M. B. Benatti[1], D. M. G. Carvalho[1], and R. P. Silva[1], [1]*Federal University of Mato Grosso, Cuiabá, MT, Brazil.*

This study aimed at evaluating the performance of cattle supplemented with different levels of total digestible nutrients (TDN), fattened on *Brachiaria brizantha* ‘Marandu’ pasture. The experiment lasted 84 d and was conducted in an area with 4 paddocks of 1.45 ha, provided with covered water fountains and feed troughs. Twenty (20) uncastrated male steers with 24 mo of age and initial live weight average of 418.48 ± 6.95 kg were used. Animals were distributed in total randomized design with 4 supplements and 5 replicates. Supplements were composed of mineral mixture, ground grain corn, soybean hulls, roasted soybeans and urea. Supplements to levels of 800, 1600 and 2400 g/animal/day, containing respectively 500, 1000 and 1500g of TDN, called S500, S1000, S1500, were provided to fulfill 300 g of crude protein (CP)/animal/day, besides the control group which received only mineral mixture. Availability of forage mass, dry matter potentially digestible and the CP content of the forage were 5.45, 3.53 t/ha and 10.59%, respectively. For the supplements S1000, S1500, S500 and MM the animal weight gain was respectively 1.071 ± 0.062; 0.960 ± 0.102; 0.914 ± 0.094 and 0.671 ± 0.079 kg/day, statistical difference was verified through orthogonal contrast only between the supplement MM and the other supplements ($P < 0.05$). The increase in the level of supplementation, with consequent increase in the supply of extra TDN, was unable to generate positive response in animal weight gain, between supplemented animals. The common characteristic between the supplements was the amount of CP provided to each animal (300 g), which probably was the key point to get superior performance compared with animals not supplemented. The supply of multiple supplements that provide 300 g of CP/animal/day,for fattening cattle during the summer promotes additional gain of 311 g/animal/day in relation to the supply of mineral mix, which is important to get a short cycle of beef production.

Key Words: beef cattle, supplementation, weight gain

M259 Different supplementation strategies to grazing beef cattle in Brazil. H. O. A. Santana[1], H. J. Fernandes*[1], M. A. Rezende[3,2], G. L. D. Feijó[2], A. Aguiar[4], E. P. Rosa[1], C. N. F. Guaraldo[1], and J. A. da Costa Lima[1], [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]*University of Florida, Gainesville.*

The objective of this study was to evaluate the effect of different supplementation strategies on the final weight and carcass characteristics of young Nellore bulls grazing *Panicum maximum* ‘Mombaça’ pastures during 426 d. Thirty-two bulls (287 ± 17.8 kg), were randomly distributed in 4 pastures, with 2.5 ha each. Treatments were: mineral supplementation (Control), continuous concentrate supplementation, concentrate supplementation on dry season, and compensatory gain (concentrate supplementation on rainy season). Concentrate supplement contained corn, soybean meal and urea (27.6% of CP and 79.8% of TDN) and was supplied at 0.5% of body weight. Mineral supplement was supplied ad libitum. At the beginning and at the end of the trial, animals were weighted (to calculate the average daily gain, ADG) and, at the end, ultrasound measurements of loin eye areas (LEA), fat thickness at the 12th rib (FTR) and at the P8 rump site (FT8) were taken. The effect of the concentrate supplementation, of the continuous or tactical (just in part of the year) concentrate supplementation, and of the season of the tactical concentrate supplementation were evaluated by the partition of the sum of squares of treatment in orthogonal contrasts. LEA and FTR did not differ (Table 1). Treatments did not affected the initial body weight ($P > 0.10$). Concentrate supplementation and continuous supplementation strategy increased the ADG and the FT8 of the animals. This result pointed to a greater sensitivity of the P8 site to assess the differences in fat deposition in the carcass, or to a difference in the site of fat deposition in animals submitted to different supplementation strategies.

Table 1. Final weight and carcass traits according to the supplementation strategy

		Conc. suppl.				*P*-value		
	Control	Dry season	Compensatory gain	Continuous	CV, %	Conc	Continuous or tactial conc.	Season of tactical suppl.
ADG, kg/d	0.460	0.487	0.533	0.590	10.1	0.005	0.006	0.144
Loin eye area, cm2	62.5	64.1	65.1	66.9	7.52	0.221	0.356	0.734
Fat thickness, mm								
at the 12th rib	3.65	4.02	3.67	3.77	17.4	0.597	0.822	0.368
at the P8 rump site	3.15	3.25	3.78	4.53	18.2	0.037	<0.01	0.184

Key Words: carcass, ultrasound, tropical production

M260 Determination of net energy requirements of growing Nellore cattle.

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In 1968 Lofgreen and Garrett introduced a net energy (NE) system designed for use in beef cattle, adopted by NRC (1996). Their equations were developed using *Bos Taurus* cattle. The objective of this study was to determine the NE requirements for maintenance and weight gain in growing Nellore cattle by calorimetry. Five Nellore bulls were confined at the Federal University of Minas Gerais (Belo Horizonte, Brazil), receiving *Cynodon* spp. hay, corn and soybean meal, from 200 to 450kg BW. Heat production (HP) was quantified by open circuit indirect calorimetry at 3 feeding levels: ad libitum, restricted and fasting. The Brouwer (1965) equation was used to estimate HP resulting from respiratory exchange and urinary nitrogen excretion: HP (kcal) = $3.866\ O_2 + 1.200\ CO_2 - 0.518\ CH_4 - 1.431\ N$. NE_m requirement was determined by linear regression between the log of HP and the metabolizable energy intake (MEI) for the ad libitum and restricted levels and also by measuring the fasting heat production (FHP) of the animals. The NE_g requirement was calculated by the difference between MEI and HP during ad libitum feeding. Data were analyzed by a repeated-measures design, using the PROC MIXED procedure of SAS (2001). The NE_m and NE_g requirements are shown in Table 1. Lofgreen and Garrett (1968) found 77 kcal/kg $EBW^{0.75}$ for NE_m, which was lower than the values found. NE_m requirements showed a decreasing trend with increasing BW. That could be explained by lower weight proportion of organs and body protein as age increases. Retained energy (ER, NE_g) values (kcal/kg $EBW^{0.75}$) obtained were within the range described by Lofgreen and Garrett (1968).

Table 1. Energy requirements (in kcal/kg EBW0.75) for maintenance (NEm) and gain (NEg) in experimental periods

	Period							
	1		2		3		4	
Item	Mean	SD	Mean	SD	Mean	SD	Mean	SD
NE_m[1]	116.03[a]	15.03	92.36[b]	15.95	91.97[b]	10.68	84.14[b]	26.44
NE_m[2]	123.53[a]	25.64	93.92[b]	3.45	98.07[b]	7.02	83.19[b]	9.30
NE_g	11.54[b]	12.81	24.79[ab]	14.84	39.23[a]	18.34	26.41[ab]	13.45

[a,b]In a row, means without a common letter differ ($P < 0.05$).

[1]Obtained by regression.

[2]Obtained by respirometric technique.

Key Words: zebu, tropical conditions, respirometry

M261 Supplementation of fattening steers on Marandu pasture in the summer: intake and digestibility.

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The objective was to evaluate intake and digestibility on fattening cattle on Marandu grass pastures supplemented with different levels of the total digestible nutrients (TDN). Four cattle, with an initial average weight of 512kg, rumen fitted and distributed in 4 paddocks, in 4x4 Latin square design, were used. The supplements were composed of mineral mixture, ground grain corn, soybean hulls, toasted soybean grain, and urea. Supplements to levels of 800, 1600 and 2400 g/animal/day, containing respectively 500, 1000 and 1500g of TDN, called S500, S1000, S1500, were provided to fulfill 300 g of crude protein (CP)/animal/day, besides the control group which received only mineral mixture. Each period lasted 17 d, 5 d for adaptation and forage collecting and 9 d for evaluation of the intake and digestibility. To estimate the intake, chromium oxide was used as external indicator and the indigestible NDF as internal indicator. Collecting of feces was made in 3 d at different collection times. SNK test was used for averages comparison. There was no statistical difference in the total dry matter intake (TDMI) and dry matter intake of pasture; however, there was a numerical increase in the TDMI with a trend to the replacement in the intake of forage for supplement. The intake of ethereal extract (EE) and non-fibrous carbohydrates (NFC) was higher for the animals fed with S1500 ($P < 0.10$), which can be explained by the increased supply of supplement.

Table 1. Intake and digestibility of cattle supplemented with levels of TDN

	Supplements				
	MM	S500	S1000	S1500	CV (%)
Intake, kg/d					
Total DM	10.22	10.86	11.15	12.11	25.59
Pasture DM	10.15	10.06	9.55	9.71	27.98
CP	1.22	1.51	1.45	1.46	25.25
EE	0.41[b]	0.51[ab]	0.55[ab]	0.61[a]	27.06
NFC	1.46[b]	1.64[b]	2.03[b]	2.51[a]	31.70
Digestibility					
OM	53.2	52.1	54.1	54.5	9.91
NDF	49.8	49.7	50.2	50.6	9.86

[a,b]Means within the row with different letters differ ($P < 0.10$).

Key Words: grazing animals, supplement

M262 Performance, feed efficiency and ultrasound carcass traits of Nellore cattle with different classes of residual gain.

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The residual gain (RG) was proposed as a measure that estimates the weight gain according to feed intake and body weight (Koch et al., 1963; J. Anim. Sci., 22:486). With the objective to verify the differences between RG classes in performance, feed efficiency and ultrasound carcass traits in Nellore cattle (bulls n = 141, 21-mo old 385 kg initial BW; steers n = 224, 20-mo old, 350 kg initial BW), we computed the average daily gain (ADG), dry matter intake (DMI), feed conversion ratio (F:G), residual feed intake (RFI) and the gain of ribeye area (GREA), gain of backfat thickness (GBFT) and gain of rumpfat thickness (GRFT) measured by ultrasound. Residual gain was calculated by regression of ADG in DMI, metabolic BW (BW superscript 0.75), contemporary group, and sex. The animals were divided into 2 classes according the standard deviation of RG (high > 0.5 SD and low < 0.5 SD). The RG class effect was analyzed by ANOVA and the means were compared with Tukey test with a 5% probability level. Only the DMI, as expected, did not differ ($P > 0.05$) between the RG classes as well as GREA. The high RG group had ($P < 0.05$) higher ADG, GBFT and GRFT and lower F:G and RFI when compared with low RG group. An improvement in the RG may increase the deposition of fat on the carcass, the weight gain and improving feed efficiency without affecting the feed intake.

Key Words: growth, *Bos indicus*, intake

M263 Effect of diet type on the expression of genes regulating ruminal epithelium function of cattle.

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The objective of this study was to investigate the effect of varying dietary concentrate to forage content on the expression of genes encoding for enzymes involved in the absorption and metabolism of VFA, ion transporters and transcription factors in ruminal epithelial tissue of cattle. Forty-eight Holstein-Friesian bull calves were assigned to one of 3 post-weaning dietary regimens; namely, grazed pasture only (n = 17; G); pasture plus 2 kg DM of concentrate (n = 16; GC) or ad-libitum concentrate plus 1 kg of straw (n = 15; C), fed indoors. Animals were slaughtered at 8 mo of age and ruminal epithelial tissue was harvested from the ventral sac of the rumen. Tissue from 10 animals per treatment was then selected for use in the current study. Total RNA was extracted and primers were designed to amplify specific regions of 25 genes involved in ruminal absorptive metabolism. Samples of rumen digesta were also collected at slaughter for VFA analysis, determined using gas chromatography. Ruminal VFA concentration was greatest for C and similar for G and GC. Acetic acid was highest for G and lowest for C (63.1 v 55.3 mol/mol VFA; $P < 0.05$). Conversely, propionic acid concentrations were greatest for C and lowest for G (32.1 v 23,2 mol/mol VFA; $P < 0.05$). The ratio of acetic:propionic was highest for G and lowest for C. There was no difference between dietary treatments ($P > 0.10$) for N-butyric, Iso-valeric or N-valeric acids. mRNA expression for Acetyl-CoA-Synthetase was greatest for C, intermediate for GS and lowest for the G treatments. Differences in expression was also detected between treatments ($P < 0.05$) for key genes involved in the ketogenesis pathway viz. Acetyl-CoA-Trans, HMGL, BDH1 and BDH2. An effect of diet type ($P < 0.05$) was also observed for genes involved in cholesterologenic homeostasis, namely ACAT2, HMGCS2 and ABCA1, with higher expression detected for C compared with GC, which in turn was higher than G. Interestingly, similar dietary effects were also observed for transcription factors PPAR-α and SREBP2 believed to regulate these biochemical events. Moreover, the relative expression values for the ion transporters NHE2, and NHE3 were greatest for C, lowest for G and intermediate for GC. These results suggest that the biochemical pathways involved in ion exchange and VFA metabolism, in particular ketogenesis and associated regulatory transcriptional coordinators were upregulated in rumen epithelial tissue, in a linear fashion, with increased concentrate allowance. This study provides further evidence for the elucidation of the molecular mechanism regulating ruminal absorptive metabolism.

Key Words: VFA metabolism, rumen, nutrient absorption

M264 Correlations between arrival plasma amino acid concentrations and feedlot performance and effects of arrival sex and antibiotic treatments in high-risk calves.

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Data from 2 experiments was pooled and used to determine correlations between arrival plasma AA concentrations and 60 d feedlot performance, and the effects of arrival sex (Bull vs. Steer) and antibiotic treatment (Trt vs. No Trt) on arrival AA concentrations. Beef calves (n = 281; BW = 259 ± 9.5 kg) were processed and administered metaphylactic treatment for control of BRD. Bulls were elastrated and all animals were allocated to individual feed intake systems (40 animals/pen; GrowSafe Systems, Ltd., Airdrie, Canada) and fed for 60 d. Cattle were observed by trained personnel for detection and treatment of disease. Twenty-three calves were administered an antibiotic treatment, and 33 bulls were elastrated. Pearson correlation coefficients were calculated using PROC CORR (SAS 9.3, Cary, NC) examining the relationship between arrival AA concentration and 60 d feedlot performance. The effects of sex and antibiotic treatment on AA concentration were analyzed using PROC GLIMMIX. Animal was the experimental unit, and the model included the fixed effect of treatment and the random effects of pen and sex nested within trial. For all cattle, glutamic acid had a negative correlation to DMI, ADG, and G:F (−0.185, −0.307, −0.272, respectively; $P < 0.05$) for the 60 d period. Serine, alanine, and 4-hydroxyproline had negative correlations ($P < 0.05$), and glycine, leucine, ornithine, and histidine had positive correlations ($P < 0.05$) to d 0–60 G:F. For calves treated, leucine and isoleucine concentrations tended to be increased ($P \leq 0.12$) compared with calves never treated. Calves that arrived as bulls had higher total, gluconeogenic, branched-chain, aromatic, and non-essential AA concentrations ($P < 0.05$) than those that arrived as steers. These data indicate that a relationship exists between arrival AA concentrations and feedlot performance, and AA concentrations are increased in bulls compared with steers. However, there appears to be no relationship between arrival AA concentrations and subsequent antibiotic treatment.

Key Words: amino acid concentration, BRD, feedlot performance

M265 Evaluation of the acid insoluble ash technique as a method for determining apparent diet digestibility in beef cattle.

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The objective was to determine if the acid-insoluble ash (AIA) method provided accurate estimates of in vivo apparent diet digestibility compared with the standard total fecal collection (TFC) method. Twelve Holstein-Friesian steers, mean LW 328 (SD 27.3) kg, were assigned to 1 of 3 blocks on a descending LW basis and randomly allocated, from within block, to 1 of 4 diets based on either whole-crop wheat (WCW) or grass silage (GS) in a 4 × 4 Latin square design. The 3 WCW silages were based (DM basis) on ratios of grain to straw plus chaff as follows: 11:89, 26:74 and 47:53. The fourth treatment was GS. Each period within the Latin square was 28 d, with all silages offered for ad libitum consumption for 15 d after which time, the amount of silage offered to each animal was limited to 0.90 of its ad libitum intake. A concentrate supplement (2.60 kg) was offered to each animal in a single feed daily.

For the last 10 d in each period diet digestibility measurements were undertaken. TFC was carried out at 08.00 h, with AIA fecal sampling carried out simultaneously. For the AIA method, fecal grab samples (200 g) were obtained per rectum and pooled for each animal at the end of the measurement period. All feed and fecal samples were assayed for DM, NDF, ADF, CP, and starch. The 2 methods were compared using graphical representation on an agreement plot and by computing a total deviation index ($TDI_{0.9}$) and coverage probability ($CP_{0.06}$). Computation was carried out using the SAS macro of Lin et al. (2002), available at http://www.uic.edu/. The $TDI_{0.9}$, which is an estimate of the deviation that covers 90% of the digestibility measurements, was 0.08 for apparent DM digestibility, with a $CP_{0.06}$ estimate of 0.75, indicating that 75% of the observations fell within the previously specified error limit of 0.06. Upon removal of GS from the analysis, the strength of the agreement between the 2 methods was increased ($TDI_{0.9} = 0.06$ and $CP_{0.06} = 0.89$). Thus, it may be concluded that the AIA method is a useful method to determine diet digestibility given the proportion of measurements that fell within the pre-specified range of acceptability.

Key Words: acid insoluble ash, total fecal collection, beef cattle

M266 Feedlot performance and carcass traits of Nellore cattle as affected by sex condition and frame size.

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Use of non-castrated (NC) males for red meat production has been a common practice in Brazil because they grow fast, utilize feed more efficiently and show high-yielding and leaner carcasses when compared with castrated males (CM). The objective of this work was to investigate the effects of sex condition and frame size (FS) on feedlot performance and carcass traits of finishing *Bos indicus* steers and bulls. Nellore bulls (n = 119; 372 ± 32kg LW) and steers (n = 122; 351 ± 36 kg LW) averaging 20-mo old, were tested for feedlot performance, being fed high-grain diets (85% of concentrate) for 56 to 140 d. Individual DMI, ADG and G:F were recorded. At the beginning of each test, animals were weighed (LW) and hip height was measured to calculate FS. In 28-d intervals, animals were weighed and ultrasound scanned for determinations of LM area (LMA) and backfat thickness (BFT) between 12th/13th ribs. At the end of test period, animals were slaughtered and hot carcass weight (HCW) and kidney, pelvic and inguinal fat (KPIF) were registered. Animal FS ranged from 4 to 9. Data was analyzed by ANOVA with year (block), FS and sex as fixed effects and time on feed (test length) as covariate. At the beginning of feedlot period, NC were heavier (369 vs 351 kg), had greater LMA (61.6 vs 59.9 cm^2) and lower BFT (0.5 vs 1.4 mm) than CM ($P < 0.0001$), respectively. Also had higher ADG (1.86 vs 1.58 kg/day), DMI (10.7 vs 10.3 kg/day) and G:F (0.176 vs 0.155 kg ADG/kg DMI) than CM ($P < 0.0001$). Steers had smaller HCW than NC (292.7 vs 320 kg, respectively) but they did not differ in dressing percentage (59.3%). Steers had higher KPIF (3.6 vs 2.8%) and BFT at slaughter (5.6 vs 4.4 mm) than NC, respectively, but they had greater final LMA than CM (79.8 vs 74.1 cm^2, respectively). FS was positively and linearly associated to initial and final LW, G:F and HCW ($P < 0.0001$) but did not affect other traits. Non-castrated and large FS finishing animals may be more profitable due to their greater weight gain and G:F. When fed high concentrate diets, NC Nellore males present carcass with adequate BFT to the meat industry.

Key Words: beef cattle, *Bos indicus*, feedlot

M267 Evaluation of a rapid determination of heat production and respiratory quotient in Holstein steers using the washed rumen technique.

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The objective of this study was to validate use of the washed rumen technique for rapid measurement of fasting heat production (FHP) and respiratory quotient (RQ), and compare this with heart rate (HR) and core temperature (CT). The experiment used 8 Holstein steers (322 ± 30 kg) under controlled temperature (21°C) as follows: 10 d diet adaptation, 1 d measurement of respiratory gases at $1.5 \times NE_m$ (Unwashed rumen), 1 d measurement of respiratory gases at fasting (Washed rumen), and 7 d for re-establishing intake. Steers were offered alfalfa cubes top-dressed with a mineral pre-mix at $1.5 \times NE_m$. At the day of measurement the reticulorumen was washed and refilled with ruminal buffer ($NaCl = 96$; $NaHCO_3 = 24$; $KHCO_3 = 30$; $K_2HPO_4 = 2$; $CaCl_2 = 1.5$; $MgCl_2 = 1.5$ mmol/kg of buffer) that was gassed with a mixture of 75% N_2 and 25% CO_2 before incubation in the rumen. Mean daily CT between unwashed and washed rumen were not different (Table 1). Mean daily HR and HP were lower for washed rumen than for unwashed rumen ($P < 0.001$). RQ was lower for washed rumen and there was an interaction ($P < 0.001$) with sampling hour. To define the plateau of RQ, dependence of RQ rate and hour on unwashed and washed rumen was fitted by a one-phase decay equation. The plateau of RQ values were calculated at 0.87 ± 0.01 and 0.72 ± 0.01 for unwashed and washed rumen, respectively. The RQ decreased to approximately 0.7, by 8 h after washing the rumen. This approach may provide an alternative to the traditional 48 h fasting time, or measurements made during the third and fourth day after starvation. Applying the washed rumen technique may be more rapid and less stressful means to predict energy required for maintenance in cattle.

Table 1. Comparison of washed and unwashed rumen models

				P-value		
Item	Unwashed	Washed	SEM	Treatment (T)	Hour (H)	T × H
CT, °C	36.91	36.91	0.07	ns	ns	ns
HR, beats/min	57.62	45.30	1.01	<0.001	ns	ns
HP, kJ/kg BW0.75	237.15	167.01	3.67	<0.001	ns	ns
RQ	0.85	0.73	0.01	<0.001	<0.001	<0.001

Key Words: fasting heat production, respiratory quotient, washed rumen

M268 Effects of lipid sources on intake and digestibility of beef cattle finished at pasture.

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This study was carried out to evaluate the effects of lipid sources in supplements on intake and apparent digestibility of finishing beef steers kept at pasture. Forty-five Nellore steers (initial average body weight of 440kg) were assigned to 5 treatments on a completely randomized design. The animals were divided in to 10 paddocks (2 paddocks per treatment) of *Brachiaria brizantha* 'Xaraés'. Different lipid sources (linseed oil, palm oil, soybean grain and calcium salts; Lactoplus) was added to the supplements (100 g/kg DM) and offered at 1.0% body weight. The control treatment was composed of a corn and soybean meal supplement with no additional fat. All the concentrate contain 200 g/kg crude protein (CP) and 100 g/kg ether extract (EE) (except the control supplement, which contained 30 g/kg EE). External markers were used to estimate fecal excretion (LIPE) and individual supplement intake (titanium dioxide, TiO_2).Calculation of dry matter intake was performed by using indegradable neutral detergent fiber (iNDF) as internal marker. The treatments were compared by analyzing variables using the GLM procedure (SAS 9.1, SAS Institute Inc., Cary, NC). Dry matter intake (DMI), pasture intake (PI) and supplement intake (SI) were not affected by the lipid sources ($P < 0.05$), with average values of 11.87, 6.87 and 4.81 kg/animal per day, respectively. The addition of linseed oil decreased dry matter and organic matter apparent digestibility ($P < 0.05$). This oil also lessen CP apparent digestibility ($P < 0.05$) relative to the other lipid treatments. Palm oil and Linseed oil presented a negative effect on neutral detergent fiber digestibility ($P < 0.05$). These results suggested that the addition of linseed oil on supplements for grazing beef cattle impair nutrient utilization, and the addition of palm oil decrease fiber degradation.

Table 1. Least squares means for apparent digestibility (g/100 g)

	Control	Palm oil	Linseed oil	Calcium salts	Soybean grain	CV (%)	*P*-value
DM	60.79^{a}	59.83^{a}	55.01^{b}	61.13^{a}	61.27^{a}	5.06	0.0007
OM	65.57^{a}	64.27^{a}	60.53^{b}	66.12^{a}	65.89^{a}	3.79	0.0006
NDF	59.23^{a}	46.17^{b}	48.20^{b}	61.87^{a}	62.04^{a}	6.16	<0.0001
CP	60.62^{b}	67.86^{a}	61.90^{b}	68.99^{a}	65.69^{ab}	5.25	<0.0001

[a,b]Values in the same row followed by different letters differed on Tukey test ($P < 0.05$).

Key Words: beef cattle, marker, oil

M269 Nutrient mass balance and performance of feedlot cattle fed barley segregated by near infrared spectroscopy.

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Crossbred yearling heifers (n = 9,617, 32 pens, 269 ± 6 kg initial BW, days on feed = 229) were assigned randomly at feedlot arrival to one of 2 treatments: LOW or HIGH starch:NDF barley. 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 on feedlot performance, animal health, carcass characteristics, and N and P mass balance. Data were analyzed using the GLIMMIX procedure of SAS, with fixed effect of treatment and random effect of replicate. Intake was 0.2 kg/d greater ($P < 0.01$) for LOW barley compared with HIGH. Gain and final BW were greater ($P < 0.01$) for LOW on a live and carcass adjusted basis, but G:F was not different ($P \geq 0.30$). Carcass weight, 12th rib fat, and marbling score were greater ($P < 0.01$) for LOW barley compared with HIGH. Percentage of carcasses grading USDA Choice was greater ($P < 0.01$) and percentage grading USDA Standard was lower ($P < 0.01$) for LOW barley compared with high, whereas the percentage of carcasses grading USDA Prime or Select was not different ($P \geq 0.36$). Feeding LOW starch:NDF barley decreased ($P < 0.01$) the percentage of YG 2 carcasses, increased ($P < 0.01$) the percentage of YG 3 carcasses, and tended to increase ($P = 0.07$) the percentage of YG 4 carcasses. No differences ($P \geq 0.19$) in morbidity outcomes were observed. Overall mortality was similar ($P = 0.79$) between the 2 barley treatments, but mortality due to miscellaneous causes was greater ($P = 0.03$) for LOW compared with HIGH. Intake, retention, and excretion of both N and P were greater ($P < 0.01$) for LOW, but removal of N, P, DM removed, as well as N and P lost were not different ($P > 0.60$) between the 2 treatments. Feeding low starch:NDF barley improved feedlot performance and carcass characteristics, had a slight negative impact on animal health, but had no effect on N and P losses.

Key Words: barley, feedlot performance, mass balance

M270 Development of a fecal starch index to predict the feeding value of barley grain for feedlot cattle.

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Fecal starch content is considered to be a good indicator of the utilization of grain by cattle fed high-grain diets. However, an accurate and rapid method for determining the starch content of feces is lacking. The objective of this study was to evaluate the relationship of in vitro gas production (GP) from feces with differing residual starch content to in vivo digestibility in an effort to develop a rapid indirect method to assess the residual starch content. Thirty-two fecal samples were collected from beef cattle in a replicated 4 × 4 Latin square study in which barley grain was processed so as to deliberately introduce variation in ruminal fermentation and total tract digestibility. Fecal samples were used as substrates in vitro. Gas production was recorded at 3, 6, 9, 15, 24, 36, 48 h and DM disappearance (DMD) was measured at 24 and 48 h of incubation. Pearson correlation coefficients of GP with fecal contents (N, NDF and starch) and in vivo feed digestibility were estimated using the CORR procedure of SAS. Ruminal contents (RI) or feces (FI) collected from 2 ruminally cannulated steers were used as inocula. Gas production (ml/g DM) was lower ($P < 0.01$) with FI than RI at 24 h (172 vs. 331) and 48 h (214 vs. 341). Dry matter disappearance was also lower ($P < 0.01$) with FI than with RI at 24 h (23 vs. 24%) and at 48 h (26 vs. 30%). In contrast, starch disappearance was higher ($P < 0.01$) with FI than with RI at 24 h (96 vs. 91%) and 48 h (99 vs. 97%). When using RI, there was no correlation of GP with either fecal starch content or in vivo starch digestibility, but there was a moderate correlation with fecal NDF content ($r = 0.45$; $P < 0.02$). However, when using FI, there was a positive correlation of GP with fecal starch content ($r = 0.5$; $P < 0.02$), and negative correlation with in vivo starch digestibility ($r = -0.48$; $P < 0.01$). The results suggest that GP from feces, using FI as an inoculum may be a good indicator on variation of residual energy value of feces. However, GP alone may not be a reliable indicator for assessing the residual starch content of feces.

Key Words: fecal starch, gas production, in vitro

M271 Effect of direct-fed microbials on utilization of ruminally degradable protein in receiving steers.

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Direct-fed microbials (DFM) have been shown to alter rumen fermentation, thus response to DFM may be influenced by supply of degradable intake protein (DIP). One hundred ninety-two crossbred beef steers (280 ± 25 kg) were used to determine if DIP supply affects response to DFM in receiving cattle. Treatments were arranged in a 5 × 2 factorial, with 5 levels of DIP (80, 90, 100, 110, 120% of DIP requirement) fed with and without DFM (1 billion cfu/hd). DIP requirement was assumed to be 11% of TDN and diets were formulated to be isocaloric and meet or exceed metabolizable protein requirement. Differences in protein degradability were achieved by altering soybean meal:treated soybean meal (Amino Plus) and urea level. DFM consisted of a mixed bacterial culture, primarily *Lactobacillus acidophilus* and *Enterococcus faecium*. BW was recorded weekly and fecal pH was determined by rectal grab on d 7 and 14. There were no DIP or DFM effects on dry matter intake

across the 56 d study. A DFM by DIP interaction ($P = 0.05$) was observed for ADG during the first 28 d of the trial, which resulted in a tendency for an interaction ($P = 0.08$) over the 56 d trial. In the absence of DFM, ADG was similar across level of DIP, whereas in the presence of DFM, ADG increased with increasing level of DIP in a cubic ($P = 0.08$) fashion. Growth efficiency (DFM×DIP, $P > 0.10$) increased linearly ($P < 0.05$) with increasing level of DIP through the first 28 d, however, this difference was not maintained over the entire 56 d ($P > 0.10$). DFM increased growth efficiency ($P = 0.05$) primarily due to increases in efficiency over the first 28 d ($P < 0.05$) of the study. A DFM by time interaction was observed for fecal pH ($P < 0.05$). In the absence of DFM pH decreased from 6.71 to 6.62 on d 7 and 14, respectively. However, in the presence of DFM there was no change in pH over time (6.64). These data show that DFM improved growth efficiency across levels of DIP, however ADG response to DFM was dependent on DIP supply. This suggests that variable responses of cattle to DFM reported in the literature may be partially explained by DIP supply.

Key Words: cattle, direct-fed microbial, rumen degradable protein

Ruminant Nutrition: Dairy I

M272 Utilizing dietary nutrients to predict nitrogen efficiency in lactating dairy cattle. N. Swanepoel* and P. H. Robinson, *University of California, Davis.*

Proactive approaches, such as monitoring dietary nutrient profiles, are methods for dairy farmers to improve efficiency of nitrogen (N) utilization (NEF) of their dairy cows and prevent excretion of excess N which can be environmentally harmful. On farm NEF (i.e., milk N/feed N) are often 20–33%, but could theoretically reach 38–40% with optimal nutrition of the total mixed rations (TMR) fed to the cows. Commercial practice suggests that formulating rations to balance essential amino acids (EAA) in metabolizable protein (MP) may further improve NEF. Our objective was to determine if analyzable dietary nutrients of 'high group' lactation TMR could be used to predict NEF, and if AA profiles of MP as predicted by 2 metabolic models (i.e., 'CPM Dairy' & 'Shield') would improve that predictability. Nutrient profiles of 16 commercial dairy cow rations were determined and then model evaluated to estimate AA profiles of MP. Correlation analysis was used to determine the predictability of NEF from single analyte levels in the TMR. The most predictive TMR nutrients were starch (ST; $P = 0.07$), crude protein (CP; $P = 0.07$) and potentially digestible CP (DCP; $P = 0.08$). Soluble CP, fat and neutral detergent fiber were non-predictive (i.e., $P > 0.35$). Multiple correlation analysis of all TMR nutrients resulted in the best fitting model being: NEF (%) = 65.7 – 1.60*(CP, %DM) – 0.48*(ST, %DM) [$r^2 = 0.49$]. That most of the predictive power from CP appeared to be from DCP suggests that it may be the EAA profile of MP that influences NEF. Thus model predicted EAA/MP ratios were added to CP and ST as potential predictors in a stepwise procedure. The final multiple prediction equations differed by model. For 'CPM Dairy': NEF(%) = 49.84 – 1.91*(CP, %DM) – 0.59*(ST, %DM) – 21.90*(Met, %MP) + 13.24*(Ile, %MP) [$r^2 = 0.65$] while for 'SHIELD' no EAA were added to the analyte based model (above). Group milk yields were a poor predictor (i.e., $r^2 = 0.05$) of NEF. This evaluation of commercial dairy rations suggests that analyzable components of TMR only predict a low amount of the variation in NEF of dairy cows but that, dependent upon model, addition of predicted EAA/MP ratios may improve it.

Key Words: amino acid, metabolic model

M273 Effects of water iron concentration, valence and source on drinking water preference of lactating cows. O. N. Genther* and D. K. Beede, *Michigan State University, East Lansing.*

Drinking water can contain high concentrations of Fe, mainly of the ferrous (Fe^{2+}) valence. Current recommended upper tolerable concentration of Fe in drinking water for cattle (0.3 mg/L) comes from guidelines for human palatability, but cattle may be able to tolerate greater concentrations. Our objective was to determine the effects of varying concentrations of ferrous (Fe^{2+}) or ferric (Fe^{3+}) iron and Fe-salt source on lactating Holstein cows' preferences for drinking water offered as choices ad libitum. In 4 separate experiments, cows were offered pairs of water treatments for 22-h periods and water intake and drinking behavior were recorded. Data were analyzed by ANOVA. In Experiment 1 treatments were: 0, 4, or 8 mg of Fe/L from ferrous lactate [$Fe(C_3H_5O_3)_2$]. Cows exhibited no preference between water with 0 or 4 mg Fe/L, but water intake tended to be less with 8 compared with 0 or 4 mg Fe/L ($P < 0.10$). Also, cows spent less time drinking water containing 8 mg Fe/L ($P = 0.01$). Total drinking duration (r = 0.62) and frequency (r = 0.55) correlated positively with water intake ($P < 0.05$) when pooled across treatments. In Experiment 2, treatments were: 0 or 8 mg Fe/L from either ferrous sulfate ($FeSO_4$) or ferric sulfate [$Fe_2(SO_4)_3$]. Water intake did not differ among treatments. Treatments in Experiment 3 were: 0 or 8 mg Fe/L from either ferrous chloride ($FeCl_2$) or ferric chloride ($FeCl_3$). Again, cows exhibited no preference among the treatments. Treatments in Experiment 4 were: 0 or 8 mg Fe/L from ferrous lactate, sulfate, or chloride. Cows preferred water without added Fe ($P < 0.05$), but did not exhibit a preference among waters containing the Fe sources with different anionic moieties. Total drinking duration and frequency were less ($P < 0.05$) when offered water containing 8 mg of Fe/L from ferrous chloride compared with ferrous lactate or sulfate. Overall, our results indicate that upon first exposure to drinking water, lactating dairy cows tolerate concentrations of Fe up to 4 mg/L without reducing water intake; however, water intake was reduced with 8 mg Fe/L. Preference was not dependent upon Fe valence or Fe source in our studies

Key Words: dairy cattle, drinking water, iron

M274 Effect of cecum starch infusion on hindgut fermentation and inflammatory response in dairy cattle. S. Li,* H. Khazanehei, E. Khafipour, and J. C. Plaizier, *University of Manitoba, Winnipeg, MB, Canada.*

To assess the effect of cecum starch infusion (CSI) on hindgut fermentation and inflammatory response, 4 dry Holstein dairy cows (BW = 610.5 ± 42.7kg) were used in a crossover trial with 2 periods. Each period consisted of 23d of adaptation followed by 3 d of CSI. Dietary treatments were: 100% grass hay diet (HF), or 60% grass hay and 40% concentrate diet (CF) that were delivered ad libitum at 0900 h. On the starch infusion days (d 1 to d 3), cows also received a dose of 600g corn starch suspended in 600mL 0.9% saline via the cecal cannula at 0900. On the day before the first starch infusion (d −1) and 3, blood and fecal samples were collected at 0900 and 1500. DMI was monitored daily. Fecal samples were used to measure pH, VFA, ammonia, and lipopolysaccharide (LPS). Inflammatory markers (serum amyloid-A and haptoglobin) concentrations were measured in peripheral blood. DMI was higher in CF than HF animals and tended to be reduced by CSI. Fecal pH was lower in CF than HF group and was reduced by CSI. Total VFA in the feces was higher in CF than HF animals due to greater molar proportion of butyrate but not that of acetate and propionate. Total VFA and molar proportion of propionate increased but acetate decreased on d 1 after CSI but the effects were disappeared by d 3. Ammonia nitrogen concentration in the feces was similar in both CF and HF animals, and only decreased in the CF group due to CSI. Endotoxin concentrations in the fecal water were similar between treatments, and only increased in CF animals following CSI challenge. Inflammatory markers were not affected by treatment and CSI. Results indicate that the increase in the hindgut

LPS concentration following a CSI challenge is greater when the diet contains more concentrate.

Table 1.

	HF diet		CF diet			*P*-value		
Item	Control	CSI	Control	CSI	SEM	CSI	Diet	CSI× Diet
DMI, kg/d	10.7	9.1	12.8	10.0	1.3	0.07	<0.01	0.49
Fecal pH	6.8	6.3	6.4	6.2	0.1	<0.01	<0.01	0.16
Fecal TVFA, mM	32.5	35.9	49.0	47.5	4.1	0.75	<0.01	0.40
Acetate, % TVFA	75.8	72.8	74.5	72.7	1.0	0.01	0.56	0.48
Propionate, % TVFA	15.0	14.4	15.5	13.9	0.5	0.25	0.90	0.12
Butyrate, % TVFA	4.1	7.4	6.5	10.4	0.9	<0.01	<0.01	0.64
Ammonia, mg/dL	8.9	8.2	10.1	7.6	1.0	0.02	0.82	0.01
Fecal LPS, EU/mL	1,654	2,069	2,705	7,495	1,498	0.05	0.02	0.12

Key Words: dairy cows, hindgut, starch infusion

M275 Hepatic triglyceride concentration and fatty acid profile in early lactation Holstein cows fed saturated medium- or long-chain fatty acids.

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Partitioning of medium-chain fatty acids (FA) in lactating dairy cows is not well understood. We examined hepatic triglyceride concentration ([TG]) and FA profile of early lactation cows fed 2 sources of saturated FA. Dietary treatments were: no added fat (CTRL); 2.7% of DM as saturated long-chain FA (Energy Booster 100; EB); 2.7% as mostly saturated, medium-chain FA (coconut oil; CNO); or, a 2.7% mixture of EB and CNO (1:1; INT). CNO diet had 47 g C12:0/kg and 30 g C14:0/kg. CTRL diet contained 36% NDF (77% from forage), 41% NFC, and 16.5% CP, DM basis. Multiparous (MP; n = 36) and primiparous (PP; n = 31) Holstein cows 10 to 14 DIM were fed 1 of 4 treatments for 16 wk. Hepatic tissue was biopsied before treatment diets were fed, and then on d 14, 28, and 112. Main effects of treatment, biopsy day (repeated measure), and their interaction were tested separately for MP and PP by least-squares ANOVA. Dietary CNO concentration increased hepatic [TG] linearly (CNO > INT > EB; $P < 0.001$). In MP, [TG] decreased linearly from d 14 to d 28 and 112 ($P < 0.001$). In PP [TG] was similar across time ($P > 0.05$). Increasing hepatic [TG] related positively to concentrations of C14:0, C16:0, C16:1, or C18:1 *cis*-9 in total hepatic FA, but negatively to C18:0, C18:2, or FA longer than 18 C ($P < 0.01$). Cows fed CTRL or EB had less than 0.1% C12:0 of total hepatic FA. In contrast, CNO increased hepatic C12:0 to 0.9% (MP) or 0.5% (PP) regardless of day of experiment. Hepatic C14:0 accumulated over time with CNO. MP cows fed EB or CTRL vs. INT or CNO had greater increase in C16:0, C16:1, and C18:1 cis-9 as hepatic [TG] increased (interaction of [TG] by treatment; $P < 0.02$). In MP, CNO decreased C18:0 concentration ($P < 0.01$). Concentration of C18:2 *trans*-10 *cis*-12 in hepatic FA accumulated in CNO and over time, presumably indicative of ruminal biohydrogenation. Dietary CNO increased hepatic [TG] in early lactation cows. Greater hepatic accumulation of C14:0 vs. C12:0 (opposite of dietary concentrations) indicates different physiological partitioning of these FA.

Key Words: fatty acid oxidation, fatty liver, coconut oil

M276 Production and metabolic response of lactating dairy cows to heat stress while supplemented with a dietary antioxidant.

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The effect of the antioxidant Agrado Ultra [dry blend of ethoxyquin and propyl gallate] on the production and metabolic response of 24 lactating dairy cows to heat stress was investigated. Holstein cows (153 ± 5 d in milk) were blocked by milk production, body condition and lactation and randomly assigned to 1 of 2 treatments: Control (Soy hulls 6.1 g/cow/day; n = 12) or AOX (Agrado Ultra Dry 6.1 g/cow/day; n = 12). Cows were housed in a free stall barn with access to Calan doors from d −2 to 14 of treatment. Cows were then housed in environmentally controlled rooms for 7 d at thermoneutral temperature (d 15 to 21; Constant at 20°C) and then 14 d of programmed 12 h cyclical heat stress (HS; d 22 to 35; Mean THI range of 72.5 ± 0.1 to 81.3 ± 0.5). Cows were returned to free stalls for 7 d of recovery (d 36 to 43). Plasma and milk were sampled 17 times during the experiment. Rectal temperature was measured daily except during HS (3 times/day). Data were analyzed using SAS by mixed model ANOVA with repeated measures. Pretreatment values were used as covariates if found to be significant. Rectal temperature increased ($P < 0.01$) during HS with a tendency for cows fed AOX to have lower rectal temperatures ($P = 0.09$). Plasma glucose concentration was greater ($P = 0.004$) in the AOX group and also responded to HS differently ($P = 0.02$) than controls. Only changes in time, particularly during HS, were observed for BHBA and NEFA ($P < 0.01$). All milk composition variables decreased during HS except for milk urea nitrogen which increased for 4 d of HS before declining to pre-HS levels by the end of study. Control cows had a greater milk fat yield ($P = 0.02$) and AOX cows had a greater percentage of milk protein ($P = 0.001$). Dry matter intake and milk yield decreased ($P < 0.01$) in both groups during HS. Live weight decreased ($P < 0.01$) by 45 ± 5 kg during the time cows were housed in the environmental rooms. Cows fed an antioxidant had a tendency to respond to HS better with lower rectal temperatures and also had greater plasma glucose concentrations and milk protein concentrations.

Key Words: dairy, antioxidant, heat stress

M277 Effect of supplemental fatty acids on production responses and hepatic fatty acid composition and gene expression of dairy cows fed diets containing low concentrations of fatty acids.

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Objectives were to evaluate the effects of supplementing diets containing low amounts of long chain fatty acids (FA, < 1.8% DM) with either mostly saturated free FA (SFA, 35% C16:0, and 52% C18:0) or with Ca salts enriched with essential FA (EFA, 27% C18:2 n-6 and 3.5% C18:3 n-3 of the FA) on production responses and hepatic FA composition and global gene expression of Holstein cows. In study 1, prepartum cows were allocated randomly to 1 of 3 dietary treatments from 60 d before to 90 d after calving. Supplementation with FA (% dietary DM) consisted of 0% (CTL, n = 26), 1.7% SFA (n = 25, Energy Booster100), and 1.9% as Ca salts of EFA (EFA, n = 25, Megalac-R). On d 14 postpartum, liver was biopsied and analyzed for FA and global gene expression. Feeding supplemental fat did not affect ($P = 0.35$) the FA content of the liver, but increased ($P = 0.02$) the content of n-6 FA (15.4, 19.0 and 19.3 g/100 g FA, respectively for CTL, SFA and EFA). Feeding EFA increased ($P < 0.01$) the content of total conjugated linoleic acid and C18:1 *trans* isomers in liver. Feeding fat upregulated genes related to T cell activation, antigen receptor-mediated signaling pathway and activation of immune response. In study 2, 30 cows at 12 DIM were allocated randomly to the same treatments as in study 1. The DMI, BW, and milk yield and composition were recorded daily for 10 wk. Supplementing the diet of cows with fat increased yields of milk and milk components, and the response was greater for EFA than SFA (Table 1). Milk composition and BW were not influenced by dietary treatment.

Table 1.

	Treatment				P-value[1]			
Item	CTL	SFA	EFA	SE	TRT	TRT*P	Fat	FA
DMI, kg/d	20.2	21.4	21.4	0.6	0.23	0.42	0.09	0.93
Milk, kg/d	37.6	40.3	43.6	0.8	< 0.001	0.56	< 0.001	<0.01
FCM, kg/d	38.9	41.4	45.4	0.9	< 0.001	0.89	< 0.001	< 0.01
Milk fat, %	3.52	3.54	3.70	0.07	0.17	0.36	0.30	0.14
Milk protein, %	2.88	2.93	2.92	0.03	0.62	0.55	0.34	0.87
Milk lactose, %	4.89	4.92	4.90	0.02	0.45	0.70	0.32	0.41
BW, kg	558.0	566.3	598.4	14.9	0.15	0.22	0.20	0.14

[1] TRT = treatment; TRT*P = treatment by parity interaction; Fat = CTL vs. EFA + SFA; FA = EFA vs. SFA.

Key Words: dairy cow, linoleic acid, gene expression

M278 Effect of lactation stage on milk production and milk quality in dairy cows in confinement.

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Milk is a rich food of high biological quality that presents important substances with anti-carcinogenic action. Some factors can affect the qualitative characteristics and milk production like animal breed, age, stage of lactation, milk production at peak lactation, health and previous nutrition. The study of factors affecting the production and milk quality were very important in economic aspect. The aim of this study was to analyze the influence of lactation stage on production, milk quality, milk production on lactation peak and period of occurrence of peak of lactation. It were used 8700 data from a commercial herd using Holstein cows in the state of Parana, Brazil. The animals were kept under confinement (free stall) during the lactation. The total ration contained 17% of crude protein in DM and the concentrate: silage proportion was 1:1 in DM. The animals were fed and milked 3 times daily. The dependent variables used were: fat correct milk (FCM), milk fat, protein, lactose and total solids (expressed in %), somatic cells count (x1000), milk production (kg), peak of production (kg) and peak occurrence (in days). The dependent variables were submitted to ANOVA using the GLM (Generalized Linear Model) procedure of SAS (2009) and means were compared using a Tukey's test at 5% probability, considering the effect of lactation stage. The percentage of protein, lactose, total solids and peak occurrence did not vary ($P > 0.05$) according to stage of lactation. However, the lactation stage on % of fat, somatic cells count, fat corrected milk and peak of milk production vary ($P < 0.05$) with stage of lactation (Table 1).

Table 1. Percentage of fat, protein, somatic cell counting, total solids (TS) and fat-corrected milk (FCM) as a function of number of lactation for Holstein cows

Lactation stage	Fat (%)	Protein (%)	SCC (x1000)	TS (%)	FCM
1	3.74^{a}	3.17^{a}	92.27^{a}	12.51^{a}	8821.08^{a}
2	3.62^{a}	3.27^{a}	135.79^{a}	12.64^{a}	9692.93^{b}
3	3.56^{a}	3.16^{a}	151.60^{a}	12.89^{a}	10603.43^{b}
4	3.82^{b}	3.12^{a}	194.96^{a}	12.13^{a}	8252.35^{a}
5	4.19^{b}	3.08^{a}	232.15^{b}	12.07^{a}	7379.20^{a}

^{ab}Values in the same column followed by same letter do not differ statistically at 5% probability by the F test.

Key Words: dairy cows, lactation number, milk quality

M279 Comparison of growth curves between two genetic compositions of dairy goats using nonlinear mixed models.

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Studies on the growth curves for animals have been used extensively to examine how body mass and others parameters of interest develop over time and in relation to the environment, genotype, diet management and other factors. The goal of this study was to evaluate which nonlinear model normally used in the literature best describes dairy goat growth, and compare the curve parameters obtained for 2 genetic compositions of dairy goats. Data used in this study were collected from the goat flock of the Universidade Federal de Viçosa, MG, Brazil, 12,573 records were used from 2,476 females collected between 1992 and 2010. Two genetic compositions of dairy goats were assessed: predominantly Alpine (+A; n = 1,458; weighings = 7,335) and predominantly Saanen (+S; n = 1,018; weighings = 5,238). The models evaluated were the Brody, Van Bertalanffy, Richards, Logistic, and Gompertz models. Random effects (μ_1, μ_2, and μ_3 were linked to the β_1 (asymptotic value), β_2 (sigmoidal curve shape parameter), and β_3 (rate of maturing) parameters, respectively. We used dummy variables to estimate curve parameters independently for each genetic composition. Residual variance and the Schwartz Information Criteria were used to evaluate the models. After selecting the model that best describes the growth curves and possesses the variance and covariance matrix previously estimated, we were able to test the equality hypotheses all parameters of the growth curve using the Wald statistic. The Brody model (+A: $\beta_1 = 56.54$; $\beta_2 = 0.9324$; $\beta_3 = 0.00258$; and +S: $\beta_1 = 58.84$; $\beta_2 = 0.9383$; $\beta_3 = 0.00244$) with 2 variance component ($\mu_1 = 23.86$ and $\mu_3 = 4.04\text{E-}07$; $P < 0.001$), provided the best fit to the data. A significant difference was detected between the estimated parameters for the 2 genotypes in selected model ($P < 0.001$). Despite the genotypes have the same origin and are often considered similar in terms of productive animals (only visibly different in their coats), differences have been found in their lactation curves, and now, in this study, in their growth parameters. There are differences in the growth patterns between the 2 genetic compositions.

Key Words: Alpine, Saanen, Wald statistic

M280 Nonlinear mixed models fitted to growth curves of dairy goats.

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Measurements taken on the same experimental unit (animal) are more closely correlated than those taken in other experiment units, as well as measures taken at closer time intervals. These relationships are inherent in animal growth data, which may disrupt the basic assumptions of statistical analysis, such as independence of errors. However, there is still controversy about which growth curve parameters normally used in the literature should be considered as random. This decision should be based on the biological interpretation of the parameters and significance of the estimated variance components. The goal of this study was to evaluate the nonlinear mixed model methodology for fitting the growth curves of dairy goat. Data used in this study were collected from the goat flock of the Universidade Federal de Viçosa, MG, Brazil, were used 12,573 records from 2,476 females. The models evaluated were the Brody, Van Bertalanffy, Richards, Logistic and Gompertz models. Random effects μ_1, μ_2, and μ_3 were linked to the β_1 (asymptotic value), β_2 (sigmoidal curve shape parameter), and β_3 (rate of maturing) parameters, respectively. In addition to the traditional fixed-effects model, we evaluated 4 combinations of random variables: all parameters linked to random effects (μ_1, μ_2, and μ_3), only the β_1 and β_2 parameters (μ_1 and μ_2), only the β_1 and β_3 parameters (μ_1 and μ_3), and only the β_1 parameter (μ_1). Residual variance and the Schwartz Information Criteria were used to evaluate the models. There was reduced residual variance in all scenarios in which random effects were considered. The Brody (μ_1 and μ_3), Van Bertalanffy (μ_1 and μ_3), and Richards (μ_1) models provided the best fit to the data. Interestingly, all 3 models have in common parameters with biologically significance linked to variance component significant ($P \leq 0.01$). A major advantage of using nonlinear mixed model methodology in fitting animal growth curves is the possibility of including population variation measurements in stochastic models to predict animal performance. Growth curves should be fitted using the nonlinear mixed model methodology, linking biologically parameters to random effects.

Key Words: stochastic, parameters, random effect

M281 Increasing doses of *trans*-10, *cis*-12 conjugated linoleic acid (CLA) and changes in milk fat content and secretion of dairy ewes. M. Baldin[1], R. Dresch[1], D. R. M. Alessio[1], J. Souza[2], M. A. S. Gama[3], M. P. Soares[4], and D. E. Oliveira*[1,5], *[1]Centro de Ciências Agroveterinárias, UDESC, Lages, SC, Brazil, [2]Esalq/USP, Piracicaba, SP, Brazil, [3]Embrapa, CNPGL, Juiz de Fora, MG, Brazil, [4]Instituto Federal Catarinense, Araquari, SC, Brazil, [5]Centro de Educação Superior do Oeste, UDESC, Chapecó, SC, Brazil.*

The aim of this study was to examine the relationship between milk fat depression and increasing levels of t10, c12 CLA fed as a rumen unprotected supplement (UnCLA, 29.9% of t10, c12) to dairy ewes. Twenty-three Lacaune ewes, 40 DIM, were used in a completely randomized design. Treatments were fed during a 14-d experimental period: Control (C): 30g of Megalac-E, n = 5; T1: 20g of Megalac-E plus 10g of UnCLA, n = 6; T2: 10g of Megalac-E plus 20g of UnCLA, n = 5 and T3: 30g of UnCLA; n = 7. The treatments provided 0, 2.99, 5.98 and 8.97 g/d of t10, c12 CLA, respectively. Ewes received after a.m. and p.m. milkings an isoproteic concentrate (1.0 kg/ewe/d) in which the fat supplements were added. Ewes were grazing paddocks of a tropical pasture. Milk samples were taken every 2d and on the last day of the experimental period for fat content and FA profile analyses, respectively. The relationships between milk fat and t10, c12 CLA-related variables were tested by linear regression analysis using the REG procedure of SAS, where Y is the variation observed in milk fat content or yield and X is the t10, c12 CLA in the diet or in milk fat. Outliers were removed from the data set. Milk fat content was decreased by 5.2, 14.1 and 26.5% and milk fat yield by 10.9, 17.9 and 26.8% in response to T1, T2 and T3, respectively. Inclusion of CLA linearly increased t10, c12 CLA content (C = 0.03; T1 = 0.10; T2 = 0.19; T3 = 0.30; $r^2 = 0.92$; $P < 0.001$) and t10, c12 CLA secretion (C = 0.03; T1 = 0.06; T2 = 0.12; T3 = 0.15; $r^2 = 0.95$; $P < 0.001$) in milk fat. Overall, estimated regression models (Table 1) show that the magnitude of milk fat depression increased linearly as t10, c12 CLA increased either in the diet or in milk fat.

Table 1. Estimated regression models

Predictors	Change in fat content (%)	Change in fat yield (%)
Dose of t10, c12 CLA (g/d)	y = 6.97 – 2.87x[1]	y = −11.57 – 1.32x
	$r^2 = 0.69$, n = 21	$r^2 = 0.44$, n = 18
Milk t10, c12 CLA (g/100g FA)	y = 7.76 – 80.61x	y = −7.56 – 60.73x
	$r^2 = 0.50$, n = 22	$r^2 = 0.84$, n = 14
Milk t10, c12 CLA (g/d)	y = 7.46 – 143.13x	y = −10.11 – 73.05x
	$r^2 = 0.43$, n = 23	$r^2 = 0.56$, n = 17

[1]All model coefficients were significantly different from zero ($P < 0.001$).

Key Words: CLA, milk fat

M282 Impacts of fat level and source on production of high producing California dairy cows. J. M. Soderstrom*[1], P. H. Robinson[1], and K. Karges[2], *[1]University of California, Davis, [2]POET Nutrition, Sioux Falls, SD.*

Addition of supplemental fat is common in total mixed rations (TMR) fed to high producing dairy cows, but these fats often have different saturations which influences their maximum dietary inclusion level. Unsaturated fats, especially those high in linoleic and linolenic acids, can affect rumen microbial activity leading to altered rumen biohydrogenation intermediates which can inhibit fat synthesis in the mammary gland. Saturated fats are less likely to affect rumen fermentation due to their high rumen stability. We determined if increasing net energy (NE) of a TMR with fat affects productive performance of high producing cows, and if unsaturated fat can be added at the same level as saturated fat without negatively affecting animal performance. The experiment was a 3 × 3 Youden square with 4 28 d periods and it was completed on a dairy farm using 3 high group pens (i.e., cows not yet confirmed pregnant), each with ~340 early lactation multiparity cows. All TMR were formulated with 75% of dry matter (DM) the same, mainly corn grain, wheat and sorghum silages, alfalfa hay, corn grain, canola meal, almond hulls and cottonseed. The other 15% of each TMR was 9% high crude protein (CP) (i.e., fat extracted) distillers dried grains with solubles (HPDDGS) and 6% beet pulp (BP) (diet LOWFAT); 15% DDGS (high fat diet with unsaturated fats: diet UNSAT); 11.1% HPDDGS, 2% BP and 1.9% rumen inert fat (high fat diet with saturated fat: diet RIFAT). The TMR had the same CP (avg. 17.3% DM), but fat levels were 3.8, 4.8, 5.0%. DM intake was highest for UNSAT ($P < 0.05$). Milk, fat and true protein yields, and milk energy output, were higher ($P < 0.01$) for RIFAT vs. UNSAT and LOWFAT. Milk fat % was lowest ($P < 0.01$) for UNSAT, highest for RIFAT and intermediate for LOWFAT. In contrast, true protein % was lowest ($P < 0.01$) for RIFAT. Change in body condition score was lowest for LOWFAT ($P < 0.01$). Whole tract digestibility of neutral detergent fiber did not differ among diets, but CP was higher for UNSAT vs. RIFAT ($P = 0.05$). Production performance and milk fat % were decreased by feeding unsaturated fat to increase diet NE but were increased by feeding rumen stable saturated fat.

Key Words: milk fat, saturated, unsaturated

M283 Meta-analysis: Impact of grain type and corn harvest and processing practices on digestion and lactation performance by dairy cows. L. F. Ferraretto* and R. D. Shaver, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

A meta-analysis was performed to evaluate the effect of cereal grain type and corn grain harvest and processing practices on intake, digestion and milk production by dairy cows using a data set comprised of 414 treatment means from 100 peer-review articles published 2000 - 2011. Categories for cereal grain type, corn processing and mean particle size (MPS) were: barley, corn and wheat; dry ground, cracked or rolled corn (DRY), high-moisture shelled or ear corn (ENS), and steam-flaked or steam-rolled corn (STM); 500–1000, 1000–1500, 1500–2000, 3000–3500 and 3500–4000 µm for DRY and <2000 or ≥2000 µm for ENS. Data were analyzed using Proc Mixed of SAS with treatments as fixed effects and trial as a random effect. Digestibility of dietary starch was lower for corn than barley ruminally, but not ($P = 0.89$) total tract (TT). The TT digestibilities of dietary DM and OM tended ($P = 0.06$ and$P = 0.09$, respectively) to be greater for corn than barley or wheat. Ruminal and TT dietary NDF digestibilities were similar among the grains ($P = 0.92$ and $P = 0.25$, respectively); actual and fat-corrected milk yields and concentrations of milk fat, protein and urea-nitrogen (MUN) did not differ ($P > 0.10$) either. The TT dietary starch digestibility was reduced ($P = 0.01$) and ruminal starch digestibility tended ($P = 0.08$) to be reduced for DRY compared with ENS or STM. Milk yield was 1.0 kg/d greater ($P = 0.01$) and DMI tended to be 1.3 kg/d lower ($P = 0.08$) for ENS than DRY. Milk fat and protein concentrations were greatest ($P = 0.05$) for DRY and STM, respectively. The TT digestibility of dietary DM, OM and starch were reduced ($P = 0.01$) for both DRY and ENS as MPS increased. The MPS, however, did not affect ($P > 0.10$) DMI or actual and fat-corrected milk yields for either DRY or ENS. Milk fat concentration decreased ($P = 0.01$) with decreasing MPS for ENS, but not ($P = 0.28$) DRY. The MUN concentration tended ($P = 0.08$) to increase with increasing MPS for DRY. Corn ensiling and particle size were major factors influencing dietary nutrient digestibilities in lactating dairy cows.

Key Words: dairy cow, meta-analysis, starch

M284 Finding a proxy for the inhibiting effects of polyunsaturated fatty acids on milk fat in dairy cows. G. Maxin*[1], H. Rulquin[1], and F. Glasser[2], *[1]INRA-Agrocampus Ouest, Rennes, France, [2]INRA, Theix, Saint-Gènes-Champanelle, France.*

Diets supplemented with plant lipids, high in polyunsaturated fatty acids (PUFA), often induce milk fat depression (MFD) in dairy cows. Several *trans* FA isomers inhibiting milk fat synthesis have been identified, but cannot fully account for diet-induced MFD. There is still debate on which FA isomers and/or other mechanisms are responsible for diet-induced MFD. The experimental approaches meet several limits (availability of pure FA isomers, simultaneous variations in several FA, and modification of rumen metabolism and other nutrients following dietary lipid supplementation), making it almost impossible to identify the FA that are involved in diet-induced MFD. The aim of this study was to identify, using a modeling approach, a proxy of the inhibiting effects of PUFA on milk fat. A database was compiled from published studies of dietary lipid addition in dairy cow diets. It included 38 responses to lipid addition (differences between a lipid-supplemented diet and a control). From diet composition and intake, using published empirical equations, we predicted the changes in nutrient flows (VFA, glucose and proteins) following lipid addition. Then, the milk fat responses to these changes in nutrient flows were predicted using another set of published empirical equations. We thus got a prediction of the milk fat changes induced by the nutrients other than FA. The prediction bias was computed for each response by difference between this prediction and the response of milk fat reported in the publications, and was assumed to be caused by the inhibiting FA. To identify proxies of the inhibiting effect of PUFA, several variables linked to lipid addition (FA intake, duodenal flows of various FA) were regressed on this bias using GLM model. The 2 best proxies (best regressors on the prediction biases of both milk fat yield and content, based on R^2 and RMSE) were the intake of 18:2+18:3 and the duodenal flow of 18:2. These results have to be confirmed on a larger database, but this modeling approach seems to be a good alternative to complement experimental studies of milk fat inhibition by dietary PUFA, and overcome some of their limits.

Key Words: dairy cow, milk fat, lipids

Ruminant Nutrition: Dairy: Calves and Heifers

M285 Crude glycerin as a replacement for corn in starter concentrate for dairy calves: Ruminal and blood parameters. G. G. O. Napoles[1,2], C. E. Oltramari[1,3], J. T. Silva[1,3], G. B. Mourão[1,3], and C. M. M. Bittar*[1,3], [1]*Escola Superior de Agricultura Luiz de Queiroz, Piracicaba, SP, Brazil,* [2]*Fapesp, São Paulo, SP, Brazil,* [3]*CNPq, Brasília, DF, Brazil.*

The purpose of the study was to evaluate the effects of crude glycerin inclusion in starter concentrate, as a replacement for corn, on dairy calves ruminal and blood parameters. Study was conducted with 24 male Holstein calves allocated into blocks according to age (3–7d of life) and initial weight (36.7kg). Animals were individually housed and fed milk replacer (Servamilk, 22% CP; 18% EE, 4L/d) and starter concentrate (21%CP; 80%TDN) with increasing levels of crude glycerin, replacing corn in the formulation (0, 5, 10%, dry matter basis). Blood samples were collected weekly until 8 weeks of age for glucose, lactate, β-hydroxybutyrate (BHBA) and total protein (TP) determination. In wk 4, 6 and 8 of age, ruminal fluid samples were collected using an oro-ruminal probe and a suction pump for pH, acetate, propionate, butyrate, and total short chain fatty acids (SCFA) determination. Plasma glucose (96.5; 90.7; 94.0 mg/dL for 0%, 5% and 10% glycerin, respectively), lactate (11.66; 11.66; 11.7 mg/dL 0%, 5% and 10% glycerin, respectively), BHBA (0.13; 0.13; 0.12 mmol/L for 0%, 5% and 10% glycerin, respectively) and TP (6.23; 6.40; 6.33 g/dL for 0%, 5% and 10% glycerin, respectively) were not affected ($P > 0.05$) by the replacement of corn by crude glycerin. However, concentrations of BHBA and TP were significantly increased with age ($P < 0.05$). Most of the ruminal parameter were also not affected by the replacement of corn by crude glycerin in the starter concentrate, except for propionic acid which presented lower molar concentrations for the 5% crude glycerin treatment (46.95; 36.03; 44.28 mmol/mL for 0%, 5% and 10% glycerin, respectively). An age effect was observed for pH and propionic acid molar concentration, but there were no significant effects for the interaction of age and treatment for these parameters. Averages were 5.25, 5.11, 5.10 for rumen pH; and 130.46; 107.86; 115.29 mmol/mL for total SCFA, for 0%, 5% and 10% glycerin treatments, respectively. The replacement of corn by crude glycerin does not affect ruminal or blood parameters of calves, being a good alternative for dairy calves solid feed formulation. Support by FAPESP.

Key Words: by-products, volatile fatty acids, solid feed

M286 Effect of feed presentation on pre- and post-weaning performance of dairy calves. E. K. Miller-Cushon[1], R. Bergeron[2], K. E. Leslie[3], G. J. Mason[4], and T. J. DeVries*[1], [1]*Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada,* [2]*Dept. of Animal and Poultry Science, University of Guelph, Campus d'Alfred, Alfred, ON, Canada,* [3]*Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada,* [4]*Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Dairy calves are typically offered feed types separately, despite commonly being fed a total mixed ration (TMR) later in life. The objective of this study was to determine how early feed presentation affects feed intake and performance of dairy calves both before and after weaning and once transitioned to a TMR. Twenty Holstein bull calves were randomly assigned at birth to 1 of 2 feed presentation treatments: they were offered chopped hay (3 - 4 cm) and concentrate at a ratio of 3:7, either as a mixture (MIX) or in separate buckets (COM). All calves received 8L/d of milk replacer for the first 4 wks. The amount of milk fed was reduced incrementally in wks 5–7 to facilitate weaning by the end of wk 7. Calves remained on their respective feed presentation treatments for 8 wks. In wk 9–11, all calves were offered the MIX diet to assess whether early feed presentation affected intake of the mixed feed. In wks 12–13, all calves were offered a novel TMR (containing haylage, corn silage, high moisture corn, and protein supplement) to assess how early feed presentation may impact acceptance of a novel feed type. Calves were weighed 2x/wk and intake was recorded daily. Data were analyzed in a repeated measures general linear mixed model. Calves had similar ADG both pre-weaning (0.75 kg/d, $P = 0.4$) and post-weaning (1.19 kg/d, $P = 0.13$), and similar weights throughout the study ($P = 0.8$). While on their respective treatments, MIX and COM calves had similar total feed intakes (average 0.54 kg/d in wks 2–8, $P = 0.8$). COM calves consumed a greater ratio of hay:concentrate than the offered ratio in wk 3,4, and 5 (7.06:7 vs. 3:7; $P < 0.04$), a similar ratio in wk 6 (3.30:7, $P = 0.3$), and a lower ratio in wks 7 and 8 (1.83:7 vs. 3:7; $P < 0.007$). When all calves were offered the MIX diet in wk 9, intake was similar between treatments (2.67 kg/d, $P = 0.7$), indicating that familiarity with feed presentation did not influence intake. Intake remained similar between treatments upon transition to the novel TMR (average 3.97 kg/d in wks 12–13, $P > 0.6$). These results suggest that dietary selectivity associated with early feed presentation may be transient, without statistically significant effects on longer-term calf intake or growth.

Key Words: dairy calf, feed presentation, growth

M287 Interactive effects of feeding frequency and feed bunk space on the 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. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada,* [2]*Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada,* [3]*Dept. of 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 effects of feeding frequency and feed bunk space on the behavior of limit-fed replacement dairy heifers. Sixteen Holstein dairy heifers (183.4 ± 9.1 d of age), divided into groups of 4, were exposed to 4 treatments, using a 2-factor 4 × 4 Latin square design with 21-d periods. The treatments were: 1) feeding 1×/d (at 1200 h) with ample feed bunk space (0.40 m/heifer), 2) feeding 1×/d with reduced feed bunk space (0.34 m/heifer), 3) feeding 2×/d (at 1200 and 1400 h) with ample feed bunk space, and 4) feeding 2×/d with reduced feed bunk space. The ration was formulated to meet nutrient requirements of a dairy heifer growing at 0.8 kg/d and fed at a rate of 2.0% of BW. Feeding and lying behavior were recorded for the last 7 d of each period. Competitive behavior was recorded on d 16, 18, and 20 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 (5.5 kg/d). Heifers fed 1×/d spent more time feeding than heifers fed 2×/d, regardless of feed bunk space (70.5 vs. 58.9 min/d; SE = 4.0, $P = 0.001$). Additionally, heifers fed 1×/d displaced each other more often than heifers fed 2×/d (4.8 vs. 2.4 displacements/d; SE = 1.3, $P = 0.008$). Feed bunk space allowance did not affect competition between heifers. Interestingly, regardless of feed bunk space or feeding frequency, all heifers maintained similar ADG

(0.9 kg/d), lying time (835.6 min/d), inactive standing time (539.8 min/d), and unrewarded time (when no feed was present) at the feed bunk (28.9 min/d). No interactions between feed bunk space and feeding frequency were found. Results suggest that feed bunk space does not affect feeding behavior or growth if heifers are allowed sufficient space to feed simultaneously. The lack of interactive effects of feeding frequency and bunk space suggests that behavioral concerns associated with limit feeding may not be addressed by increased feeding frequency when limit-fed dairy heifers are provided with reduced feed bunk space.

Key Words: dairy heifer, feeding behavior, limit feeding

M288 Effect of physical form of forage on performance, feeding behavior, and digestibility of Holstein calves.

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The physical form of forage may influence rumen development, and consequently BW gain, DM consumption, digestibility, and welfare of dairy calves. The objective of this study was to determine the effect of different physical forms of forage on performance, apparent digestibility, and feeding behavior of young calves. Twenty Holstein male calves (46.8 ± 1.2 kg) were randomly assigned at birth to 1 of 2 feeding treatments, in which they were exposed to a mixed ration containing (on a DM basis) 90% crumb starter concentrate and either 1) 10% chopped (3–4 cm) grass hay (COARSE; n = 10), or 2) 10% ground (2 mm) grass hay (FINE; n = 10). All calves were offered 8 L/d of milk replacer (MR; 1.2 kg of DM) from birth, which was incrementally reduced after 5 wk to enable weaning by the end of wk 7. The study finished after wk 8. Consumption of mixed ration, MR, and water was recorded daily, and calves were weighed twice weekly. Samples of feed and orts were taken in wk 7 and 8 for nutrient content analysis. Behavioral data of each calf were obtained 2 h per day during wk 6 and 8. Total feces were collected during wk 8 to determine apparent digestibility. Calves exposed to COARSE had a greater ($P < 0.05$) DMI than FINE calves (2.70 vs. 2.45 kg/d, respectively) during the week after weaning (wk 8). Body weight gain was similar between treatments, despite COARSE calves having a numerically greater gain than FINE calves (0.94 vs. 0.89 ± 0.03 kg/d). Interestingly, COARSE calves tended ($P = 0.09$) to have a greater gain to feed ratio than FINE calves (0.68 vs. 0.63 ± 0.02 kg/kg). No differences were observed in CP, soluble protein, and ADF consumption between treatments; however, COARSE calves tended ($P = 0.09$) to consume more NDF than FINE calves during the last week of study (719.2 vs. 610.5 ± 25.84 g/d). Calves receiving COARSE sorted in favor of NDF to a greater extent than FINE calves ($P < 0.05$), whereas FINE calves sorted in favor of CP to a greater extent than COARSE calves ($P < 0.05$). Apparent DM, CP, NDF, and ADF digestibilities were greater ($P < 0.05$) in COARSE than in FINE calves (72.3, 77.4, 40.7, and 42.7% vs. 69.2, 74.5, 34.0, and 35.6%, respectively). Calves fed FINE spent more ($P < 0.05$) time performing non-nutritive oral behaviors than those fed COARSE, and FINE calves tended to spend less time idle (either lying or standing) than COARSE animals. In conclusion, providing chopped hay to young calves improves feed intake, improves DM, CP, NDF, and ADF digestibility after weaning, and reduces non-nutritive oral behaviors.

Key Words: feeding behavior, forage, physical form

M289 Effects of age on gene expression of transport proteins in ruminal epithelia of milk-fed calves.

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The objective was to evaluate effects of age of milk-fed calves on expression of genes coding for epithelial transport proteins that facilitate absorption of fermentation acids from the rumen. Eighteen Holstein bull calves were individually housed and fed whole milk twice daily (4L/d) and offered texturized calf starter ad libitum. The calves were harvested at week one (n = 6), 3 (n = 5), or 6 (n = 7) after birth, and ruminal epithelial tissue was harvested; the epithelium was manually peeled off from the muscle layer, rinsed in PBS (pH 7.4), snap-frozen in liquid nitrogen, and kept at −80°C until analysis. Total RNA was extracted, and real-time RT-PCR was performed for monocarboxylate transporter isoform 1 (*MCT-1*; co-transporter exporting protons and dissociated VFA), Na^+/H^+ exchanger (anti-porter importing Na^+ and exporting protons) isoforms 1 (*NHE-1*), 2 (*NHE-2*) and 3 (*NHE-3*), putative anion transporter isoform 1 (*PAT-1*; anti-porter importing dissociated VFA and exporting bicarbonate), and downregulated in adenoma (*DRA*; anti-porter importing dissociated VFA and exporting bicarbonate). The expression of each targeted gene was normalized using 3 internal control genes: ribosomal protein large P0, β-actin, and glyceraldehyde-3-phosphate dehydrogenase. Ruminal epithelia harvested from 3 or 6 wk old calves had higher mRNA abundance of *DRA* (0.44 and 0.39 vs. 0.07 units; $P < 0.05$) and *MCT-1* (1.08 and 0.81 vs. 0.26 units; $P < 0.05$) compared with samples from one-wk old calves. Abundance of *NHE-2* mRNA was greater for 6-wk old calves compared with one-wk old calves (0.72 vs. 0.21 units; $P < 0.05$). However, mRNA abundance of *NHE-1*, *NHE-3*, and *PAT-1* was not affected by age at harvest. Dissociated VFA are transported across apical membrane via *DRA* and basolateral membrane via *MCT-1*, and both *MCT-1* and *NHE-2* regulate intracellular pH by exporting protons generated from absorption of undissociated VFA. These results indicate that ruminal epithelia of calves initiate metabolic adaptations at a molecular level within 3 wk after birth to facilitate absorption of fermentation acids from the rumen.

Key Words: calf, rumen epithelia, transport protein

M290 Ruminal and blood parameters of dairy calves managed on different milk-feeding programs.

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The objective was to evaluate the effect of different milk-feeding programs on dairy calves ruminal and blood parameters. After birth, 30 male Holstein calves were utilized in a randomized block design and assigned to 3 milk-feeding programs: 1) Conventional (C): 10% birth weight (BW) (4L/d); 2) Step-down (SD): wk 1: 10% BW (4L/d); wk 2 to 6: 20% BW (8L/d), and wk 7 and 8: 10% BW (4L/d); 3) Intensive (I): 20% BW (8L/d). Animals were individually housed, had water free-choice, starter concentrate fed ad libitum (18% CP; 80% TDN), and milk replacer (MR) (20% CP, 16% EE, 12.5% solids; Sprayfo Violeta, Sloten do Brasil Ltda.) fed according to milk-feeding program. Coast-cross hay was fed after weaning (eighth week). Blood samples were collected weekly until 10 weeks of age for glucose and β-hydroxybutyrate (BHBA) determination. In wk 4, 8 and 10 of age, ruminal fluid samples were collected using an oro-ruminal probe and a suction pump for pH

and short chain fatty acids (SCFA) analysis. Plasma glucose (88.8; 89.8; 92.4 mg/dL for C, SD and I programs, respectively) were not affected ($P > 0.05$) by milk-feeding program, but concentrations decreased as animals aged ($P < 0.0001$). Concentrations of BHBA (0.155; 0.122; 0.101 mmol/L for C, SD and I, respectively) were affected ($P < 0.05$) by milk-feeding program, as well as by age ($P < 0.02$), with similar values up to the 6th week but increasing values thereafter; and by the interaction of age and milk-feeding program ($P < 0.02$). Observed effects for BHBA reflect the observed starter concentrate intake according to milk-feeding programs (722.5; 552.0; 435.7 g/d for C, SD and I, respectively), with higher concentrations of BHBA for treatments with higher starter intake. Average ruminal pH (5.47; 5.51; 5.46 for C, SD and I, respectively), and total SCFA (106.6; 112.5; 105.4 mmol/mL for C, SD and I, respectively) were not affected by milk-feeding program. However, an age effect ($P < 0.001$) was observed for pH, with decreasing values; and for acetate, propionate, butyrate and total SCFA, with increasing concentrations as calves aged. An interaction of age and milk-feeding program effect was observed for propionate ($P < 0.2$), butyrate ($P < 0.6$), and for the total SCFA ($P < 0.05$), with lower concentrations for calves on intensive milk-feeding program at wk 8. Effects of milk-feeding program on starter intake affect rumen and plasma parameters. Support by FAPESP.

Key Words: β-hydroxybutyrate, milk replacer, volatile fatty acids

M291 Effects of kelp meal on performance and structural growth of conventional and organic dairy calves.

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Kelp meal (KM) is a dried seaweed product used in dairy farms particularly in organic operations. The current study examined the effects of KM (*Ascophyllum nodosum*) on performance and structural growth of 36 heifer calves [18 conventional Holsteins (Trial 1) and 18 organic Jerseys (Trial 2)]. We hypothesized that the high mineral content and salty flavor of KM enhances diet palatability and DMI in calves. Animals were blocked by calving date and, within breed, randomly assigned to 2 treatments: Control (calf starter) or KM (calf starter + 25 g of KM). Approximately 5.7 and 3.8 L of milk were fed daily to Holsteins and Jerseys, respectively. Grass hay was offered ad libitum and orts were collected daily. Body weight and growth were measured twice a week from wk 1–7 and wk 1–8 of age in Holsteins and Jerseys, respectively. Except for whiter height, which was higher ($P = 0.05$) for Holsteins fed the control vs. the KM diet, no other significant treatment differences were observed on Trial 1. However, data from Trial 2 showed that KM significantly increased DMI and ADG compared with the control. No differences ($P > 0.05$) in structural growth were observed for calves fed the control or the KM diet in Trial 2, suggesting that dietary energy was utilized for body fat deposition rather than skeletal growth. A 2-fold difference in ash concentration between the conventional (9.04%) and the organic starter (5.68%) suggests the latter was lacking minerals. Because KM is rich in minerals and adds a salty flavor to the diet, increased DMI in Jerseys may be explained by enhanced diet palatability and/or an animal need to meet mineral requirements. Research is needed to investigate the interaction between KM and the starter nutrient profile on body composition and structural growth of dairy calves.

Table 1. Effects of kelp meal (KM) on performance and growth of dairy calves

	Holsteins (Trial 1)				Jerseys (Trial 2)			
Item	Control	KM	SED	P>F	Control	KM	SED	P>F
DMI, kg/d	1.34	1.39	0.12	0.77	0.93	1.16	0.04	<0.01
ADG, kg/d	0.73	0.76	0.03	0.55	0.49	0.61	0.03	0.01
ADG:DMI	0.50	0.55	0.02	0.11	0.53	0.53	0.03	0.98
Final BW, kg	60.5	61.5	1.05	0.52	40.7	44.7	1.00	0.02
Whiter height, cm	85.3	84.4	0.31	0.05	74.8	75.0	0.60	0.73
Hip height, cm	89.1	88.3	0.35	0.11	77.1	77.8	0.44	0.36
Body length, cm	65.0	63.7	0.77	0.26	59.2	59.4	0.51	0.85

Key Words: dairy calves, kelp meal, organic dairy

M292 Total serum protein in calves is not correlated with future milk performance.

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It is well established that calves with poor passive transfer of immunoglobulins have increased risk of diarrhea, respiratory problems, and mortality. Furthermore, there are some studies that have linked plasma immunoglobulin concentrations or colostrum provision early in life with improvements in future performance. The improvements have been attributed to potential lactocrine mechanisms mediated by hormones present in the colostrum. The objective of this study was to determine whether total serum protein (TSP) in calves was correlated with future milk performance in the first lactation. A total of 6,172 calves born between 2005 and 2009 in the same herd were fed 3 L of colostrum within 1 h after birth followed by 2 additional liters 8 h later, and blood-sampled within 48 h of life to determine TSP. Determinations of TSP were performed by an experienced veterinarian using a refractometer (Jorvet J-351, Jorgensen Laboratories, Inc. CO). Then, total milk produced by the animals in their first lactation was recorded. A categorical variable was constructed including TSP below 5.4 (n = 1,962), between 5.4 and 6.4 (n = 2,324), and above 6.4 mg/dl (n = 1,886). A mixed-effects model that accounted for the random effects of year of birth and sire (father of each heifer considered) plus the fixed effects of the 3 TSP categories and the lactation length as a covariate was run to evaluate any potential relationship between TSP and milk yield in the first lactation. In the first lactation, calves that had TSP below 5.4 mg/d produced 10,551 ± 230 kg, those with TSP between 5.4 and 6.4 mg/dl produced 10,499 ± 229 kg, and those with TSP above 6.4 mg/dl produced 10,445 ± 230 kg. There was no relationship ($P = 0.13$) between TSP and future milk production. These results indicate that either TSP is not a valid proxy to assess the adequacy of colostrum feeding, or that the amount of colostrum offered during the first 2 d of life has no impact on future animal performance.

Key Words: colostrum, metabolic imprinting, performance

M293 Intake and performance of Holstein heifers transitioned to group housing from individual pens using differing grain mixes with or without hay the first two weeks after moving. D. Ziegler*[1], D. Schimek[2], B. Ziegler[2], H. Chester-Jones[1], M. Raeth-Knight[3], and G. Golombeski[4], [1]*University of Minnesota Southern Research and Outreach Center, Waseca,* [2]*Hubbard Feeds Inc., Mankato, MN,* [3]*University of Minnesota, St. Paul,* [4]*Hubbard Feeds Inc., Iowa City, IA.*

One-hundred twelve 57- to 60-d-old Holstein heifers (82.6 ± 1.32 kg) were assigned to 1 of 4 treatments in 4 replicate pens (7 heifers/pen) for 112 d. Treatments were fed d 1–14 and included 1) free choice (FC) 18% CP texturized grain mix without hay (TXT); 2) same as TXT but with FC hay (TXTH); 3) FC 16% crude protein whole corn/pellet grain mix without hay (WCP); 4) same as WCP but with FC hay (WCPH). Then from d 15–112 all heifers were fed a common diet of 16% CP GM (2.73 kg/d d 15–56 and 2.27 kg/d d 57–112) with FC hay. Intakes were taken daily from d 1–28 and then weekly from d 29–112. Daily grain mix dry matter intake and gain/feed did not differ from d 1–14, 2.30 ± 0.05 kg and 0.38 ± 0.006 kg gain/kg feed, respectively. Hay dry matter intake for d 1–14 was 0.06 and 0.11 kg/d for TXTH and WCPH, respectively. There were significant grain mix x hay interactions for ADG ($P < 0.05$) and total dry matter intake ($P = 0.0003$) but no differences in gain to feed from d 1–112 (0.29 ± 0.002 kg gain/kg feed). No differences were observed in body condition score (112 d avg. 3.25) or hip height (112 d avg. 112.2 cm; $P > 0.05$). Under conditions of this study feeding differing grain mixes with or without hay for 14 d in group pens after moving from individual nursery pens had minimal effect on heifer performance.

Key Words: grain mixes, Holstein heifers, performance.

M294 Precision-feeding dairy heifers with different levels of dietary fiber and F:C. Effects on protein utilization, N efficiency, and rumen fermentation. G. J. Lascano*[1] and A. J. Heinrichs[2], [1]*The California Polytechnic State University, San Luis Obispo,* [2]*The Pennsylvania State University, University Park.*

The objective of this experiment was to determine the effects of manipulating dietary fiber level with differing forage to concentrate (F:C) ratios on protein rumen utilization of precision-fed dairy heifers. Six cannulated Holstein heifers (486.98 ± 15.07 kg BW) were randomly assigned to 2 levels of concentrate, HC (45% forage) and LC (90% forage) and to a forage type sequence [33% grass hay and wheat straw HS, 67% corn silage CS (Low fiber); 50% HS, 50% CS (Medium fiber); and 67% HS, 33% CS (High fiber)] within forage level administered according to a split-plot 3 × 3 Latin square design (21-d period). Similar N intake and rumen degradable protein (RDP) were provided (1.20 g N/kg BW 0.75), and casein was added to supply additional N to provide 1.80 g N/kg BW 0.75. Heifers fed HC had greater apparent total tract organic matter (OMD), neutral detergent fiber (NDF), and cellulose apparent digestibility (AD) than those fed LC diets ($P \leq 0.01$). Nitrogen AD was not different between F:C or with increasing levels of HS in diets, but N retention tended to decrease linearly as HS was increased in the diets ($P = 0.09$). Protozoa numbers were not different between F:C treatments, but HS interacted linearly. The HC-fed heifers had a greater VFA concentration ($P \leq 0.05$). Mean pH was not different among F:C rations. Increasing dietary fiber through HS affected RDP utilization and decreased DM, OM, NDF, ADF and cellulose AD linearly ($P \leq 0.05$). Microbial protein synthesis predicted from urinary purine derivatives decreased linearly with HS addition resulting in a linear decrease in N retention with HS addition ($P = 0.03$), which was opposite to rumen NH_3N and BUN, reflecting the inefficiency in N utilization as more HS was added to the diets. Rumen fermentation parameters, DM and fractional passages (solid and liquid) rates support the reduction in protein utilization and retention, microbial protein synthesis and AD observed as more dietary fiber is added to the rations of precision-fed dairy heifers.

Key Words: heifers, fiber, protein degradability

M295 Insulin response is affected by the level of milk replacer offered to young calves. A. Bach*[1,2], Ll. Castells[2], C. Montoro[2], and M. Terre[2], [1]*ICREA, Barcelona, Spain,* [2]*Department of Ruminant Production, IRTA, Barcelona, Spain.*

Eight male Holstein calves (40.6 ± 2.9 kg of BW and 7.8 ± 1.6 d of age) individually housed were allocated to either a LOW milk replacer (MR) allowance of 2 daily doses of 2 L each (478.5 g/d of DM from MR), or to a HIGH allowance of 2 daily doses of 4 L (957.0 g/d of DM from MR). In addition all calves had ad libitum access to the same starter feed and water. At d 7, 30, and 60 of experiment all calves were submitted to a glucose tolerance test (GTT) that consisted on an i.v. infusion of 180 mg/kg of BW of glucose at 4 h after the morning MR offer. Blood was harvested at −15, −5, 0, 4, 8, 12, 25, 35, 45, and 60 min relative to glucose infusions. Blood samples collected at −15 and −5, and 0 relative to glucose infusion were used as baseline concentrations of glucose and insulin. Then, the area under the curve (AUC; concentration/min) for glucose and insulin was calculated as the increase with respect to the baseline. Next, the clearance rates of insulin (CRI, %/min) and glucose (CRG, %/min) were computed. The increase in blood glucose following the GTT (assessed as AUC) was similar in both LOW and HIGH calves, which indicates that all animals were able to control glycemia effectively. Similarly, CRG and CRI were no different between LOW and HIGH calves. However, calves in the HIGH group needed a substantially greater ($P < 0.001$) serum insulin concentration (98.7 ± 13.2 μU/ml) than LOW calves (41.5 ± 13.2 μU/ml) to control glycemia. Furthermore, as age increased, the rise in serum insulin elicited by the GTT continued to increase ($P = 0.01$) in HIGH but not in LOW calves. Insulin to glucose ratio was greater ($P < 0.001$) in HIGH (157.5 ± 7.8 μU/mg) than in LOW (46.7 ± 7.8 μU/mg) calves. This ratio increased with age ($P < 0.01$) and in a more pronounced ($P = 0.03$) fashion in HIGH than in LOW calves. It is concluded that offering 8 L/d of MR in 2 separate doses decreases insulin sensitivity of young calves. Research is needed to assess whether the impaired glucose responsiveness of calves can be minimized by feeding milk more frequently.

Key Words: calf, glucose, metabolism

M296 Optimizing particle size and moisture in diets for dairy heifers. M. A. Khan[1], A. Bach[2,3], Ll. Castells*[3], D. M. Weary[1], and M. A. G. von Keyserlingk[1], [1]*Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada,* [2]*ICREA, Barcelona, Spain,* [3]*Deparment of Ruminant Production, IRTA, Barcelona, Spain.*

Little research to date has addressed diets for growing dairy heifers. In 2 experiments involving 36 replacement heifers (181 ± 7 kg of BW and 175 ± 7 d of age) we tested the effects of forage particle length and DM of a TMR on DMI, feeding rate and feed sorting. Each experiment used a replicated 3 × 3 Latin square design, testing 9 heifers in each of 2 replications for 3 periods of 9 d each. Each group of heifers was housed in a pen with access to 3 electronic feed bins. In Exp. 1, a TMR was formulated using the same ingredients but where the hay component was provided at 3 different lengths resulting in a TMR with 72 (LONG), 64.2 (MEDIUM), or 60% (SHORT) of the particles above 19 mm. In Exp. 2, heifers were provided access to a TMR with different moisture contents (obtained by adding water): LOW (65% DM), MODERATE

(50% DM), and HIGH (35% DM). In both experiments, data from the last 5 d of each period were analyzed using a mixed-effects model accounting for the fixed effects of treatment and period, and the random effects of replication, animal within treatment, and period. In Exp. 1, DMI tended ($P = 0.09$) to increase and time spent feeding decreased ($P = 0.05$) as the particle size of TMR increased. Feeding rate also tended ($P = 0.07$) to increase as particle size of the TMR decreased. Heifers fed the LONG diet selected ($P < 0.05$) in favor of long particles (>19 mm) and against short (1.18–8mm) and fine (<1.18 mm) particles; heifers fed the SHORT diet selected ($P < 0.05$) against long particles and in favor of short and fine particles. In Exp. 2, heifers consuming the LOW moisture diet tended ($P = 0.09$) to have greater DMI than those fed the MODERATE and HIGH diets, with no differences in feeding behavior or sorting activity. We conclude that TMRs with particle sizes similar to the MEDIUM diet minimize sorting. Adding water to achieve moisture contents of a TMR >35% can reduce DMI in heifers.

Key Words: eating rate, feeding behavior, sorting

M297 Replacing processed grains with whole corn in starter diet did not affect the performance of dairy calves.

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We compared the effects of replacing processed grains in conventional texturized starter with whole corn on the performance of dairy calves. Individually housed Holstein heifer calves (n = 24) were fed whole milk (8 l/d) for 28 d of age and gradually weaned during d 29 to 39. At 7 d of age, calves were randomly assigned to one of the 2 starter diets i.e., conventional (textured; contain processed grains) starter (n = 12) or whole corn (whole corn replaced the grain component of conventional diet) starter (n = 12). Starter diets were fed ad libitum for 70 d. Daily starter intake in calves fed either conventional or whole corn starter was similar during pre-weaning (0.21 ± 0.02 vs. 0.22 ± 0.02, kg; $P = 0.73$) and post-weaning (2.10 ± 0.07 vs. 1.99 ± 0.10; $P = 0.46$) periods. Overall during the experiment, total (milk solid plus starter) DMI (98.0 ± 3.0 vs. 95.7 ± 3.7, kg; $P = 0.63$), BWG (53.5 ± 2.2 vs. 53.1 ± 2.4, kg; $P = 0.92$) and feed efficiency (0.56 ± 0.01 vs. 0.57 ± 0.02, BWG/DMI; $P = 0.67$) were similar in calves fed either conventional or whole corn starter. Calves fed whole corn starter visit the feeder more frequently (186.5 ± 9.4 vs. 153 ± 15.3, visit/d; $P = 0.02$) than those fed conventional starter. However, daily time spent eating was not affected (3.57 ± 0.17 vs. 3.45 ± 0.19, h/d; $P = 0.18$) by diet. Calves on both treatments did not ($P > 0.05$) preferentially select feed particles (grains or pellets) from the starter diet. Ruminal pH was similar (5.68 ± 0.16 vs. 5.43 ± 0.07, $P = 0.20$) in calves fed whole corn based starter compared with those fed conventional starter. Concentrations of blood glucose and blood BHBA were similar ($P > 0.05$) in calves fed both starter diets. In conclusion, replacing processed grains with whole corn in starter diets did not affect the feed consumption, feed particle sorting, growth and feed efficiency in dairy calves however; it fails to alleviate the severe acidic conditions in the rumen of developing calves. Use of whole corn in starter could potentially lower the rearing cost of heifers by reducing the processing cost of grains.

Key Words: whole corn, starter, rumen development

M298 Performance of dairy calves managed on different milk-feeding programs.

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The objective was to evaluate the effect of different milk-feeding programs on performance of calves until 10 weeks of age, abruptly weaned at 8 weeks of age. After birth, 30 male Holstein calves were utilized in a randomized block design and assigned to 3 milk-feeding programs: 1) Conventional (C): 10% birth weight (BW) (4L/d); 2) Step-down (SD): wk 1: 10% BW(4L/d); wk 2 to 6: 20% BW (8L/d), and wk 7 and 8: 10% BW (4L/d); 3) Intensive (I): 20% BW (8L/d). Animals were individually housed, had water free-choice, starter concentrate fed ad libitum (18% CP; 80% TDN), and milk replacer (MR) (20% CP, 16% EE, 12.5% solids; Sprayfo Violeta, Sloten do Brasil Ltda.) fed according to milk-feeding program. Coast-cross hay was fed after weaning (eighth week). Fecal scores, starter and milk replacer intake were evaluated daily. Calves were weighted and growth measurements were taken weekly until the tenth week of age. Starter daily intake was affected ($P < 0.05$) by the milk-feeding program with lower intake observed for the intensive fed calves as compare with calves fed by the conventional program, with no difference with the step-down program (722.5; 552.0; 435.7 g/d for C, SD and I, respectively). Measured average MR intake was 3.94; 6.02; 7.30 L/d for C, SD and I programs, respectively. Despite the higher MR intake for the step-down and intensive programs, weight gain (469.1; 455.0; 466.4 g/d for C, SD and I, respectively), average body weight (50.6; 51.6; 52.7 kg for C, SD and I, respectively), and final weight (69.7; 68.6; 69.6 kg for C, SD and I, respectively) were not affected by milk-feeding. Even though average and final body weight were not affected, heart girth was affected ($P < 0.05$) (84.3; 86.2; 87.2 cm for C, SD and I, respectively), suggesting effects on growth other than weight gain. However, other body measurements (hip width: 23.1; 23.4; 23.8 cm and withers height: 82.3; 82.1; 83.0 cm for C, SD and I, respectively), were not affected ($P > 0.05$). Average hay intake was affected ($P < 0.05$) with lowest intake for calves on the step-down program (461.0; 150.5; 307.4 g/week for C, SD and I, respectively). Fecal scores were higher for the step-down and intensive programs (1.44; 2.8; 2.1 for C, SD and I, respectively). Support by FAPESP.

Key Words: milk replacer, liquid feeding, weight gain

M299 Effect of increasing intake of linoleic acid in milk replacer on Holstein calf performance.

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The aim was to evaluate the linoleic acid (LA) requirement of unweaned Holstein calves from birth to 60 d of age. Within 2 h of birth, calves (n = 88) were fed 4 L of colostrum (>60 g of IgG/L) harvested from cows delivering the experimental calves. Calves were blocked by gender and assigned randomly to 1 of 4 treatments. Soybean and coconut oils were mixed with an emulsifier and added to a basal milk replacer (MR; 7% fat and 28% CP) at the time of feeding (0600 and 1200 h) to supply 0.064, 0.128, 0.256, or 0.512 g of LA/kg of metabolic BW, T1 to T4, respectively. Final MR fed was 15% fat. Amount of MR fed was adjusted based on weekly BW. Blood was collected weekly. A low LA grain mix (18% CP, 2.87 Mcal of ME/kg, and 1.6% fat) was offered starting at 31 d of age. Birth weight and height were covariates for analysis of gain and growth respectively. During the period of feeding MR alone, T2 males gained more BW (5.3 kg) compared with males fed T1, T3, or T4 (2.8, 2.8, and 2.7 kg, respectively, SE = 0.5) whereas BW gain by females did not differ (2.6, 3.1, 3.3, and 3.4 kg; cubic by gender interaction, $P = 0.04$). Increased gain by T2 males was accompanied by increased intake of MR (19.7 vs. 19.2, 19.0, and 19.2 kg, SE = 0.2). Intake of grain mix (480 g/d; SE = 55) and BW gain (21.2 kg, SE = 1.4) between 31 and 60 d of life did not differ among treatments. At 60 d of life, calves fed diets T2 and T3 had greater wither height (82.6, 83.6, 84.0, and 83.2 cm, SE = 0.7, $P = 0.08$) and hip height (87.6, 88.7, 88.9, and 87.9 cm, SE = 0.7; quadratic effect, $P = 0.04$). Mean concentrations of plasma glucose (90.3 mg/dL, SE = 1.5) and insulin (2.2 ng/mL, SE = 0.3) were unaffected by diet. Total cholesterol concentrations in plasma increased linearly ($P = 0.05$) with increasing intake of LA (72.6, 75.2, 79.0, and 80.4 mg/dL, SE = 4.1) whereas plasma concentrations of BHBA tended ($P = 0.10$) to be greater for T1 calves compared with others (0.82 vs. 0.74, 0.72, and 0.76 mg/dL, SE = 0.05). Supplementing LA in MR at >0.064 g/kg of metabolic BW during the first 60 d of life improved growth but not BW of underperforming female Holstein calves.

Key Words: calves, milk replacer, linoleic acid

M300 Effect of feeding increasing amounts of linoleic acid on health and immunity of unweaned Holstein calves. M. Garcia,* J. H. Shin, A. Schlaefli, D. Wang, J. E. P. Santos, and C. R. Staples, *University of Florida, Gainesville.*

The aim was to evaluate the effect of increasing intake of linoleic acid (LA) on measures of health and immunity of Holstein calves from birth to 60 d of age. Within 2 h of birth, calves (n = 88) were fed 4 L of thawed colostrum (minimum of 60 g of total IgG/L) harvested from cows delivering the experimental calves. Calves were blocked by gender and assigned randomly to 1 of 4 treatments. Soybean and coconut oils were mixed with an emulsifier and added to a basal milk replacer (MR; 7% fat and 28% CP) at the time of feeding (0600 and 1200 h) to supply 0.064, 0.128, 0.256, or 0.512 g of LA/kg of metabolic BW, T1 to T4, respectively. Final MR fed was 15% fat. A grain mix of low LA concentration (18% CP, 2.87 Mcal of ME/kg, and 1.6% fat) was offered starting at 31 d of age. Blood was sampled weekly. Serum IgG (g/L) on the day after birth was used as a covariate for health measures. As LA intake increased, fecal firmness tended ($P = 0.07$) to increase linearly as well as age at first day of diarrhea (7.0, 7.3, 7.5, and 7.5 d, SE = 0.3). The % of days with fever (>39.5°C) during the first 14 d of age did not differ (5.7%, SE = 2.3) nor did % of days (4.5%, SE = 1.0) with severe diarrhea throughout the 60-d study. Mean plasma concentration of acid soluble protein tended ($P = 0.06$) to decrease linearly (102.0, 96.5, 91.7, and 92.6 mg/L) with increasing LA intake. Mean plasma concentration of haptoglobin decreased (treatment by age, $P = 0.04$) to a greater extent at first evidence of diarrhea for T1 calves. Mean concentration of TNFα in mitogen-stimulated blood did not differ among treatments (375 pg/mL, SE = 64), but that of IFNγ tended to be greater in T2 and T3 calves (258, 342, 319, and 238 pg/mL, SE = 67; quadratic effect, $P = 0.09$). A similar quadratic response to LA supplementation was detected for % of blood neutrophils undergoing phagocytosis (62.1, 66.6, 64.1, and 62.8%, SE = 2.3; $P = 0.07$) and oxidative burst (51.5, 55.8, 53.6, and 50.4%, SE = 2.5; $P = 0.04$). Feeding LA in MR between 0.128 and 0.256 g/kg of metabolic BW appeared to increase several markers of pro-inflammatory response in unweaned Holstein calves.

Key Words: calves, linoleic acid, immunity

M301 Jersey calf blood metabolites in response to liquid feeds with varied fatty acid profiles. V. A. Swank,* W. S. Bowen, K. M. O'Diam, M. L. Eastridge, and K. M. Daniels, *Department of Animal Sciences, The Ohio State University, Columbus.*

Most commercially available Jersey calf milk replacers (MR) use edible lard as the primary fat source. Edible lard lacks medium chain fatty acids (MCFA) whereas pasteurized saleable whole milk (pSWM) from Jersey cows contains many MCFA. The objective was to determine whether altering the FA profile of MR with the inclusion of coconut oil (CO), rich in MCFA, would alter blood metabolite profiles in Jersey calves over time. This trial was conducted as a randomized complete block design. Male (n = 18) and female (n = 32) Jersey calves were randomly assigned at birth to 1 of 4 liquid diets: pasteurized Jersey saleable whole milk (pSWM; 27.9% CP, 33.5% fat, DM basis); MR containing 100% of fat as edible lard (100:00; 29.3% CP, 29.1% fat); MR containing 20% of fat as CO (80:20; 28.2% CP, 28.0% fat); MR containing 40% of fat as CO (60:40; 28.2% CP, 28.3% fat). Calves were fed 2L of their respective liquid diet twice daily (0600h and 1800h) from 2d of age until 7wk of age, and once daily until weaning (8wk of age). Once a week, a subset of calves (n = 34) were fasted overnight for 12h and jugular blood samples were taken; immediately before morning feeding which occurred at 0600h, 0800h, 1200h, and immediately before the evening feeding at1800h. These samples were collected at 1wk, 3wk, and 6wk of age. Blood samples were used to determine concentrations of triglycerides (TG), glucose, plasma urea nitrogen (PUN), and total protein (TP). Data were analyzed using the mixed procedure of SAS. TP was not different throughout the trial. The interaction of diet and week was significant for TG and glucose concentrations; both variables changed over time in a complex pattern for animals on a given treatment (significant linear and quadratic contrast effects). Treatment, week, and time of collection had a significant effect on intensive PUN concentrations, with all 3 having a linear effect. Moreover, pSWM was significantly different than 80:20, with 6.17mg/dl and 5.76mg/dl, respectively ($P = 0.036$). Given that calves on this trial grew the same (companion abstract) our results here measuring concentrations of blood metabolites are as expected.

Key Words: fatty acids, Jersey calf, milk replacer

M302 Ponderal development of dairy heifers fed sugarcane and increasing crude protein levels. M. F. S. Queiroz*[1], T. T. Berchielli[2], R. D. Signoretti[3], and J. A. S. Morais[4], *[1]Universidade Federal da Paraíba, CCHSA/UFPB, Bananeiras, Paraíba, Brazil, [2]Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal, São Paulo, Brazil, [3]Agência Paulista de Tecnologia dos Agronegócios, Colina, São Paulo, Brasil, [4]Universidade Federal de Sergipe (UFS), São Cristovão, Sergipe, Brazil.*

Twenty-four Holstein × Zebu crossbred heifers with average age of 19 months and 250 kg fed sugarcane and four different protein levels diets were used. The sugarcane (IAC 862480) was evaluated during August to November (winter/spring) and the diets concentrate was compound by corn meal, soybean meal, urea, ammonia sulfate and mineral mix, in different proportions, to obtain the protein levels (13, 15, 19 and 22% of crude protein) in 70:30 relation forage and concentrate. The animals were maintained in an individual stall and ad libitum fed twice a day (8 and 16 h) during the adaptation and experimental period, 15 and 62 days, respectively. The experimental design was completely randomized blocks, consisting of 3 blocks and 4 treatments. The heifers were weighed and their thoracic perimeter; withers and hip height, and body score were determined at the beginning and at the end of the experimental period, at every 21 days. There was no diet effect ($P > 0.05$) on ponderal development and body score. The heifers had an average growth of 0.05 cm/day withers height and 0.04 cm/day hip height and 0.17 cm/day of heart girth during the experimental period.

Table 1. Means of crossbred dairy heifers ponderal development

	Diet CP level (%)					P-value[1]	
Item	13	15	19	22	CV	LE	QE
Weight (kg)	279.1	275.6	268.9	277.1	13.3	ns	ns
Withers height (cm)	120.1	121.1	119.3	119.6	4.2	ns	ns
Hip height (cm)	124.0	124.9	123.6	123.0	3.9	ns	ns
Thoracic perimeter (cm)	158.1	155.7	155.8	156.3	5.0	ns	ns
Initial BCS[2]	2.5	2.6	2.6	2.6	8.2	ns	ns
Final BCS[2]	2.8	2.8	3.0	2.8	9.0	ns	ns

[1] LE = linear effect; QE = quadratic effect.

[2] Scale 1 to 5.

Key Words: body score, feedlot, heifer reraising

M303 Pre- and postweaning performance and health of dairy calves when sodium butyrate is fed in milk replacer and/or calf starter during the summer months.

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One-hundred eight (2–4 d old) individually fed Holstein heifer calves (39.3 ± 0.64 kg) were randomly assigned to 1 of 4 treatments to evaluate pre- (d 1–42) and post weaning (d 43–56) calf performance and health when fed sodium butyrate in milk replacer and/or calf starter. All calves were fed a non-medicated 20% fat:20% protein milk replacer (MR) at 0.284 kg in 1.99 L water (12.5% solids) 2X daily for the first 35 d and 1X daily from d 36 to weaning at 42 d. Calf starter (CS; 18% CP) and water were fed free choice d 1 to 56. Day 1 to 14, 1:1 neomycin:oxytetracycline was added to the MR solution to provide 22 mg/kg BW/d. Treatments (Trt) were 1), Control MR and CS with rumensin (R; 33 mg/kg); 2), MR with 0.3% sodium butyrate (NaB; Adimix-Pro) and CS with R; 3), Control MR and CS with 0.33% NaB (Adimix-30C); and 4), MR with 0.3% NaB and CS with 0.33% NaB. Ambient temperatures averaged a high of 27.2°C (range 18.9 to 38.3°C) and a low of 16.9°C (range 10.6 to 26.1°C) during the study (June, July, August, 2011). Calves fed MR with NaB (Trt 2,4) had greater pre-weaning ADG ($P = 0.02$) and gain/feed ($P = 0.001$) than those fed MR without NaB (Trt 1,3). Similar trends ($P = 0.09$) were observed for d 1–56 ADG. Calves fed Trt 1 had reduced gain/feed and tended to have lower pre-weaning and overall ADG ($P = 0.07$) vs. Trt 2, 3, and 4. The addition of NaB or R to starter did not affect starter intake pre- or post-weaning. There were also no differences in total DMI between treatments averaging 0.78 kg/d and 1.76 kg/d during the pre- and post-weaning periods, respectively. There were no pre- or post weaning scouring days and treatment cost differences due to treatments. Under the conditions of this study there were benefits to calf performance of adding NaB to non-medicated MR during the summer months. Using NaB in CS appeared to be an acceptable alternative to R.

Key Words: Holstein calves, performance, sodium butyrate

M304 Limiting amino acids for pregnant heifers fed corn silage-based diet.

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Two experiments were conducted to determine limiting amino acids (AA) for pregnant heifers fed corn silage-based diet. In experiment 1, four 21-mo-old Holstein Heifers (BW = 450 ± 20kg) fitted with ruminal, proximal duodenal and terminal ileal cannula were used to determine flows of AA into the duodenum and apparent intestinal AA digestibilities. These data were used to calculate amounts of total essential amino acids (TEAA) that should be infused into the duodenum to match the requirements of AA of growing and pregnant heifers according to calculations, which suggested that 8, 15, 20, 5, 15, 15, 20, 5, 10 and 5 g/d of methionine, histine, lysine, arginine, threonine, valine, leucine, isoleucine, phenylalanine and tryptophane were required, respectively, to be supplemented to the duodenum. In experiment 2, three 23-mo-old Holstein Heifer (BW = 470 ± 25kg) fitted with ruminal, proximal duodenal and terminal ileal cannula were used in a duplicate 3 × 3 Latin square design experiment, and the 3 treatments were continuously duodenal infusion of a mixture of methionine, Histine, lysine, arginine, threonine, valine, leucine, isoleucine, phenylalanine and tryptophane at 8, 15, 20, 5, 15, 15, 20, 5, 10 and 5 g/d, respectively (TEAA, from experiment 1), or replacement of histine (−15 g histine) or lysine (−20 g lysine) respectively from the TEAA mixture. Data were analyzed using MIXED procedures. When cows were fed corn silage diet, there was no significant effect ($P > 0.05$) of amino acids infusion on nitrogen retention plasma amino acid and plasma urea nitrogen. Replacement of lysine reduced lysine concentrations in plasma ($P < 0.01$). Replacement of histine reduced histine concentrations in plasma ($P = 0.07$). Replacement of lysine increased phenylalanine and valine concentrations in plasma ($P < 0.05$). Collectively, these data suggest that for pregnant heifers fed corn silage-based diet, lysine was likely the first limiting amino acid, followed by histine.

Key Words: limiting amino acid, lysine, plasma amino acids

Ruminant Nutrition: Dairy: Feed Additives I

M305 Effect of live yeast on milk yield and related responses in a commercial dairy herd. G. E. Higginbotham*[1], A. R. Castillo[2], J. M. Heguy[3], and H. A. Rossow[4], *[1]University of California Cooperative Extension, Madera, [2]University of California Cooperative Extension, Merced, [3]University of California Cooperative Extension, Modesto, [4]University of California School of Veterinary Medicine, Tulare.*

Two pens with approximately 220 early lactating Holstein cows (averaging 70 DIM) were used to investigate the effect of supplementing their diets with a live *Saccharomyces cerevisiae* yeast (Yeast) versus no yeast supplementation (Control). Both treatment pens were fed a TMR 2x daily composed of 2.3% wheat hay, 4.0% alfalfa silage, 16.0% alfalfa hay, 26.2% corn silage, 16.0% earlage, 8.4% wet distillers grains, 4.0% whey, 4.8% rolled corn, 18.3% concentrate mix composed of 56.5% canola meal, 21.7% whole cottonseed, 2.2% EnergII, 8.7% high-fat product and 10.9% mineral mix. Total DM offered per cow was 28.5 kg/d. The yeast supplement was fed at the rate of 4.0g/cow/day in the TMR. Cows were milked 2 times daily and housed in freestalls with access to an open dry-lot. Milk yield and composition were recorded by weekly milk weights during the 8-wk trial. Only cows that were in the experimental pens during the complete duration of the trial were used for data analysis (n = 154-control; n = 149-yeast). Milk production of cows before entering treatment pens were used as a covariant. Adjusted mean milk and FCM production was significantly higher ($P < 0.01$) for Yeast versus Control cows, 45.5 vs. 43.3 kg/d (milk) and 43.8 vs. 42.7 kg/d (3.5% FCM). No differences in milk fat (mean 3.28%) or MUN (mean 11.8 mg/dL) were shown. Ruminal fluid pH, total VFA concentration and blood urea N (BUN) were measured twice at one-week intervals from 10 cows per treatment. BUN concentrations were significantly ($P < 0.001$) higher for yeast fed cows, 14.5 vs. 13.7 mg/100mL. Rumen acetic acid was significantly higher ($P < 0.01$) for control, 67.3 vs. 58.5 Mmol/l. Rumen NH3 was significantly ($P < 0.01$) higher for Control versus Yeast fed cows, 16.1 vs. 11.5 mg/100mL. Under the conditions of this field trial, live yeast increased milk production and other parameters (rumen and blood) were affected.

Key Words: milk production, rumen fermentation, yeast

M306 Effects of corn shredlage on lactation performance by dairy cows. L. F. Ferraretto* and R. D. Shaver, *University of Wisconsin-Madison, Madison.*

The objective of this trial was to determine the effects of feeding a TMR containing corn shredlage (SHRD) or processed corn silage (KP) on lactation performance by dairy cows. The KP was harvested using conventional rolls at 3 mm roll gap and the chopper set at 19 mm of theoretical length of cut (LOC). The SHRD was harvested using novel cross-grooved rolls at 2.5 mm roll gap and the chopper set at 30 mm LOC. The SHRD and KP were harvested from one field on 2 consecutive d and stored in separate silo bags for 30 d before the feeding trial. The DM of SHRD and KP during feed-out averaged 35%. One hundred and 12 cows (116 ± 36 DIM and 700 ± 20 kg of BW at trial initiation) were stratified by breed and parity and randomly assigned to 14 pens each with 8 cows. Pens were randomly assigned to the 2 treatment TMR in a completely-randomized design. A 2-wk covariate adjustment period with cows fed a 50:50 mixture of the treatment diets was followed by an 8-wk treatment period with cows fed their assigned treatment diet. The TMR contained (DM basis) KP or SHRD (50%), alfalfa silage (10%), concentrate mixture (40%). Data were analyzed using Proc Mixed in SAS with covariate, treatment, wk, and treatment x wk interaction as Fixed effects and pen within treatment as a Random effect. Cows fed SHRD tended ($P < 0.08$) to consume 0.7 kg/d more DM than KP. Milk yield (43.2 kg/d) did not differ ($P > 0.10$) between treatments. Fat- and energy-corrected milk (FCM, ECM) yields tended ($P < 0.07$ and $P < 0.10$, respectively) to be 1.0 kg/day greater for cows fed SHRD. A treatment by wk interaction ($P < 0.04$) was detected for both FCM and ECM yields; similar ($P > 0.10$) during wk 2, a tendency ($P < 0.10$) for SHRD to be greater during wk 4 and 6, and greater ($P < 0.05$) for SHRD at wk 8. Milk composition did not differ ($P > 0.10$) between treatments. The TMR particle size (15.6+2.9% vs. 3.5+1.4% of particles retained on a 19 mm screen) was greater for SHRD than KP, and feed sorting was minimal and did not differ ($P > 0.10$) between treatments. Feeding corn shredlage tended to increase dry matter intake and fat- and energy-corrected milk yields compared with processed corn silage.

Key Words: corn silage, dairy cow, shredlage

M307 Could live yeast supplement improve milk composition of mid lactating Holstein cows during heat stress? M. Dehghan-Banadaky*[1], R. Motameni[2], and M. Ebrahimi[1], *[1]University of Tehran, Karaj, Tehran, Iran, [2]Islamic Azad University, Tehran, Iran.*

Fifty-six Holstein cows with averaged 145 d postpartum, were used to investigate the effects of live yeast supplement (4 g/cow daily of Probio-Sacc with 15×10^9 cfu) on productivity during hot summer conditions (average thermo humidity index, THI = 78.07). Cows were fed in pens a control diet without or with 4 g of live yeast/cow daily for 4 weeks. The diet as a total mixed ration on dry matter (DM) basis included: corn silage (18.4%), alfalfa hay (21.6%), and a concentrate mix (60%). Live yeast added to the total mixed ration at the time of feeding. Milk production (35.56 and 35.67 kg/d, for control and live yeast treatment, respectively), 3.5% fat-corrected milk (32.20 and 32.96 kg/d), DM intake (22.84 and 22.52 kg/d) were similar for cows fed control and live yeast diets ($P > 0.05$). Greater milk fat percentage (3.02 vs. 3.18) was observed for cows fed live yeast compared with control group ($P < 0.05$). Also milk urea nitrogen (MUN) concentration in cows fed live yeast were lower compared with control group (16.67 vs. 18.75 mg/dl). Other milk components were similar in both groups. Body weights and body condition score changes were similar in both groups. The results suggested that the live yeast cannot improve productivity of heat stressed dairy cows in mid lactation but improved milk fat percentage and decreased MUN.

Key Words: heat stress, lactating cows, live yeast

M308 Investigation of live yeast supplement on blood metabolites and nutrient digestibility in mid lactating Holstein cows. M. Dehghan-Banadaky*[1], R. Motameni[2], and M. Ebrahimi[1], *[1]University of Tehran, Karaj, Tehran, Iran, [2]Islamic Azad University, Tehran, Iran.*

Present study conducted to investigate the effects of live yeast (4 g/cow daily of Probio-Sacc with 15×10^9 cfu) on dietary nutrient digestibility and blood metabolites of mid lactating Holstein cows during hot summer conditions (average thermo humidity index, THI = 78.07). Fifty-six Holstein cows with averaged 145 d in milk, were used in a complete random design with 2 treatments and 28 replicates for 35 d. Cows were fed in pens a control diet without or with 4 g of live yeast/

cow daily. The diets as TMR in dry matter (DM) basis included: corn silage (18.4%), alfalfa hay (21.6%), and a concentrate mix (60%). The live yeast supplement added to the total mixed ration at time of feeding. Blood samples were taken in 2 subsequent days in last week. Feed, ort and fecal samples were taken during 3 subsequent days in last week for nutrient digestibility assay. Acid insoluble ash used as an internal marker. Cows fed live yeast had higher blood glucose (76.60 vs. 66.50 mg/dL, $P < 0.05$) and numerically higher total protein concentration (10.69 vs. 9.73 g/d, $P = 0.07$) compared with control. Blood urea nitrogen was lower for cows fed live yeast compared with control ($P < 0.05$). Nonesterified fatty acids, β-hydroxybutyrate (BHBA), triglyceride, and total cholesterol were similar for both groups. The apparent digestibility of NDF was higher for cows fed live yeast compared with control (53.50 vs. 49.30%, $P < 0.05$) but, the apparent digestibility of DM, OM, CP, and ADF were similar for both diets. Results suggested that live yeast supplement can improve nutrient digestibility and blood metabolites of heat stressed dairy cows in mid lactation.

Key Words: blood metabolites, heat stress, live yeast

M309 Influence of *Salix babylonica* extract on daily milk production and composition as well as in vitro gas production in dairy cows. A. Z. M. Salem*[1], R. Rojo[2], M. Ronquillo[1], H. Gado[3], N. Pescador[1], and F. Peralta[2], [1]*Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma del Estado de México, Toluca, Estado de Mexico, Mexico,* [2]*Centro Universitario UAEM Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, Estado de México, México,* [3]*Department of Animal Production, Faculty of Agriculture, Ain Shams University, Cairo, Egypt.*

A 3 × 3 Latin square design was used to evaluate the effect of 0, 150, and 300 mL of *Salix babylonica* extract on daily milk production and composition in dairy cows. Cows (3 cows for each treatment, 390 ± 10 kg) were fed on 5 kg of commercial concentrate (14% CP and 33% NDF- to meet 70% of their daily metabolizable energy) and oat hay ad libitum. Experiment was carried out in 3 experimental periods of 21 d (14 d of adaptation and 7 d for samples collection). Extract doses were mixed daily morning with a small amount of concentrate (approximately 1 kg) and fed to cows. Daily feed intake, water consumption, milk production and composition (solids not fat, fat, protein and lactose) were determined. In vitro gas production of the diet fed to cows (40: 60, concentrate: Oat hay) was recorded after 2, 4, 6, 8, 10, 12, 24, 48, 72 and 96 h of incubation with 0, 06, 1.2 and 1.8 mL extract/g DM. Rumen liquor was collected from 2 Brown Swiss cows (450 kg BW) and fitted with permanent cannulas. Milk production was increased ($P < 0.05$) with the extract addition at 150 or 300 mL/d while all the milk composition parameters were not affected by the extract addition. Milk energy output (Mcal/d) and milk density were also increased ($P < 0.05$) with extract addition at the 2 doses. Milk efficiency (kg DM/kg of milk) was improved ($P < 0.05$) with the extract doses versus control (1.59, 1.56 and 1.35, for 150, 300 and 0 mL extract/d, respectively). In vitro gas production of the diet fed to cows was increased ($P < 0.05$) dramatically with the 2 levels of extract with a short lag time and high rate of gas production per hour versus control (i.e., 0 mL). Addition of *Salix babylonica* extract improved milk production by 12%, without effect on milk composition in dairy cows probably due to its positive impact of ruminal microorganism's activities.

Key Words: cow, milk production, *Salix babylonica*

M310 A novel approach to measure the bioavailability of rumen protected l-lysine. K. B. Cunningham*[1], J. A. Davidson[1], S. E. Boucher[2], and B. L. Miller[1], [1]*LongView Animal Nutrition Center, Land O' Lakes Purina Feed, Gray Summit, MO,* [2]*Kemin AgriFoods North America, Des Moines, IA.*

This experiment includes 2 studies to determine bioavailability of a rumen protected L-lysine (Lys) product, USA Lysine (Kemin Industries Inc., Des Moines, IA), in cattle through the use of plasma lysine concentrations [p-Lys] affected by L-lysine (i-Lys) infused in the small intestine and fed as USA Lysine. Study 1 was a 4 × 4 Latin square design with 7 d periods. Four, duodenally cannulated steers (290 ± 18 kg) were fed a TMR twice daily (14.9% CP, 2.75 Mcal/kg ME) ad libitum with 60% of the TMR offered at 0800 h and remainder 12 h later. One of 4 Lys levels, 0, 30, 60 or 90 g, was infused daily into the duodenum of each steer for 22 h. On the 7th day, plasma was collected through jugular veinipuncture at 0, 2, 4, 6 and 8 h post-feeding. Each plasma sample was analyzed for L-lysine content. SAS linear regression analysis was applied to [p-Lys] versus g/d of i-Lys. Regression utilizing natural log-transformation of [p-Lys] as a percent of baseline values yields a predication equation of $[\text{p-Lys}] = 0.01146 *(\text{i-Lys}) + 4.60958$, $r^2 = 0.602$. This relationship between [p-Lys] and supplemented Lys infused to the small intestine is useful to predict bioavailability of USA Lysine in study 2. Study 2 was a replicated 4 × 4 Latin square design using 8 steers (276 ± 24 kg) fed the basal diet of study 1 and followed a similar feeding regimen, sampling and analyses. Dietary Lys treatments were offered as USA Lysine and supplied as 3 types of incorporations into the grain mix: hand mixed (50 and 100 g; H50 and H100), mechanical mixed (100 g; M100) and pellet (100 g; P100). Results of H50 did not increase [p-Lys] over the basal diet. Plasma Lys concentrations of H100, M100 and P100 were different from the basal diet ($P < 0.0001$). Mechanical mixing and pelleting of USA Lysine in the top-dress did not affect [p-Lys] compared with hand mixed. Regardless of dietary incorporation method, the regression equation applied to the [p-Lys] of steers fed 100 g of USA Lysine, predicts at least 50% bioavailability of Lys from USA Lysine.

Key Words: bioavailability, cattle, lysine

M311 Determining the bioavailability of lysine in AjiPro-L using the plasma free amino acid dose response method. N. L. Whitehouse*[1], E. S. Fletcher[1], A. F. Brito[1], C. G. Schwab[2], and I. Shinzato[3], [1]*University of New Hampshire, Durham,* [2]*Schwab Consulting LLC, Boscobe,* [3]*Ajinomoto Heartland Inc., Chicago, IL.*

Six multiparous ruminally cannulated Holstein cows averaging 108 d in milk were used in a 6 × 6 Latin square study with 7-d periods. Samples were collected during the last 3 d. The 6 treatments were: 1) control (0 g/d L-Lys), 2) 30 g/d of abomasally infused Lys, 3) 60 g/d of abomasally infused Lys, 4) 30 g/d of feed supplemented Lys, 5) 45 g/d of feed supplemented Lys, and 6) 60 g/d of feed supplemented Lys. An L-Lys HCl product containing 80% Lys and assumed to be 100% bioavailable was used for the infusions. The AjiPro-L (Ajinomoto Co. Inc., Tokyo), which contains 40% Lys (as fed basis) was mixed with 454 g of concentrate and offered to the cows 1 h before each of the 3 daily feedings. The basal diet was formulated to meet the Lys requirements and contained 36% corn silage, 14% grass silage, 3% alfalfa hay and 47% concentrate. Four blood samples were collected from the tail vein at 2-h intervals starting at 0700 h; samples were centrifuged, deproteinized, and composited by cow/day with plasma stored at −80°C for AA analysis. Data were analyzed using the MIXED and PROC REG procedures of SAS. Milk yield and composition, and DMI were not different among treatments. Lysine was the only plasma AA that increased linearly (*P*

≤ 0.05) in response to infused or feed supplemented Lys. The slopes for the infused and feed supplemented Lys were 0.0224 ($r^2 = 0.98$) and 0.0078 ($r^2 = 0.94$), respectively, when the concentration unity μg/mL was used for expressing the concentration of plasma Lys relative to that of total AA. When the concentration unity μM was chosen to express plasma Lys as a proportion of total AA, the slopes were slightly lower for the infused (0.0183; $r^2 = 0.97$) and feed supplemented (0.0068; $r^2 = 0.93$) treatments. The calculated bioavailabilities for AjiPro-L using the 2 different sets of slopes (0.0224 and 0.0078 μg/mL vs. 0.0183 and 0.0068 μM) were relatively similar averaging 35% (0.0078/0.0224 × 100) and 37% (0.0068/0.0183 × 100), thus indicating marginal impact of concentration unity (μg/mL vs. μM) on the outcome of Lys bioavailability values using the in vivo plasma response method.

Key Words: amino acids, lysine, bioavailability

M312 Microencapsulated sodium selenite supplementation in dairy cows: Effects on selenium status. E. Grilli*[1], P. Fantinati[2], M. Morlacchini[3], and A. Piva[1], [1]*DISMVET, Facoltà di Medicina Veterinaria, Ozzano Emilia, Italy,* [2]*Vetagro SpA, Reggio Emilia, Italy,* [3]*Centro Ricerche per la Zootecnia e l' Ambiente, San Bonico, Italy.*

The objective of the study was to assess the selenium status of dairy cows fed with 3 different sources of selenium; that is, free or microencapsulated sodium selenite and yeast selenium. Thirty dairy cows were divided in 5 groups and fed the same total mixed ration with 5 different supplementations of selenium: the control group (CTR) received sodium selenite at 0.3 mg/kg DM; M1 and M2 group received lipid microencapsulated sodium selenite at 0.3 mg/kg, and 0.5 mg/kg DM, respectively; Y1 and Y2 group received selenized yeast providing selenium at 0.3 mg/kg and 0.5 mg/kg, respectively. Cows were fed the supplements for 56 d during which milk, blood, and fecal samples were collected weekly to perform selenium content analysis and glutathione peroxidase 1 (GPx-1) activity. Data measured over time were subjected to ANOVA using the repeated measures in the mixed procedure of SAS in a complete randomized design. The statistical model included the fixed effect of treatment, time of measurement and (treatment x time) interaction. The random variable was the cow within treatment. Pre-experimental variables were subjected to analysis of covariance for adjustments. Cows fed with 0.3 mg/kg of microencapsulated selenium had 6.6% and 5.7% higher total plasma selenium concentration than CTR and Y1 group, respectively. Also, milk selenium concentration was higher in M1 group compared with CTR and Y1 group (+38.2% and 13.1%, respectively; source effect). The increment was more pronounced at the highest inclusion rate (0.5 mg/kg, M2 group). Despite the higher selenium content in body fluids observed in animals fed the microencapsulated form, GPx-1 activity was not significantly affected by treatments. The results showed that lipid microencapsulation is a suitable technique to protect nutrients from ruminal reduction of bioavailability and that microencapsulated sodium selenite is absorbed and incorporated in tissues (plasma and milk) in a more efficient way than in the free form. Microencapsulated sodium selenite resulted also comparable to Se-yeast in terms of availability and incorporation in milk when fed at 0.3 mg/kg DM, whereas the inclusion in the diet at 0.5 mg/kg DM resulted more advantageous for the microencapsulated form.

Key Words: dairy cow, microencapsulation, selenium

M313 Effects of dietary amylase and sucrose on productivity of cows fed low-starch diets. C. F. Vargas*[1], M. Engstrom[2], and B. J. Bradford[1], [1]*Kansas State University, Manhattan,* [2]*DSM Nutritional Products, Parsippany, NJ.*

Recent studies have observed positive effects of both sucrose and exogenous amylase on fiber digestion and productivity of dairy cattle. Our objective was to evaluate direct effects and interactions of amylase and sucrose on DMI, milk production, and milk components. Forty-eight multiparous Holstein cows between 70 and 130 DIM were randomly assigned to each of 4 pens (12 cows/pen). Pens were randomly assigned to treatment sequence in a 4 × 4 Latin square design balanced for carryover effects. The treatments were a control diet (36% NDF, 21% starch), the control diet with amylase (0.5 g/kg DM; Rumistar, DSM), a diet with sucrose replacing corn grain at 2% of DM, and the sucrose diet with amylase (0.5 g/kg DM). All data were analyzed with mixed models including the fixed effect of treatment and the random effects of period and pen. Milk data included the random effects of cow nested within pen and pen × period to provide the error term for the pen-level analysis. DMI was not affected by treatments. Milk yield and milk composition were not altered by the inclusion of sucrose or amylase; however, a tendency for an amylase by sucrose interaction was observed for milk protein content ($P = 0.06$), reflecting slightly lower milk protein concentrations for amylase and sucrose treatments (3.00 and 2.99 ± 0.03%) compared with control and amylase + sucrose treatments (3.02 and 3.03 ± 0.03%). Solids-corrected and fat-corrected milk yield variables were not significantly altered by treatment, although the direct effect of amylase approached significance for both variables (both $P = 0.13$), suggesting possible small increases with amylase supplementation (~0.5 kg/d). Feed efficiency (ECM/DMI) numerically increased with either amylase (1.57 ± 0.12) or sucrose (1.60 ± 0.12) treatment, but the combination of the 2 (interaction $P = 0.19$) resulted in feed efficiency similar to the control treatment (both 1.50 ± 0.12). The inclusion of amylase or sucrose did not significantly affect DMI, productivity, or feed efficiency in mid-lactation cows fed low-starch, high-fiber diets.

Key Words: sugar, enzyme, lactation

M314 The effect of essential oil/botanical product on performance and health of calves. B. L. Miller, T. J. Earleywine,* and T. E. Johnson, *Land O' Lakes Inc., Webster City, IA.*

One hundred seven (107) 3- to 10-d-old Holstein bull calves with an average initial weight of 47.3 kg (SD = 3.44 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility. Calves were randomly assigned according to BW and blood gamma globulin to either a control or experimental milk replacer (MR) diet offered in a 15% solids solution. Both diets utilized a 22% all milk protein/20% fat non-medicated MR powder. The experimental diet was the same as the control with an essential oil/botanical product (Digestarom, Micro-Plus Konzentrate; Stadtoldendorf, Germany) included at 0.05% active ingredient. Calves were fed to provide 681 g DM feeding rate daily in 2 feedings at 0700 and 1615 h. Calves were offered 340.5 g in one feeding at 0700 h during the last week. Calf starter (18% crude protein, as fed basis) was fed ad libitum throughout this 42 d trial. Data were analyzed by Mixed procedures of SAS. Calves offered no essential oil/botanical product were inferior ($P = 0.10$) in total weight gain, MR intake ($P = 0.07$), feed efficiency ($P < 0.05$), scour scores ($P < 0.01$) and scour days ($P < 0.01$) when compared with calves receiving essential oil/botanical product. Essential oil/botanical product improved calf performance and health.

Table 1. Performance of calves offered MR without (Diet 1) or with (Diet 2) essential oils/botanical product

Item	Diet 1	Diet 2	*P*-value	SE
BW gain, kg	20.6	22.8	0.10	0.914
MR (DM), kg	24.1	25.0	0.07	0.342
Starter (DM), kg	20.2	20.9	0.66	1.070
Feed/Gain	2.28	2.10	0.04	0.060
Scour score,[1] 2 wk avg	1.35	1.22	0.01	0.030
Scour days, 2 wk	4.53	3.03	0.01	0.388

[1]Scour score = 1 to 4 scale; 1 = normal to 4 = watery with dehydration.

Key Words: calves, milk replacer, essential oils/botanical

M315 Effects of two sources of rumen-protected fat associated or not with conjugated linoleic acid (CLA) on milk fatty acid profile in dairy ewes. E. Ticiani[1], J. De Souza[2], F. Batistel[2], M. Baldin[3], R. Dresch[3], M. A. S. Gama[4], F. C. F. Lopes[4], and D. E. Oliveira*[1,3], *[1]Universidade do Estado de Santa Catarina, CEO, Chapecó, Santa Catarina, Brazil, [2]Universidade de São Paulo, ESALQ, Piracicaba, São Paulo, Brazil, [3]Universidade do Esatado de Santa Catarina, CAV, Lages, Santa Catarina, Brazil, [4]Embrapa Gado de Leite, Juiz de Fora, Minas Gerais, Brazil.*

The aim of this study was to evaluate the associative effects of 2 sources of calcium salts of fatty acids (Agelac 84 or Megalac E) and an unprotected CLA (UnCLA) supplement (Luta-CLA60) on milk fatty acid profile in dairy ewes. Thirty-nine Lacaune and 36 East Friesian ewes in mid lactation (70 ± 7 DIM) received for 53 d one of the following dietary treatments in a 2 × 2 factorial design:1) 27g of Agelac 84; 2) 30g of Megalac E; 3) 27g of Agelac 84 + 20g of UnCLA; and 4) 30g of Megalac E + 20g of UnCLA. The UnCLA supplement contained 29.9% of trans-10, cis-12 and 29.8% of cis-9, trans-11. Ewes grazed Panicum maximum Jacq. cv. Aruana grass and were fed an isoproteic concentrate (1 kg DM/d) in which the fat supplements were added. Milk samples were collected on the 14th day of the experimental period and analyzed for fatty acid profile by gas chromatography. Data were analyzed using the PROC MIXED of SAS. There was no interaction between treatments and breed. The concentration of fatty acids < 16C in milk fat was reduced by CLA and Megalac E (Table 1). Milk fat trans-10, cis-12 CLA was increased by 861% in ewes fed CLA (0.026 vs 0.224 g/100g of FA, $P < 0.001$) with no fat and fat x CLA effects. Milk fat cis-9, trans-11 was increased 18% (0.99 vs 0.84 g/100g of FA) and 0.7% (0.84 vs 0.83 g/100g of FA) by CLA and Megalac E ($P < 0.01$), respectively and there was an interaction between CLA x fat (Megalac E +UnCLA = 1.09 vs Agelac 84 +UnCLA = 0.89 g/100g of FA, $P < 0.02$). All desaturase indexes were reduced by CLA, and Megalac E reduced C16:1/C16:0 and CLA/trans-11 C18:1 ratios. The milk fatty acid profile of ewes was altered by dietary supplementation with UnCLA and different sources of rumen-protected fat.

Table 1. Milk fatty acid profile of dairy ewes fed two sources of rumen-protected fat (Agelac 84 or Megalac E) associated or not with UnCLA

	Treatment				*P*-value		
Item	Agelac 84	Megalac E	Agelac 84 + UnCLA	Megalac E + UnCLA	UnCLA	Fat	CLAxFat
Ratio							
<C16	30.9	30.0	25.7	24.4	0.01	0.03	0.91
C16+C16:1	26.2	25.2	25.8	23.4	0.02	0.01	0.05
>C16	43.1	45.5	48.7	51.6	0.01	0.01	0.82
Desaturase Index							
14:1/14:0+14:1	0.013	0.011	0.009	0.008	0.01	0.05	0.75
16:1/16:0+16:1	0.036	0.029	0.027	0.022	0.01	0.02	0.56
18:1/18:0+18:1	0.604	0.585	0.542	0.534	0.01	0.11	0.44
CLA/t1118:1+CLA	0.322	0.301	0.276	0.265	0.01	0.01	0.41

Key Words: dairy ewes, fatty acid profile, desaturase index

M316 Feeding protected lysine to lactating dairy cows improved milk protein yield. J. A. Davidson*[1], S. E. Boucher[2], and B. L. Miller[1], *[1]LongView Animal Nutrition Center, Land O' Lakes Purina Feed, Gray Summit, MO, [2]Kemin AgriFoods North America, Des Moines, IA.*

The objective was to determine if increasing metabolizable Lys with either blood meal (BM) or a rumen protected lysine source, USALysine (Kemin Industries, Des Moines, IA), improved milk yield and milk protein yield of dairy cows. Twenty-four cows averaging 90 DIM (blocked by parity, milk yield, and DIM) were assigned to one of 3 treatments varying in metabolizable Lys supply (g/d): Control (Ctrl, 180 g/d), BM (200 g/d), or USALysine (204 g/d). All diets were formulated with Dynamic Nutrition System model of Land O' Lakes Purina Feed with a minimum of 0.14 kg/h/d of BM and 22 g/h/d of Smartamine M (Adisseo, Antony, France) to provide 60 g/d of metabolizable Met. To increase Lys, the BM treatment included an additional 0.27 kg/h/d of BM. Smartamine M was added to diets to maintain a 3:1 ratio of Lys:Met. Cows were individually fed with Calan door system for 28 d. Data from d 5 to 28 were analyzed with repeated measures procedure of SAS. No differences were detected for main effect of day or interactions with day, thus data were pooled across day. Dry matter intake was 22.1 for cows fed additional BM and 23.1 and 23.8 kg/d for Ctrl and USALysine, SE 0.58, $P = 0.13$). Adjusting for actual DMI, cows consumed 165, 177, and 184 g/d of metabolizable Lys and 56, 52 and 54 g/d of metabolizable Met for Ctrl, BM and USALysine, respectively. Cows fed USALysine had greater milk protein concentration (2.92%) and yield (1.30 kg/d) than Ctrl (2.77% and 1.22 kg/d) and BM (2.75% and 1.19 kg/d) fed cows (SE 0.04 and 0.03, respectively, $P < 0.05$). Energy-corrected milk yield tended to be greater for USALysine cows (42.1 kg/d, SE 0.88, $P = 0.07$) compared with the other groups (40.6 and 39.3 kg/d for Ctrl and BM). However, daily milk yield was not statistically different (41.9, 42.0, and 44.1 kg/d for Ctrl, BM, and USALysine, respectively, SE 1.51). Increasing metabolizable Lys with BM numerically decreased DMI, thus no improvements in milk or milk protein yield were observed. Utilizing USALysine to deliver additional metabolizable Lys increased milk protein concentration and yield. USALysine is a protected source of Lys that can be used to improve lactation performance when Lys supply is limiting.

Key Words: dairy cows, milk protein, protected lysine

M317 The effect of treating corn stover silage with cellulase and *Lactobacillus* on nutritive value of silage in dairy cows. H. Ma, J. Q. Wang,* 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.*

Corn stover silage is a major forage source for dairy cows during the winter season in the northern China due to its low cost and high content of carbohydrates. But its crude protein concentration and digestibility are low. The aim of this study was to determine if the nutritive content and digestibility in the total gastrointestinal tract of corn stover silage could be improved by addition of cellulase and *Lactobacillus* preparations at ensiling. Corn stover after harvest was ensiled with untreated or treated with commercial cellulase (1.0 g/kg of fresh forage) and *Lactobacillus* (1 × 100,000 cfu/g of fresh forage) in laboratory silos. Three ruminally cannulated Holstein dairy cows were used in a 3 × 3 Latin square design of three 21-d periods. The data were analyzed using the GLM procedure of SAS 9.1. Duncan's multiple range tests were used to detect statistical significance between treatment groups. Treatment with cellulase and *Lactobacillus* increased CP concentrations of corn stover silages ($P < 0.05$), and decreased neutral detergent fiber (NDF) and acid detergent fiber (ADF) concentrations of silages ($P < 0.05$) compared with the untreated group. In addition, silages treated with cellulase had lower concentrations of NDF and ADF compared with silages treated with *Lactobacillus* ($P < 0.05$). In situ ruminal DM, CP, NDF and ADF degradability of silages were improved by treated with cellulase and *Lactobacillus* ($P < 0.05$). Similarly, digestibility of DM, CP, NDF and ADF in the total tract were also improved by treated with cellulase and *Lactobacillus* ($P < 0.05$). Moreover, ruminal degradability and digestibility in the total tract of DM and NDF were higher in silages treated with cellulase than in untreated and treated with *Lactobacillus* group ($P < 0.05$). The results indicate that when applied at ensiling, cellulase and *Lactobacillus* can improve the degradability and digestibility of corn stover silages in dairy cows. In the experimental conditions of the current trial, nutritive value of corn stover silage treated with cellulase was superior to treatment with *Lactobacillus*.

Key Words: corn stover silage, dairy cow, nutritive value

M318 Degradation of L-arginine and N-carbomyl glutamate and their effect on rumen fermentation in vitro. B. Chacher,* D. M. Wang, H. Y. Liu, and J. X. Liu, *Institute of Dairy Science, MoE Key laboratory of Molecular Animal Nutrition, College of Animal Sciences, Zhejiang University, Hangzhou, China.*

Arginine is a versatile amino acid and plays an important role in urea cycle and protein synthesis, but the high cost limits its use in dairy production. *N*-carbomyl glutamate (NCG) is a metabolically stable analog of *N*-acetyl glutamate, which is an essential allosteric activator of carbamoyl phosphate synthase-I, and may be substituted for endogenous synthesis of arginine. The objective of this experiment was to determine the degradation rates of L-arginine (L-arg) and NCG and to examine their effects on rumen fermentation. The in vitro gas test based on syringes was employed and rumen liquor were collected from 3 rumen-fistulated dairy cows that were fed 55% roughage and 45% concentrate mixture, plus premix (minerals and vitamin). Syringes were filled with 30 mL of medium (10 mL rumen liquor and 20 mL buffer solution) and then aerobically incubated in 3 replicates with 1 mmol/L of L-arg, NCG or control (without L-arg and NCG) at 39°C. At incubation for 0, 2, 4, 6, 12 and 24 h, gas production and pH value were recorded and rumen fluid samples were collected in separate tubes to determine the contents of L-arg and NCG. At 24 h, concentrations of ammonia N, volatile fatty acids and microbial protein were measured. Degradation rates of L-Arg were 0, 32.0, 47.1, 52.8, 99.3 and 100%, while NCG degradation in rumen fluid was 0, 7.8, 12.8, 13.3, 14.2 and 17.8% during 0, 2, 4, 6, 12 and 24 h, respectively. Gas production and ratio of acetate to propionate were higher in groups treated with L-arg and NCG than that in the control ($P < 0.01$). Ammonia N concentration was higher ($P < 0.01$) in group added with L-arg than that in NCG and control group. Microbial protein concentration diminished in groups treated with L-arg and NCG, compared with the control ($P < 0.01$). In summary, the effects of L-arg and NCG on rumen fermentation were numerically relatively similar. Rapid degradation of L-arg in rumen indicates nutritionally wasteful process, and it should be protected from rumen degradation, while NCG can be fed to ruminants with no need for coating.

Key Words: L-arginine, N-carbomyl glutamate, rumen fermentation

M319 Folic acid and vitamin B12 supplement enhances energy metabolism of dairy cows in early lactation. M. Duplessis*[1,2], C. L. Girard[2], D. E. Santschi[3], D. M. Lefebvre[3], and D. Pellerin[1], [1]*Université Laval, Département des sciences animales, Québec, Qc, Canada,* [2]*Agriculture and Agri-Food Canada, Sherbrooke, Qc, Canada,* [3]*Valacta, Ste-Anne-de-Bellevue, Qc, Canada.*

The purpose of this study was to measure the effects of folic acid and vitamin B12 supplement on milk production and components, and indicators of energy balance of dairy cows from 3 wk before expected calving date until 8 wk after parturition. Commercial dairy herds (n = 15) were involved in this project. From February to December 2010, every 2 mo and within each herd, cows (n = 805) were randomly assigned, according to parity, predicted 305d milk production, and calving interval to receive weekly intramuscular injections (5 mL) of 1) saline 0.9% NaCl (C) or 2) 10 mg of vitamin B12 + 320 mg of folic acid (V). Milk production and components were obtained from the DHI agency (Valacta, Ste-Anne-de-Bellevue, Qc, Canada). Only milk production and components data for the first 60 DIM are presented. Cows with less than 2 tests were not included in the analysis. Body weight (BW) was measured by chest girth 3 wk before calving, and 1 and 8 wk after parturition. Body condition score (BCS) was evaluated on a 1 to 5 scale by the same individual every 2 wk until 100 DIM. Data were analyzed using the MIXED and GLIMMIX procedures of SAS. The 305d milk production before the study was similar between treatments (9663 ± 114 kg; $P = 0.97$). Average milk production for C and V was 36.9 ± 0.4 kg/d ($P = 0.99$). Milk fat concentration was 4.19 and 4.03 ± 0.04% for C and V, respectively ($P = 0.007$). Milk protein concentration was 3.09 and 3.15 ± 0.02% for C and V, respectively ($P = 0.02$). The vitamin supplement increased by 8.3% the number of cows with a protein:fat ratio greater than 0.75 ($P = 0.009$). From 1 to 8 wk after parturition, V cows lost 7.4 ± 2.6 kg BW less than C cows ($P = 0.007$). There was no treatment effect ($P = 0.45$) on BCS before calving (3.45 ± 0.04) but after parturition, the vitamin supplement tended to reduce BCS loss (treatment x time, $P < 0.07$). The observed reduction in BW and BCS losses and milk fat secretion without effect on milk production suggest that supplementary folic acid and vitamin B12 lessened the negative energy balance in early lactation. This effect was possibly due to an improved efficiency of energy metabolism.

Key Words: folic acid, vitamin B12, dairy cow

M320 The potential benefits of supplementing corn-based dairy diets with Zado or yeast for milk yield and production efficiency in dairy cows. H. Gado*[1], B. E. Borhami[2], and A. Z. M. Salem[3,2], [1]*Ain Shams University, Cairo, Egypt,* [2]*Alexandria University, Alexandria, Egypt,* [3]*Universidad Autónoma del Estado de México, Estado de México, México.*

The objective of this study was to verify the potential benefits of supplementing corn-based dairy diets (T0, control diet without any supplementation) with Zado (T1, contains 2.32 U/g Xylanase, 61.5 U/g α-Amylase, 7.05 U/g cellulase and 29.2 U/g protease) or yeast (T2) for milk yield and production efficiency in dairy cows. Sixty lactating Holstein dairy cows were randomly assigned to the 3 treatments and housed in pens (20 cows for each). All cows were fed the control diet for 4 weeks, followed by 8-weeks period on their assigned diets. The control diet consisted of 25% corn silage, 25% alfalfa silage, 6% alfalfa hay, and 44% of a ground corn-based concentrate (DM basis). Zado was added to concentrates to provide 40 g/head/day for (T1). Active dry yeast was added to the concentrate to provide 0.5 g Levucell/d per animal (T2). There was no difference in final BW (600 ± 22 vs. 610 ± 25 and 608 ± 20 kg; $P = 0.85$) for T0 vs T1 and T2, respectively. Meanwhile, there were differences for net energy (NE) output (34.1 ± 0.05 vs. 37.5 ± 0.07 and 35.3 ± 0.08 Mcal/d; $P < 0.05$), or efficiency of NE output (1.61 ± 0.03 vs. 1.42 ± 0.07 and 1.63 ± 0.04 Mcal/kg DMI; $P = 0.04$) for cows on T0 vs T1 and T2, respectively. There were differences in dry matter intake (21.3 ± 0.12 vs. 24.7 ± 0.14 and 21.0 + 0.18 kg/d; $P < 0.07$), 3.5% FCM (31.2 ± 0.41 vs. 36.6 ± 0.46 and 31.4 ± 0.38 kg/d; $P < 0.08$), and efficiency of fat corrected milk (FCM) production (1.63 ± 0.12 vs. 1.44 ± 0.24 and 1.68 ± 0.18 kg FCM/kg DMI; $P < 0.06$) for cows fed on T0 vs T1 and T2. In conclusion, cows fed on diet supplemented with Zado increased milk production in comparison to control or YEAST supplemented diets.

Key Words: milk production, yeast, Zado

M321 The effect of carnitine on growth and performance of calves fed milk replacer. B. L. Miller,* T. J. Earleywine, and T. E. Johnson, *Land O' Lakes Inc., Webster City, IA.*

Fifty-eight (58) 3–10 d old Holstein bull calves with an average initial weight of 45.7 kg (SD = 2.14 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility. Calves were randomly assigned according to BW and blood gamma globulin to either a control or experimental milk replacer (MR) diet offered in a 17.6% solids solution. Both diets utilized a 28% all milk protein/20% fat non-medicated MR powder. The experimental diet was the same as the control with added carnitine, (International Animal Technologies, Marion, TX). Calves were fed to provide 1135 g DM feeding rate daily in 2 feedings at 0700 and 1615 h. Calves were offered 567.5 g in one feeding at 0700 h during the last week. Calf starter (22% crude protein, as fed basis) was fed ad libitum throughout this 49 d trial. Data were analyzed by Mixed procedures of SAS. Calves offered no Carnitine were inferior ($P < 0.05$) in total weight gain, starter feed intake ($P < 0.05$) and feed efficiency ($P = 0.11$) when compared with calves receiving carnitine. Carnitine improved calf growth and performance.

Table 1. Performance of calves offered MR without (Diet 1) or with (Diet 2) carnitine

Item	Diet 1	Diet 2	*P*-value	SE
BW gain, kg	30.9	34.9	0.02	1.11
MR (DM), kg	44.7	45.4	0.43	0.61
Starter (DM), kg	10.6	13.8	0.02	0.94
Feed/Gain	1.81	1.73	0.11	0.04

Key Words: calves, carnitine, milk replacer

M322 Effects of a solid oil supplement (Oralac) on milk fatty acid composition of grazing dairy cows. G. A. Gagliostro*[1], L. E. Antonacci[1], J. Ballistreri[2], E. Bonina[2], M. R. Williner[3], and C. A. Bernal[3], [1]*Instituto Nacional de Tecnología Agropecuaria, INTA, Balcarce, Buenos Aires, Argentina,* [2]*Tecnuar SRL, Rosario, Santa Fé, Argentina,* [3]*Universidad Nacional del Litoral, Santa Fé, Santa Fé, Argentina.*

Oralac (OR) is a lipid supplement (90% DM, 68.6% fat) for ruminants containing vegetable and marine oils. The fatty acid (FA) composition of OR is palmitic (11.25%), stearic (4.65%), oleic (31.7%), linoleic (44.7%), linolenic (2.45%), EPA (0.6%) and DHA (1%). The effect of OR on milk FA composition was tested on 20 multiparous Holstein cows in mid lactation. Cows consumed pasture (70% of total DM intake) and were offered concentrates (7.2 kg DM/cow) with increased OR content: OR-0, OR-8.75, OR-11.25 and OR-15%. Intake of OR was 0.666; 0.798 and 0.826 owing to concentrate refuse in OR-11.25 (6.9%) and OR-15 (27%). Intake of C18:2 was 0.13, 0.15 and 0.16 kg/cow/day in OR-8.75, OR-11.25 and OR-15. Fat intake was 1.75% of total DMI in OR-8.75 and 2.40% in the other 2 treatments. Milk yield was lower in OR-0 (27.4 kg/cow/d) than the average yield of 30.6 kg in OR supplemented cows ($P < 0.55$). Milk fat content (g/kg) was 33.5 in OR-0 and 30.2 in OR treatments ($P < 0.44$). Milk protein averaged 35.2 g/kg in all treatments. Milk concentration (g/100g) of C12:0 decreased (−32%) after OR feeding from 3.35 in OR-0 to 2.23 and 2.34 in OR-11.25 and OR-15 ($P < 0.03$) respectively. Basal (OR-0) concentration (g/100g) of C14:0 (9.82) decreased (−13%) in OR-11.25 and OR-15 (8.51) ($P < 0.21$). Basal C16:0 concentration (23.45 g/100g) decreased (−14%, $P < 0.02$) in OR-8.75 and OR-11.25. The atherogenicity index of milk in OR-11.25 and OR-15 (1.47) tended ($P < 0.09$) to be lower (−23%) than in OR-0 (1,92). Basal concentration (g/100g) of vaccenic acid (2.75) increased ($P < 0.0002$) after OR feeding (6.75). Concentration (g/100g) of rumenic acid was 1.23 in OR-0 increasing up to 2.75 in OR treatments (+124% over basal). The highest values were observed in OR-8.75 (3.01) and in OR-11.25 (2.96). Concentration of trans-10C18:1 in OR-0 (0.77 g/100g) remained low after OR feeding (1.88 g/100g) ($P < 0.58$). Basal concentration of trans-9 C18:1 averaged 0.23 g/100 g and was not affected by OR feeding ($P < 0.17$). The n-6/n-3 ratio was 3.5 in OR-0 ranging from 3.12 to 2.78 in OR treatments ($P < 0.58$). Basal OR-0 saturated/unsaturated FA ratio (1.62) was reduced ($P < 0.04$) in OR-8.75 (1.14) and OR-11.25 (1.28). Results suggested a positive effect of OR at very low doses of total oil intake on milk yield, FA composition and functional-healthy value of milk.

Key Words: grazing dairy cows, functional milk, conjugated linoleic acid

M323 Combination of bacterial and yeast probiotics: A step forward to unravel their mode of action. J. Chiquette*[1], J. Lagrost[2], C. L. Girard[1], S. Li[3], J. C. Plaizier[3], and G. Talbot[1], [1]*Dairy and Swine Research and Development Centre, Sherbrooke, Quebec, Canada,* [2]*Institut Supérieur d'Agriculture Rhône-Alpes, Lyon, Rhône-Alpes, France,* [3]*University of Manitoba, Winnipeg, Manitoba, Canada.*

Four ruminally fistulated Holstein dairy cows averaging 616 ± 38 kg body weight and 81 ± 5 d in milk were assigned to the following experimental treatments in a 4 × 4 Latin square design: 1) *Enterococcus faecium* (2.5×10^9 cfu/g; EF); 2) EF + *Saccharomyces cerevisiae* (1×10^9 cfu/g; EFSC; Probio Precise, Chr. Hansen, Milwaukee, WI); 3) EF + *Lactococcus lactis* O 224 (2.8×10^9 cfu/g; EFO); 4) No probiotics (C). Probiotics were given at the rate of 80 mg/ kg DM intake, twice a day before each meal. They were introduced directly into the rumen through the fistula. Each experimental period consisted of 18 d of adaptation, 3 d of subacute rumen lactic acidosis (SARA) challenge and 7 d of rest during which they received the same TMR than during adaptation but without probiotic. Our previous research has shown that EFSC could stabilize rumen pH when dairy cows were submitted to a SARA challenge. The objectives of this study were to: 1) compare EFSC with the bacteria EF alone or with EF and *L. lactis* O 224 as a replacement for the yeast, on rumen pH regulation during SARA; 2) examine the effect of yeast probiotic on redox potential and 3) as vitamin B12 is produced only by bacteria, detect if ruminal concentration of this vitamin could be affected during SARA. Each treatment was compared with EFSC. Milk yield drop during SARA was lower with EFSC (- 0.8 kg/d), compared with C (-7.5 kg /d; $P = 0.03$) and similar to that of EF or EFO (-0.9 kg/d). During SARA, mean pH was greater with EFSC (5.55) than with C (5.43; $P = 0.03$) and tended to be lower than with EFO (5.66; $P = 0.07$). Time with pH <6.0 tended to be lower with EFSC (13.3 h) than with EF (15.4 h; $P = 0.08$) and greater than with EFO (11.1 h; $P = 0.07$). During adaptation, time with pH <5.5 was lower with EFSC (0.2 h) than with EF (5 h; $P = 0.02$) or EFO and C (3 h) ($P = 0.08$ and 0.09, respectively). Redox potential was greater during SARA (−150 mV) than adaptation (−180 mV; $P < 0.001$) or rest (−176 mV; $P = 0.04$). During SARA, EFSC maintained the rumen concentration of vitamin B-12 in the rumen whereas it decreased with other treatments. In conclusion, both EFSC and EFO provided pH regulation during SARA but only EFSC prevented the drop of vitamin B12. Probiotics decreased milk drop during SARA.

Key Words: *Enterococcus faecium* and *Saccharomyces cerevisiae*, *Lactococcus lactis* O224, subacute ruminal acidosis

M324 Effect of live yeast supplementation on milk yield, milk components, and rumen pH in dairy cows. M. B. de Ondarza[1], A. Hall[2], J. Sullivan[2], and E. Chevaux*[2], [1]*Paradox Nutrition LLC, West Chazy, NY,* [2]*Lallemand Animal Nutrition, Milwaukee, WI.*

The trial objective was to determine the effect of supplemental live yeast (LY; 0.5 $g \cdot cow^{-1} \cdot d^{-1}$; *Saccharomyces cerevisiae* CNCM I-1077) vs. sodium bicarbonate (BC; 170 $g \cdot cow^{-1} \cdot d^{-1}$) on milk yield, milk components, and rumen pH in high-producing, multiparous cows. Half of the cows (n = 57) received LY and half (n = 54) received BC. The study was 11 wk in length with 6 wk of diet adaptation and 5 wk of data collection. Treatment groups were housed in separate pens with ad libitum access to TMR. Cow groups were balanced pre-trial for parity, DIM, and pre-trial 14-d average milk yield. Daily milk yield of individual cows was recorded. Milk was sampled on wk 8, 9, and 10 and analyzed for components. The statistical model included treatment, DIM category, and lactation category as fixed effects with cow as the random effect. Pre-trial production data were included as covariates. There was a trend ($P = 0.09$) for higher milk yield with LY treatment (41.9 and 39.8 kg/d for LY and BC, respectively (SE = 0.86)). Percent milk fat, milk fat yield, 3.5% FCM, and energy-corrected milk were not affected ($P > 0.10$) by treatment. Percent milk true protein and milk urea nitrogen (mg/dl) were not affected ($P > 0.10$) by treatment but milk true protein yield tended ($P = 0.09$) to be higher for cows fed LY (1.24 vs. 1.18 kg/d for LY vs. BC, respectively (SE = 0.02)). Somatic cell count (SCC x 1000) was lower ($P < 0.05$) for cows supplemented with LY (80.09) (SE = 49) than for cows supplemented with BC (245.48) (SE = 49). Four cows per treatment were used to measure rumen pH every 5 min using rumen bolus probes. Live yeast significantly increased ($P < 0.0001$) mean daily pH (6.22 vs. 6.03 for LY vs. BC, respectively; SE = 0.01), minimum daily pH (5.54 vs. 5.34 for LY vs. BC, respectively; SE = 0.01), and maximum daily pH (6.98 vs. 6.81 for LY vs. BC, respectively; SE = 0.02). The area under the pH 5.8 curve (pH x min/d) was less ($P < 0.0001$) for cows fed LY (19.5 vs. 80.1 for LY vs. BC, respectively; SE = 4.3). Live yeast reduced the risk of rumen acidosis and tended to increase milk yield.

Key Words: live yeast, rumen pH, sodium bicarbonate

***M325 Enterococcus faecium* as a probiotic for lactating ruminants.** I. K. Hindrichsen,* M. Raun, N. L. Milora, B. Struer-Lauridsen, M. M. Jensen, and E. Upton Augustsson, *Chr. Hansen A/S, Hørsholm, Denmark.*

High-yielding dairy cows often suffer from sub-acute diseases triggered by typical dairy cow diets. These results in ill-thrift and production losses. Sub-acute hindgut acidosis was recently shown to significantly affect the health of dairy cattle. Supplementing high-yielding dairy cows with the probiotic *Enterococcus faecium* has in several studies resulted in improved production and/ or well being parameters. In the current study, the aim was to unravel some of the possible mode of action of *E. faecium* has on dairy cows, using genome sequencing and in vitro assays. First, the survival of 3 *E. faecium* strains under digestion challenges were tested, including high volatile fatty acid, pH and challenge with bile. Optical density (OD) test showed that all 3 *E. faecium* strains survived in a pH range between 2 and 7. At pH 2 the lag time increased, however after 24 h the max OD was the same as for pH 7. *E. faecium* could be shown to withstand up to 9.5% bile concentration with a reduced growth. It was further illustrated that all tested *E. faecium* showed active bile salt hydrolase activity, indicating that *E. faecium* can utilize bile as a substrate in the lower tract. The genome sequencing revealed that all tested *E. faecium* had genes associated with adhesion ability, while only one strain showed genes for producing the 2 bacteriocins enterocin A and enterocin B. The bacteriocin producing strain was superior in inhibiting *S. bovis*, as well as other pathogens such as *C. perfringens*, *S. aureus* and *L. monocytogenes* compared with the none-bacteriocin producing E. faecium. It has been shown that these 2 bacteriocins have synergistic effect in reducing pathogens. It is hypothesized that the positive effect of *E. faecium* on production parameters of dairy cows may be due to the reduction of *S. bovis* in the rumen, the possibility of surviving digestive challenges and passing down to the lower tract where it actively inhibits certain pathogens. These features can significantly affect the occurrence of subacute hindgut acidosis.

Key Words: dairy cows, *Enterococcus faecium*, pathogen

M326 Effect of oral calcium bolus supplementation on early lactation health and milk yield in commercial dairy herds.

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The objective of this study was to evaluate the effect of supplementation with oral calcium (Ca) boluses after calving on early lactation health and milk yield. Second lactation or greater cows (n = 927) from 2 large dairies in Wisconsin were enrolled during the summer of 2010. Both herds fed supplemental anions during the pre-fresh period and treated less than 1% of fresh cows for clinical signs of hypocalcemia. Prior to calving, cows were scored for lameness and body condition, then randomly assigned to either control or oral Ca bolus supplemented groups. Control cows received no oral Ca boluses around calving. Cows in the oral Ca bolus group received 2 oral Ca boluses (Bovikalc, Boehringer Ingelheim, St. Joseph, MO) - one bolus 0 to 2 h after calving and the second 8 to 35 h after calving. The oral Ca bolus administration schedule was designed to be feasible for large commercial dairies and did not require that cows be locked up more than once daily. Early lactation health events were recorded and summed for each cow. There were only 6 cases (0.6% of calvings) of clinical milk fever during the trial, and only 14% of cows tested were hypocalcemic (ionized Ca less than 1.0 mmol/L) at 8 to 35 h after calving. Subgroups of cows with significant responses to oral Ca bolus supplementation were identified based on significant interactions between oral Ca bolus supplementation and covariates in mixed multiple regression models. Lame cows supplemented with oral Ca boluses had 0.34 fewer health events in the first 30 d in milk compared with control cows. Cows with a higher previous lactation milk yield (greater than 105% of herd rank) produced 2.9 kg more milk when supplemented with oral Ca boluses. Results of this study indicate that lame and higher producing cows respond favorably to supplementation with oral Ca boluses using a protocol that is practical to implement in large commercial dairies, and that oral Ca bolus supplementation to targeted groups of cows is beneficial even for dairies with a very low incidence of hypocalcemia.

Key Words: oral calcium boluses, milk fever, hypocalcemia

M327 Effect of dietary buffers and magnesium oxide on intake, milk yield and composition, and blood metabolites of lactating dairy cows.

J. K. Bernard,* J. W. West, and N. A. Mullis, *University of Georgia, Tifton.*

Forty-eight lactating Holstein cows were used to determine the effect of feeding different buffers on nutrient intake, milk yield and composition, and select metabolic indices of health of early lactation Holstein cows. Treatments included a negative control (NEG), positive control supplemented with sodium bicarbonate (POS), acid buffer (AC, CalMin, Celtic Sea Minerals, Cork, Ireland) or acid buffer plus MgO from seawater (ACM, CalMin16, Celtic Sea Minerals). A basal diet provided similar concentrations of energy and protein and treatments added at feeding provided varying concentrations of Ca, Cl, Na, and DCAD. Beginning at approximately 21 ± 4 DIM cows were fed the NEG diet for 14 d and cows were assigned randomly to one of 4 treatments for the following 10 wk. Contrast statements compared 1) NEG with all other diets, 2) POS with AC and ACM, and 3) AC with ACM. The DMI tended to be higher ($P = 0.07$) for POS compared with AC and ACM. No differences ($P > 0.10$) were observed for milk yield, concentration or yield of milk fat, protein, lactose, or SNF. Concentrations of MUN were lower ($P = 0.01$) for NEG compared with the other treatments and ACM compared with AC ($P = 0.005$). Serum concentrations of total protein ($P = 0.04$), globulin ($P = 0.03$), glucose ($P = 0.0004$), and creatinine kinase ($P = 0.06$) were highest for NEG compared with other treatments. No ($P > 0.10$) differences were observed in serum concentrations of Ca, P, Mg, K, Na, Cl, or bicarbonate. No deleterious effects were observed for cows fed NEG, but cows were not exposed to heat stress during the trial. The POS diet had lower concentrations of dietary Cl (0.52% of DM) compared with the other treatments (0.63% of DM) which could explain the trend for higher DMI. Overall the acid buffers supported similar performance as sodium bicarbonate.

Table 1. Intake, milk yield, composition, and select blood metabolites

Item	NEG	POS	AC	ACM	SE
DMI, kg/d	22.9	24.0	23.0	21.8	0.6
Milk, kg/d	43.8	45.7	44.6	43.3	1.4
Fat, %	3.55	3.56	3.83	3.69	0.13
Protein, %	2.68	2.58	2.57	2.59	0.04
Lactose, %	4.66	4.66	4.68	4.69	0.02
SNF, %	8.24	8.18	8.21	8.21	0.05
MUN, mg/dL	10.3	11.1	12.0	10.6	0.3
Serum metabolites					
Total protein, g/dL	7.50	7.25	7.28	7.15	0.11
Globulin, g/dL	3.70	3.41	3.45	3.32	0.01
Glucose, mg/dL	61.69	56.37	55.60	53.05	1.39
Creatinine kinase, U/L	278.60	133.58	147.14	152.93	60.25

Key Words: buffers, milk yield, milk composition

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M328 Milk fatty acids composition responses to dietary short-medium chain fatty acids and long chain fatty acids in lactating dairy cows. Y. Sun, D. P. Bu, J. Q. Wang,* H. Cui, X. W. Zhao, X. Y. Xu, P. Sun, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

De novo synthesis of short-medium chain fatty acids (SMCFA), which inhibited by the exogenous long chain fatty acids (LCFA), might be promoted by dietary addition of SMCFA. Our objective was to evaluate the effects of different ratios of SMCFA to LCFA on milk fatty acids (FA) composition in dairy cows. The experiment lasted for 9 wks. Thirty-six lactating Holstein dairy cows (183 ± 46 DIM) were blocked base on average daily milk yield, DIM and parity, and were randomly assigned to 1 of 3 treatments. Cows were fed total mixed ration with 1 of 3 fat supplements: 80 g/d SMCFA and 320 g/d LCFA (20S80L); 400 g/d of butterfat (40S60L); 240 g/d SMCFA and 160 g/d LCFA (60S40L), and the ratios of SMCFA to LCFA were 20:80, 40:60, and 60:40 respectively. The FA compositions of the SMCFA mixture (a blend of 6% caproic acid, 4% caprylic acid, 9% capric acid, 10% lauric acid, 32% myristic acid and 39% palmitic acid) and the LCFA mixture (a blend of 59% cocoa butter, 16% olive oil, and 25% palm oil) were identical to those found in milk fat. Analysis of data was conducted using the MIXED procedures of SAS 9.0. As the ratios of SMCFA to LCFA in the supplements increased, concentrations of C < 16:0 (25.39, 27.58, and 27.39%; $P = 0.08$) tended to increase linearly ($P = 0.06$), C14:0 percentage (10.39, 11.18, and 11.90%; $P < 0.05$) increased linearly ($P < 0.05$), and polyunsaturated FA percentage (4.12, 4.68, and 4.31%; $P < 0.05$) was increased quadratically ($P < 0.05$). However, concentration of C16:0 (32.16, 32.01, and 31.91%; $P > 0.05$), C > 16:0 (42.08, 39.78, and 40.28%; $P > 0.05$), saturated FA (68.26, 69.81, and 69.10%; $P > 0.05$), and monounsaturated FA (27.64, 25.51, and 26.59%; $P > 0.05$) were not affected. In conclusion, dietary supplementing different ratios of SMCFA to LCFA influenced milk FA synthesis and caused the alteration of milk FA composition.

Key Words: long chain fatty acids, milk fatty acids composition, short-medium chain fatty acids

M329 Effect of sorghum grain supplementation levels on ruminal volatile fatty acids: Comparison between cattle and sheep. M. Aguerre*[1], C. Cajarville[2], L. Assandri[2], A. Gonzalez[1], 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 = 16; 210 ± 42.5 kg), and lambs (n = 16; 45.6 ± 6.2 kg), were used to compare the response on ruminal VFA concentration and profile 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, 12.6% CP, 41.8% NDF). After 30d, ruminal liquor samples were taken every 1h from 0 to 6h post-supplementation, to determine acetate, propionate and butyrate concentrations by HPLC, while total VFA (TVFA) were determined as the sum of the above VFA. Mean values and linear regressions were compared between species with the MIXED procedure (SAS). Mean TVFA was lower in cattle than in sheep (94.4 vs. 112 ± 6.81 mMol/L; $P = 0.008$). Increasing supplementation levels similarly increased TVFA in both species (Table 1). Proportion in TVFA of acetate was higher (70.7 vs. 63.7 ± 0.70 mMol/100mMol; $P < 0.001$), while propionate and butyrate were lower in cattle than in sheep (15.8 vs. 20.6 ± 0.83 mMol/100mMol and 13.5 vs. 15.9 ± 0.62 mMol/100mMol; $P < 0.001$, propionate and butyrate respectively). Increasing supplementation levels affected differently acetate and butyrate proportion in TVFA in both species (P<0.001; Table 1), leading to more pronounced changes in acetate and butyrate proportions in sheep than in heifers. However, propionate proportion in TVFA was not affected. In conclusion, increasing levels of sorghum supplementation determined a similar rose in TVFA in cattle and in sheep. However, sheep showed more drastic changes in VFA profile than heifers.

Table 1.

Item	Cattle	Sheep	*P*-value[1]
Total VFA (mmol/L)	$y = 77.6 + 23.0x$; $R^2 = 0.12$, $P < 0.001$	$y = 108 + 30.7x$; $R^2 = 0.21$, $P < 0.001$	0.355
VFA, mmol/100 mmol			
Acetate	$y = 72.7 - 2.49x$; $R^2 = 0.13$, $P < 0.001$	$y = 68.8 - 6.48x$; $R^2 = 0.40$, $P < 0.001$	<0.001
Butyrate	$y = 12.1 + 1.92x$; $R^2 = 0.09$, $P = 0.003$	$y = 10.9 + 6.72x$; $R^2 = 0.53$, $P < 0.001$	<0.001

[1]*P* of the comparison of regressions.

Key Words: bovine, ovine, fresh pasture

M330 Effects of different ratios of short-medium chain fatty acids to long chain fatty acids on milk composition in dairy cows. Y. Sun, D. P. Bu, J. Q. Wang,* H. Cui, X. W. Zhao, X. Y. Xu, P. Sun, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Dietary addition of long chain fatty acids (LCFA) inhibits milk fat de novo synthesis in dairy cows, whereas short-medium chain fatty acids (SMCFA) may promote this process. This study evaluated the effects of supplementation of different ratios of SMCFA to LCFA on milk composition in dairy cows. Thirty-six lactating Holstein cows (183 ± 46 DIM) blocked by average daily milk yield, DIM and parity, were randomly assigned to 1 of 3 treatments. During the 9 wks experimental period, cows were fed total mixed ration 3 times daily, and supplemented with 1 of 3 supplements: 80 g/d SMCFA and 320 g/d LCFA (20SM80L); 400 g/d of butterfat (40SM60L); and 240 g/d SMCFA and 160 g/d LCFA (60SM40L). The ratios of SMCFA to LCFA in the supplements were 20:80, 40:60, and 60:40 respectively. The FA composition of the SMCFA mixture (a blend of 6% caproic acid, 4% caprylic acid, 9% capric acid, 10% lauric acid, 32% myristic acid and 39% palmitic acid) and of the LCFA mixture (a blend of 59% cocoa butter, 16% olive oil, and 25% palm oil) were representative of those found in milk fat. Data was analyzed by MIXED procedures of SAS 9.0. Dry matter intake (16.3, 16.1, and 16.0 kg/d; $P > 0.05$), milk yield (23.5, 23.9, and 21.8 kg/d; $P > 0.05$), 3.5% fat corrected milk (25.9, 26.8, and 25.4 kg/d; $P > 0.05$), milk protein percentage (3.46, 3.43, and 3.48%; $P > 0.05$) and yield (0.83, 0.82, and 0.76 kg/d; $P > 0.05$) were not affected among the treatments. As the ratios of SMCFA to LCFA increased in the supplements, milk fat percentage (4.01, 4.20, and 4.41%, $P = 0.06$) tended increase in a linear fashion ($P < 0.05$) and milk total solids proportion (13.09%, 13.26%, and 13.55%; $P < 0.05$) increased linearly ($P < 0.05$), while milk fat yield (0.97, 0.99, and 0.97 kg/d; $P > 0.05$) was not different. In conclusion, dietary supplementing SMCFA might compensate the inhibitory effects of LCFA on milk fat synthesis.

Key Words: short-medium chain fatty acids, long chain fatty acids, milk composition

M331 Effects of different fatty acid mixtures on milk fatty acid composition and oxidative stability of milk fat. X. W. Zhao, J. Q. Wang,* D. P. Bu, Y. Sun, H. Cui, X. Y. Xu, L. Y. Zhou, and P. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Unsaturated fatty acids (UFA) as the main function components in milk fat, have beneficial effects on health maintenance and disease prevention. More and more people are concerning to improve UFA content in milk. However, the rich content of UFA, especially polyunsaturated fatty acids (PUFA) in milk fat will increase the risk for developing spontaneous oxidized off-flavor (SOF). The experiment was carried out to determine the effects of different fatty acids mixture on milk fatty acids composition and milk fat oxidation changes. Thirty 6 dairy cows were used in a completed design experiment for 8 wk. Cows supplement 3 types of dietary fatty acids mixture: 1) short- and medium-chain fatty acids (SMCFA), 2) butterfat, and 3) long-chain fatty acids (LCFA). Data were analyzed using the MIXED procedure of SAS. Relative to SMCFA, the C12:0, C14:0 and C16:0 concentration in milk fat from cows on butterfat and LCFA were significantly decreased ($P < 0.05$). The proportions of *cis*-C18:1, *trans*-C18:1 and *cis*-C18:2 were increased by 16.0, 45.6, and 8.8% ($P < 0.05$) in milk fat from cows on LCFA compared with cows on SMCFA. Similar increases in *trans*-C18:1, *cis*-C18:2 and C18:3 were 31.6, 11.9 and 13.6% ($P < 0.05$) in butterfat treatments, respectively. Furthermore, the activities of superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GSH-Px) tended to decrease when increased long-chain FA in cow′ diet, while the concentration of malondialdehyde (MDA) tended to increase in bovine milk. Our results indicated that long-chain FA tended to exhibit positive effects on milk fatty composition, but may decrease the oxidative stability of milk fat.

Key Words: milk fatty acids composition, oxidation changes, milk fat

M332 Endogenous contribution and urinary recovery of purine derivatives in Nellore cattle. A. M. Barbosa*[1], R. F. D. Valadares[2], S. de C. V. Filho[2], D. do Santos Pina[3], and M. A. Fonseca[2,4], *[1]Universidade Federal da Bahia, Salvador, Bahia, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal do Mato Grosso, Sinop, Mato Grosso, Brazil, [4]Texas A&M University, College Station.*

This study was conducted with the objective to evaluate the endogenous contribution of purine derivatives (PD) urinary excretion in Nellore cattle, fed in a single diet with different levels of DM. The trial was performed using 8 cannulated (rumen and abomasum; moreover 4 of those had ileum cannula) heifers with average BW of 258 ± 20 kg. The animals were allocated on individual stalls and fed twice a day. The statistical analyses were performed using 2 balanced Latin square designs (4 × 4). Treatments were constituted of 4 DM offer levels: 1.2, 1.6, 2.0 and 2.4% of BW. The endogenous losses of PD and the purine bases recovery as PD were estimated by the regression between the daily excretion of PD (dePD) in urine, and purine bases in the abomasum (X), expressed as mmol/kg$^{0.75}$. The endogenous contribution and the purine recovery of PD are represented by the coefficient of the regression and the intercept, respectively. Additionally, the endogenous losses were evaluated by the regression between excretion of PD, in mmol/kg$^{0.75}$, and DMI, in g/kg$^{0.75}$. The equation obtained ($P < 0.001$) was: dePD = 0.0196 X + 0.2421. Daily excretion of PD, mmol/kg$^{0.75}$, as a function of RNA flux into the abomasum, mmol/kg$^{0.75}$, was adjusted ($P < 0.001$) to the regression, dePD = 0.8601 X + 0.4603 ($r^2 = 0.661$) where 0.86 represents the recovery of DP in urine, and 0.4603 represents the endogenous contribution. The conclusion was for the different methods utilized was found the estimatives of 0.46 mmol/kg$^{0.75}$ and 0.24 mmol/kg$^{0.75}$ for endogenous excretion of PD in Nellore cattle; the true digestibility of RNA in small intestine was 0.93, which is higher than the classic value adopted in the literature for microbial production calculation.

Key Words: flux RNA abomasum, level of intake, ruminant nutrition

M333 Effects of dietary inclusion of tannin and polyethylene glycol supplementation on nitrogen metabolism in Saanen dairy goats. A. Rahimi[1], A. A. Naserian[1], R. Valizadeh[1], A. Tahmasbi[1], B. Saremi*[2], and A. R. Shahdadi[3], *[1]Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran, [2]Institute of Animal Science, Physiology & Hygiene Unit, University of Bonn, Germany, [3]Agricultural Sciences & Natural Resources, University of Gorgan, Gorgan, Golestan, Iran.*

Tannins reduce the protein degradation in the rumen, shift the site of N metabolism from rumen to the lower digestive tract and large intestine. Shifting excretion pattern of nitrogen from urine to faces and formation of tannin–protein complex are beneficial environmentally. High levels of tannins in the diet may have negative effects on feed intake and digestibility of nutrients and polyethylene glycol (PEG) could eliminate it. We aimed to evaluate the effects of feeding pistachio hull (PH, source of tannin) and PEG on nitrogen metabolism in Saanen dairy goats. Nine animals were used in a 3 × 3 Latin square design. Treatments were: T1) Control, without PH, T2) 30% PH (DM basis) that provided 18.1 g condense tannin per kg DM of diet, and T3) 30% PH + 1% PEG (DM basis). In T2 and T3, PH replaced alfalfa hay. Statistical analysis was performed using the MIXED procedure of SAS ($P < 0.05$). Addition of PH in T2 and T3 (despite of addition PEG) reduced the nitrogen intake. In addition, urinary nitrogen excretion was significantly decreased and fecal nitrogen excretion was increased by addition of PH in T2 and PEG supplementation in T3 increased or decreased them respectively but not to the similar values like control group. Milk nitrogen excretion was not affected by experimental diets. Nitrogen digested was significantly decreased by substitution of PH in diet in T2 and T3 (despite of addition PEG). Nitrogen retained was not affected by experimental diets. To sum up, using of high levels tannin in the diet could alter protein metabolism positively from an environmental aspect and supplementation with PEG could reduce possible negative effectsof tannin on performance.

Table 1.

Nitrogen metabolism	Alfalfa	30% PH	30% PH+PEG	SEM	*P*-value
Nitrogen Intake (g/d)	54.47^{a}	53.01^{b}	53.96^{b}	0.360	0.050
Nitrogen excretion from urine (g/d)	12.42^{a}	9.90^{b}	11.52^{ab}	0.553	0.049
Nitrogen excretion from fecal (g/d)	14.46^{b}	15.43^{a}	15.00^{ab}	0.135	0.011
Nitrogen excretion from milk (g/d)	7.21	6.63	7.18	0.427	0.102
Nitrogen digested (g/d)	38.52^{a}	35.51^{b}	36.73^{b}	0.448	0.013
Nitrogen retained (g/d)	20.36	21.03	20.25	0.794	0.820

^{a,b}Means within the same row with different letters are significantly different ($P < 0.01$).

Key Words: tannin, nitrogen metabolism, goats

M334 Intake and apparent total tract digestibility of dry matter and nutrients in Nellore steers fed with whole raw soybean.

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This study was conducted to evaluate the effects of whole raw soybean on intake and apparent total tract digestibility of dry matter and nutrients in Nellore steers. Twelve steers were assigned to 3 Latin squares in individual pens. Based on dry matter the diets were: T0 with 0% of soybean, T8 with 8% of soybean, T16 with 16% of soybean and T24 with 24% of soybean. Fourteen days were necessary for adaptation and 4 d for evaluation. The individual intake was evaluated by weighing the leftovers of the previous day. Leftovers and feces were collected in the d 14 to 16 to determine the intake and the apparent total tract digestibility of dry matter and nutrients. This material was dried and sampled for posteriori analysis on dry and mineral matter, ether extract, neutral detergent fiber, acid detergent fiber, crude protein and lignin. The total amount of excreted fecal dry matter was estimated by the method of acid detergent fiber indigestible (FDAi). Samples of feces, food and leftovers were placed and subsequently incubated in 3 cannulated Nellore for 312 h. Treatment effects were evaluated by Proc Mixed SAS software. The inclusion of whole raw soybean provided linear effect ($P < 0.05$) for intake of dry matter, organic matter, non-fibrous carbohydrates and total carbohydrates. There was a quadratic effect on crude protein ($P < 0.05$) and the lowest value on the diet with 16% soybean differing from the one with 24% and total control. There was a linear increase ($P < 0.001$) for ether extract intake and all treatments differed. There was no effect ($P > 0.05$) on apparent total tract digestibility of dry matter, organic matter, crude protein, neutral detergent fiber and non-fibrous carbohydrates. However, there was a quadratic effect of soybean on the total apparent digestibility in ether extract with highest digestibility for the 24% soybean. There was a linear decrease ($P < 0.05$) of total carbohydrate in apparent digestibility. Changes in the dry matter and nutrient intake in digestibility were noticed according to the levels of inclusion of whole raw soybean but these effects were not negative to the animals.

Key Words: digestibility, protein source, ruminant

M335 Evaluation of published models for predicting dry matter intake of lactating dairy cows.

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Accurate prediction of dry matter intake (DMI) is pre-requisite for ration formulation software and a precision feeding program. The equations commonly used for predicting DMI are empirical models, developed on the basis of experimental data obtained more than a decade ago. Considering increases in genetic potential of dairy cows and dairy management, there is an interest in evaluating the model using recent data to see if the published models are still applicable to the field. The objective of this study was thus to evaluate 6 published empirical equations widely used for predicting DMI of lactating dairy cows using recently published experimental observations. A literature database based on the research articles published in the *Journal of Dairy Science* from January 2006 until June 2011 (volumes 89 through 94) was constructed. The database is composed of a total of 525 treatment means from 143 studies, and contains wide ranges of DMI, milk yield and week of lactation. Six published models include NRC (NRC, 2001), Brown (Brown et al., 1977), Chase (Chase and Sniffen, 1985), Rayburn (Rayburn and Fox, 1993), Roseler (Roseler et al., 1997) and Fuentes-Pila (Fuentes-Pila et al., 2003), and they were statistically evaluated using the constructed database. The coefficient of determination and root mean square prediction error (RMSPE) were used to examine precision and accuracy of the model, respectively. Residual analysis was also conducted to assess the mean and slope bias of a model. The NRC, Brown, Chase, Rayburn, Roseler and Fuentes-Pila models explained 49, 39, 48, 41, 51 and 41% of the variations in the evaluation data set, and the RMSPE were 2.59, 2.97, 2.75, 2.08, 3.44 and 3.61 kg, respectively. All of the models showed significant mean bias ($P < 0.01$): the highest absolute mean bias was observed with the Roseler equation (2.336) while the lowest value with the NRC equation (0.450). Among the equations, only the Roseler and the NRC predicted the observed DMI without slope bias ($P > 0.05$). The NRC model was highly ranked among the tested models in all of the evaluation criteria. The accuracy of the NRC model prediction, however, may be reduced with recent observations.

Key Words: dairy cows, dry matter intake, evaluation

M336 Effects of roughage source and dietary level of inclusion on total tract apparent digestibility in Nellore cattle.

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Six ruminally cannulated Nellore steers were allotted in a 6 × 6 Latin square to investigate the effects of roughage source and dietary inclusion on nutrient digestion. The 6 diets were composed of fiber sources: negative control (NC) with 10% NDF from corn silage (50.2% NDF, DM basis), positive control (PC) with 20% NDF from corn silage and 4 diets containing 10% NDF from corn silage and 10% NDF from: sugarcane (SC; 46.8% NDF); sugarcane bagasse (SCB; 81.0% NDF); soybean hulls (SH; 75.1% NDF) and low oil cottonseed meal (LOCM; 49.2% NDF). Total fecal collections, during 4 d consecutively in each period, were used to determine total tract apparent digestibility coefficients (TTAD) of DM, CP, NDF, ADF. Lower inclusion of forage fiber (CN) in the diet presented higher digestion coefficients of DM ($P \leq 0.05$) in comparison with diets containing double amount of fiber sources (20% of NDF). When fiber sources with low amount of CP (SC and SCB) were included in the diets, TTAD of CP were 12.32% lower than diets containing corn silage, SH or LOCM. Fiber digestibility was influenced ($P \leq 0.05$) by roughage sources and inclusion level on TTAD. Although similar DMI ($P \leq 0.05$) was observed between treatments CP, SC, SH e HOCM, differences among TTAD values can be explained either by differences in solid passage rate, ruminal retention time or chemical composition of fiber when different roughage sources replaced each other. In spite of the lower TTAD values of NDF of NC in comparison to PC (6 percentage units), the higher inclusion of concentrate (NC) improved the DM digestibility by 8.3 percentage units.

Table 1. Effects of roughage source and level on total-tract apparent digestibility in Nellore cattle

Total-tract apparent digestibility, %	Diet[1]						
	NC	PC	SCB	SC	SH	LOCM	SE
DM	77.1^{a}	68.7^{b}	69.6^{b}	70.2^{b}	71.9^{b}	70.8^{b}	1.8
CP	74.4^{a}	68.3^{a}	58.2^{b}	58.4^{b}	71.0^{a}	68.8^{a}	1.9
NDF	60.3^{bc}	66.3^{a}	53.8^{bc}	52.3^{bc}	61.7^{ab}	50.5^{c}	2.5
ADF	47.4^{abc}	52.6^{ab}	45.4^{bc}	45.8^{bc}	54.8^{a}	43.6^{c}	2.3

[abc] Means lacking common superscripts differ ($P \leq 0.05$).

[1] NC = negative control; PC = positive control; SCB = sugarcane bagasse; SC = sugarcane; SH = soybean hulls; LOCM = low oil cottonseed meal.

Key Words: digestibility, forage, Nellore

M337 Intake and digestibility of diets with different levels of concentrates in cattle feedlot Nellore. C. S. Ribeiro Junior,* Y. T. G. Salcedo, R. C. Canesin, T. T. Berchielli, M. Machado, L. M. Delevatti, E. San Vito, I. P. C. de Carvalho, J. F. Lage, and G. Fiorentini, *São Paulo State University, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil.*

The increased meat demand in the world market amplified the production system. For that reason, the use of confinement systems is an option and the inclusion of grains in the diet is essential. Based on these assumptions, this study aimed is to evaluate the intake and digestibility of diets with different forage: concentrate. We used 8 Nellore, male, castrated, with an average weight of 320 ± 44 kg. The animals were divided into 2 latin square 4x4, with 4 treatments and 4 replications. The treatments consisted of 4 diets with different forage: concentrate (70:30, 60:40, 40:60, 20:80), balanced to maximize microbial protein synthesis and increase the use of urea. The forage used was fresh chopped sugar cane and the concentrates consisting of corn bran, soybean meal, urea and mineral salt. The experiment was divided into 4 periods of 22 d each: the first 15 d for the diet adaptation of animal and the other days for data collection. Data were analyzed statistically by SAEG statistical program (Statistical Analysis System), using the Tukey test at 5% probability in comparison of means. The dry matter intake as a function of body weight was greater in relations 60:40 (1.9%) and 40:60 (1.8%), differing significantly ($P < 0.05$) dry matter intake in relations 70:30 (1.6%) and 20:80 (1.7%). The organic matter intake was higher in the 60:40 ratio (6.3 kg/d), differing from the others ($P < 0.05$). As for the digestibility of dry matter and organic matter the highest values were observed in the 40:60 ratio, and the smaller the ratio 20:80. It is concluded that the forage: concentrate ratio 40:60 had a better digestibility of dry matter and organic matter and a higher dry matter intake, with high nutritional value. In this experiment 40:60 ratio is more suitable for feeding beef cattle.

Key Words: digestibility, sugar cane, nutritive value

M338 Voluntary intake, apparent digestibility and blood urea levels in hair sheep fed *Cynodon nlemfuensis* grass mixed with *Leucaena leucocephala* and supplemented with rumen fermentable energy. V. A. Arjona-Alcocer, A. Ruiz-Gonzalez, E. Briceño-Poot, A. J. Ayala-Burgos, N. Ruz-Ruiz, and J. C. Ku-Vera,* *FMVZ-Universidad Autonoma de Yucatan, Merida, Yucatan, Mexico.*

Tropical grasses supply insufficient amounts of energy and protein for grazing sheep, resulting in low productive performance. Silvopastoral systems supply good quality forages (CP, fermentable energy) to grazing sheep. However, in silvopastoral systems there may be an imbalance among energy and nitrogen availability in the rumen leading to the loss of nitrogen from this organ. Four hair lambs housed in metabolic crates were used in a 4 × 4 Latin square design. Sheep were fed *Cynodon nlemfuensis* grass and foliage of the legume *Leucaena* leucocephala mixed in a ratio 50:50 on a dry matter basis. Increasing levels of cane molasses were supplied: 0, 0.24, 0.72 and 1.2 Mcal per lamb daily. The ration was served twice daily at 10:00 and 15:00 h divided in 2 halves. Response variables were DM intake, DM digestibility and concentration of urea in blood and excretion of urea in urine. The experiment lasted for 48 d with 4 periods of 12 d, 7 d for adaptation and 5 d for sampling. Results were analyzed with the statistical package SAS. DM intake was increased by energy supplementation, although DM digestibility was unaffected by treatment (Table 1). There was a trend for energy supplementation to decrease urea concentration in blood and urinary excretion of urea in sheep.

Table 1. DM intake, apparent digestibility of DM and levels of urea in blood and urine of lambs fed a mixture of C. nlemfuensis and L. leucocephala and supplemented with three levels of energy

	ME (Mcal/d) supplied as molasses			
Item	0	0.24	0.72	1.2
DMI, g/head/d	1047.91^{c}	1184.13^{b}	1268.46^{ab}	1316.17^{a}
DMI, g/kg$^{0.75}$/d	93.14^{c}	103.66^{b}	109.72^{ab}	115.43^{a}
ADDM, %	66.62	63.93	63.85	63.97
Blood urea, mg/dL	68.25^{a}	60.27^{ab}	56.45^{bc}	48.25^{c}
Urinary urea, g/sheep/d	42.34	41.72	36.67	28.34

^{a,b}Different superscripts in the same row differ ($P < 0.05$).

Key Words: hair sheep, energy, supplementation

M339 Rumen ammoniacal nitrogen and pH from cattle supplemented with levels of replacement of soybean meal by sunflower cake. R. G. F. Silva,* J. T. Zervoudakis, L. S. Cabral, D. P. Sousa, L. K. H. Zervoudakis, M. F. Costa Filho, R. S. Gomes, F. M. Negrão, and J. F. W. Koscheck, *Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil.*

This study aimed at evaluating the replacement levels of the protein from soybean meal by the protein from sunflower cake in multiple supplements on the rumen ammoniacal nitrogen (RAN) and rumen pH of beef cattle. The experiment was conducted during the Brazilian rainy season. Five Nelore breed animals, uncannulated, submitted to grazing *Brachiaria brizantha* 'Marandu' were used, they were divided into individual paddocks of 0.24 ha. The average initial age and weight were 15 mo and 257 kg, respectively. The treatments were: 0% of replacement (0%SC), 25% of replacement (25%SC), 50% of replacement (50%SC), 75% of replacement (75%SC) of the protein from soybean meal by the protein from the sunflower cake, isoprotein with 30% crude protein and one more control treatment of commercial mineral mixture (MM). One kg of fresh matter/animal/day was provided for the supplemented treatments and the control treatment was provided ad libitum. A Latin square design 5x5 was used. Rumen fluid was collected and the pH was measured right before the supplementation (0 h) and 4 h after the supplementation. The availability of forage in the dry matter ranged on average from 5678 kg in the 1st period to 9743 kg in the 5th period. There was no effect of the treatments on rumen pH ($P > 0.05$), however there was a time effect on rumen pH ($P < 0.05$), in which at time 0 the average was 6.75 and 6.50 at time 4, both within the levels considered physiologically normal. For RAN, there was effect of treatment and time ($P < 0.05$), in the study within the time the RAN concentrations were 5.42 and 12.22 mg/dL for the time 0 and 4 respectively. In the study within the treatments the RAN concentrations were 9.38; 9.89; 9.25; 9.98 and 5.61 mg/dL, respectively, for the treatments 0% SC, 25% SC, 50% SC, 75% SC and MM. Therefore, it is concluded that the inclusion of sunflower cake for beef cattle grazing in the rainy season can be carried out without affecting the activity of rumen microbiota. Furthermore, fermentation quality improves when supplemented, as compared with the control treatment.

Key Words: grazing, forage, supplementation

M340 Comparison of three different methods in determination of accurate soluble fraction in feeds for CPM Dairy formulation to improve efficiency and milk prediction accuracy. P. Yu, B. Liu,* Z. Niu, and D. A. Christensen, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

The CPM dairy software is the major software used in Saskatchewan for milk production prediction and diet formulation for dairy producers and for researchers. However, the key information that we need to accurately predict the milk production is lacking, which is the soluble protein fraction. Without accurate feed soluble fractions in the CPM model, we get the poor milk predictions because we only estimate soluble fractions in Saskatchewan feeds. The objectives of this study were to compare 3 available methods to determinate accurate soluble fractions in dairy feed and diet for the CPM dairy formulation to improve feed utilization efficiency and prediction accuracy of milk production. The 3 methods that were accessed to determine protein soluble fractions in Saskatchewan feeds included (1) CNCPS V6.1 method; (2) Dutch 2007 DVE method; (3) In situ Method. The 14 different types of feeds were used in this study. The data normality, correlation, CRD and paired-*t*-test were analyzed using SAS. The results showed that the CNCPS method and In situ method produced similar soluble protein fractions, both methods produced higher soluble fractions than the Dutch-2007 DVE method (35.6 vs. 34.2 vs. 18.0% of CP, $P < 0.05$). Paired-*t*-test between any 2 methods also showed significant differences ($P < 0.01$) between the CNCPS and Dutch-2007 DVE method and between the In situ method and Dutch-2007 DVE method, but showed no difference between the CNCPS and In situ Methods. Although there were significant differences between the methods, the correlation analysis showed significant correlated between any methods with correlation coefficients r = 0.82 (between the CNCPS and in situ methods), 0.81 (between the CNCPS and Dutch-2007 DVE methods) and 0.59 (between the Dutch-2007 DVE method and in situ method).

Key Words: solubility methods, soluble protein fractions of Saskatchewan feeds, dairy cows

M341 Economic analysis of the inclusion of macauba pie of dietary lactating dairy cows.

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The objective of this study was to analyze the economic feasibility of substitution of corn meal for macauba pie (MP) in the total diet of lactating dairy cows. We used 8 animals with a live weight of 480 kg and average production of 25 kg of milk per day. The animals were divided into 2 4x4 Latin square with 4 treatments with 4 levels of inclusion of in dry matter (0, 10, 20 and 30%) and 4 periods of 21 d, 14 adaptation and 7 d of evaluation. The animals were kept in tie stall and fed ad libitum corn silage and concentrate, the concentrate was composed of corn, soybeans, cottonseed, and increasing levels of macauba pie. Intake of total dry matter (DMI), milk yield (MY), the daily cost of each diet and economic return of the diets. Data were analyzed statistically by SAEG statistical program (Statistical Analysis System), using the tukey test at 5% probability in comparison of means. The dry matter intake as a function of body weight was higher with 0% (4.07%), decreasing significantly in the treatment 30% (3.46%) ($P < 0.05$), the same was observed in the production of milk, where the animals who received treatment 0% produced 26.20 kg of milk per day, against 18.36 kg of milk per day treatment in 30% ($P < 0.05$). The reduction of DMI decreased cost of maintenance, however, this result was not sufficient to compensate the decline shown in milk production, resulting in reduced net margin per kg of milk and less profit for the inclusion in diets for MP dairy cows. For the production of milk, it is necessary that the price adopted per kg dry matter MP is 68.35% of corn.

Key Words: dairy cattle, economic analysis, macauba pie

M342 Survey of nutritional recommendations used by feedlot nutritionists in Brazil in 2011.

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This survey was designed to describe nutritional and management recommendations of Brazilian feedlot nutritionists in 2011. Thirty-three feedlot nutritionists, responsible for about 2,658,000 animals, completed the survey within 1-mo, which was available on line (www.surveymonkey.com) and consisted of 81 questions. The mean inclusion of roughage and inclusion in finishing diets by nutritionists was 21.0 ± 10.2% and 79.0 ± 19.4%, respectively. The level of grains included in the finishing diets recommended by 12 nutritionists (36.4%) ranged between 51% and 60%, but 11 (33.3%) nutritionists recommended diets with 61% to 80%, and 10 (30.3%) used less than 51% grains. Corn was the primary source of grain used in feedlot diets (n = 29; 87.9%), followed by sorghum (n = 4; 23.1%). Most of the corn fed in Brazilian feedlots was of the flint type (n = 28; 96.5%). The primary grain processing method adopted was coarsely grinding and fine grinding, which were used by 19 (57.6%) and 12 (36.4%) nutritionists, respectively. Whole cottonseed was the primary co-product included in finishing diets, being used by 17 (41.5%) of the nutritionists. Use of soybean hulls was reported by 8 (24.2%) nutritionists, whereas citrus pulp pellets was reported by 7 (21.2%), and soybean residues were used by 1 (3%) of the participants. Corn silage was the primary roughage source, being used by 9 (27.3%) of the respondents, followed by sorghum silage, which was used by 8 (24.2%) of the nutritionists, and sugarcane bagasse by 7 (21.2%), fresh chopped sugarcane by 5 (15.2%), and grass silage by 4 (12.1%) of the nutritionists. In addition, average recommended concentrations of NDF for finishing diets in Brazil were 21.1 ± 12.3%. The average CP, urea and true protein concentrations (DM basis) recommended for finishing diets in Brazil was 13.4 ± 2.5%, 1.4 ± 0.3% and 8.1 ± 1.7%, respectively. The primary source of plant-based protein used by the nutritionists was cottonseed meal (n = 19; 57.6%). The present survey provides an overview of nutritional recommendations currently applied by feedlot nutritionists from all regions in Brazil. These data may facilitate the design of industry-oriented research.

Key Words: Brazil, feedlot, survey

M343 Effects of different ratios of short-medium chain fatty acids to long chain fatty acids on plasma fatty acids profiles in lactating dairy cows.

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The objective of this current study was to evaluate the response of plasma fatty acids (FA) profiles to different ratios of short-medium chain fatty acids (SMCFA) to long chain fatty acids (LCFA) in lactating dairy cows. Thirty-six lactating Holstein dairy cows (183 ± 46 DIM), blocked by average daily milk yield, DIM and parity, were randomly assigned to 1 of 3 treatments and fed total mixed ration, which supplemented with 1 of 3 lipids supplements. The supplements were: 80 g/d SMCFA and 320 g/d LCFA (20S80L; the ratio of SMCFA to LCFA is 20:80); 400 g/d of butterfat (40S60L; the ratio of SMCFA to LCFA is 40:60); 240 g/d SMCFA and 160 g/d LCFA (60S40L; the ratio of SMCFA to LCFA is 60:40). The FA compositions of SMCFA mixture (a blend of 6% caproic acid, 4% caprylic acid, 9% capric acid, 10% lauric acid, 32% myristic acid and 39% palmitic acid) and LCFA mixture (a blend of 59% cocoa butter, 16% olive oil, and 25% palm oil) were identical to those found in milk fat. Blood samples were collected from the coccygeal vein at 3 h after the morning feeding. Data was analyzed as a randomized block design with repeated measures using MIXED procedure in SAS 9.0. As the ratios of SMCFA to LCFA in the supplements increased, percentages of $C > 16:0$ (85.66, 86.75, and 85.75%; $P < 0.05$), saturated FA (27.68, 25.55, and 27.85%; $P < 0.05$), and polyunsaturated FA (62.31, 66.05, and 62.49%; $P < 0.05$) increased quadratically ($P < 0.05$). Concentrations of $C < 16:0$ (2.81, 2.21, and 2.69%; $P > 0.05$) and monounsaturated FA (10.00, 8.40, and 9.66%; $P > 0.05$) were not different among the treatments. The results suggested that changes of blood FA composition, which induced by lipid supplements, might be one of the reasons for milk FA profile alternation.

Key Words: long chain fatty acids, plasma fatty acids profiles, short-medium chain fatty acids

M344 Effects of total solids in drinking water and milk yield per cow on milk mineral concentrations from California dairy farms.

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Knowing the quantity of specific minerals secreted in milk by dairy cows is important to comply with Nutrient Management Plans. Forty dairies in Merced, California (mean 787 ± 592 lactating cows/farm) were selected to study the effect of drinking water total solids (TS) contents and milk yield per cow (MY) on milk mineral content. Data was analyzed as 2 × 2 factorial with high TS (HTS; average 809 mg/L) and low TS (LTS; average 307 mg/L), and high MY (HMY; average 36 kg/d) and low MY (LMY; average 27.6 kg/d) as main factors. Milk yield was estimated from DHIA records. Dairy farm water troughs and am-pm bulk tank milk samples were taken by duplicate on 2 non-consecutive days and assayed for TS (water) and concentrations of Ca, P, Mg, Cl, K, Na, S, Cu, Fe, Mn, Se, and Zn (milk). Average milk mineral composition (mg/L) and standard deviation was: Ca 1008 ± 34.8; P 906 ± 34.4; Mg 100 ± 5.4; K 1534 ± 50.1; Na 397 ± 28.1; Cl 1045 ± 79.7; S 308 ± 11.3; Cu 0.036 ± 0.010; Fe 0.159 ± 0.020; Mn 0.016 ± 0.003; Zn 3.28 ± 0.208; Se 33.4 ± 7.54. No interactions between water TS and MY were observed. Milk from dairies with HTS water had lower ($P < 0.1$) concentrations of K (−2%), S (−2%), and Mn (−15%). In dairies with HMY, milk had significantly lower concentrations of Ca (−2.3%), P (−3.1%), Na (−5%), S (−3%), and Cu (−14%). The MY response was likely associated with dilution. More research is needed to evaluate water TS effects. Our results indicate that milk mineral contents might be affected by drinking water TS contents and MY.

Key Words: milk mineral contents, milk yield, drinking water

M345 Effects of supplementing different sources of fatty acids on lipid metabolism and endocrine responses in mid-lactation dairy cows.

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The objective of this study was to evaluate the effects of supplementing different sources of fatty acids on lipid metabolism and endocrine responses in mid-lactation dairy cows. Thirty-six Chinese Holstein cows were blocked based on milk yield, DIM and parity and randomly assigned in 3 groups. The animals were fed with diets containing 0 or 400g/d short and medium chain fatty acids(SMCFA, containing 6.0% C6:0, 4.0% C8:0, 9.0% C10:0, 10.0% C12:0, 32% C14:0 and 39% C16:0) and 400g/d long chain fatty acids (LCFA, containing 59% cocoa butter, 16% olive oil, and 25% palm oil) for group1(control), group2 and group3, respectively. The experiment lasted 8 weeks and at the last day of the experiment, blood samples were collected from tail vein of the cows. The results showed that serum triglyceride, high-density lipoprotein, low-density lipoprotein, growth hormone and insulin were not affected by supplementing different fatty acids ($P > 0.05$). The concentration of cholesterol increased by supplementing fatty acids, but no differences were observed among all the groups ($P > 0.05$). In group 3, the concentration of non- esterified fatty acid was significantly higher than that in group1 ($P < 0.05$). Compared with the control and group3, supplementing SMCFA significantly decreased the concentration of insulin-like growth factor by 16.9% ($P < 0.05$) and 9% ($P > 0.05$). In conclusion, supplementing SMCFA significantly decreased insulin-like growth factor, which may suggest SMCFA may have some negative effects on lipid metabolism.

Key Words: endocrine, fatty acids, metabolism

M346 Effect of replacing legume/grass silage with corn silage in dairy cow diets on enteric methane production.

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The objective of this study was to determine the effect of replacing legume/grass silage with corn silage in the TMR of dairy cows on enteric CH_4 emissions. Nine lactating cows (DIM = 75 ± 19; BW = 688 ± 66 kg) used in a triplicated 3 × 3 Latin square (31-d periods, 14-d adaptation) were fed (ad libitum) TMR (60:40, forage:concentrate ratio) with the forage portion being either legume/grass silage (0% CS), corn silage (100% CS) or a 50:50 mixture (50% CS). Diets were formulated to be isonitrogenous (CP = 16.4%) and isocaloric ($NE_L = 1.62$ Mcal/kg). Production of CH_4 was determined (3 consecutive days) using respiration chambers. Digestibility and milk performance were determined over 6 consecutive days. Linear (L) and quadratic (Q) contrasts (Proc MIXED; SAS) were used to determine the effects of treatments. Significance was declared at $P \leq 0.05$. Dry matter (DM) intake (21.7, 23.0, and 22.8 kg/d) and DM digestibility (69.7, 70.6 and 71.3% for 0, 50 and 100% CS, respectively) increased linearly as the proportion of CS in the diet increased while a quadratic effect ($P_Q < 0.01$) was observed for milk yield (32.3, 35.3, and 34.3 kg/d for 0, 50 and 100% CS, respectively). Milk protein yield increased ($P_L < 0.01$) and milk fat yield decreased ($P_L < 0.01$) as the proportion of CS increased in the diet. Fat corrected milk (FCM) yield was not affected by treatments and averaged 31.3 kg/d. Methane emissions were lower ($P_Q < 0.01$) in cows fed 0% CS (440 g/d) and 100% CS (434 g/d) than in cows fed 50% CS (483 g/d). When adjusted for DM intake, CH_4 production was lowest ($P_Q < 0.01$) with 100% CS than with the 2 other treatments (20.3, 20.7, and 17.7 g/kg for 0, 50 and 100% CS, respectively). When expressed relative to FCM, CH_4 production was lower ($P_Q = 0.01$) in cows fed 0% CS (14.3 g/kg) and 100% CS (14.6 g/kg) compared with cows fed 50% CS (15.3 g/kg). Results from this study suggest that using corn silage as the sole forage source in dairy cow diets offers a means to decrease (−13%) enteric CH_4 emissions (g/kg DM intake) compared with using legume/grass silage or 50:50 mixture of both forages.

Key Words: corn silage, legume/grass silage, methane

M347 Effects of supplementing different ratios of short-medium chain fatty acids to long-chain fatty acids on the immune function in mid-lactating dairy cows.

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It is well known that fatty acids as the composition of immune cell membrane can modulate immune functions. The objective of this study was to investigate the effects of supplementing different ratios of short-medium chain fatty acids (SMCFA) to long-chain fatty acids (LCFA) on the immune function in mid-lactating dairy cows. Seventy-two Chinese Holstein cows were blocked based on milk yield, DIM and parity and randomly assigned in 6 groups. The animals were fed 0g/d, 400g/d LCFA, 80g/d SMCFA and 320g/d LCFA, 400g/d butter fat, 240g/d SMCFA and 160g/d LCFA and 400g/d SMCFA respectively on the basis of ordinary diets for group1 (control), group2 and group3, group4, group 5 and group 6. The supplementing mixtures consisted of different ratios of fatty acids: 1) SMCFA (C6:0–6.0%, C8:0- 4.0%, C10:0- 9.0%, C12:0- 10.0%, C14:0- 32%, and C16:0- 39%), 2) butter fat (amount to 40% SMCFA plus 60% LCFA), and 3) LCFA (59% cocoa butter, 16% olive oil and 25% palm oil). The experiment lasted 8 weeks and on the last day, blood samples were collected to determine the concentrations of serum immunoglobulin (Ig) A, IgG, IgM, prostaglandin (PG) E2 and cytokines. The results showed that the concentrations of IgA in group 2 and group 5 were higher than that in group 6; but no differences were observed with the control ($P > 0.05$). Among all the groups, IgM and PGE2 were not affected by supplementing fatty acids ($P > 0.05$). Compared with the control, the concentrations of IgG, interleukin 4 and 10 increased after supplementing fatty acids, especially in group 5. In conclusion, supplementing fatty acids which consisted of 240g/d SMCFA and 160g/d LCFA can improve the immune functions in mid-lactating dairy cows well.

Key Words: fatty acids, Holstein cows, immune function

M348 Effects of supplemental extruded full-fat soybean (ESB) on ruminal fermentation, nutrient digestion, blood parameters and productive performance of early lactation dairy cows.

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Four ruminally cannulated early lactation Holstein dairy cows, with similar days in milk (DIM, 23.6 ± 4.4), body weight (BW, 587 ± 46 kg) and body condition score (BCS, 2.95 ± 0.08), were used a in 4 × 4 Latin square design to determine the effects of supplemental ESB [0 kg/d (control), 1.0 kg/d, 2.0 kg/d or 3.0 kg/d] on ruminal fermentation, nutrient digestion, blood parameters and productive performance. The basal TMR diet was formulated to meet or exceed the predicted requirements (NRC, 2001), contained (DM basis) 13.6% alfalfa hay, 22.8% corn silage, 13.7% Chinese wildrye, and 49.9% concentrate mainly from corn, bran, rapeseed meal, cottonseed meal, soybean meal and DDGS. Extruded full-fat soybean contained 91.0%DM, 38.7% crude protein (CP), 20.6% ether extract (EE), 23.6% neutral detergent fiber (NDF), 12.4% acid detergent fiber (ADF) and 6.20%Ash. Each experimental period was 21-d, including 10-d adaptation period and 7-d sampling period. With the increase of the supplemental ESB, ruminal pH tended to decrease ($P = 0.062$), but ruminal NH3-N, propionate, valerate and isovalerate concentrations increased significantly ($P < 0.05$). Compared with control, test group′s dietary apparent digestibility of CP and EE increased ($P < 0.001$), and that of DM tended to increase ($P = 0.061$), N retention increased significantly ($P < 0.01$). Milk yield tended to increase after ESB supplementing ($P < 0.10$), while milk solids-not-fat (SNF) percentage and milk urea nitrogen (MUN) concentration increased significantly ($P < 0.05$), but milk fat content tended to decrease ($P = 0.081$). Test group′s plasma urea nitrogen (PUN) concentration increased significantly ($P = 0.002$), and the 2.0 kg/d group plasma total bilirubin concentration tended to decrease ($P = 0.072$), indicated that cows′ liver injury was alleviated. Under the conditions of this trial, supplementing ESB during early lactation could improve cows′ productive performance and healthy condition, and 2.0 kg/d amount might be appropriate choice.

Key Words: early lactation, extruded full-fat soybean

M349 Intake and digestibility by lactating cows fed different levels of palm kernel cake.

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Sixteen multiparous dairy cows of the Holstein × Gir crossbreed, with an average weight of 436.6 kg (±59.7), were tested to determine the most appropriate amount of palm kernel cake in a dietary supplement for lactating cows at pasture. The experiment was conducted at the Experimental Farm of the Federal University of Bahia, Brazil, during August to October 2009. A Latin square design was utilized, with the cows distributed in 4 Latin squares (4 × 4 simultaneous; 4 treatments × 4 periods × 4 animals in each treatment). Intake and digestibility were analyzed for cattle with a dietary supplement containing 0, 25, 50, and 75% palm kernel cake, and grazing Massai grass (*Panicum maximum* ‘Massai’). Indigestible neutral detergent fiber (iNDF) was used as an internal indicator of the measure of intake. Intake of DM, CP, ether extract, NDF, NFC, total carbohydrates, and total digestible nutrients within the supplement, as well as the intake of total crude protein, total ether extract, and total NFC, were negatively influenced by level of palm kernel cake supplementation. The forage mass during the experiment was, on average, 8.72 kg DM/ha, with an average supply of 8.32% of live BW in forage DM. The digestibility of DM, OM, CP, NFC, and total carbohydrates was significantly reduced with an increased percentage of palm kernel cake in the supplement. A decrease in the digestibility of CP and NFC indicates that palm kernel cake is not an adequate ingredient in nutritional supplements for dairy cows at pasture. Thus, one should be cautious in using supplements with palm kernel cake and its use must to be very careful. The high fiber content (NDF, 71.13%) and the expressive content of lignin (17.03%), that together comprise a difficult material degradation, associated with the low NFC (12.10%) of palm kernel cake, create the need for a greater period of residence in the rumen to provide a greater degree of breakdown. Therefore, lower percentages of palm kernel cake in the supplement result in a greater availability of nutrients.

Key Words: Massai grass, nutrients, pasture

Ruminant Nutrition: Rumen Function and Digestion

M350 Comparison of three marker systems and three sites of digesta sampling to estimate the rumen outflow in bulls fed with corn silage or sugar cane. P. P. Rotta,* S. de C. V. Filho, L. F. C. Silva, F. A. C. Villadiego, and E. M. Galindo, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

The aim of this study was to evaluate the rumen outflow and the rumen and intestinal digestibility of dry matter and digesta components in crossbred bulls by use of sampling in 3 places (abomasum, omasum or reticulum) evaluating 3 marker systems (single, double or triple) with bulls feeding corn silage or sugar cane in different ratios. Eight crossbred bulls fitted with ruminal and abomasal cannulas and with 24 mo, weighting 353 ± 36.94 kg were separated in 2 4 × 4 Latin squares design. The experimental diets were: 1) 60% of corn silage + 40% of concentrate; 2) 40% of corn silage and 60% of concentrate; 3) 60% of sugar cane + 40% of concentrate; 4) 40% of sugar cane + 60% of concentrate. Eight digesta samples were collected in each experimental period with intervals of 9 h. At the end of each experimental period the samples were pooled and they were appointed to the 3 marker systems (single system: sample without separation; double system: filtered sample; and triple system: filtered and centrifuged sample). The whole reticular digesta composition was different ($P < 0.0001$) in comparison with the others to ether extract (EE), neutral detergent fiber (NDF) and indigestible NDF. The digesta sampled at the abomasum and omasum presented similar ($P > 0.05$) values to rumen outflow to dry matter (DM), organic matter (OM) and NDF. Similarly, the abomasal and omasal digesta were similar ($P > 0.05$) to estimate of ruminal digestibility of DM, OM, crude protein (CP) and NDF. Digesta sampled at abomasum and omasum presented similar ($P > 0.05$) values to estimations of intestinal digestibility of OM, CP and NDF. The omasal sampling is recommended as an alternative to abomasal sampling. Due to no difference among the marker systems to ruminal and intestinal digestion for NDF and intestinal digestion for CP, any marker systems can be used. Whereas that there are few differences to rumen outflow and digestions by estimating with double and triple marker systems, it is recommended the use of double marker system (indigestible NDF and Co-EDTA), that can be accessible to any research center.

Key Words: abomasal digesta, ruminal digestibility, omasal digesta

M351 Comparison of in situ nylon bag protocols for analysing ruminal degradation of dry matter and crude protein in forages. H. van Laar*[1], J. Doorenbos[1], J. D. Steckley[2], and J. A. Metcalf[2], *[1]Nutreco R&D, Boxmeer, the Netherlands, [2]Nutreco Canada Agresearch, Guelph, ON, Canada.*

This experiment compared degradation of forages between different in situ nylon bag protocols in 2 laboratories. In laboratory 1 fresh forages were cut to <2cm, 5g DM was weighed into nylon bags and incubated by time point in the rumen of 3 fistulated cows for 0, 3, 8, 16, 32, 56, 96 and 336 h in a net bag with a 1.5kg weight. In laboratory 2 forages were dried and ground over a 2 mm sieve, 5g DM was weighed into polyester bags and incubated in the rumen of 4 fistulated cows for 0, 1, 2, 4, 8, 16, 24 and 72 h attached to a 5 foot long nylon belt with a 1kg weight at the end. Forages were 5 grass silages, 5 grass hays, 5 haylages, 5 mixed hays (both a mix of alfalfa and grass) and 10 corn silages. After incubation samples were pooled by time point within cow and analyzed for dry matter and crude protein content. Degradation characteristics, Washable (W), Degradable (D), Undegradable (U) and degradation rate (K_d) were estimated with PROC NLIN of SAS. Effective degradability (ED) was calculated assuming a passage rate of 0.045/h. Differences between laboratories were analyzed by a paired *t*-test. PROC REG of SAS was used to estimate linear regression coefficients and r-square. For DM and CP (all forages combined), U and residues at 0, 8 and 16 h were lower (all $P < 0.02$) whereas W and ED were higher (all $P < 0.0001$) for laboratory 2. D fractions for DM and CP did not differ whereas K_d for DM was higher ($P < 0.05$) in laboratory 2. The r^2 of the comparison between laboratories for U, D, W, K_d and ED was 0.29, 0.07, 0.74, 0.23, and 0.87 for DM and 0.73, 0.09, 0.53, 0.41, and 0.59 for CP. When analyzed by forage type, correlation for ED of DM and CP between laboratories was good ($r^2 > 0.5$) only for grass hay (0.99, 0.96), haylage (0.92, 0.88) and mixed hays (0.94, 0.55), whereas correlations were poor ($r^2 < 0.5$) for grass and corn silages. The different in situ procedures result in a higher ED for laboratory 2, with acceptable correlation between degradation parameters taking all forages together; however, correlation between laboratories is not acceptable for all individual forage types.

Key Words: in situ, forage, rumen degradation

M352 Methane emissions and diet digestibility for sheep offered diets varying in fat content and forage quality. E. J. Mc Geough,* Y.-H. Chung, K. A. Beauchemin, S. M. McGinn, and T. A. McAllister, *Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada.*

The objective of this study was to determine DMI, diet DM digestibility (DMD) and methane (CH_4) emissions for sheep offered diets varying in fat content and forage quality. The study was a replicated (4 square) Latin Square design with 4 experimental treatments based on 2 levels of fat inclusion (low fat = 21.5, high fat = 59.6 g/kg DM) and 2 basal forages varying in nutritive quality. Fat was derived from the inclusion of canola meals and oil. To achieve variability in diet quality, oat hulls (LQ) and beet pulp (HQ) were chosen as the basal forages, accounting for 400 and 500 g/kg of diet DM, respectively. Twenty 4 Canadian Arcott sheep (16 male and 8 female), initial BW 60.4 (SD 4.80) kg, were assigned to 1 of the 4 treatments. Within treatment, sheep were assigned to 1 of 2 groups based on LW and sex to facilitate measurements in climate-controlled open circuit respiration chambers over 2 subsequent 4 d periods within each period of the Latin square. Each period consisted of 17 d of dietary adaptation followed by 4 d to measure CH_4 production and DMD. Three sheep were assigned to each chamber and housed individually in metabolism crates. Apparent total tract digestibility was determined by collecting total feces and urine for 4 d from group 1. Data were analyzed using PROC MIXED of SAS. Improving forage quality reduced DMI, on average 16.2%, ($P < 0.05$) for both low and high fat diets, but addition of fat did not affect DMI ($P = 0.17$) within forage type. Dry matter digestibility was also higher ($P = 0.001$) for HQ than LQ forage (on average 19.7%) regardless of dietary fat level. Increasing the fat content of LQ diets increased ($P < 0.05$) DMD, however DMD of the HQ diet was not affected ($P = 0.64$) by fat content. Improving the quality of forage in the diet increased ($P < 0.001$) CH_4 emissions (per kg DMI) from both low fat (13.1–15.0 g/CH_4) and high (14.0–16.5 g/CH_4) fat diets. Fat content did not affect CH_4 output ($P = 0.17$) for LQ diets, however CH_4 emissions from HQ diets were increased (9.2%; $P < 0.05$) with the higher level of fat inclusion.

Thus, dietary supplementation of fats may not be an effective means to mitigate CH_4 emissions in high quality forage diets.

Key Words: fat, forage quality, methane

M353 Leucaena diets with or without polyethylene glycol affecting rumen fermentation and methane emission in sheep. Y. Soltan*[1,2], A. Morsy[1,3], R. Lucas[1], S. Sallam[2], H. Louvandini[1], and A. Abdalla[1], [1]*Centre for Nuclear Energy in Agriculture, University of Sao Paulo, Piracicaba,Sao Paulo, Brazil,* [2]*University of Alexandria, Alexandria, Egypt,* [3]*Animal Production Research Institute, Cairo, Egypt.*

This study evaluated the effect of leucaena (*Leucaena leucocephala*) diet with or without polyethylene glycol (PEG) on rumen fermentation and methane (CH4) emission in vivo. Six adult rumen cannulated Santa Inês sheep (70 ± 2.5 kg of BW) divided in to 3 experimental diets completing a double Latin square design [3 treatments, 3 periods (17 d each), 6 animals] as follow: control (CNTRL- 70% Tifton hay (*Cynodon* spp.) + 21% ground corn, 9% soybean meal); leucaena diet that consisted of the control diet replaced by 0.50 of Tifton hay with leucaena (LEUC −123 and 8.8 g/kg DM of total tannins and condensed tannins respectively) and leucaena diet plus 20 g/day/animal of PEG (LPEG). Leucaena diets (LEUC and LPEG) decreased ($P < 0.0001$) the CH4 emission per kg digested organic matter by 0.14 and 0.11, respectively as well as decreased ($P < 0.0001$) the rumen acetate:propionate ratio compared with CNTRL, however LPEG increased butyrate ($P = 0.0034$) when compared with the LEUC. No differences ($P > 0.05$) were detected for rumen pH or protozoa count for all the experimental diets while LEUC showed the lowest ($P < 0.0001$) rumen ammonia concentrations (20.4, 19.6 and 24.3 (SEM = 1.350) mg/100 mL respectively for CNTRL, LEUC and LPEG). These results showed that leucaena diets either with or without PEG addition reduced methane emission by manipulating rumen fermentation.

Key Words: tannins, polyethylene glycol, methane

M354 Biometrics digestive tube of kids suckled up to 60 days fed different goat milk replacers. L. S. Knupp, M. I. Marcondes,* C. S. Cunha, T. S. Oliveira, J. G. L. Regadas Filho, J. C. M. Lima, L. C. Lacerda, and C. M. Veloso, *Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

There are few studies on the development of the digestive tract of goats. The study of non-carcass parts is important, because they tend to vary with diet, directly affecting carcass yield and weight gain. This work aimed to evaluate the biometrics of the digestive tract of goats suckled up to 60 d fed different goat milk replacers. Twenty-four Saanen (12) and Alpine Brown (12) kids were randomly assigned to treatments and were slaughtered at 60 d. They were offered coast-cross hay, starter ad libitum, and one liter of milk, or replacer, per day. The treatments were: goat milk (GM), cow milk (CM), fermented cow colostrum (FC) and lactal - commercial milk replacer (LAC).The organs were separated and weighed without digesta. The parameters analyzed were: Rumen, omasum, abomasum, small and large intestine. Data were analyzed using a complete randomized design, using the initial weight as a covariate. When a treatment effect was observed, the Tukey test was applied to evaluate the least squares means, using a significance level of 5%. The treatments did not affect any of the evaluated parameters ($P > 0.05$). The averages of rumen weight for kids who received CM, LAC, GM, and FC, respectively, were: 0.231, 0.185, 0.207, 0.163 kg; the average omasum weights were: 0.019, 0.012, 0.015, 0.009 kg; the average abomasum weights were: 0.090, 0.077, 0.085, 0.082 kg; the average small intestine weights were: 0.358, 0.296, 0.297, 0.262 kg; and the average large intestine weights were: 0.179, 0.263, 0.157, 0.129 kg. We concluded that all evaluated goat milk replacers can be used for feeding goats up to 60 d without affecting the development of their digestive tract. Supported by CNPq/INCT-CA.

Key Words: abomasum, omasum, rumen

M355 Comparative influence of solvent extracted-peanut meal and soybean meal on apparent digestibility of diets for finishing lambs. L. R. Flores*[1], A. Camacho[1], N. E. Villalba[2], J. J. Lomelí[1], and R. Barajas[1], [1]*FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México,* [2]*Agricola Ganadera Mojolo, Culiacán, Sinaloa, México.*

Four hair lambs 22.3 ± SE 0.5 kg were used to compare influence of solvent extracted-peanut meal and soybean meal on apparent digestibility of diets for finishing lambs. In an experiment with a Crossover design, lambs were assigned to consume one of 2 diets in that consisted the treatments: 1) Diet containing 19.6% CP, integrated (DM basis) with soybean meal 27%, corn 57%, corn straw 8.3%, sugar cane molasses 5.0%, and 2.7 of mineral premix (SBM); or 2) Diet containing 21.4% CP, where SBM was completely substituted by solvent extracted peanut meal (SEPM). The crude protein content of SEPM was 52.3% and its ether extract value was 2.2%. Each 11-d experimental period was integrated for 7 d adaptation phase and 4 d total feces collection phase. Lambs were fed 95% of appetite to prevent refusals. Dry matter intake, crude protein intake, dry matter excreted in feces, and crude protein excreted in feces were similar between treatments ($P > 0.30$). Apparent digestibility of dry matter was no affected by treatments ($P = 0.78$) with mean values of 82.2 and 82.7% for SBM and SEPM, respectively. Crude protein apparent digestibility was similar in both protein-meal sources ($P = 0.80$), with means values of 83.3 and 83.9% for soybean meal-diet and peanut meal-diet, respectively. Digestible energy of diets was unaffected by treatments ($P = 0.78$). Using substitution method and soybean meal as ingredient of reference, true CP-digestibility of peanut meal was calculated in 95% and its digestible energy content in 3.8 Mcal/kg of DM. It is concluded, that peanut meal can substitute soybean meal completely in finishing lambs diets without altering nutritional value of the diet. The true CP-digestibility of peanut meal is 95% and its digestible energy content is 3.8 Mcal/kg of DM.

Key Words: digestibility, lambs, peanut meal

M356 Development of a new marker for utilization in digestibility studies. C. C. C. Couto Filho[1], E. O. S. Saliba*[1], M. N. Pereira[2], N. M. Rodriguez[1], and N. N. Morais Júnior[3], [1]*Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil,* [2]*Universidade Federal de Lavras, Lavras, MG, Brazil,* [3]*Instituto Federal de Educação Ciência e Tecnologia do Espírito Santo, Colatina, ES, Brazil.*

A new marker using nanoparticles was developed by a research group at the Federal University of Minas Gerais. This trial was conducted to evaluate the estimates of fecal output and digestibility in dairy cattle with this new marker. Ten Holstein cows were used in the trial, which had consisted of 14 d for adaptation to the diet, 10 d of adaptation to chromic oxide and 2 d to nanomarker. The markers were also provided during the collection period. The markers were administered separately in capsules containing 500 mg of nanomarker and 10 g of chromic oxide. The fecal output and the digestibility were determined by total collection and by different markers, by sampling at intervals for 6 h, directly from the rectum of each animal, between fifteenth and nineteenth days.

Feces for the analysis of the nanomarker were collected during 24 h, starting on the sixteenth day. The dry matter content (AOAC, 1995), chromic oxide (Williams et al., 1962) and the nanomarker (near infrared reflectance spectroscopy - NIRS) in feces was determined. The statistical design was randomized blocks, with the animals being the blocks. The chromic oxide overestimated fecal output and consequently underestimated digestibility, fact which can be evidenced by the incomplete recovery of this marker in the feces (Table 1). In contrast, the results obtained with the nanomarker does not differ from the total collection method, showing complete fecal recovery (Table 1). The highest velocity dispersion of nanoparticles in the gastrointestinal tract provided a better homogenization of the material in the digesta, allowing a steady state faster. Thus, the nanomarker can be used as an marker in digestibility trials to replace the total collection.

Table 1. Fecal output, fecal recovery and digestibility by different techniques

Technique	Fecal output (kg)	Fecal recovery (%)	Digestibility (%)
Total collection	6.6[a]	100.0[a]	72.1[a]
Nanomarker	6.5[a]	100.8[a]	71.9[a]
Chromic oxide	9.0[b]	139.3[b]	62.2`
SEM	0.17	2.88	0.93
P value	<0.001	<0.001	<0.001

[a,b]Means followed by different letters in the same column differ (P < 0.05) by Tukey test.

Key Words: fecal output, markers, nanotechnology

M357 Effects of vitamin B_{12} on in vitro rumen fermentation and microbial enzyme activity.

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This study was conducted to investigate the effects of vitamin B_{12} (VB_{12}) on rumen fermentation and microbial enzyme activity in an in vitro study with a 3 × 3 factorial arrangement of treatments. Substrates were designed with 3 ratios of forage and concentrate (C/F, 35:65, 50:50 and 65:35) and 3 doses of VB_{12} (0, 40 and 90 ng/mL). Rumen fluid was collected from 3 rumen cannulated Hu sheep fed a diet consisting of Chinese wildrye hay and concentrate mixture (60:40) twice daily. Cobalt was not added into the incubation medium (mixture of rumen fluid and buffer solution) so that it did not interfere in the effect of vitamin B_{12}. Gas pressure measurements were recorded at 2, 4, 6, 9, 12 and 24 h of incubation and then converted to gas volume. Ammonia N, pH, volatile fatty acids, microbial protein, and activities of carboxymethylcellulase, xylanase and amylase were determined at 24 h incubation. Data were analyzed using the GLM procedure of SAS. Terminal pH varied within normal range (6.52 to 6.65) regardless of treatment or substrate. With the increasing C/F ratio and additional doses of VB_{12}, gas production at 24 h incubation was enhanced ($P < 0.01$) and VB12 had a linear effect. Addition of VB_{12} to the substrate at C/F ratio of 35:65 did not have effects on all the rumen fermentation parameters ($P > 0.05$), while ammonia-N, volatile fatty acids, and microbial protein increased ($P < 0.05$) at 40 and 90 ng/mL VB_{12} when the C/F ratio was at 50:50 and 65:35. Activities of carboxymethylcellulase, xylanase and amylase increased ($P < 0.05$) at 40 and 90 ng/mL VB_{12} for the C/F ratio of 35:65 and 50:50, and at 90 ng/mL VB_{12} for C/F ratio of 65:35. Although the C/F ratio and VB_{12} dose had varying effects on in vitro rumen fermentation, the results of this study indicate that addition of VB_{12} can improve rumen fermentation through enhancing microbial enzyme activity with pronounced effect at higher C/F ratio.

Key Words: microbial enzyme activity, rumen fermentation, vitamin B_{12}

M358 Urinary recovery of purine derivatives and microbial production in Nellore cattle.

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The objectives of this study were to estimate the abomasum proportion of purines recovered as purine derivatives (PD) in urine, and verify the effect of intake level on microbial production (Nmic) in Nellore cattle. The animals were fed with one diet with different levels of DM offer. The trial was performed using 8 cannulated (rumen and abomasum; moreover 4 of those with ileum cannula) heifers with average BW of 258±20 kg. The animals were allocated on individual stalls and fed twice a day. The statistical analyses were performed using 2 balanced Latin square designs (4 x 4). Treatments were constituted of four levels of DM offer: 1.2, 1.6, 2.0 and 2.4% of BW. The average of RNA apparent digestibility coefficient obtained was 75.63%, but it was not affected ($P>0.05$) by the levels of DM offered in diet. The daily flux of RNA, and the Nmic into the abomasum as a function of DM offered in the diet presented quadratic behavior. Estimates were maximum of 1.50 mmol/kg$^{0.75}$ and 55.20 g Nmic for the DMI of 2.43 and 2.45% of BW. Daily urinary excretion of PD, in mmol/kg$^{0.75}$, increased linearly ($P>0.05$) with the level of DM offered in diet. When the excretion of PD, expressed in mmol/day basis, was related with TDN intake, kg/day, was observed ($P>0.0001$) an excretion of 32.15 mmol for each kg of TDN consumed. Microbial production estimated by PD in urine as a function of the level of DM offered in the diet, presented linear behavior ($P>0.05$). The recovery of the absorbed PD in urine was 0.86.

Key Words: level of intake, RNA, ruminant nutrition

M359 Methane emission potential, chemical composition and degradability of banana crop wastes for ruminants.

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Five substrates, consisting of banana leaves hay, banana pseudostem hay, coastcross hay and 50% substitution levels of coast-cross hay to leaves or pseudostem banana hay were evaluated for the chemical composition, cumulative gas production, methane emission potential and degradability. The semi-automated in vitro gas production technique was employed to determine the cumulative gas production with 2, 4, 6, 8, 12, 16, 20, 24, 30, 36, 48, 72 and 96 h after incubation in ruminal fluid of sheep and cattle. Each sample included 3 repetitions per inoculum, with 6 replicates to evaluate the dry matter degradability in 2, 6, 12, 24, 48 and 96 h. After 24 and 48 h the gas was storage to evaluate the methane concentration using gas chromatograph. The experimental design was completely randomized in 5 × 2 factorial, with substrates and inoculum factors. Data for cumulative gas production, degradability and volume of methane were subjected to variance analysis and the means compared by Tukey test (5%). The fermentation kinetics parameters was estimated using the France model. The banana leaves hay had the highest crude protein content (13.8%), while in pseudostem hay this nutrient level was lower (3.5%). This last substrate had small values of neutral detergent fiber (64.6%) and acid detergent fiber (36.2%) and high proportion of non-fibrous carbohydrates (28.4%), when compared with the coastcross hay. After 24 h fermentation, the pseudostem hay had cumulative gas production higher than others substrates ($P < 0.05$), reflecting their greater effective degradability (76.3%). The lowest rate of effective degradability was observed for the coastcross hay (46.3%), resulting in low gas production. The 50% addition level of leaves or pseudostem banana hay to the coastcross hay improved the fermentative quality of the substrate, being observed increase in effective degradability, up 10.6%, and in maximum potential gas production, up 14.7 mL/g of dry matter. The methane emission was lower ($P < 0.05$) for banana leaves and coastcross hay, both not differing from each other ($P > 0.05$).

Key Words: alternative forages, methane, ruminant nutrition

M360 Corn grain or citrus pulp associated with glycerin in Nellore feedlot steers: intake and ruminal fermentation. V. R. Fávaro,* J. M. B. Ezequiel, J. R. Paschoaloto, M. T. C. Almeida, A. P. D'Áurea, A. C. Homem Junior, and V. C. Santos, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

In most studies glycerin has been evaluated as an energy source replacing the corn of the diet. In Brazil, citrus pulp represents an interesting alternative for feedlot cattle, due to its nutritional characteristics, good availability and lower price when compared with corn. The objective of this research was to evaluate the association of corn grain or citrus pulp with glycerin in diets for Nellore feedlot steers on dry matter intake, rumen pH and rumen ammonia concentration. Five rumen cannulated Nellore steers (420 ± 20 kg BW) were used in a 5x5 Latin square design. Experimental diets consisted of 30% corn silage and 70% concentrate (corn grain, citrus pulp, soybean hulls, urea and glycerin) and were labeled as (DM basis): diet with no added glycerin (CON), 30% of corn grain with 10% of glycerin (CG10), 25% of corn grain with 15% of glycerin (CG15), 25% citrus pulp with 10% of glycerin (CP10), 20% of citrus pulp with 15% of glycerin (CP15). To determine pH and ammonia concentration, rumen fluid samples were taken through the rumen cannula at the time of feeding and, 1, 2, 4, 6 and 8 h after feeding. Statistical analysis was performed using the MIXED procedure of SAS. Orthogonal contrasts were used to determine the effect of 0% glycerin vs glycerin treatment, CG10 vs CG15, CP10 vs CP15 and corn grain vs citrus pulp treatments. For pH, and ammonia data the time of harvest was included as a repeated measure. The rumen pH and ammonia concentrations were not influenced ($P > 0.05$) by the treatments. The mean values of pH and ammonia concentration were respectively 6.38 and 17.99 mg/dL. DM intake decrease ($P < 0.009$) when corn grain treatments was compared with citrus pulp treatments, the mean values were 7.27, 7.55, 7.24, 5.50 and 6.56 kg/day respectively for CON, CG10, CG15, CP10 and CP15. These data suggest that the use of glycerin at 10 or 15% with corn or citrus pulp does not affect the rumen pH neither ammonia concentration but, diets with more citrus pulp proportion causes decrease in dry matter intake.

Key Words: biodiesel, byproducts, feedlot cattle

M361 Assessment of the in vitro fermentation pattern of native forage from the Brazilian semiarid region. D. K. A. Silva*[1,2], L. O. Tedeschi[2], M. A. Fonseca[3,2], N. F. De Paula[3,2], K. P. Pereira[1], G. R. Medeiros[4], J. C. B. Dubeux Junior[1], and D. P. V. Silva[1], *[1]Federal Rural University of Pernambuco, Academic Unit of Garanhuns, Garanhuns, Pernambuco, [2]Texas A&M University, Department of Animal Science, College Station, [3]Federal University of Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [4]National Institute of Semiarid, Campina Grande, Paraíba.*

This work was aimed to evaluate the in vitro gas production (IVGP) and the fermentation kinetic parameters of 6 Brazilian native forages from the semiarid region in 2 seasons (PY) of the year: rainy (RS) and dry (DS) seasons. The forages analyzed were *Calotropis procera* (AS), *Croton sonderiamus* Müll Arg (M), *Caesalpinia pyramidalis* Tul. (CA), *Macroptilium martii* Benth. (OO), *Ipomoea glabra* Choisy (JIT), and *Herissantia crispa* (L.) (MB). The statistical analyses were performed using a random coefficient model assuming PY as a random variable and forage as a fixed variable. The IVGP technique was used to determine the total gas production (TGP). The results indicated that only PY affected TGP ($P < 0.05$) (Table 1). JIT had a greater value during the RS than DS season. During the RS period, AS and CA had the greatest and M had the lowest TGP values. During the DS period, AS and OO presented the greatest while JIT and M had the lowest TGP values. The greatest fractional rate of fermentation (kf h^{-1}) was observed for AS, which also had the greatest lag time (1,351 ± 0,24), suggesting that microbes needed more time to start the fermentation of AS but they were able to ferment it quickly. This is likely because either AS had greater amounts of nonfiber carbohydrates or a specific group of secondary compounds that interfered on the in vitro fermentation. These results indicated that these forages, except for JIT, have the potential to be used as alternative feed sources with no disadvantage in the ruminal fermentative aspects throughout the year under the Brazilian semiarid region.

Table 1. In vitro gas production and fermentation parameters of Brazilians semiarid native forages

	Forages					
PY	AS	CA	JIT	OO	MB	M
Rainy season IVGP (mL/100 g DM)	26.83 ±1.09^{A,a}	25.31 ±1.08^{A,b}	24.65 ±0.92^{A,ab}	23.05 ±0.99^{A,b}	24.07 ±1.08^{A,b}	17.25 ±0.99^{A,c}
Dry season IVGP (mL/100 g DM)	26.60 ±0.99^{A,a}	22.91 ±0.99^{A,b}	19.18 ±0.92^{B,c}	24.24 ±0.92^{A,ab}	22.73 ±0.92^{A,b}	19.87 ±1.22^{A,c}
kf (h^{-1})[1]	0.165 ±0.01^{a}	0.099 ±0.01^{cd}	0.106 ±0.01^{cd}	0.106 ±0.01^{c}	0.133 ±0.01^{b}	0.086 ±0.01^{b}

$^{a\text{–}d}$Values within rows with same lowercase letters do not differ (P > 0.05).

^{A,B}Values in columns (for IVGP) with same uppercase letters do not differ (P > 0.05).

[1] Fractional rate of fermentation.

Key Words: Brazilian semiarid, IVGP, lag time

M362 An in vitro evaluation of rumen fluid type on hydrogen sulfide production of common beef cattle feedstuffs. K. L. Neuhold*[1], J. J. Wagner[2], K. S. Sellins[1], and T. E. Engle[1], *[1]Colorado State University, Fort Collins, [2]Southeast Colorado Research Center, CSU, Lamar, CO.*

Rumen fluid from fistulated steers receiving a high roughage (ROU; 50% alfalfa hay, 50% corn silage) or a high concentrate-based diet (CON; 70% rolled corn, and 30% corn silage) was utilized to examine in vitro hydrogen sulfide (H_2S) production of common beef cattle feedstuffs. Rumen fluid was collected and combined in equal amounts from 2 rumen fistulated steers that had ad libitum access to ROU and mixed at a 3 to 1 ratio of artificial saliva to rumen fluid. Fermentation substrates included: corn, alfalfa, consolidated corn distillers soluble, dried distillers grains (DDG), and wet distiller's grain (WDG). Individual substrates (700mg) were added to separate 125 mL glass serum bottles (in triplicate) with 50 mL of rumen fluid-artificial saliva mixture. Fermentation bottles were capped with an air tight rubber stopper and incubated in a water bath for 24 h at 39°C. After 24 h of incubation, the total volume of gas produced was measured and a 5-mL gas sample was obtained. Gas samples were then analyzed for H_2S concentration, after gas sampling, pH and dry matter disappearance (DMD) were determined. This experiment was then repeated using rumen fluid from steers fed CON. A feedstuff by rumen fluid type (ROU vs. CON) interaction ($P < 0.001$) was detected for μmol of H_2S produced per mg of DMD. Consolidated corn distillers soluble substrate produced less H_2S per mg of DMD when incubated with CON compared with ROU rumen fluid while corn, alfalfa, DDG and WDG produce greater μmol of H_2S per DMD when incubated in CON compared with ROU rumen fluid. Across diets (ROU vs. CON) fermentation of corn produced the lowest pH and fermentation of alfalfa produced the highest pH and across feedstuff ROU had a higher pH when compared with the CON rumen fluid. These data suggest that type of rumen fluid (ROU vs. CON) and feedstuff can influence the production of H_2S. Understanding factors that influence H_2S production within the rumen may be useful when formulating beef cattle diets.

Key Words: hydrogen sulfide, in vitro, sulfur

M363 In vitro methane production and dry matter degradability of citral.

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Citral, a major component of lemongrass oil has several applications in industry and also antibacterial, antifungal, and anticarcinogenic effects. The aim of this study was to determine the in vitro effect of different concentrations of citral from 2 different industries (sources S_1 and S_2) on methane production and ruminal degradability of a ruminant diet using a semi-automatic gas production technique. A total mixed ration (50% maize silage and 50% concentrate) was incubated with buffered rumen fluid and different levels of citral (0, 15, 30, 45 and 60μL/mL) at 39°C for 72h. Gas production was measured at 4, 8, 12, 16, 24, 30, 36, 48, 60 and 72h of incubation and the dry matter disappearance at 12, 24, 48 and 72h. Data were analyzed using PROC MIXED of SAS 9.1. Differences were observed for sources ($P = 0.017$) and doses ($P = 0.001$). The inclusion of citral increased dry matter degradability (DMD) for $S_1(\text{DMD} = -0.0006S_1^2+0.0921S_1+21.611;\ R^2 = 0.58)$ and for $S_2(\text{DMD} = -0.0076S_2^2+0.5949S_2+20.968;\ R^2 = 0.99)$, but the S_2 was more efficient. Unlike what has been expected, the citral, regardless of source, increased production of methane. There was quadratic effect in the methane production to $S_1(CH_4 = 3.186+2.077S_1\text{-}0.021S_1^2;\ R^2 = 0.91;\ P = 0.001)$, 4.69; 23.61; 55.09; 47.73; 52.49 mL/g DMD and S_2 ($CH_4 = 4.228+2.603S_2\text{-}0.032S_2^2;\ R^2 = 0.83;\ P = 0.001$), 4.71; 30.96; 64.63; 43.67; 45.37 mL/g DMD, respectively to doses 0, 15, 30, 45, 60, and the interaction of citral doses and sources was significant ($P \leq 0.001$). Ammonia-N concentration was not altered with inclusion of citral at different doses. There was significant effect of citral on the methane production and dose containing 45 and 60 μL/mL decreased significantly ($P \leq 0.05$) the production. The effects of citral would not be nutritionally beneficial to the ruminal energetic metabolism. Fapesp project number 2011/06260-9.

Key Words: degradation, gas production, lemongrass

M364 Estimated microbial production, efficiency and nitrogen balance in sheep fed high concentrate varying amounts of glycerin from soybean biodiesel.

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The objectives of this study were to evaluate the effect of glycerin from soybean biodiesel in high-concentrate diets on ammonia concentrations, nitrogen balance, excretion of purine derivatives, and microbial production (Pmic) and efficiency (Efmic). Animals were housed in individual pens, randomly allocated in a 5 × 5 Latin square design, and the dietary treatments were: 0, 5, 10, 15 and 20% of glycerin on diet DM. The glycerin used was derived from soybean biodiesel production (98% glycerol, 19.2% fat, 0.98% methanol, 0.18% ethanol, 101 mg KOH/g). Five male sheep, castrated and cannulated in the rumen, with initial body weight of 56.0 ± 9.02 kg were used in this study, and fed isoproteic diets (12.5% CP), containing 25% corn silage and 75% concentrate, on DM basis. For each 50 mL of ruminal fluid collected, 1 mL of 50% sulfuric acid was added to preserve samples during freeze. Feed, refusal, total fecal and urinary output was collected on 16 d through 20 d of each period. Feces were collected with canvas bag and the urine was collected into plastic vessels containing 50 mL of 20% v/v sulfuric acid for each 450 mL of urine to perform the nitrogen (N) balance, estimates of Pmic and Efmic from the total excretion of purine derivatives in urine. Ammonia concentrations were no effect by glycerin ($P > 0.11$), with an average of 17.24 mg/dL. There was a quadratic effect ($P < 0.11$) on nitrogen (N) intake and absorption, with maximum values of 9.32 and 9.67% glycerin, respectively, but without influence ($P > 0.11$) on N retention (10.28 g/d), which corresponded to 56,35% of the absorbed. Fecal and urinary excretion of N were not affected ($P > 0.11$), with average values of 4.73 and 7.37 g N/d, in the same order. Allantoin, uric acid, xanthine + hypoxanthine excretions ($P > 0.11$) were 7.68, 0.50 and 0.29 mmol/d, respectively, which corresponded to 89.25, 6.35 and 4.39% of total purines. Purine derivatives excretion (8.48 mmol/d) were not affected ($P > 0.11$) resulting in a Pmic of 46.03 g/d and Efmic of 45.45 g CP/kg TDN. Inclusions up to 20% glycerin could be recommended without compromising nitrogen balance, microbial production and efficiency in high-concentrate diets to sheep.

Key Words: ammonia concentrations, glycerol, purine derivative

M365 Microbial kinetics, fermentative and chemical characteristics in solid-state fermentation of apple bagasse.

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Nutritional characteristics of solid wastes, and its further utilization as an animal feed, can be improved by solid-state fermentation (SSF). This technology is an efficient way to improve degradation of lignocellulosic compounds and enhance the amount and quality of protein fraction. The aim of this trial was to evaluate the effect of incubation time on the fermentative profile and chemical content of fermented apple residues collected after industrial processing for juice extraction. Apple waste was ground and mixed with (as % fed basis) 1.5 urea, 0.2 of ammonium sulfate, 0.9 calcium carbonate and 0.5 of a mineral salt mixture. Calcium carbonate was added to promote a slight alkaline substrate. These ingredients were mixed and then 340g (as fed basis) as substrate were distributed to separate sterile 500mL flasks plugged with cotton and incubated under static conditions at 32°C for 0, 12, 24, 36, 48 and 72h. A completely randomized design was used with 4 replications at each incubation time and data was analyzed with the GLM procedure of SAS. The pH values decreased ($P < 0.0001$) progressively over time and lactic acid increased ($P < 0.0001$) through time of incubation. Yeast cell counts (expressed in log10) also increased in the first 48h and decreased subsequently ($P \leq 0.0001$; 7.02, 7.19, 7.64, 7.78 and 7.26 cfu/mL).Lactobacilli colonies increased to the 36h and then decreased ($P \leq 0.0001$; 7.86, 8.71, 9.80, 9.69 and 9.54 cfu/mL). Dry matter content (%) was increased in the first

12h ($P < 0.001$; 18.98, 20.28, 20.08, 20.51, 20.33 and 20.53). Crude and true protein content (%) increased ($P \leq 0.0001$) also over time (31.7, 33.9, 33.8, 34.9, 35.0 and 35.2; 15.8, 18.8, 21.1, 19.2, 22.6 and 23.9 respectively). Neutral detergent fiber (%) was not affected in the first 12 h ($P \geq 0.05$), but diminished from 12 to 36 h ($P < 0.002$). According to these results it can be concluded that a 48-h time of fermentation was enough to accomplish an adequate yeast cell growth and obtain an improvement of the protein fraction of fermented residues of the apple industry.

Key Words: apple bagasse, nutritional, solid-state fermentation

M366 Evaluation external and internal markers for digestibility studies.

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The objective of this experiment was to evaluate complexed chromium (Cr-EDTA) and ytterbium chloride ($YbCl_3$) as external markers, and indigestible neutral detergent fiber (INDF) such internal marker digestibility in comparison with total fecal collection (TC). Eight crossbred heifers (Holstein/Zebu) with 202.12 kg ± 11.54 of BW, were used. The experimental design was a replicated 4 × 4 Latin square. The diets were isonitrogenous (13% CP), and were composed by different protein sources: soybean meal (60% sugar cane, 15% soybean meal, 23.5% corn grain, 1% mineral and 0.5% urea); cottonseed meal (60% sugar cane, 14.2% cottonseed meal, 23.8% corn grain, 1% mineral and 1% urea); peanut meal (60% sugar cane, 13% peanut meal, 25.3% corn grain, 1% mineral and 0.7% urea); and sunflower meal (60% sugar cane, 16.2% peanut meal, 21.75% corn grain, 1% mineral and 0.85% urea). Each period consisted of 7 d of adaptation and 21 d of sample collections. Total feces were collected for 5 consecutive days during each period. Composite diet and fecal samples were analyzed for nutrients (chemical composition), and concentration of chromium and ytterbium was obtained in atomic absorption spectrophotometer and INDF in 11 d ruminal incubation (non-woven textile bags, 20 mg DM/cm^2). Apparent total digestibilities of all nutrients were lower for INDF compared with Cr-EDTA, $YbCl_3$ and TC. Digestibility estimated using Cr-EDTA, $YbCl_3$ or TC were not different (Table 1). In conclusion, using INDF as a digestibility marker yielded greater fecal output estimates and consequently lower apparent digestibility values for all dietary nutrients compared with TC or Cr-EDTA, $YbCl_3$. In the conditions of this experiment, Cr-EDTA and $YbCl_3$ was a more appropriate digestibility marker than INDF.

Table 1. Comparisons of methods for determining total tract apparent digestibility

	Method					
Item	TC	Cr-EDTA	$YbCl_3$	INDF	*P*-value	SEM
DM	67.62^a	66.86^a	67.01^a	63.62^b	<0.001	4.61
OM	65.23^a	64.80^a	65.54^a	61.30^b	<0.001	6.68
CP	67.20^a	65.11^a	66.29^a	62.57^b	<0.001	8.24
NDF	50.53^a	49.07^a	48.83^a	44.43^b	<0.001	8.06

[a,b]Means within a row followed by different letters are different ($P < 0.05$) by Tukey test.

Key Words: digestibility, heifers, markers

M367 Addition of fumarate reducing bacteria on in vitro fermentation.

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Fumarate reducing bacteria utilized hydrogen which is one of the main substrate in methanogenesis. This study was conducted to determine if addition of these bacteria on in vitro fermentation can reduce methane, increase volatile fatty acids (VFA) production, and effect on its microbial diversity. The ruminal samples were collected from Holstein cows, mixed with a basal medium (1:3), transferred into 50-mL serum vials containing rice straw and filled under a stream of O_2-free N_2 gas. *Mitsuokella jalaludinii* and *Veillonella parvula* were added to the serum vials and incubated. After incubation, pH, total gas production, VFA, and methane emission were measured. Moreover, diversity of microorganism was determined by DGGE using universal and specific primer. All data were analyzed using SAS (2003). *M. jalaludinii* significantly reduces methane at 48 h of incubation. In addition, *M. jalaludinii* significantly increases succinate at 12, 24 and 48 h of incubation followed by *V. parvula* and then control. Furthermore, total volatile fatty acid was significantly higher in *V. parvula* at 24 h of incubation. These results suggest that addition of fumarate reducing bacteria to ruminal fermentation reduces methane, increases succinate and total volatile fatty acid, and changes the rumen microbial diversity.

Key Words: fumarate reducing bacteria, in vitro, DGGE

M368 Rumen wall morphology of lambs fed high concentrate diets.

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High concentrate diets results in high rumen fatty acids concentrations which stimulates epithelium proliferation of papillae causing parakeratosis and increased occurrence of injury and inflammation. To evaluate different forms of corn grain processing on the rumen wall and papillae morphology 23 Santa Inês × Dorper male lambs with mean BW of 28 kg and 90 d old were fed a high concentrate diet (75% corn, 20% protein and mineral mix and 5% coast cross hay), with whole corn grain (WCG), high moisture corn (HMC) or ground corn grain (GCG). After 65 d of feeding animals were slaughtered and the rumen content (RC) was weighed and its pH measured. The incidence of ruminitis (IR) was classified according to a 0 to 10 scale. Fragments of 3cm^2were taken from the cranial sac of the rumen and kept in buffer for macroscopic measurements of papillae number (PN), papillary area (PA) and absorption surface (AS). PN was measured by 3 evaluators and PA and AS were measured on scanned images of the papillae and parietal surface fragments using the UTHSCA Image Tool free software. The average BW at slaughter was 47 ± 1.44kg. There were no significant differences among treatments for ADG (mean = 0.32 kg). The RC was higher for WCG (4.5 kg; $P = 0.02$) when compared with GCG (3.5 kg) and HMC (3.4 kg) with no differences between GCG and HMC. The rumen pH was smaller ($P < 0.0001$) for WCG (5.4) when compared with GCG (6.5) and HMC (6.6) with no differences between the last 2 treatments. There was no difference among treatments in IR (mean = 0.48%) and PN (mean = 43 papilla/cm^2). The treatment WCG, expressed as a percentage of rumen wall surface, had greater PA (95%; $P = 0.04$) then HMC (93%) but was similar to GCG (94%) with no differences between GCG and HMC. The AS was greater for treatment WGC (19cm^2) than for HMC (14cm^2; $P = 0.05$) with no difference between GCG (17cm^2) and HMC treatments. Although WCG may be interesting because the grain needs no processing and has a small effect on rumen wall morphology, it may result in an unfavorable rumen environment.

Key Words: feedlot, ruminant, sheep

M369 Growth rate of mixed ruminal bacteria as a function of energetic substrate concentration in bath culture.

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The objective of this study was to evaluate levels of sucrose on microbial growth. Roll tubes were filled with 15.6 mL of buffer Chen, 1 mL of inocula (rumen fluid from fistulated steer at pasture), 1 mL of Trypticase or hydrolyzed casein (1 g/L as final concentration) and 2.4 mL of sucrose solutions (0.00, 0.37, 0.75, 1.5, 3.0, 6.0, 12.0, and 24.0 g/L), in triplicate. The pH was 5.56 at 0 h and 4.6 after 6 h, and 5.83 in 0 g/L and 4.18 above 1.5 g/L of sucrose. The optical density (OD-600 nm) and microbial protein (MP-595 nm) tended to stabilize after 12 h and 6 g/L of sucrose, with no interaction between them. The OD (6 h to 24 h mean values) was curvilinear (hyperbolic), as a function of sucrose concentration, followed the saturation kinetics of Michaelis-Menten, which is typical of enzymes systems, and was described by the following Lineweaver-Burk equation: $1/OD = 0.508*(1/sucrose) + 1.15$, $R^2 = 0.99$. The theoretical maximum microbial growth (1/a = kmax) was 0.87 OD and the concentration of sucrose to reach half of kmax (b/a = Ks) was 0.44 g/L of sucrose. The microbial growth was affected by incubation time, substrate concentration, and culture medium acidification.

Key Words: Lineweaver-Burk, Michaelis-Menten, saturation kinetics

M370 Nutrient digestibility of pregnant WAD ewe fed Mexican sunflower leaf meal (MSLM) based diets.

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Fifteen days before parturition, studies was conducted using 16 West African Dwarf (WAD) ewes weighing between 22.8 and 26.0kg on a basal diet of *Panicum maximum* were allotted into 4 treatment groups A, B, C and D of 4 replicates each. The Mexican sunflower leaf meal (MSLM) replaced wheat bran (WB) gravimetrically at 0, 15, 30 and 45%. Treatment A served as control, while animals in treatments B, C and D received MSLM at 15, 30 and 45% respectively. The experiment lasted for one week. Digestibility was determined using a 6-d total fecal collection. Ewes were given ad libitum access to feed and water and routine vaccination and medication followed standard procedures. The 16 ewes were previously brought to heat (estrus) by synchronization and served by 2 rams (1:8). Parameters measured were voluntary dry matter intake (VDMI), which comprised concentrate dry matter intake (CDMI) and grass dry matter intake (GDMI), apparent digestibility coefficients of dry matter(DM), crude protein(CP), ether extract (EE), nitrogen-free extract (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), organic matter (OM), energy and feed conversion ratio (FCR). Data were analyzed using descriptive statistics and ANOVA .The VDMI (g/d) varied from 392.3 - 695.0 for ewes during digestibility. CDMI (g/d) varied from 191.4 – 565.0 and GDMI (g/d) varied from 137.5 – 227.3 for ewes and this was significant ($P < 0.05$) with animals on treatment B having the highest CDMI while animals on treatment C having the highest GDMI respectively. Apparent digestibility coefficients of EE, NDF, ADF, ADL, OM, energy and FCR were similar. Approximately 75.5 ± 1.1% of the VDMI came from the supplement. Diets containing 15% MSLM was superior to others for CDMI (191.4 – 565.0 g/d), C P absorbed (42.1 – 99.5 g/d), CP apparent digestibility (86.5 – 91.5%), digestible DMI (52.3 – 85.2 g/d/kg$W^{0.75}$) and digestible CPI (14.3 – 28.4 g/d/kg$W^{0.75}$) while GDMI (137.5 – 227.3 g/d) for diets containing 30% and 45% MSLM were significant ($P < 0.05$). Therefore, MSLM could suitably replace wheat bran in the diets of pregnant ewe up to 30% level of inclusion without eliciting any adverse effect.

Key Words: Mexican sunflower, nutrient digestibility, pregnant West African dwarf ewe

M371 Rumen bacteria growth and pH of culture medium on different substrate concentrations.

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The objective was to evaluate the response on rumen bacteria growth rate as a function of increasing substrate. Incubations were performed in glass jars saturated with carbon dioxide gas and hermetically sealed, containing 6 mL of rumen liquid, 24 mL of artificial saliva, and substrate weights of 1.2; 0.6; 0.3; 0.1; 0.05 and 0 g, being half of each weight corresponding to sucrose and half soybean meal. The tubes were incubated in triplicate for 72 h at 39°C and the pH and optical density were evaluated at 0, 6, 12, 18, 24, 42 and 72 h of incubation. The experiment was analyzed as completely randomized design as a function of substrate concentration, time of incubation and the respective interaction. Bacterial growth reached high values after 6 h ($P < 0.01$), but with strong depression at 48 and 72 h, associated with the low pH of culture medium and microbial lyses. It was observed increase in microbial growth ($P < 0.01$) with increase in the level of substrate. There was substrate * time interaction in microbial growth ($P < 0.01$), in which there was decrease in microbial growth with increase in time in low substrate levels, due to microbial lyses. Linear regression analyses of the reciprocal of the rate of microbial growth versus reciprocal supply of nutrients were made for the 48 times and 72 h of incubation, which had already reached the maximum growth, technique called Lineweaver-Burk equation. The theoretical maximum growth rate was 1.08 and substrate concentration required to achieve half of the maximum response was 0.128 g. The low observed K_s shows that bacteria affinity for sucrose is high, leading to rapid fermentation of substrate, lowering the pH values below the level tolerable by the predominant microbial population in rumen. This effect takes, consequently the microbial lyses and reduction of optical density. In this experiment it was found that the curvilinear response of saturation kinetics is due to first order kinetics in low levels of nutrients (excess enzymes and/or low substrate) and because of the zero order kinetics in high levels of nutrients (saturated microbial enzyme activity by fermentation products). Supported by FAPEMIG (Fundação de Amparo à Pesquisa do Estado de Minas Gerais).

Key Words: growth rate, saturation kinetics, sucrose

Small Ruminant: Nutrition

M372 Effect of breed and sex on fatty acid composition of fat-tailed and tailed lambs. A. Yousefi,* H. Kohram, A. Z. Shahneh, M. Sadeghi, and M. Poorhamdollah, *University of Tehran, Karaj, Tehran, Iran.*

The objective of this study was to compare fatty acid profile of longissimus dorsi (LD) between fat-tailed Chall (14 male and 15 female) and tailed Zel lambs (15 male and 15 female). All of lambs were pastured with average age of 10–12 mo and BW of 36.5 ± 1.6 (Kg). LD muscles were dissected 24h after slaughtering to evaluation fatty acid composition. Data of fatty acid profile and intramuscular fat of LD muscle were analyzed by SAS 9.2 software and GLM procedure where HCW was used as covariate and breed and sex were used as fixed effect. Results showed (Table 1) that Zel and female stored more intramuscular fat than Chall ($P < 0.001$) and male lambs ($P < 0.0001$), respectively. Oleic (C18:1) acid was lower ($P < 0.001$) and linolenic acid (C18:3n-3) was higher ($P < 0.01$) in Chall compared with Zel lambs. Although percentage of linoleic acid (C18:2n-6) and SFA were not significant ($P > 0.05$) between breeds, LD muscle of Chall contained more percentage of PUFA and PUFA/SFA ratio ($P < 0.05$) rather than Zel lambs. LD muscle of male lambs showed higher percentage of PUFA ($P < 0.05$) and lower proportion of n-6/n-3PUFA ($P < 0.001$). Considering n-6/n-3PUFA, LD muscle of Chall lambs showed lower ratio ($P < 0.01$) than Zel lambs whereas sex did not show significant difference ($P > 0.05$). In conclusion, results indicated that meat produced by Fat-tiled and male lambs was more close to recommended nutritional quality for human.

Table 1. Mean ± SE fatty acid and chemical components analysis

	Breed			Sex			Effect	
Trait (mg/100g)	Chall	Zel	SEM±	Male	Female	SEM±	Breed	Sex
C16:0	26.3	26.6	0.47	25.3	26.91	0.47	NS	NS
C18:1	36.9	40.2	0.64	38.7	38.41	0.65	***	NS
C18:3n-3	0.05	0.53	0.05	0.65	0.60	0.05	**	NS
C18:2n-6	5.98	5.47	0.24	6.25	5.20	0.24	NS	**
PUFA	9.33	7.61	0.46	9.24	7.70	0.46	*	*
PUFA/SFA	0.19	0.16	0.01	0.20	0.15	0.01	*	**
n-6/n-3PUFA	4.77	6.12	0.35	5.37	5.52	0.34	**	NS
Intramuscular fat	1.82	2.83	0.24	1.98	2.97	0.21	**	***

*P <0.05; **P <0. 01; *** P < 0.001; NS = not significant.

Key Words: fatty acid composition, fat-tailed lamb, tailed lamb

M373 The energetic efficiency of growing lambs fed high-concentrate diets with different roughages. D. B. Galvani[1], A. V. Pires*[2], I. Susin[2], V. N. Gouvea[2], A. Berndt[3], L. J. Chagas[2], J. R. R. Dórea[2], A. L. Abdalla[4], and L. O. Tedeschi[5], [1]*EMBRAPA Goats and Sheep, Sobral, CE, Brazil,* [2]*University of São Paulo, "Luiz de Queiroz" College of Agriculture, Piracicaba, SP, Brazil,* [3]*EMBRAPA Southeast Livestock, São Carlos, SP, Brazil,* [4]*University of São Paulo, Center for Nuclear Energy in Agriculture, Piracicaba, SP, Brazil,* [5]*Texas A&M University, Department of Animal Science, College Station.*

Poor quality roughages have been widely used as fiber source in high-concentrate diets for ruminants. Because roughage quality is associated with the efficiency of energy use in high-forage diets, the objective of this study was to determine whether using roughages with different quality in high-concentrate diets could change the energy requirements of growing lambs. Eighty-two Dorper × Santa Ines ram lambs (18.0 ± 3.3 kg BW) were individually penned and divided into 2 groups according to the diet roughage quality: low quality (sugarcane bagasse; SCB) or good quality [coastcross hay (*Cynodon* sp.)]. Diets were formulated to be isonitrogenous (2.6% N) and to meet the minimum requirement of physically effective NDF (peNDF = 20%). After a 10-d ad libitum adaptation period, 7 animals from each group were randomly selected and slaughtered (baseline). Twenty one animals in each group were fed ad libitum and slaughtered at 25, 35, or 45 kg BW. The remaining 28 lambs were submitted to one of 2 levels of feed restriction: 70 or 50% of the ad libitum intake. Retentions of body fat, N, and energy were determined. Additionally, 6 ram lambs (52.3 ± 6.9 kg BW) were kept in cages to estimate diet ME content. There was no effect of intake level on diet ME content, but it was greater in the SCB diet than in the hay diet (3.18 vs. 2.94 Mcal/kg, respectively; $P < 0.01$). Animals fed the SCB diet had greater body fat and energy concentrations as a response of a larger visceral fat deposition ($P < 0.05$). Using poor quality roughage in high-concentrate diet for growing lambs did not change NE_m and the efficiency of ME use for maintenance, which averaged 72.9 kcal/kg$^{0.75}$ BW and 0.64, respectively. On the other hand, the greater ME content of the SCB diet resulted in a 17% better efficiency of ME use for gain (k_g = 0.41 vs. 0.35; $P < 0.05$), which was associated with a greater partial efficiency of ME retention as fat (k_f = 0.73 vs. 0.58; $P < 0.01$). In a meat production scenario, however, this increased nutritional efficiency should be viewed with caution because it is related to visceral fat deposition, a non edible tissue.

Key Words: efficiency of gain, energy retention, visceral fat

M374 Intake and feeding behavior of Morada Nova lambs fed different energy levels. D. A. Camilo[1], E. S. Pereira*[1], P. G. Pimentel[1], M. S. S. Carneiro[1], I. Y. Mizubuti[2], M. R. G. F. Costa[1], G. M. B. Moreno[1], and J. N. Rocha Junior[1], [1]*Federal University of Ceara, Fortaleza, Ceara, Brazil,* [2]*State University of Londrina, Londrina, Parana, Brazil.*

The eating behavior of ruminants, such as feed intake, ruminating time and number of chews, varies by feed type and physical characteristics and has an important effect on the digestive physiology of the ruminant. The objectives of this study were to evaluate the effects of ME levels on nutrient intake and ingestive behavior of Morada Nova lambs. Forty Morada Nova lambs were used with an initial BW of 12.2 ± 2.05 kg. Five treatments were defined according to the ME levels (0.96, 1.28, 1.72, 2.18 and 2.62 Mcal/kg DM). Diets were composed of Tifton 85 hay as roughage and concentrates based on corn grain, soybean meal, urea, sodium chloride, calcium carbonate, dicalcium phosphate and mineral premix and offered as a total mixed ration. The experimental model was a randomized block design. Regression equation was adjusted when 0.05 significance was observed, using PROC REG SAS (9.0).Linear effect ($P < 0.0001$) of ME levels was determined for DMI, OM, CP, total carbohydrates (TC), non-fibrous carbohydrates (NFC) and TDN in g/day. Quadratic effect was determined for neutral NDF ($P < 0.017$) and non fibrous carbohydrate intake ($P < 0.003$). Eating, ruminating and total chewing times, expressed in h/d, decreased linearly ($P < 0.0001$) with the energy levels of experimental diets. Idle time increased linearly ($P < 0.0001$) with the increase of energy levels of the rations. Feeding and rumination efficiencies were influenced by the energy levels (($P < 0.0001$) when expressed in g of DM/h. The number of ruminal boluses, number of chews and chews per ruminal bolus were not affected by the levels of ME. However, the time spent chewing per ruminal bolus was influenced ($P < 0.0014$). Increase in ME levels of diets influences nutrient intake and feeding behavior of Morada Nova lambs during the growing period.

Key Words: eating time, feeding level, rumination time

M375 Different supplement treatments for lactating meat goat does grazing grass/forb pastures.

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Lactating meat goats grazing 0.4-ha grass/forb pastures were used to determine effects on performance of different supplement treatments. Boer does (32) with 1 or 2 kids were used in a study with 4 4-wk periods (PR) starting 22 ± 2.0 d after birth. Two groups were subjected to treatments of no supplementation (CO), access to a 20% CP supplement block (SB), and placement in a supplement pasture with mimosa (*Albizia julibrissin*) trees for 6 h 1 d/wk (1×) or twice weekly for 3 h/d (2×). All groups received access to the same mineral-vitamin supplement. Available forage DM in non-supplement pastures averaged 3,477, 3,448, 3,353, 2,802, and 2,423 kg/ha initially and after PR 1, 2, 3, and 4, respectively; hand-plucked forage samples averaged 15 and 67% CP and NDF, respectively. Treatment did not affect doe ADG (−23, −42, −23, and −15 g; SE = 11.5), FAMACHA score, or fecal egg count, although kid ADG in the first 3 PR differed ($P < 0.05$) between type of supplement and frequency of supplement pasture access (121, 111, 120, and 134 g for CO, SB, 1×, and 2×, respectively; SE = 3.3). Spanish does (32) nursing 2 kids were used in a study with three 4-wk PR starting 66 ± 0.8 d after kidding. The same CO and SB treatments were employed, but access to supplement pastures was for 24 h 1 d/wk (1×) or 2 d for 6 h/d (2×). Forage DM averaged 1,530, 842, 791, and 750 kg/ha initially and after PR 1, 2, and 3, respectively), and 0.6 kg/d (as fed) per doe of grass hay (7 and 67% CP and NDF, respectively) was fed after PR 1. Hand-plucked forage samples averaged 14 and 64% CP and NDF, respectively. Treatment did not affect doe or kid FAMACHA score. Kid ADG in PR 1 and 2 was not affected by treatment. Doe ADG was affected by supplementation ($P < 0.05$) and supplement type ($P < 0.09$; −44, −33, −23, and −12 g; SE = 5.5), which resulted from effects ($P < 0.05$) in PR 3 after weaning (−87, −69, −16, and −2 g for CO, SB, 1×, and 2×, respectively; SE = 14.3). In conclusion, use of the SB was not beneficial, and infrequent access to supplement pastures had relatively small effects on ADG perhaps because forage availability and nutritive value were not severely limiting.

Key Words: goats, grazing, supplementation

M376 Effects of level and length of supplementation on BW and harvest characteristics of yearling Boer and Spanish wethers.

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Spanish (S; 28 - 40 wk of age) and Boer (B; 33 - 46 wk) wethers were used to determine effects of level (SL) and length of supplementation on BW and harvest characteristics. The experiment started in January, with wethers residing in 4 pastures primarily with warm season grasses. Alfalfa hay was given free-choice, and a pelleted diet (16% CP and 60% TDN) was group supplemented at 0.5 or 1.5% BW (DM basis; L and H, respectively). Five S and 6 B were harvested initially, and 12 per breed (BR) and SL were harvested after 110 and 218 d (PR 1 and 2, respectively). Data were analyzed by GLM procedures. There were BR differences ($P \leq 0.06$) in initial BW (33.3 and 23.7 kg), carcass weight (15.4 and 10.9 kg), and mass of noncarcass components (NCC; 11.7 and 9.2 kg for B and S, respectively) but not in mass of NCC relative to empty BW (EBW). The ADG was greatest ($P < 0.05$) among PR-BR treatments for PR 1-B (139, 74, 63, and 56 g for PR 1-B, PR 1-S, PR 2-B, and PR 2-S, respectively; SEM = 5.23). The BW was affected ($P < 0.05$) by SL (48.2 and 43.1 kg for H and L), BR (53.1 and 38.2 kg for B and S), and PR (41.8 and 49.3 kg in 1 and 2, respectively). There were corresponding differences ($P < 0.05$) in weight of the carcass (23.6 and 20.4 kg for H and L; 25.5 and 18.5 kg for B and S; 20.3 and 23.8 kg for PR 1 and 2, respectively) and NCC (16.9 and 15.0 kg for H and L; 18.4 and 13.5 kg for B and S; 15.1 and 16.8 kg for PR 1 and 2, respectively). Digestive tract mass was similar between BR and lowest ($P < 0.05$) among SL-PR treatments for PR 2-H (7.21, 7.19, 6.31, and 7.51% EBW for PR 1-H, PR 1-L, PR 2-H, and PR 2-L, respectively). Liver mass was similar between BR and less ($P < 0.05$) for H than for L (2.15 and 2.30% EBW) and for PR 2 vs. 1 (2.11 and 2.34% EBW). Mass of internal fat was greatest ($P < 0.05$) among SL-PR treatments for PR 2-H (6.72, 6.36, 8.61, and 5.95% EBW for PR 1-H, PR 1-L, PR 2-H, and PR 2-L, respectively). In summary, advantages of B in BW and carcass weight were similar after PR 1 and 2, BR had little effect on NCC mass relative to EBW, and H increased mass of internal fat after PR 2 but not PR 1.

Key Words: meat goat, breed, supplement

M377 Energy requirements for growth of male and female Saanen goat kids.

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Nutritional requirements could be affected by several factors, including sex. However, studies evaluating the effect of sex on body composition and nutritional requirements in goats are scarce. The aim of this study was to evaluate the effect of sex on energy requirement for maintenance and gain of Saanen goat kids, using comparative slaughter technique. A total of 66 animals (24 non-castrated males, 18 castrated males and 24 females) with initial BW of 4.93 ± 0.1 kg were used. Six non-castrated males and 6 females were slaughtered at beginning of the experiment (baseline animals) and 18 randomly selected kids (6 of each sex) were slaughtered when they reached 10 kg BW (intermediate slaughter). The reminder was randomly allocated into 12 groups (blocks) of 3 animals of the same sex, subjected to 0, 25 and 50% of feed restriction. A group was slaughtered when the animal set in the 0% restriction reached 15 kg BW. Initial body composition was determined using equations developed from the energy composition of the baseline kids. The energy maintenance requirement was estimated using the animals subjected to feed restriction (0, 25, and 50% of feed restriction). Animals fed ad libitum (baseline, intermediate and 0% of feed restriction) were used to estimate body composition and requirements for gain. There was no effect of sex on the energy requirements for maintenance and gain. The overall NE_m calculated was 56.3 kcal/kg$^{0.75}$ EBW (47.3 kcal/kg$^{0.75}$ BW). The overall ME_m for maintenance (88.05 kcal/kg $^{0.75}$ EBW) was calculated by iteration assuming heat produced is equal to ME intake at maintenance. Therefore, the partial efficiency of use of ME to NE for maintenance was 0.64. Net energy (NE_g) requirements for gain ranged from 2.07 to 2.30 Mcal/kg empty weight gain (EWG) for kids weighting 5 and 15 kg BW, respectively. These findings suggested that sex did not influence energy requirements of Saanen goat kids at early growth stages.(FAPESP project number 2008/58351–5)

Key Words: gain, sex, maintenance

M378 Influence of reducing starch and increasing digestible fiber on glucose tolerance test of lactating ewes. R. S. Gentil*[1], I. Susin[1], A. V. Pires[1], E. M. Ferreira[1], A. Cannas[2], D. Eysink[1], M. V. Biehl[1], and C. P. Nolli[1], *[1]Universidade de São Paulo/ESALQ, Piracicaba, São Paulo, Brazil, [2]Università degli Studi di Sassari, Sassari, Sardegna, Italy.*

Thirty-three lactating Santa Ines ewes (68 ± 3 initial BW and 13.2 ± 3 DIM; mean ± SD), assigned to a randomized complete block design, were used to define an optimal combination between carbohydrates sources (starch and high digestible fiber) that can favor energy partitioning toward milk production at different lactation stages. Ewes were housed individually for a period of 10 wks from the second wk of lactation. Animals were fed a 60:40 (concentrate:roughage ratio). Soybean hull (SH) replaced corn by 0, 20 or 40% (DM basis). At the end of the lactation trial, 9 ewes (3 animals/treatment) were used for the glucose tolerance test (GTT). Prior to GTT, ewes were removed from feed and weighed 24 h before glucose infusion (0.25 g of glucose/kg of BW, delivered in a 50% dextrose solution). Fasting values of glucose and insulin were determined at 0 min before administration of the glucose bolus. Additional blood samples were collected at 5, 10, 20, 40 and 80 min after the glucose infusion. A colorimetric assay was used to determine plasma glucose concentrations. Plasma insulin concentrations were measured using RIA. Glucose disappearance rate was calculated by regression of glucose concentration over time from 5 to 80 min post glucose infusion. Incremental area under the curve (AUC) for glucose (transformed logarithmically, Ln) was determined using a trapezoidal summation method. Data were analyzed by the PROC MIXED (SAS, 2002). Both, insulin and glucose concentrations showed effect ($P < 0.01$) on the time post glucose infusion. Fasting glucose (53.2; 57.7; 60.4 mg/dL) and insulin (1.4; 3.0; 5.3 μIU/mL) concentrations and peak insulin increased (22.4; 25.9; 35.1 μIU/mL) ($P < 0.05$) with inclusion of the SH. Additionally, peak glucose (247.5; 236.3; 184.7 mg/dL) and glucose clearance rate (2.04; 1.44; 1.11 mg/dL.min) decreased ($P < 0.05$) in the animals fed more SH. Glucose tolerance (measured as glucose AUC) was not affected ($P > 0.05$) by replacing corn by SH. Sheep fed more corn demonstrated greater ability to decrease the concentration of glucose.

Key Words: insulin, ovine, soybean hulls

M379 Soybean meal supplementation of lambs grazing native pastures in the summer-fall season. L. Piaggio[1], M. L. delPino[1], H. Deschenaux[1], and M. de J. Marichal*[2], *[1]Secretariado Uruguayo de la Lana, Montevideo, Uruguay, [2]Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay.*

The objective of this study was to evaluate the effect of soybean meal (SBM) supplementation on growth rate of lambs grazing natural pastures in the summer-fall season. The experiment was conducted at Research Center (S 33° 52’, W 55° 34’) of the Secretariado Uruguayo de la Lana from January 17 to April 27 (15 d of adaptation period plus 85 d of measurements). Thirty-six 3-mo-old weaned Corriedale lambs were divided into 12 homogenous groups according to sex and live weight. Animals were allocated in one paddock of natural pastures (10 lambs ha^{-1},1864 kg of initial available DM ha^{-1}; 8.8 and 70.4% CP and NDF, respectively) and assigned (3 groups of lambs/treatment) to one of the following treatments: continuous grazing (T0), Control + SBM (150 g $lamb^{-1}d^{-1}$; 46.7 and 20.9% CP and NDF, respectively; T1), Control + SBM (250 g $lamb^{-1}d^{-1}$; T2), Control + SBM (350g $lamb^{-1}d^{-1}$; T3). Lambs were weighed at the beginning of the experiment (average 17.8 ± 2 kg), and at every 15 d thereafter. Initial and final BW, and ADG, were analyzed (PROC GLM, SAS) in a completely randomized design (Tukey test), considering the group of lambs by replicate as the experimental unit. Treatment effects ($P = 0.02$) were registered in final weights (FW). Greater ($P = 0.04$) FW was registered in T3 than T0 (22.7 and 28.6 kg, respectively), presenting T1 and T2 intermediate and with similar ($P = 0.19$) values (24.5 and 26.4 kg, respectively). No differences ($P = 0.14$) among treatments were observed for the ADG of lambs at d 14 after the beginning of the measurement period (56, 65, 71 and 109 g $lamb^{-1}d^{-1}$ for T0, T1, T2 and T3, respectively). Differences ($P = 025$) in ADG were first registered on d 28, presenting lambs in T3 greater ($P = 0.004$) in ADG than T0 (126 and 57 g d^{-1}, respectively), and T2 and T3 having similar ($P = 0.16$) values (78 and 101gd^{-1}, for T1 and T2, respectively). These differences were maintained from this point forward. In the overall measurement period, ADG were 56, 78, 101, and 127 g $lamb^{-1}d^{-1}$, for T0, T1, T2 and T3 ($P < 0.05$). Soybean meal supplementation appeared as an effective supplement to improve growth in lambs grazing natural pastures.

Key Words: lambs, soybean meal supplementation, grazing

M380 Nutritional quality, intake, and apparent digestibility of mulberry (*Morus alba*) and star grass (*Cynodon nlemfuensis*) in goats. J. A. Elizondo-Salazar* and J. Rodríguez-Zamora, *Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, Costa Rica.*

The objective of the study was to evaluate the quality, intake, and apparent digestibility of mulberry and star grass offered to goats in fresh or partially dehydrated form. The experiment was carried out at the "Alfredo Volio Mata" Experiment Station of the University of Costa Rica. Forage was fed to 12 Saanen, Toggenburg, and Lamancha nonlactating and non-pregnant goats with an average live weight of 37 ± 5 kg. A 2x2 factorial design was used with 2 forage species (star grass and mulberry) and 2 moisture levels (fresh and partially dehydrated). Thus, treatments were fresh star grass, partially dehydrated star grass, fresh mulberry, and partially dehydrated mulberry. Forage was offered chopped to the animals. The GLM procedure of SAS was used to analyze the data. There were some nutritional differences among treatments. Dry matter content was different ($P < 0.05$) between treatments (28.2, 37.5, 36.7, and 43.1%, respectively). Mulberry had the lowest NDF content (65.7%) but also had the highest lignin concentration (13.0%). Daily DMI was not different when considering water concentration within forages but it was different ($P < 0.05$) for forage type. The levels of intake were 0.93, 0.76, 1.17, and 1.12 kg/animal for fresh star grass, partially dehydrated star grass, fresh mulberry, and partially dehydrated mulberry, respectively. This represented 2.62, 2.09, 3.17, and 3.13% of BW. Crude protein intake was lower for partially dehydrated star grass and greater for fresh mulberry (75.2 vs. 135.4 g/d). Apparent digestibility was not different between treatments and averaged 49.2% for DM, 59.8% for CP, 57.8% for NDF, and 55.3% for ADF. This study demonstrated that forage species significantly affected voluntary DMI in goats; however, DM content of the forages used in this study did not affect DM intake.

Key Words: intake, dry matter, digestibility

M381 Effect of dietary supplementation of ferrous sulfate on performance and carcass characteristics of meat sheep. G. Abdelrahim*[1], J. Khatiwada[2], and A. Gueyec[3], *[1]Alabama A&M University, Huntsville, [2]North Carolina A&T State University, Greensboro, [3]Mount Ida College, Newton, MA.*

The overall objective of this study was to gain a thorough understanding of the impact of increasing the concentration of $FeSO_4$ in meat sheep diets. The specific objective was to investigate the effects of elevated levels of $FeSO_4$ inclusion on DMI, growth, and carcass characteristics of meat sheep. Twenty-four Gulf Coast wether lambs (26.3 ± 3.63 kg initial BW, and 8 to 9 mo of age) were blocked by BW and were randomly assigned within block to 1 of the 3 dietary treatments, giving 8 lambs per treatment. Animals were grouped in 2 pens (replicates) per treatment (4 lambs/pen) with pen serving as the experimental unit. Lambs were fed dietary treatments containing 0, 75, or 150 mg/kg of DM (as-fed basis) supplemental FeSO4. Control diets contained dry-rolled corn, SBM, and fescue/bermudagrass hay. The concentrate mixes were formulated to be isonitrogenous and isocaloric and to meet or exceed the NRC requirements of a finishing lamb. Lambs were slaughtered, and data were collected after a 48-h chill. Both growth and carcass quality data were analyzed using the GLM procedures of SAS. Dry matter intake, final BW, and ADG were not different among treatments ($P = 0.5$, 0.9, and 0.7, respectively). Also, no differences were observed in HCW ($P = 0.9$), cold carcass weight ($P = 0.8$), body wall fat ($P = 0.6$), 12th rib fat ($P = 0.9$), K&P fat ($P = 0.9$) and REA ($P = 0.7$) among treatments. These results support our hypothesis that the addition of 75 or 150 mg $FeSO_4$/kg in finishing lamb diets do not affect DMI, growth rate, and carcass characteristics of meat sheep.

Key Words: iron, meat sheep, growth

M382 Effects of diets with different qualities of roughage on fatty acids metabolism in mammary glands of lactating dairy goats.

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The objectives of this study were to determine the effects of diets with different qualities of roughage on milk-fat percentage, daily yield of milk fat and fatty acids metabolism in mammary gland. Eight multiparous lactating GuanZhong dairy goats (BW = 45.6 ± 2.5 kg, DIM = 90 ± 12 d) fitted with external pudendal artery (EPA) and subskin abdominal vein (SAV) intubation were assigned to 2 treatments in a crossover design. Animals received same concentrate and different roughage, concentrate-roughage ratio was 40:60. Treatments were: 1) hay (30%), corn silage (20%) and alfalfa (10%) (HCA; CP: 10.6%, NDF: 50.4% and ME: 2.24 Mcal/kg); 2) hay (30%), corn straw (30%) (HCS; CP: 14.2%, NDF: 39.7% and ME: 2.39 Mcal/kg)(DM basis). Each period lasted for 3-wk. At the last 3 d of each period, milk and blood samples from EPA and SAV were collected for FA analysis. Data were analyzed by the PROC MIXED procedure of SAS 9.0. The milk fat percentage of HCA was greater than HCS (3.04 vs. 2.84%; $P = 0.01$), while daily yields of milk fat were not affected (15.3 vs. 14.5 g/d). Compared with HCS, HCA tended to increase total percentage of long-chain FA (>16c) which known as major precursor of de novo milk fat synthesis in mammary gland (35.0 vs. 33.0%, $P = 0.16$); the concentration and profile of FAs in the blood of EPA, SAV and milk were not affected. However, percentage of total milk SFA by HCA was statistically lower than HCS (71.7% vs. 73.4, $P = 0.15$); percentage of milk UFA by HCA was higher than HCS (28.29 vs. 26.59%, $P = 0.15$). Compared with HCS, HCA tended to increase EPA plasma concentration of total FA (0.73 vs. 0.57, $P = 0.32$), and increased SAV plasma concentration of total FA (0.62 vs. 0.44, $P = 0.02$), especially the concentration of C18:0 and C18:2c6 (0.1 vs. 0.08, $P = 0.12$; 0.12 vs. 0.09, $P = 0.11$). No differences were found on the extraction rate of specific FA in 2 groups. Compared with HCS, HCA increased plasma concentration of long-chain FA in EPA and SAV, which might result in higher milk fat percentage.

Key Words: milk fat concentration, FA composition, dairy goat

M383 Effects of diets with different forage profiles on the gene expression of enzymes related to fatty acid synthesis in the mammary gland of lactating dairy goats.

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The objective was to determine the effects of 2 diets with different forage profiles on the key gene expression of enzymes related to fatty acid synthesis in the mammary gland of GuanZhong dairy goats. Analysis of mRNA expression for acetyl-coenzyme A carboxylase- α (ACACA), fatty acid synthesis (FASN), stearoyl coA desaturase (SCD), and lipoprotein lipase (LPL) were performed. Eight multiparous lactating goats (BW = 45.6 ± 2.5 kg, DIM = 90 ± 12 d) were assigned to 2 treatments in a crossover design. Animals were fed diets with different forage profiles, the concentrate-roughage ratio in the treatments were 40:60. Diets were: 1) hay (30%), corn silage (20%) and alfalfa (10%) with additional 40% of concentrate (HCA; CP: 10.6%, NDF: 50.4% and ME: 2.24Mcal/kg); 2) hay (30%), corn straw (30%) with additional 40% of concentrate (HCS; CP: 14.2%, NDF: 39.7% and ME: 2.39Mcal/kg), on DM base. Mammary gland biopsies were performed after milking on the last day of each period. The mammary tissue biopsy (50 mg/animal) was immediately frozen in liquid nitrogen and stored at-80°C until RNA isolation. Samples of total RNA were reverse transcribed to cDNA to determine the expression of key genes for fatty acid synthesis by the method of RT-PCR. Statistical analysis was performed using a paired *t*-test on the difference between treatments. Compared with HCS, in HCA animals mammary mRNA abundance of LPL, which is involved in fatty acid uptake was increased by 39% ($P < 0.01$); ACACA and FASN, which are involved in de novo fatty acid synthesis were increased by 18, and 20%, respectively ($P < 0.01$); SCD, which is involved in fatty acid desaturation was increased by 50% ($P < 0.01$). The data demonstrated that diet with high quality roughage (HCA) can increase the gene expression of enzymes that are related to milk fat synthesis in the mammary gland of dairy goats.

Key Words: mammary gland, milk fatty acid, dairy goat

M384 Performance of Ile de France lambs fed with diets containing different percentages of mulberry hay.

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Among the concentrated feeds most used in ruminant feeding, stand out the corn and the soybean meal, and the high cost of this feeds limit their use. Efforts have been made in the search for alternative feeds among them the mulberry hay, being fundamental to evaluate the performance of lamb fed with such feeds. The objective of this study was to evaluate the performance of lambs fed with diets containing different percentages of mulberry hay. A total of 20 4 lambs, Ile de France breed, with 25 kg of BW, 3 mo old were used and kept in individual stalls, in a completely randomized design, with 3 treatments and 8 repetitions, in which the data were analyzed using SISVAR statistical software, and when statistical differences were observed, a mean comparison was done using the Tukey test. The treatments were: T1: sugarcane + concentrate with 0% mulberry hay; T2: sugarcane + concentrate with 25% mulberry hay; T3: sugarcane + concentrate with 50% mulberry hay. The sugarcane used was the forage variety IAC 86–2480, and the total diet had forage:concentrate ratio of 50:50 given ad libitum. The remains of the diets were collected, weighed and subtracted from the total provided to quantify the feed consumed by the animals individually. The ADG (0.26 kg/d), DMI (0.82 kg/d), feed conversion (3.21 kg

DM/kg BW), feed efficiency (0.31 kg BW/kg DM) and feedlot period (66 d) were not affected ($P > 0.05$) by different percentages of mulberry hay in the concentrate. The use of mulberry hay partially substituting the concentrate did not affect the performance of feedlot lambs. This research is in progress (Fapesp process number 2011/18362–0).

Table 1. Initial body weight (IBW), final body weight (FBW), daily weight gain (DWG), dry matter intake (DMI), feed conversion (FC), feed efficiency (FE) and days of feedlot (DF) of lambs fed with diets containing different percentages of mulberry hay

Item	T1	T2	T3	CV (%)
IBW (kg)	15.5	15.5	15.5	0.50
FBW (kg)	32.1	32.1	32.3	1.69
DWG (kg/day)	0.26	0.25	0.25	6.53
DMI (kg/day)	0.83	0.80	0.82	9.88
FC (kg DM/kg BW)	3.21	3.21	3.22	7.99
FE (kg BW/kg DM)	0.31	0.31	0.31	7.22
DF	64.8	66.8	66.4	7.14

Key Words: feedlot, feed conversion, weight gain

M385 Effect of metabolizable protein supplementation to ewes during late gestation on wether offspring feedlot performance, carcass characteristics, and nitrogen balance.

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Our objective was to determine the effect of metabolizable protein (MP) supplementation to ewes during late gestation on wether offspring nitrogen (N) balance, feedlot performance, and carcass characteristics. Maternal dietary treatments were isocaloric and contained 60% (60), 100% (100), and 140% (140) of MP requirements for ewes bearing twins during the last 50 d of gestation. Feedlot (28 ± 7 kg) and N balance wethers (29 ± 3 kg) were fed a common feedlot ration (84.7% whole corn, 15.3% commercial market lamb pellet). The N balance trial was 21 d in length and consisted of an adaptation period on d 1 through 14 and on d 15 through 21 feed, orts, urine, feces, and blood samples were collected and composited by lamb. Statistical analysis was accomplished utilizing the MIXED procedures of SAS. Maternal dietary treatment did not affect ($P \geq 0.36$) initial and final BW, ADG or G:F of wether offspring. Hot carcass weight, dressing percentage, longissimus muscle area, 12th rib fat depth, body wall thickness, leg score, conformation score, flank streaking, USDA quality grade, yield grade, and percent boneless, closely trimmed retail cuts were not different ($P \geq 0.40$) due to maternal dietary treatment. For the N balance trial, daily DMI, daily NDF intake, daily N intake, total tract digestibility of DM, NDF, and N, daily N excretion in the feces and urine, daily N balance, daily digested N retained, and serum urea-N concentrations were not different ($P \geq 0.46$) due to maternal dietary treatment. There was a day effect ($P = 0.02$) for serum urea-N concentrations. Days 15 and 17 of the collection period had increased serum urea-N concentrations compared with d 20 ($P = 0.001$ and $P = 0.02$, respectively) and 21 ($P = 0.004$ and $P = 0.04$, respectively); and d 15 also had increased ($P = 0.04$) concentrations compared with d 18. Maternal MP restriction or excess during late gestation did not affect wether offspring performance in the feedlot, carcass characteristics, or N retention.

Key Words: metabolizable protein, performance, wethers

M386 Effects of sources of oil on intake, performance and carcass characteristics of feedlot sheep.

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Crossbred uncastrated male lambs (Santa Inês × Dorper, n = 24, 24.9 ± 2.4 kg BW) were used to evaluate intake, feedlot performance and carcass characteristics when fed diets containing supplementary oil sources. Treatments (3 diets) consisted of a control diet containing 40% corn silage, 10.8% corn grain, 9.8% soybean hulls, 37.45% sunflower meal, 0.55% urea, 0.4% limestone, and 1% supplement, and 2 diets containing additional 6% soybean oil or 6% residual soybean frying oil (DM basis). Lambs were vaccinated against common viral and clostridial diseases, weighed and assigned randomly to 24 individual feedlot pens (8/treatment). Over a period of 21 d, lambs were transitioned from diets containing 20% concentrate to their respective 60% concentrate finishing diets, using 3 step-up diets that contained, progressively, greater proportions of concentrate. Final diets provided 18.5% CP, 2.6 kcal ME/kg, 0.85% Ca, and 0.60% P, and the animals were harvested when reached 35 kg BW. Data analysis were performed as a completely randomized block design (initial BW as block), using GLM procedure of SAS, and the contrasts control vs. oil treatments and soybean oil vs. frying oil were evaluated. Adding oil sources decreased DMI ($P \leq 0.01$), and the decrease were more severe in animals fed frying oil ($P = 0.02$). This oil source also promoted lower ADG ($P \leq 0.01$) and increased days on feed ($P = 0.05$), compared with other treatments. However, the addition of both sources of oil increased G:F ($P = 0.02$). Carcass weight were unaffected ($P > 0.05$) by diets, but dressing percentage were lower in treatment with soybean oil ($P \leq 0.01$). LM area and BF thickness were not affected by oil addition ($P > 0.05$). Including supplementary oil to sheep diets decreased DMI and improved feed efficiency but when the source of oil is residual frying oil, it decreased performance, by increasing days on feed.

Key Words: by-products, lambs, frying oil

M387 Lipid sources in diets for feedlot sheep: Blood parameters.

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Twenty-four crossbred uncastrated male lambs (Santa Inês × Dorper, 24.9 ± 2.4 kg BW), were used to evaluate the effects of adding lipid sources (soybean oil or residual frying soybean oil) on blood parameters. Lambs were vaccinated against common viral and clostridial diseases, weighed and assigned randomly to 24 individual feedlot pens (8/treatment). Over a period of 21 d, lambs were transitioned from diets containing 20% concentrate to their respective 60% concentrate finishing diets, using 3 step-up diets that contained, progressively, greater proportions of concentrate. Corn silage was the roughage, and concentrate was composed of corn grain, soybean hulls, sunflower meal, urea, mineral supplement, antioxidant, soybean oil or residual frying oil and diets provided 18.5% CP, 2.6 Mcal ME/kg, 0.85% Ca, and 0.60% P. Treatments were labeled as 1 - Control, without added oil, 2 - Soybean, with 6% added soybean oil, and 3 - Frying, with 6% added used frying oil. The animals were kept in a feedlot barn, equipped with individual pens for up to 105 d. Blood sampling was performed with jugular vein puncture on d 59 and serum glucose, triglycerides, cholesterol, total protein, and liver enzymes AST (aspartate aminotransferase), GGT (gamma glutamyltransferase) and ALP (alkaline phosphatase) were determined. Data analysis were performed as a completely randomized block design (initial BW as block), using GLM procedure of SAS, and

the contrasts control vs. oil treatments and soybean oil vs. frying oil were evaluated. The addition of oil increased cholesterol ($P \leq 0.01$) and AST ($P \leq 0.01$). When the residual frying oil was used it was observed a tendency to increase ALP ($P = 0.06$). Serum glucose, triglycerides and total protein were unaffected by the diets ($P > 0.05$). Addition of 6% soybean oil or residual frying oil in feedlot sheep diet increases concentrations of serum liver enzymes, suggesting over activity of the organ. However, such changes, observed to this feedlot period, are not sufficient to cause damage to animal health.

Key Words: frying oil, lambs, liver enzymes

M388 Relationship between phosphorus fluids concentration and phosphorus flows in growing ruminants. R. M. Patiño*[1], T. Soares da Silva[3], J. C. da Silva Filho[2], D. M. S. S. Vitti[3], J. A. Moreira[4], and E. H. van Cleef[5], *[1]University of Sucre, Sincelejo, Colombia, [2]Federal University of Lavras, Lavras, MG, Brazil, [3]Nuclear Energy Center for Agriculture, Piracicaba, SP, Brazil, [4]Federal University of Rio Grande do Norte, Natal, RN, Brazil, [5]State University of São Paulo, Jaboticabal, SP, Brazil.*

The objective of this work was to study the relationship between phosphorus (P) concentration in body fluids and the flows between plasma and organs, and P concentration in liver and bone, in growing sheep fed diets with increasing levels of P. An experiment was carried out using 24 male sheep, initial BW of 33.6 ± 1.6 kg, assigned to 4 treatments (0, 2, 4 and 6 g/d of supplementary P). The animals were injected with 7.4 MBq of ^{32}P and slaughtered 168 h later. The flows were quantified using isotopic dilution technique and applied a compartmental model, to define the flows between the digestive tract and plasma (F_{21}), plasma and digestive tract (F_{12}), plasma and bone (F_{42}), bone and plasma (F_{24}), plasma and soft tissues (F_{32}) and soft tissue and plasma (F_{23}). P concentration in plasma, saliva, ruminal fluid, feces, urine, liver, and bone were determined. Principal components and regression analysis were used. In all cases the first component explained more than 80% of the variation, indicating the effect of P intake on P concentration in fluids and P kinetics, principally when P supplementation exceeded 4 g. F_{12} and F_{21} flows were correlated ($P = 0.002$), as well as the flows F_{23}, F_{32}, F_{24} and F_{42} ($P < 0.05$), however, no correlation was observed ($P > 0.05$) between the 2 groups of variables. The concentration of P in plasma, saliva and urine was related to the flows between compartments, with the exception of F_{21} and F_{12}, however, P concentration in urine (PU) was the better predictor ($P < 0.003$) [F_{23} (g/d) = 5.75 + 0.31 × PU (mg/100 mL) ($R^2 = 0.42$); F_{32} (g/d) = 5.65 + 0.28 × PU (mg/100 mL) ($R^2 = 0.34$); F_{42} (g/d) = 1.58 + 0.06 × PU (mg/100 mL) ($R^2 = 0.47$) and F_{24} (g/d) = 0.79 + 0.05 × PU (mg/100 mL) ($R^2 = 0.44$)]. The equation, P liver (% DM) = 9.87 + 3.36 × P saliva (mg/100 mL) ($R^2 = 0.26$; $P = 0.01$), explained the relation between P concentration in urine and liver. It is concluded that the increase in P intake affects P kinetics in growing sheep. P concentration in plasma, saliva, and urine predicts the flows between organs, principally urine, with the exception of flows between plasma and digestive tract, and vice versa.

Key Words: metabolism, mineral, lamb

M389 Mineral requirements for gain in Saanen goats of different sexes. A. N. Mendonca,* C. J. Härter, I. A. M. A. Teixeira, O. Boaventura Neto, S. F. Souza, and D. Oliveira, *UNESP/Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil.*

There is evidence that sex plays an important role on body composition and requirements of animals; however, there are few studies evaluating the effect of sex on the mineral requirements of goats, thus the objective of this study was to estimate the net calcium (Ca), phosphorus (P) and magnesium (Mg) requirements for growth of Saanen goat kids, using the comparative slaughter technique. A total of 48 Saanen animals, 18 females, 18 males, and 12 castrated males with BW ranging from 5 to 15 kg were used. At the beginning of the experiment 6 intact males and 6 females with approximately 5 kg BW were slaughtered. No castrated males were slaughtered with 5 kg BW, because castration occurred when they were about 15 d old, then the males slaughtered at 5 kg BW were considered for the construction of the equations of both, castrated and intact males. The remainder of the kids, from each sex, were randomly assigned to 2 treatment groups (slaughter weight; 10 and 15 kg BW). The experiment was conducted in a completely randomized design in a factorial scheme (3 × 2). Body composition was estimated using the logarithmized allometric equation (Log y = a + b log x). The equations ($P < 0.0001$) for estimating Ca and Mg body composition were different for males and females (Table 1). There was no sex effect on P body composition (Table 1). The net Ca and Mg requirements for weight gain were influenced by the sex of goats in the early growth phase. On the other hand, kids of different sex had similar net P requirement. FAPESP project number 2011/05176-4.

Table 1. Allometric equations to estimate Ca, Mg, and P body composition of female, intact, and castrated male goat kids

	5 kg	10 kg	15 kg	Equation	RMSE
Ca (g/kg)					
Males	1.74	2.07	2.27	log Ca = 0.99+1.19 log EBW	0.071
Females	1.83	2.06	2.20	log Ca = 1.31+0.83 log EBW	0.071
Castrated	1.74	2.08	2.29	log Ca = 0.94+1.26 log EBW	0.071
Mg (g/kg)					
Males	0.28	0.64	0.86	log Mg = -0.53+1.29 log EBW	0.057
Females	0.36	0.62	0.78	log Mg = -0.24+0.95 log EBW	0.057
Castrated	0.27	0.65	0.87	log Mg = -0.58+1.35 log EBW	0.057
P (g/kg)	1.64	1.95	2.15	log P = 0.91+1.15 log EBW	0.051

Key Words: goats, growth requirements, major minerals

M390 Effect of chromium supplementation on ruminal parameters of Mahabadi goat kids. A. Emami, A. Zali, M. Ganjkhanlou,* A. Hojabri, and A. Akbari, *University of Tehran, Tehran, Iran.*

The objective of this study was to evaluate the possible effects of supplementing chromium-methionine (Cr-Met) on different ruminal parameters in growing kids. Thirty-two male kids (BW = 22 ± 2 kg, 4mo) were used in a completely randomized design to one of 4 treatments: 1) control (without Cr), 2) 0.5, 3) 1.0 and 4) 1.5 mg Cr as Cr-Met/animal/d. Diets were formulated for NRC requirements with forage (alfalfa and corn silage):concentrate ratio of 30:70 in TMR form. Diets were the same, except for top-dress addition of Cr-Met fed in 2 equal meals (0800 and 1600 h). Animals were kept in individual pens with self-mangers for 90 d. Ruminal fluid samples were taken from the rumen at 3 h after the morning meal the last day of the experiment to determine rumen concentration of ammonia nitrogen (NH3-N) and VFA. Rumen contents were sampled 5 times during the trial to measure ruminal protozoa and pH. Protozoa counts were determined using light microscopic numeration with a hematocytometer. Protozoa and pH data were analyzed by MIXED MODEL procedure and rumen NH3-N and VFA with GLM MODEL procedure and adjusted Tukey-Kramer (SAS 9.1). Cr supplementation increased rumen pH ($P = 0.03$). Treatment failed to have statistically significant effects on rumen NH3-N and VFA ($P > 0.05$), but there was a higher butyrate concentration in kids receiving 1 mg Cr as Cr-Met/animal/d compared with other groups ($P = 0.009$). There was a negative relationship between Cr supplementation and protozoa count ($P = 0.0079$). These results indicate that supplementation of goat kid diets with chromium-methionine decreased protozoa, and increased pH and butyrate concentration without altering other VFAs.

Table 1. Characteristics of ruminal parameter in kid fed chromium-methionine

	Treatment, mg of Cr				
Trait	Control (0.0)	0.5	1.0	1.5	SEM
pH	6.23^{b}	6.16^{b}	6.45^{a}	6.22^{b}	0.07
Total VFA, mmol/L	48.3	39.7	48.1	60.0	6.25
Acetate, mmol/L	25.7	19.4	24.4	32.1	4.68
Propionate+Isobutyrate, mmol/L	15.0	14.4	12.5	15.3	2.81
Butyrate, mmol/L	5.77^{b}	4.76^{b}	8.77^{a}	4.72^{b}	0.76
Valerate, mmol/L	1.15	0.36	0.75	5.3	2.36
Protozoa count (10^4)	70.0^{a}	67.0^{a}	54.0^{b}	65.2^{a}	3.55

^{a,b}Means in each row with different superscripts were statistically different ($P > 0.05$).

Key Words: goat kids, chromium-methionine, ruminal VFA

M391 Effect of feeding tannin-containing pine bark on performance, parasite load and blood metabolites in goats.

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The objective of this study was to assess animal performance, parasite load and blood parameters of goats fed condensed tannin (CT)-containing pine bark (PB) diet. Pine bark is one of the abundant forest by-products in Southern US and contains 11–13% CT on a DM basis. Thirty-two Kiko-cross meat goats (*Capra hircus*; BW = 28.0 ± 1.0 kg) were randomly assigned to 2 experimental diets: 1) 0% PB and 30% wheat straw (WS) and 2) 30% PB and 0% WS. Grain mixes were fed at 85% with the remaining 15% provided as bermudagrass hay. Animals were strategically dewormed and one half of each diet group was inoculated with 5000 infective stage (L3) *Haemonchus contortus* larvae (n = 8). Feed intake, refusals, and performance were monitored for 87 d. Blood samples were taken twice, once at the beginning and once at the end of the experiment. Fecal egg counts (FEC) were determined approximately every 2 wk. At the end of the experimental period, goats were slaughtered and carcass characteristics were determined. Total stomach worms were identified and counted. Overall, there were no differences ($P > 0.10$) in DMI, animal performance and carcass characteristics among diet groups or inoculation groups, but ADG (76.8 vs. 97 g/d), G:F (0.05 vs. 0.07), HCW (14.2 vs. 15.8 kg), and cold carcass weight (13.3 vs. 14.8 kg) tended to increase ($P = 0.15$ to 0.18) with PB supplementation compared with WS diet within artificially inoculated groups, respectively. The LM area was lower ($P = 0.02$) for inoculated groups. Goats fed PB had greater ($P = 0.001$) blood urea nitrogen and lower serum triglyceride and cholesterol ($P = 0.03$). Mean red blood cells, hemoglobin, and hematocrit (packed cell volume) were greater ($P = 0.03$) for goats fed PB diets. Mean FEC, coccidia counts, and total worm counts were lower ($P < 0.05$) for goats that were fed PB diet. The results indicated that ground PB as a feed ingredient has the potential to decrease internal parasite infection, and worm burdens while improving animal performance by altering feed efficiency, especially in parasitized goats.

Key Words: goats, internal parasites, pine bark

M392 Lamb performance feeding diets with different crude protein level.

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Thirty 6-mo old Dorset × Ramboullet lambs with 21.3 ± 4.48 kg BW were used to study the effect of CP level in the diet on feed intake, DM digestibility, ADG, feed efficiency, and water intake during a 50 d feeding period. Lambs were stratified by BW and randomly assigned to one of 3 levels of CP in the diet (12, 14 or 16% with 2.59 Mcal ME/kg DM). After the 50 d feeding period, digestibility of DM was determined with 5 lambs per treatment in metabolic cages. An economic balance was performed including only the feed cost of the total diet consumed. Data was analyzed as a completely randomized design of treatments using the GLM procedure of SAS. No significant differences were detected in DM intake among treatments neither during the pen feeding phase (3.8, 4.2, and 4.2%; 88, 98, and 96 g/kg metabolic BW, respectively), nor when fed in cages (3.1, 3.0, and 3.3%; 75, 76, and 82 g/kg metabolic BW, respectively). Water intake was not affected ($P > 0.05$) by CP level in both phases (pen: 3.21, 3.10, and 3.16 g water/g DM; metabolic cages: 3.22, 3.80, and 3.47 g water/g DM, respectively). Dry matter digestibility was similar among CP levels (74, 72, and 74%, respectively). Feed conversion (6.83, 6.67, and 5.33) and ADG (214, 291, and 276 g/anim/d) were not significantly different among CP levels. Results of this study indicated that even though lambs fed the diets with 14 and 16% CP had numerically higher ADG, there were no differences among CP levels for the variables studied. The economic balance showed that lambs fed the 14% CP diet had the greatest return.

Key Words: lambs, crude protein

M393 Effect of copper and zinc on nutrient digestibility and growth performance in goats.

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Copper (Cu) and zinc (Zn) are elements that have specific health functions in animal production; they play an indispensable role in physiological processes. In this study, a growth assay was conducted to evaluate the addition of copper and zinc to a total mixed ration (TMR) for improving of nutrient digestibility and performance of goat. Sixteen Boer crossbred male goats were randomly assigned to the following treatments (mg/kg DM): Cu-Zn (860.7–224.1); Cu (860.7); Zn (224.1) and control (no added trace minerals). Data were analyzed as a completely randomized design. Cu and Zn improved ($P < 0.01$) DM, OM, CP and ADF digestibility. DMI (g/d) was not affected ($P = 0.216$) by the micro-minerals addition. Animals on Cu-Zn treatment presented the highest ($P < 0.01$) ADG (g/d), Cu and Zn, with intermediate values while the control group had the lowest response. Feed conversion ratio was greater ($P = 0.023$) in the diet where Cu-Zn were added. Ruminal pH was not affected by treatments ($P = 0.435$). Copper and Zinc addition improved the nutrient digestibility and performance of growing male goats.

Table 1. Nutrients digestibility (g/kg DM) and growth performance of male goats consumed a total mixed ration supplemented with copper and zinc

Item	Cu + Zn	Cu	Zn	Control	SEM	*P*-value
Digestibility						
DM	702.9^{a}	697.9^{a}	705.6^{a}	675.6^{b}	5.89	0.001
OM	716.1^{a}	714.8^{a}	720.1^{a}	692.6^{b}	6.28	0.03
CP	670.8^{a}	682.9^{a}	685.1^{a}	597^{b}	10.39	0.01
ADF	374.7^{a}	363.3^{a}	387.3^{a}	277.9^{b}	9.09	0.01
AVG (g/d)	104.2^{a}	81.7^{b}	80.9^{b}	57.5^{c}	2.10	0.01
FCR	8.0^{a}	11.2^{ab}	10.5^{ab}	13.6^{b}	0.69	0.02
	6.1	6.3	6.1	6.2	0.21	0.43

[a,b]Mean values within each row for micromineral addition with different letters differ (P <0.05).

Key Words: copper, zinc, performance of male goats

M394 Growth and carcass characteristics of lambs fed high-concentrate diets containing increasing levels of crude glycerin. D. M. Polizel,* R. S. Gentil, E. M. Ferreira, M. O. Maia, C. P. Nolli, D. Eysink, A. V. Pires, and I. Susin, *Escola Superior de Agricultura Luiz de Queiroz (ESALQ)/University of São Paulo (USP), Piracicaba, São Paulo, Brazil.*

Crude glycerin is a co-product of biodiesel production with a high concentration of glycerol. Due to the high production of biodiesel, there is a wide availability of crude glycerin and it is becoming an interesting ingredient in animal nutrition. The objectives of this trial were to determine the effects of partial replacement of corn by crude glycerin on growth and carcass characteristics of lambs fed high-concentrate diets. Forty Santa Inês ram lambs (initial BW 24.1 ± 0.6 kg and 97 ± 2 d old) were used in a randomized complete block design according to initial BW and age. Lambs were penned individually during 56 d and fed an isonitrogenous (15% CP, DM basis) total mixed ration composed of 90% concentrate and 10% coastcross hay. Levels of crude glycerin (89.7% glycerol, DM basis) were 0, 5, 10, or 15% in experimental diets G0, G5, G10 and G15, respectively. There was a quadratic response for DMI, ($P < 0.04$) and ADG, ($P < 0.06$) with no effect on G:F. Dry matter intake was 1.03, 1.18, 1.12 and 1.09 kg/d while ADG was 250, 293, 294 and 272 g for G0, G5, G10 and G15, respectively. Carcass characteristics (dressing percentage, LM area, backfat thickness and body wall thickness) were unaffected by experimental diets. Dietary crude glycerin up to 10% increases DMI and ADG in feedlot lambs.

Key Words: co-product, glycerol, sheep

M395 Ruminal fermentation, kinetics and digestibility of hair lambs supplemented with cull pinto bean. F. Castillo, G. Villalobos,* D. Domínguez, J. A. Ortega, and L. Cortés, *Universidad Autónoma de Chihuahua, Chihuahua, Chihuahua, México.*

Cull pinto bean (*Phaseolus vulgaris*) is an ingredient used in ovine feeding in northern Mexico. The objective was to evaluate the effect of 3 levels of cull pinto bean (CPB) on feed intake, ruminal fermentation, kinetics, and nutrient digestibility of hair lambs. Six crossbred (Dorper × Pelibuey and Charolais × Pelibuey) rumen fistulated lambs averaging 56.6 ± 3.8 kg were used. Lambs were randomly assigned to 1 of 3 treatments. Treatments were (DM basis): 1) 0% of CPB of the supplement (CON); 2) 25% of CPB of the supplement (F25); and 40% of CPB of the supplement (F40). Dry matter intake, ruminal pH, ruminal NH_3 and VFA, methane production, Kp, MRT, DMD, CPD, and NDFD were evaluated. Data were analyzed with the MIXED procedure of SAS in a Latin square design 3 × 3 repeated in line. Estimates used for Kp, and MRT were obtained by a non linear regression model (PROC NLIN, SAS). There was a difference in DMI (kg; $P \leq 0.05$) among treatments, F25 (1.62 ± 0.08) and F40 (1.62 ± 0.08) were lower probably due to anti-nutritional factors in CPB. Ruminal pH and NH_3 (mg/100 mL of ruminal fluid) were not different ($P \geq 0.05$) among treatments. Differences were found ($P \leq 0.03$) for ruminal VFA (mM) concentration (CON: 60.4 ± 2.1; F25: 68.4 ± 2.1; F40: 64.2 ± 2.1). Higher DMI of CON did not affect total VFA. The higher value in F40 could be due to its greater oligosaccharide content. Acetate: propionate ratio was greater ($P \leq 0.0001$) for F40 (CON: 2.34 ± 0.073; F25: 2.2 ± 0.07; F40: 2.9 ± 0.07). CH_4 production (mM/ml) was different ($P \leq 0.03$) among treatments (CON: 29.1 ± 0.75; F25: 27.6 ± 0.75; F40: 32.9 ± 0.75). Kp (%/h) (CON: 3.6 ± 1.9; F25: 2.9 ± 1.9; F40: 5.9 ± 1.9%) and MRT (h) (CON: 36.3 ± 13.7; F25: 57.7 ± 13.7; F40: 36.2 ± 13.7 h) were similar ($P \geq 0.42$) among treatments. Digestibility of DM, CP, and NDF was similar ($P \geq 0.26$) among treatments. Cull pinto bean reduced DMI, although it did not affect ruminal pH and NH_3 production. The inclusion of 25% of CPB in the diet of hair lambs allowed having an appropriate nutrient digestibility without affecting Kp and MRT, and this increased the molar proportion of VFA without increasing methane production maintaining acetate:propionate ratio.

Key Words: cull pinto bean, hair lamb, ruminal fermentation and kinetics

M396 Effect of clinoptilolite (zeolite) substituting for soybean meal on apparent digestibility and energy concentration of feed in growing Pelibuey sheep. A. Estrada-Angulo,* S. A. Serrano-Cebreros, V. Martinez-Cruz, J. Cazarez-Rocha, A. Rubio-Angulo, B. I. Castro-Perez, H. Davila-Ramos, J. C. Robles, and F. G. Ríos, *FMVZ-UAS, Culiacan, Sinaloa, Mexico.*

To determine the effect of clinoptilolite (zeolite) substituting for soybean meal on apparent digestibility and energy concentration of feed in growing Pelibuey sheep, 6 male Pelibuey sheep (BW = 25.0 ± 1.1kg) were used in a Cross Over design with the following diets: 1) 3 animals received control treatment (without zeolite) 18.0% CP and 3.68 Mcal DE/kg, and contained 10.0% sudan hay, 49.0% cracked corn grain, 14.0% soybean meal, 14% DDGS, 8.0% sugarcane molasses, 2.5% animal fat, and 2.5% mineral premix; 2) like control, 3 animals received diet with zeolite, had 17.2% CP and 3.60 Mcal of DE/kg, but contained 1.5% zeolite and 12.5% soybean meal. Dry matter intake was adjusted at 1000 g/day/head (500 g am and 500 g pm). Total collection of feces was used in 2 periods under crossover experimental design. Data were analyzed with ANOVA. The OM excreted in feces was greater ($P <$ 0.05) in control treatments (86.4 vs. 83.1%) in comparison with zeolite treatment. The apparent digestibility of OM for control and zeolite treatments was similar ($P > 0.05$) with 85.5 and 84.0%, respectively. Ashes excreted in feces were greater ($P < 0.05$) in sheep with zeolite treatment in respect to control (16.9 vs. 13.6%, respectively). N excreted in feces was minor 12.7% in zeolite treatment. There was no difference in DE concentration of diet ($P > 0.05$) between treatments (3.5 vs. 3.4 Mcal/kg of DM) for control and zeolite treatment, respectively. The observed/expected DE ratio was similar for treatments (0.95 and 0.94 for control and zeolite treatments, respectively). It is concluded that clinoptilolite (zeolite) can substitute soybean meal at 1.5% of the diet increasing the apparent digestibility of OM and without effect on energy concentration in diets for growing Pelibuey sheep. Further, zeolite can diminish the N excreted in feces when it is included in diets for growing hair sheep.

Key Words: clinoptilolite, apparent digestibility, pelibuey sheep

M397 Influence of level of protein and energy on growth performance and tissue composition of feedlot hair lambs. F. G. Rios[1], H. Davila-Ramos*[1], A. Estrada-Angulo[1], A. Plascencia[2], J. J. Portillo[1], and J. C. Robles[1], [1]*FMVZ-UAS, Culiacan, Sinaloa, Mexico,* [2]*IICV-UABC, Mexicali, BC, Mexico.*

Forty-eight Pelibuey × Katahdin (23.9 ± 2.84 kg) crossbred male lambs were used in a 84-d feeding trial (6 pens per treatment in a randomized complete block design) to evaluate the influence of protein and energy supplementation level on growth performance and tissue composition. Lambs were fed with cracked corn-based finishing diet. Treatments were HPHE: 18% CP/2.99 Mcal ME/kg DM; HPLE: 18% CP/2.79 Mcal ME/kg DM; LPHE: 15% CP/2.99 Mcal ME/kg DM, and LPLE: 15% PC/2.79 Mcal ME/kg DM. Final live weight (FLW), DMI, ADG, G:F, slaughter weight (SW), HCW, dressing percentage (DP), LM area, Fat thickness (FT), kidney-pelvic fat (KPF), primal performance and carcass tissue composition were determined. The values were analyzed by ANOVA for a complete block design with 2 × 2 factorial arrangement; for carcass traits, slaughter live weight was used as a covariate. The means were compared using Tukey-Kramer test. FLW was greater ($P < 0.05$) in HPLE by the effect of protein level (49.8 vs. 48.0 kg), DMI was lower ($P < 0.05$) in HPHE and LPHE by the effect of energy level (1.15 vs. 1.27 kg); ADG (0.29 kg/d) and (G:F) (4.27) was not affected ($P > 0.05$) by treatments. SW was greater ($P < 0.04$) in HPHE (46.6 vs. 45.1) due to the protein level, KPF was higher ($P < 0.05$) for HPHE by the effect of energy level (1.03 vs. 0.79 kg). Carcass tissue composition was not modified by the effect of protein and energy level, nor by the factor's interaction. The results of this experiment suggested that 15% protein in the diet is sufficient to optimize the carcass traits of the finishing lambs with high energy diets, on the other hand providing higher levels of protein, does not improve carcass dressing percentage and carcass traits.

Key Words: protein level, hair lambs, carcass composition

Swine Species I

M398 Neutral semi-purified glycerin in starting pigs feeding in Brazil.

I. Moreira*[1], A. G. Gallego[1,2], P. C. Pozza[1], P. L. O. Carvalho[1], L. M. Peñuela-Sierra[1,3], and L. M. Huepa[1,2], [1]*Universidade Estadual de Maringá, Maringá, Paraná, Brazil,* [2]*Universidad del Tolima, Ibagué, Tolima, Colombia,* [3]*Universidad Cooperativa de Colombia, Ibagué, Tolima, Colombia.*

Two experiments were carried out to investigate the use of neutral semi-purified glycerin - NSPG (obtained from soybean oil), in starting piglet diets. Chemical composition (as-fed-basis) of NSPG: DM = 88.11%; glycerol = 80.2%; CP = 0.90%; GE = 3,535 kcal/kg; Methanol = 0.01%; NaCl = 5.86% and Ash = 6.18%. A digestibility trial (Experiment I) was conducted using 30 crossbred barrows with an initial BW of 42.91 ± 1.58 kg. The digestible (DE) and metabolizable energy (ME) values of glycerin were estimated by regression of DE and ME intake vs. glycerol intake (Adeola, 2001). For concentrations (4%, 8%, 12% and 16%) of NSPG in a corn + soybean meal (CSM) basal diet were fed. The values (as-fed basis) of DE and ME (kcal/kg) obtained were 3,298 and 2,531, respectively. The results indicate that the glycerin is a highly available energy source for feeding starting pigs. In the performance trial (experiment II), 100 piglets (BW = 15.14 ± 0.06 to 30.28 ± 0.70 kg) were allotted in a completely randomized block design, with increasing levels (0, 3.5, 7.0, 10.5, and 14.0%) of NSPG in a CSM diet. There were 10 pens per diet with 2 pigs per pen. Experimental diets were formulated according to NRC (1998). No effects ($P \geq 0.05$) of NSPG inclusion on piglet performance (Table 1) were observed by regression analysis. It can be concluded that using up to 14% of NSPG (2,531 kcal of ME/kg) in diets for starting piglet is feasible, without impairing performance.

Table 1. Piglet performance fed on neutral semi-purified glycerin (NSPG)

	Inclusion of NSPG ,%							*P*-value	
Item	0	3.5	7.0	10.5	14.0	Mean	± SE	Linear	Quadratic
ADFI, kg	1.314	1.248	1.331	1.241	1.305	1.287	±0.131	0.99	0.99
ADG, kg	0.729	0.683	0.727	0.706	0.711	0.711	±0.039	0.99	0.99
Feed/gain ratio	1.81	1.83	1.83	1.77	1.84	1.82	±0.021	0.99	0.99

Key Words: biodiesel, co-product, glycerol

M399 Brazilian neutral semi-purified glycerin on growing and finishing pigs feeding.

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This study was carried out to evaluate the use of Brazilian Neutral Semi-purified Glycerin - NSPG, on growing and finishing pigs performance. The chemical composition (as-fed-basis) of the NSPG was: DM = 88.11%; Glycerol = 80.2%; CP = 0.90%; GE = 3,535 kcal/kg; Methanol = 0.01%; NaCl = 5.86% and ash = 6.18%. Eighty growing (BW = 30.31 ± 0.47 to 60.41 ± 0.87 kg) and finishing (BW = 60.41 ± 0.87 to 90.99 ± 0.87 kg) pigs were used in the performance trial. Pigs (one per pen) were allotted in a completely randomized block design, with increasing levels (3.5, 7.0, 10.5, and 14%) of NSPG in a corn-soybean meal diet, resulting in 16 replicates per treatment. Additionally a control diet was formulated containing no glycerin (0%). Experimental diets were formulated according to NRC (1998). The regression analysis indicates no effects ($P \geq 0.05$) of NSPG inclusion on pigs performance and carcass traits (backfat thickness and loin depth) (Table 1). It can be concluded that using up to 14% of NSPG (2,531 kcal of ME/kg) on growing and finishing pig diet is feasible, without impairing performance and carcass traits.

Table 1. Pig performance fed on Brazilian neutral semi-purified glycerin (NSPG)

	NSPG level, %						
Item	0	3.5	7.0	10.5	14.0	Mean	±SE
Growing							
ADFI, kg	1.68	1.73	1.58	1.76	1.64	1.66	±0.028
ADG, kg	0.74	0.73	0.72	0.72	0.72	0.72	±0.035
F:G	2.25	2.25	2.37	2.40	2.32	2.32	±0.044
Finishing							
ADFI, kg	2.05	2.01	2.01	1.98	2.02	2.01	±0.026
ADG, kg	0.74	0.74	0.73	0.73	0.72	0.73	±0.067
Feed/gain ratio	2.78	2.75	2.78	2.75	2.82	2.78	±0.044
BT-P2,[1] mm	12.07	11.87	11.94	11.00	13.00	11.98	±0.334
Loin depth, mm	55.27	52.00	52.75	51.27	50.88	52.43	±0.817

[1] BT-P2 = backfat thickness.

Key Words: carcass traits, co-product, glycerol

M400 Performance and carcass traits of finishing pigs fed on crude glycerin in Brazil.

I. Moreira*[1], P. L. O. Carvalho[1], L. M. Piano[1], J. B. Toledo[1], A. G. Gallego[1,2], and L. M. Peñuela-Sierra[1,3], [1]*Universidade Estadual de Maringá, Maringá, Paraná, Brazil,* [2]*Universidad del Tolima, Ibagué, Tolima, Colombia,* [3]*Universidad Cooperativa de Colombia, Ibagué, Tolima, Colombia.*

This experiment was carried out to investigate 2 types of crude glycerin which were obtained from soybean oil (CGS) and animal fat + soybean oil (CGA) on finishing pigs performance. Chemical composition (as-fed-basis): CGS (DM = 97.46%; Glycerol = 55.95%; CP = 0.06%; GE = 5,247 kcal/kg;Fatty acid = 23.3%; Methanol = 10.96% and Ash = 4.45%); NaCl = 3.52 and CGA (DM = 94.55%; Glycerol = 55.45%; CP = 0.05%; GE = 5,242 kcal/kg; Fatty acid = 21.5%; Methanol = 5.05%; NaCl = 3.01 and Ash = 4.26%). In the performance trial, 63 pigs (BW = 60.35 ± 2.25 to 89.91 ± 5.23 kg) were allotted (one per pen) in a completely randomized design in 2 × 4 factorial scheme, with increasing levels (3, 6, 9, and 12%) of 2 types of crude glycerin (CGS and CGA) in the diet. Additionally a control diet was formulated containing no glycerin (0%). Experimental diets were formulated according to NRC (1998). The regression analysis indicates no effects ($P \geq 0.05$) of CGS and CGA inclusion on pigs performance and carcass traits (Table 1). It can be concluded that using up to 12% of CGS and CGA (4.480 and 4.707 kcal of ME/kg, respectively) on finishing pigs diet is feasible, without impairing performance and carcass traits.

Table 1. Pig performance and carcass traits fed on crude glycerin (CGS and CGA)

	Inclusion of crude glycerin, %								
	CGS					CGA			
	0	3	6	9	12	3	6	9	12
ADFI, kg	2.31	2.28	2.47	2.40	2.50	2.27	2.15	2.58	2.30
ADG, kg	0,81	0.83	0.85	0.81	0.89	0.75	0.76	0.87	0.82
F:G	2.86	2.79	2.98	2.98	2.83	3.02	2.86	3.02	2.85
BT, cm	2.63	2.59	2.69	2.61	2.66	2.50	2.46	2.67	2.34
LM area, cm^2	36.20	36.48	35.39	35.70	37.01	35.62	36.22	32.96	35.79
Carcass lean,%	75.29	75.54	73.08	75.05	74.63	76.46	76.15	71.14	76.22

CGS = made from soybean oil; CGA = made from animal fat + soybean oil; BT = backfat thickness.

Key Words: biodiesel, co-product, glycerol

M401 Determination of optimal dose and time of administration of intravaginal triptorelin gel for synchronizing ovulation in weaned sows.

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The effect of dose and time of administration of intravaginal triptorelin gel (TG) on synchronization of ovulation in weaned sows was evaluated in 3 experiments. Sows were weaned and treated intravaginally with TG. Estrus was detected twice daily and ultrasound performed to assess ovulation at 8-h intervals. Sows were inseminated each day during estrus. In expt. 1, sows (n = 131) received 0 (control), 25, 100, or 200 μg of TG at 96 h after weaning. Wean to estrus and duration of estrus were correlated ($P < 0.0001$) and wean to estrus was shorter and duration was longer in TG ($P < 0.05$) compared with controls. More sows ovulated ($P < 0.05$) by 48 h post-treatment with 200 (91%), 100 (70%) and 25 μg (68%) of TG compared with controls (35%). Farrowing rate and total born did not differ. In expt. 2, sows (n = 126) received 200 μg of TG at 72, 84, or 96 h after weaning or served as untreated controls. Wean to estrus and duration of estrus did not differ from controls but wean to ovulation interval was shortened ($P < 0.05$) by TG at 72 and 84 h compared with 96 h and controls. More sows ovulated by 48 h after treatment ($P < 0.05$) with TG at 96 h (73.1%) compared with 72 (32%) and 84 h (43%) while tending ($P = 0.10$) to differ from controls (50%). Farrowing rate was lower ($P < 0.05$) for sows assigned to TG at 72 and 84 h compared with 96 h and Controls, while liveborn did not differ. In expt.3, sows (n = 113) were assigned to OvuGel (200 μg TG given intravaginally at 96 h after weaning), no treatment (Controls) or placebo (Placebo). Wean to estrus did not differ but duration of estrus tended to be shorter following OvuGel compared with other treatments ($P < 0.10$). More sows ovulated ($P < 0.001$) by 48 h following OvuGel (80%) compared with Control (46%) and Placebo (37%). Farrowing rate and liveborn did not differ among treatments. The results of these studies indicate that 200 μg of TG given intravaginally at 96 h after weaning (OvuGel) synchronizes ovulation and results in fertility similar to controls. This methodology will aid in development of single and timed AI procedures for use in swine.

Key Words: OvuGel, sows, ovulation

M402 The effects of arginine supplementation of weanling pig diets on growth performance and IGF expression.

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Young piglets have a high requirement of arginine for growth and metabolic function, but the sow milk or endogenous synthesis cannot provide enough arginine for maximal growth. Dietary arginine supplementation can improve the immunity of early-weaned piglets and enhance the skeletal muscle synthesis for growth. The insulin-like growth factor (IGF) signaling pathway is an important regulatory factor in regulating fetal and placental growth, proliferation, differentiation, migration and aggregation, and inhibits apoptosis of mammalian cells. However, the role of arginine in altering IGF expression in newly weaned pigs is not clear. This study was conducted to investigate the effect of dietary arginine supplementation in modulation of the IGF system of weanling piglets. Twelve, 21-d-old healthy piglets (Landrace × Yorkshire) with a mean body weight (BW) were assigned randomly to 2 treatments representing diets supplemented with 0.6% L-arginine or 1.23% L-alanine (isonitrogenous control). At 28 d of age, 12 piglets were killed and samples were collected. In arginine group, ADG was increased significantly, and Gain: Feed obviously decreased compared with control group ($P < 0.05$). However, ADFI were not different ($P > 0.05$). The liver, kidney, heart, spleen and lung weight relative to body weight were lower in arginine group than in control, but not significant ($P > 0.05$). The weight of small intestine in arginine group was 33.4% heavier than that in control ($P < 0.001$).Components of IGF signaling pathway (IGF1, IGF1R, IGF2, IGF2R and IGFBP5) mRNA expression were examined in 3 tissues by RT- PCR method. IGF1 was increased in muscle, liver and kidney tissues of arginine group ($P < 0.05$). IGF2 was significantly increased in muscle of arginine group ($P < 0.01$). Both muscle and liver had a higher concentration of IGFBP5 with arginine supplementation ($P < 0.05$). These data suggest an important role of arginine in modulating the IGF signal pathway and the involvement in improving growth performance.

Table 1. Performance of weanling piglets fed diets containing 0.6% l-arginine or 1.23% l-alanine (control)[1]

Item	Control	l-Arginine
Initial weight(g)	5370 ± 53	5230 ± 203
Finish weight (g)	5870 ± 210	6503 ± 208*
ADG (g/d)	70 ± 23	167 ± 31*
ADFI (g/d)	183 ± 12	187 ± 21
Gain: Feed	2.61 ± 0.47	1.07 ± 0.18*

[1]Data are means ± SEM, n = 6.

Key Words: arginine, early-weaned piglets, IGF

M403 Assessment of zero-tannin faba bean and co-fermented corn and wheat DDGS in diets of growing-finishing pigs.

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A grow-finish feed trial was conducted to determine the impact on growth performance and carcass characteristics of feeding diets containing co-fermented corn and wheat DDGS (cwDDGS) from and zero-tannin fava beans (ZTFB) as substitutes for corn DDGS (cDDGS) and some soybean meal. A total of 16 diets were tested containing one of 2 DDGS Sources (cDDGS or cwDDGS) at 2 levels (10% or 30%) of inclusion, with either 0% or 15% ZTFB and with 0 ppm or 62.5 p.m. of yucca extract (YE) in a full factorial design. Feed was delivered 3 times daily to 120 pens of 21 pigs to provide ad libitum feeding by robotic feeders (FeedLogic Corporation; Willmar, MN, USA). Diets, formulated to meet NRC (1998) recommendations, were provided in 5 phases and were not split-sex fed. Pigs were tagged, weighed individually on wk 1, 4, 8, 12, 14 and 16 and were shipped to Maple Leaf Foods (Brandon, MB, Canada) at 123–129 kg BW. Slaughtered pigs were tattooed by pen and data for carcass weight, fat and loin thickness, carcass index, and lean yield was recorded and used to calculate carcass value. There was an interaction effect between DDGS source and DDGS level on days to market (DTM) ($P < 0.05$), standardized feed cost per kg BW gain (SFC/kg) ($P < 0.05$), carcass weight ($P < 0.05$) and a trend for carcass value ($P < 0.10$). The DDGS level only affected responses in cwDDGS and not cDDGS in which case 30% cwDDGS resulted in 3 more DTM, $0.036 lower SFC/kg, 2.15 kg lower carcass weight and $3/hog reduced carcass value. Pigs fed diets containing 15% ZTFB had ($P < 0.05$) lower ADG, and higher FCR, SFC and DTM than pigs fed diets without ZTFB. However, when 62.5ppm of YE was added to the diet, performance was similar to pigs fed diets without ZTFB. These results suggest that ZTFB can be used in grow-finishing swine diets as long as YE is also included and that cwDDGS, when compared with cDDGS, has a negative effect on growth when used at 30% inclusion.

Key Words: zero-tannin faba beans, grow-finish pigs, DDGS

Monday, July 16, 2012

SYMPOSIA AND ORAL SESSIONS
Graduate Student Competition: ASAS Western Section Graduate Student Paper Competition

17 Effect of supplementing activated charcoal on intake of honey mesquite leaves by lambs. P. Mayagoitia*[1], D. Bailey[1], and R. Estell[2], [1]*New Mexico State University, Las Cruces,* [2]*USDA-ARS Jornada Experimental Range, Las Cruces, NM.*

A study was conducted to determine if intake of honey mesquite (*Prosopis glandulosa* Torr.) leaves by sheep could be increased by supplementing activated charcoal at 0.0, 0.33, 0.67 or 1.00 g / kg of body weight. Twenty wether lambs (36.6 ± 0.6 kg) were randomly assigned to the 4 treatment levels. Lambs were fed low-quality Sudan-grass hay at 2% of BW plus 80 g/d of molasses for 7 d, and Sudan-grass hay at 1.9% of BW plus 80 g/d of molasses mixed with the assigned level of activated charcoal for 16 d (d 8 to 23). On d 8 to 23, lambs were also given ad libitum access to honey mesquite leaves that had been previously harvested, frozen, and thawed immediately before feeding. Repeated measures analyses were used to determine if level of activated charcoal fed to lambs affected daily intake of mesquite leaves. No differences ($P = 0.52$) in intake of mesquite leaves were detected. Mean intake of mesquite leaves was 20.7 ± 3.7, 23.8 ± 3.8, 20.2 ± 3.7, and 27.3 ± 3.7 g/d for 0.0, 0.33, 0.67 and 1.0 treatment levels, respectively. Consumption of mesquite leaves varied greatly among lambs, ranging from 1.4 to 7.4% of their diet during the last 8 d of the study. No differences in hay intake ($P = 0.23$) or lamb weight gain ($P = 0.58$) were detected among supplemental charcoal treatments. Future studies examining the consumption of honey mesquite leaves by sheep should consider the potential variability in intake among individual animals.

Key Words: sheep, rangeland, secondary compounds

18 Pre-breeding β-hydroxybutyrate concentration influences conception date in young postpartum range beef cows. J. T. Mulliniks*[1], M. E. Kemp[1], R. L. Endecott[2], S. H. Cox[1], E. J. Scholljegerdes[1], T. W. Geary[3], and M. K. Petersen[3], [1]*New Mexico State University, Las Cruces,* [2]*Montana State University, Miles City,* [3]*USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.*

Cows in negative energy balance after calving often have reduced reproductive performance, which is suggested to be mediated by metabolic signals. The objective of this 3-yr study was to determine the association of serum metabolites, resumption of estrus, milk production, cow BW change, BCS, and calf performance on conception date in 2- and 3-yr-old beef cows (n = 131) grazing native range at the Corona Range and Livestock Research Center. Cows were classified by conception date in a 60-d breeding season as early conception (EC; conceived in the first 15 d of breeding) or late conception (LC; conceived during the last 45 d of breeding). Date of conception was calculated from the subsequent calving date. Beginning on d 30 postpartum, blood samples were collected twice/wk for serum metabolite analysis and progesterone analysis to estimate days to resumption of estrous cycles. As a chute-side measure of nutrient status and glucose sufficiency, whole-blood β-hydroxybutyrate (BHB) concentrations were measured 2 wk before breeding. A random subsample of cows from groups was mechanically milked approximately 57 d postpartum. Whole-blood BHB and serum glucose concentrations were lower ($P \leq 0.04$) in EC cows than LC cows. Serum insulin concentrations were greater ($P = 0.03$) in EC cows relative to LC cows. Serum NEFA and urea N concentrations were not different ($P \geq 0.32$) between EC and LC cows. Initial calving date during the year of the study was not different ($P = 0.19$) between EC and LC cows. The postpartum anestrous interval was shorter ($P = 0.04$) in EC cows, indicating that the earlier conception was due partially to an earlier return to cyclicity. Milk production was not different ($P = 0.28$) between EC and LC cows. Cow BW and BCS and were not different ($P \geq 0.12$) at any period between EC and LC cows. Calf weaning (205-d) BW was not different ($P = 0.67$) between EC and LC cows. This study indicates that blood BHB concentrations before breeding may provide a sensitive indicator of energy status for rebreeding success in young beef cows as measured by interval to conception.

Key Words: beef cows, conception date, β-hydroxybutyrate

19 Effects of algal meal supplementation to finishing wethers on performance and carcass characteristics. M. G. Dib,* T. E. Engle, H. Han, I. N. Roman-Muniz, and S. L. Archibeque, *Colorado State University, Fort Collins.*

Crossbred wethers (n = 40; initial BW = 45.3 kg + 3.5) were used in a randomized complete block design to evaluate the effects of titrated concentrations of algal meal as a protein supplement on live performance, live health status and carcass characteristics. Wethers were blocked by time and randomly assigned to one of the 5 treatments. Treatments included (1) soybean meal and rice meal as protein supplementation sources (CON); (2) 5% of algae meal on a DM basis as a protein replacement (5%A); (3) 10% of algae meal on a DM basis as a protein replacement (10%A); (4) 15% of algae meal on a DM basis as a protein replacement (15%A); and (5) 20% of algae meal on a DM as a protein replacement (20%A). All diets were isocaloric and isoproteic. All wethers were fed a high concentrate finishing diet once daily in individual stalls. Wethers were individually weighed on d −1, 0, 21, and 28. On d 21, wethers were transported to metabolic crates for determination of nutrient digestibility and retention. On d 28, animals were transported to a commercial abattoir for harvest. Initial (45.4 kg) and final (44.5 kg) BW, ADG for feedlot period (0.24 kg/d), ADG for metabolism period (−0.84 kg/d), DMI (1.38 kg/d), and G:F (0.187) were similar ($P > 0.05$) across treatments. Furthermore, hot carcass weight, subcutaneous adipose depth, Longissimus muscle area, calculated YG, marbling score, dressing percentage, muscle percentage, body wall thickness, Leg score, Leg circumference, flank streaking, quality grade, carcass conformation and carcass length were also similar ($P > 0.05$) across treatments. Research results suggest that feeding up to 20% of algae co-product meal as a replacement protein source to finishing wethers is feasible with limited impact on performance and carcass characteristics as compared with the standard protein sources that have been used by the industry. Further research may be necessary to determine the response of different levels of supplementation of algal meal for sheep, effects on animals in a different physiological stage or effects on other ruminants in the finishing diet on performance and carcass merit.

Key Words: algae, protein, co-product

20 Influence of the level of dried distillers grains with solubles on feedlot performance, carcass characteristics, serum testosterone concentrations, and semen quality of growing rams. M. L. Van Emon*[1,2], K. A. Vonnahme[2], P. T. Berg[2], R. R. Redden[2], M. M. Thompson[1], J. D. Kirsch[2], and C. S. Schauer[1], *[1]Hettinger Research Extension Center, North Dakota State University, Hettinger, [2]Department of Animal Sciences, North Dakota State University, Fargo.*

The objective of this study was to evaluate the effects of dried distillers grains with solubles (DDGS) on ram lamb feedlot performance, carcass characteristics, serum testosterone concentration, and semen quality. One hundred 20 ram lambs (40.4 ± 9.1 kg; western whiteface × Suffolk) were used in a completely randomized design to determine the effects of DDGS on feedlot performance and carcass characteristics. Rams were allotted into one of 4 dietary treatments (n = 4 pens/treatment; 10 rams/pen): 1) 0DDGS: 85% corn and 15% commercial market lamb pellet; 2) 15DDGS: 15% DDGS substituted for corn on a % DM basis, 70% corn, and 15% commercial market lamb pellet; and 3) 30DDGS: 30% DDGS substituted for corn on a % DM basis, 55% corn, and 15% commercial market lamb pellet. Rams were weighed on consecutive days at the beginning (d 0, 1) and end (d 96, 97 and d 116, 117) of the trial. Scrotal circumference was measured on all rams on d 84, 96, and 116. Semen and blood samples were collected on a subset of 48 rams (4 rams/pen; 16 rams/treatment; n = 4). Blood samples were collected every 14 d throughout the study. Semen samples were collected on d 84, 98, and 112. Rams were fed to market weight, shipped to a commercial abattoir, and harvested for carcass data collection. Initial BW, final BW, change in scrotal circumference, days on feed, carcass characteristics, serum testosterone concentrations, and semen score were not different ($P \geq 0.11$) due to dietary treatment. However, DMI increased linearly ($P < 0.001$) as DDGS increased in the ration, resulting in a linear increase ($P = 0.02$) in ADG. Additionally, sperm count decreased linearly ($P = 0.05$) as DDGS concentration increased in the ration. Increasing DDGS in the diet did not have a negative effect on ram feedlot performance or carcass characteristics; however, in this preliminary study, sperm production may have been negatively affected, necessitating the need for additional research on the effect of distillers grains on ram development.

Key Words: dried distillers grains with solubles, rams, semen quality

21 Effect of weaning method on welfare and performance of beef calves during receiving. E. A. Bailey*[1], J. R. Jaeger[2], J. W. Waggoner[2], L. W. Murray[3], G. W. Preedy[1], L. A. Pacheco[1], D. L. Davis[1], and K. C. Olson[1], *[1]Department of Animal Sciences & Industry, Kansas State University, Manhattan, [2]Western Kansas Agricultural Research Center, Kansas State University, Hays, [3]Department of Statistics, Kansas State University, Manhattan.*

We evaluated receiving performance and welfare of beef calves that had been subject previously to 1 of 3 ranch-of-origin weaning methods 28 d in duration: drylot weaning + dam separation (D), pasture weaning + fence-line contact with dams (PF), and pasture weaning + fence-line contact with dams + supplemental feed delivered in a bunk (P+S). Calves assigned to D were fed a diet designed to promote a 1 kg ADG at a DMI of 2.5% of BW (17.7% CP, 0.92 Mcal NE_g/kg); PF calves had access to native forage only (6.8% CP, 43% ADF); and P+S calves had access to native forage and received a ration of the diet fed to D at a rate of 1% of BW 3 × weekly. Weaning-phase ADG tended ($P = 0.10$) to be greater for D than for PF or P+S; however, incidence of undifferentiated fever during weaning was similar ($P = 0.22$) between treatments. At the end of the weaning phase, all calves were transported 4 h to a feedlot, were penned according to treatment (n = 8 pens/treatment), and were fed a receiving diet (14.9% CP, 0.93 Mcal NE_g/kg) ad libitum. Feed intake, growth, and health were monitored during a 60-d receiving period. Observations of calf behavior were made 3 × daily for the first 7-d of receiving; the proportion of calves in each pen that were eating, resting, or pacing was recorded by 2 trained observers and reported as a pen average. During the first 30 d of receiving, ADG was less ($P < 0.01$) for PF than for D and P+S; however, ADG of D was greater ($P < 0.01$) than that of PF and P+S during the entire 60-d receiving phase. Diet DMI and G:F were greater ($P \leq 0.01$) also for D than for PF or P+S during receiving. Fewer (treatment × day - $P < 0.01$) PF calves were observed at the bunk during the first 4 d of receiving than D or P+S calves; however, the proportions of calves observed at the bunk were similar (treatment × day - $P = 0.64$) between treatments by d 6. Incidence of undifferentiated fever was similar ($P = 0.50$) between treatments during receiving. We interpreted these data to suggest that animal performance and welfare during the receiving period were not improved by pasture weaning + fence-line contact with dams compared with drylot weaning + dam separation. Best-management practices for animal welfare may involve initiating diet transitions from forage to grain at the ranch of origin.

Key Words: animal welfare, preconditioning, weaning

22 Effects of timing of vaccination (day 0 versus day 14 of a receiving period) with a modified-live respiratory viral vaccine on performance, feed intake and febrile response of beef heifers. K. P. Sharon*[1], G. C. Duff[1], M. M. Harbac[1], J. A. Paterson[1], J. A. Carroll[2], and J. W. Dailey[2], *[1]Department of Animal and Range Sciences, Montana State University, Bozeman, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective of this study was to evaluate the effects of timing of administration of a modified-live respiratory viral vaccine (IBR-PI_3-BRSV-BVD) on d 0 or on d 14 of a receiving period on performance, feed intake and febrile response in beef heifers. Our hypothesis was vaccine timing will alter febrile response and feed intake of feeder cattle. Thirty-six heifers (Angus and Angus crosses; initial BW = 265 ± 20 kg) were ranked by BW and assigned to treatment pens (9 pens total) in a completely randomized design. Treatments (3 pens/treatment with 4 heifers/pen) included no vaccine (CON), vaccination on d 0 (DO), and a delayed vaccination on d 14 (D14) of the receiving period. Heifers were fed in 6 × 12 m pens with GrowSafe feeding systems. Daily intakes were recorded and BW measured on d −1, 0, 14, 27, and 28. Temperature probes were attached to controlled intrauterine drug release devices (CIDR; active compound was removed) and vaginal temperatures were recorded every 5 min for the experiment; vaginal temperatures were then averaged for every h before data analysis. All data were analyzed using pen as the experimental unit. No differences ($P > 0.10$) among treatments were observed for initial BW, final BW, ADG for d 0 to end, or overall G:F. A treatment x d interaction ($P < 0.05$) was observed for feed intake. Daily intake was decreased for D14 versus D0 on d 14 ($P < 0.01$) and 15 ($P < 0.10$) and decreased ($P < 0.05$) on d 15 for the average of vaccinated calves versus CON. Eating rate (grams consumed/eating duration) was decreased ($P < 0.05$) on d 14 for D14 versus D0. A treatment x d interaction ($P < 0.01$) was observed for vaginal temperature. Vaginal temperature was increased ($P < 0.10$) on d 1 for D0 versus D14 heifers and increased for D14 versus D0 on d 14 ($P < 0.01$), 15 ($P < 0.05$) and 16 ($P < 0.05$). Our results suggest that time of administration of a modified-live respiratory viral vaccine can alter feed intake and vaginal temperature in feeder heifers.

Key Words: beef heifers, respiratory vaccines, feed intake

23 Assessment of chestnut tannin extract supplementation on animal performance and ruminal fermentation profiles in feedlot finishing diets. J. M. Sieg*[1], J.-S. Eun[1], D. R. ZoBell[1], and B. R. Min[2], [1]*Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan,* [2]*Department of Agricultural and Environmental Sciences, Tuskegee University, Tuskegee, AL.*

The objective of this study was to assess animal performance and ruminal fermentation when feedlot finishing beef steers were fed with supplementation of chestnut tannin extract (CTE). Eight Charolais-cross steers (average BW = 495 kg) were used in a duplicated 4 × 4 Latin square experiment with a 2 × 2 factorial arrangement of treatments. The 4 animals in one of 2 squares were surgically fitted with a ruminal cannula. Within squares, animals were randomly assigned to a sequence of 4 diets during each of the 4 21-d periods (14 d of treatment adaptation and 7 d of data collection and sampling); CTE supplementation (without vs. with CTE) and ionophore (ION; monensin administered as a Rumensin) supplementation (without vs. with ION). Animals were fed a finishing diet consisting of 8.0% alfalfa hay, 7.0% corn silage, 77.0% rolled barley grain, 3.0% CTE or wheat straw, and 5.0% feedlot supplement without or with ION. Intake of DM/d was not affected by CTE supplementation or ION, whereas DMI/kg BW tended to increase ($P = 0.08$) by CTE supplementation. Supplementation of CTE increased ADG ($P = 0.01$), but ION did not influence ADG. Total VFA concentration did not differ in response to supplementing CTE or ION. Additionally, molar proportions of acetate and propionate were similar between dietary treatments. Molar proportion of butyrate tended to increase ($P = 0.10$) by CTE supplementation, but not by ION. Mean ruminal pH measured for 48 h averaged 6.39 across dietary treatments, but was not influenced by dietary treatments. In contrast, daily episodes with ruminal pH <5.80 tended to increase ($P = 0.10$) by CTE supplementation, while ION increased the daily episodes only with CTE supplementation, resulting in an interaction between CTE and ION ($P = 0.03$). Supplementation of CTE had minor impacts on ruminal fermentation, except that CTE affected total buffering capacity of finishing beef steers. Further research is needed to investigate positive effects on animal performance by CTE supplementation in feedlot finishing diets.

Key Words: chestnut tannin extract, beef finishing steers, ruminal fermentation profiles

24 Evaluation of the incidence, causes, and potential solutions for the occurrence of disabled or non-ambulatory cattle within the California beef and dairy industries. M. V. Sis*[1], J. K. Ahola[1], H. A. Foster[2], D. L. VanOverbeke[3], and D. A. Daley[4], [1]*Colorado State University, Fort Collins,* [2]*California Beef Council, Sacramento,* [3]*Oklahoma State University, Stillwater,* [4]*California State University-Chico, Chico.*

A survey was conducted to evaluate how California beef and dairy operations sell market cows and bulls and identify key contributors to these animals becoming disabled or non-ambulatory (NA). Surveys were mailed to 9,778 California beef and dairy producers using the California Beef Council mailing list. Twenty-nine questions were included to evaluate beef and dairy producer demographics, the incidence of NA cattle on-farm or on-ranch, management and marketing practices utilized for market cows and bulls, and reasons animals become NA. Response rate for the mailed portion of the survey was 3.9%. Completed surveys were received from 446 producers (n = 403 beef, n = 43 dairy). The mean age (±SD) for survey respondents was 62 ± 12.3 yr for beef producers and 55 ± 13.1 yr for dairy producers. Survey responses clearly indicated that most beef (77.5%) and dairy producers (62.5%) market their animals at a livestock auction market, which was more ($P < 0.05$) than any other option. The direct sale of market cows and bulls to a beef packer was ($P < 0.05$) the next most common outlet among both beef (11.7%) and dairy (22.9%) respondents. Rates of culling, euthanasia, and death loss among cows were 10.8, 1.2, and 1.3%, respectively, for beef respondents, and 33.1, 2.1, and 3.3%, respectively, for dairy respondents. However, 35.6% of beef and 95.2% of dairy respondents indicated they had at least 1 non-ambulatory cow in the previous 12 mo. The majority ($P < 0.05$) of beef and dairy survey respondents indicated they would consider on-farm euthanasia (92.1 and 88.1%, respectively), and gunshot was identified as the primary method ($P < 0.05$) of euthanasia among beef (76.2%) and dairy (78.0%) producers. Dystocia was reported to be the primary cause ($P < 0.05$) of NA status in cows among beef (46.5%) and dairy (79.1%) respondents. These data suggest that management of potential causes of NA status continues to be a challenge among beef and dairy cattle producers and solutions to reduce NA incidence are needed.

Key Words: beef cattle, dairy cattle, non-ambulatory

25 Effect of two, four, and six-hour intervals between two prostaglandin $F_{2\alpha}$ injections administered with five-day CO-Synch + CIDR protocol on pregnancy rate in beef cows. C. J. Berrett*[1], J. L. Seabrook[1], G. E. Seidel Jr[1], J. C. Whittier[1], J. K. Ahola[1], R. K. Peel[1], and A. V. Grove[2], [1]*Colorado State University, Fort Collins,* [2]*AG Research LLC, White Sulphur Springs, MT.*

At the time this study was conducted, it was recommended when using the 5-d Co-Synch protocol that two 25 mg PG injections at 12-h intervals be given because it was assumed that an immature 5-d CL would not be successfully regressed by a single 25 mg PG injection. Therefore, the objective of this study was to compare fixed-time AI (TAI) pregnancy rates resulting from intervals of 2-, 4-, or 6-h between two 25 mg prostaglandin (PG) $F_{2\alpha}$ injections administered following CIDR removal in the 5-d CO-Synch + controlled internal drug-release device (CIDR) estrous synchronization protocol. Angus and Angus-crossbred cows (n = 901) maintained on native pasture at 3 locations were randomly assigned to one of 3 experimental treatments after blocking for BCS and postpartum interval (PPI). All cows received gonadotropin-releasing hormone (GnRH) and CIDR on d −5, PG with CIDR removal and 25 mg PG on d 0, and GnRH with TAI 72 h after the initial PG injection. Cows also received a second 25 mg injection of PG either 2-, 4- or 6-h after the first injection of PG. Timed AI pregnancy rates were determined by ultrasonography 40 ± 2 d following TAI. Fixed-time AI pregnancy rate was lower ($P \leq 0.05$) in cows receiving 2 PG injections separated by 2- (50.6%) and 4-h (51.4%) intervals, compared with cows receiving 2 PG injections separated by a 6-h (59.7%). Reducing the interval between PG injections from 6 to 2 h resulted in a 9-percentage point (15%) reduction in TAI pregnancy rates for cows synchronized with a 5-d CO-Synch + CIDR protocol. Based on these data the interval between PG injections should be a minimum of 6-h to maintain acceptable pregnancy rates in beef cows when using the 5-d CO Synch + CIDR protocol.

Key Words: beef cow, CIDR, fixed-time AI

26 Effects of pain mitigation and method of castration on behavior and feedlot performance in cull beef bulls. P. E. Repenning*[1], J. K. Ahola[1], R. J. Callan[2], J. T. French[1], R. L. Giles[1], R. K. Peel[1], J. C. Whittier[1], J. T. Fox[3], and T. E. Engle[1], [1]*Department of Animal Sciences, Colorado State University, Fort Collins,* [2]*Department of Clinical Sciences, Colorado State University, Fort Collins,* [3]*JBS Five Rivers Cattle Feeding LLC, Greeley, CO.*

The objectives of this study were to evaluate the effects of castration method (band vs. surgical) and use of analgesia on behavior and feedlot performance in cull bulls. Angus, Hereford, and Angus crossbred bulls (n = 20; initial BW 384 ± 59.3 kg; 336 ± 20.0 d old) were housed in feedlot pens equipped with the ability to measure individual daily feed intake. A balanced randomized block design using a 2 × 2 factorial arrangement of treatments was utilized. Factors included: 1) castration method, and 2) analgesia presence. A multimodal analgesia protocol (MMA) was used and consisted of subcutaneous ketamine-stun containing butorphanol (0.01 mg/kg), xylazine (0.02 mg/kg), ketamine (0.04 mg/kg), and a local 2% lidocaine hydrochloride anesthetic block of the spermatic cords (10 mL per cord) and scrotum (10 mL) on d 0. Flunixin meglumine (1.2 mg/kg) intravenously (iv) on d 0, 1, 2 and 3. Cattle were stratified to treatments based on breed, BW, age and a temperament score. Treatments included: 1) band castration without analgesia (BAND), 2) band castration with analgesia (BAND-MMA), 3) surgical castration without analgesia (SURG), and 4) surgical castration with analgesia (SURG-MMA). Chute exit velocity (EV) and time in chute (TIC) were collected on d −9, 0, 1, 2 and 13. Willingness-to-enter-chute (WTE) score, rectal temperature (TEMP), heart rate (HR), and respiration (RESP) were collected on d 0, 1, 2, 3 and 13. Cattle were weighed on d −9 and 13 while feeding behaviors were collected continuously for 57 d pre-castration and 28 d post-castration. There was a tendency ($P < 0.09$) for ADG to be greater in cattle receiving analgesia. Both SURG treatments exhibited greater ($P < 0.001$) TEMP on d 1 and on d 2 ($P < 0.05$) when compared with BAND treatments. Mean DMI was greater ($P = 0.02$) in MMA treatments when compared with non-medicated treatments. The SURG treatment, when compared with SURG-MMA and BAND, exhibiting greater ($P = 0.04$, $P = 0.04$, respectively) meal size. Results suggest that pain mitigation reduces the impact of castration on ADG and DMI.

Key Words: bulls, castration, ketamine-stun

27 Fetal and maternal induction of angiogenic factors during early pregnancy.

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Early pregnancy, when most embryonic losses occur, is a critical period in which vital placental vascularization is established. Adequate vascular development supports embryonic survival and subsequent fetal growth. Vascular endothelial growth factor (VEGF) is the most potent inducer of angiogenesis, and factors regulating VEGF may ultimately affect vascularization. Activation of chemokine receptor 4 (CXCR4) by CXCL12 increases VEGF synthesis and secretion, which in turn stimulates CXCL12 and CXCR4 production. This synergistic regulation may drive placental vascularization. Our laboratory reported elevated CXCR4 in endometrium during early pregnancy in sheep, but the relationship between the CXCL12/CXCR4 signaling pathway and angiogenic factors such as VEGF, Fibroblast growth factor (FGF2), and Angiopoietin 1 (ANG1) is lacking in ruminants. We hypothesized CXCL12, CXCR4, and select angiogenic factors and their receptors would increase in placental tissue during early pregnancy. To test this hypothesis, caruncle and fetal extraembryonic membrane tissues were collected on d 20, 25 and 30 of pregnancy, with d10 of the estrous cycle as a control. Real time PCR was used to assess relative mRNA levels. Expression levels were normalized by standard methods, and subjected to ANOVA with Newman-Keuls post hoc test to determine significant differences ($P < 0.05$). In caruncles, CXCL12 and CXCR4 increased on d20 in pregnant ewes. FGF2 increased during early to mid-placentation in caruncle tissue. In fetal extraembryonic membranes, CXCL12, CXCR4, ANG1 and VEGF were induced with advancing pregnancy, whereas FGF2 and VEGFR2 peaked on d25. The increase of angiogenic factors in fetal placenta during implantation and placentation highlights the concept that the fetus regulates its vascularization in synergy with the maternal placenta. The relationship between VEGF and CXCL12/CXCR4 underscores the potential role for this chemokine system in placentation. These results provide strong support for enhanced signaling between chemokines and angiogenic factors within the fetal-maternal interface.

Key Words: chemokine, vascularization, pregnancy

28 Effect of swath grazing on forage intake and wastage by ewes.

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Sixty non-pregnant and nonlactating mature white faced ewes (Targhee 65.4 ± 5.84 kg BW in 2010 and Rambouillet 61.9 ± 6.28 kg BW in 2011) were used in a 2 yr study to evaluate intake, wastage, and nutrient composition of a pea/barley forage fed either as baled hay in confinement (CONFINEMENT) or swathed and left to graze (GRAZE). Forage intake was estimated using IVDMD and chromic oxide as a marker for estimating fecal output. Forage wastage was estimated by sampling and weighing the initial swath, standing, and baled forage, and weighing the forage again after a 7-d collection period, and subtracting the estimated forage DMI. Baled, swathed, and any standing forage was sampled once per month from the date the forage was swathed (early August) until October. Samples were analyzed for DM, OM, CP, NDF, ADF, and in situ dry matter digestibility (ISDMD). There was no main effect of treatment or year ($P \geq 0.23$) for DMI ($kg \cdot ewe^{-1} \cdot d^{-1}$); however, there was a treatment x year interaction ($P < 0.04$). In 2010, DMI ($kg \cdot ewe^{-1} \cdot d^{-1}$) was greater ($P < 0.10$) by CONFINEMENT compared with GRAZE (2.4 vs 1.7 kg/d). Forage wasted as a percent of beginning available forage did not differ ($P \geq 0.28$) between GRAZE and CONFINEMENT within both years. In 2010, OM was greatest ($P < 0.10$) in baled forage, intermediate in standing forage, and lowest in swathed forage. In 2011, OM did not differ ($P = 0.99$) for baled and swathed forage, but both were greater ($P < 0.10$) compared with standing forage. In 2010, CP was greatest ($P < 0.10$) in swathed forage (12.0%), intermediate in baled forage (10.3%), and lowest in standing forage (8.2%). In 2011, CP was greater ($P \leq 0.05$) in baled forage compared with swathed and standing forage. In both years, NDF and ADF were lower ($P < 0.10$) in baled forage compared with swathed and standing forage. In 2010, ISDMD was greater ($P < 0.10$) for swathed forage compared with baled forage. In 2011, percent ISDMD was greater ($P < 0.10$) in baled forage compared with swathed or standing forage. Forage intake and percent wastage were not affected by treatment, but forage quality was lower in the GRAZE treatment compared with the CONFINEMENT treatment.

Key Words: confinement, ewes, swath

29 Maternal diet restriction in beef cows alters fetal cardiovascular hemodynamics and fetal and placental development during early pregnancy.

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Objectives were to examine the effects of maternal nutrient restriction on fetal cardiovascular hemodynamics, and fetal and placental development during early gestation. On d 30 of pregnancy, multiparous beef cows were randomly assigned to dietary treatments of 100% (CON; n = 6) or 60% of NRC recomendations (RES; n = 6). Cows were individually-fed once daily using Calan gates at 1000 h. On d 85 of gestation, fetal blood flow was determined via Doppler ultrasonography followed by cow slaughter. Ultrasound measurements included fetal heart rate (HR), umbilical blood flow (uBF), pulsatility index (PI), and resistance index (RI). Fetal PI and RI were not affected ($P \geq 0.19$) by maternal restriction, while fetal HR was decreased ($P = 0.006$) in RES vs. CON fetuses. Umbilical BF, uBF relative to placental weight, and uBF relative to cotyledon weight were not affected by maternal nutrient restriction, while uBF relative to fetal weight was decreased ($P = 0.03$) in RES vs. CON. Fetal weight tended to be greater ($P = 0.07$) in RES vs. CON fetuses. Total placentome weight was greater ($P = 0.002$) in RES vs. CON cows; however, cotyledon weight, caruncle weight, fetal membranes, and chorioallantoic/amniotic fluid volume were not different ($P > 0.27$) between treatments. Placental efficiency (fetal weight: placentome weight ratio) tended to be greater ($P = 0.10$) in CON vs. RES cows. Heart girth and ponderal index were increased ($P = 0.004$) in RES vs. CON fetuses, while biparietal distance and crown rump length were not different ($P \geq 0.28$) between treatments. Maternal nutrient restriction during early gestation increased fetal growth and placentome weight, while uBF was decreased relative to fetal weight. Therefore, it would appear that maternal nutrient restriction leads to compensatory fetal and placental development during early gestation.

Key Words: maternal restriction, pregnancy, umbilical blood flow

30 Serum exosome profile as related to early pregnancy status in the mare.

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During early pregnancy the conceptus and mare must communicate to establish and maintain pregnancy. This is most pronounced between d 12 and 16 post-ovulation. The mechanism behind successful establishment of pregnancy in the mare is unknown. Recently, cell-secreted vesicles, called exosomes, were detected in high amounts in serum of pregnant women. Exosomes are 50–100 nm vesicles containing bioactive materials such as mRNA, miRNA, and protein that can mediate immune-responses through membrane protein interaction and delivery of products into cells. Exosomes have been described in body fluids, including urine, milk, and serum. We hypothesized that exosomes are present in mare serum and that their amount differs with pregnancy status. To test this, we determined the presence and relative amount of exosomes in serum of pregnant and non-pregnant mares. Serum samples were obtained from mares in a crossover design, with each mare serving as a pregnant treatment and non-mated control (n = 3/d). Blood samples were obtained on d 12, 14, 16, and 18 post-ovulation. Serum was removed and stored at −80°C. Exosome isolation, for flow-cytometry and transmission electron microscopy (TEM), was performed using ExoQuick (System Biosciences, Inc.), a precipitation solution designed to isolate exosomes. Samples were analyzed using flow cytometry with 100 nm sized beads as a size control and a counting bead standard for relative amount determination. Flow cytometry analysis revealed exosomes in both pregnant and non-pregnant mares and the presence of 2 distinct size populations, one of exosomes smaller (<100 nm) than previously described, which were more abundant in mare serum from d 12 of pregnancy, and the second of the expected 100 nm size at each day examined. TEM analysis validated the results from the flow cytometry as each population was characterized visually. Along with the 100 nm and slightly smaller sized vesicles, TEM also revealed the presence of vesicles slightly larger than 100 nm, with small amounts of vesicles ~200 nm in size, indicating the presence of microvesicles as well. We conclude that exosomes are present in mare serum and further characterization of such populations can provide clues about the intercellular mode of communication in early pregnancy.

Key Words: mare, pregnancy, exosome

31 Effects of natural service and artificial insemination breeding systems on pregnancy rates and days to conception.

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Four hundred 80 crossbred beef cows and 86 crossbred beef heifers were used to compare the effects of 2 breeding systems on pregnancy rates and days to conception. Cattle were stratified by age and BCS, and assigned randomly to 1 of 2 treatments: 1) Females exposed to natural service bulls for the duration of the breeding season (NS; n = 284), or 2) females exposed to estrous synchronization and a fixed-timed AI (d 0; 7-d Co-Synch + CIDR), followed by exposure to natural service bulls for the duration of the breeding season (AI, n = 282). Bulls were introduced on d 1 and both treatments were managed as a cohort in the same pastures. Blood samples were collected on d −20 and −10 to determine cyclic status. On d 49 and again at least 40 d after bull removal from pastures, transrectal ultrasonography was used to determine pregnancy status and fetal age. Overall, 42.8% of cattle were cyclic at the beginning of the breeding season. Treatment × cyclic status interactions ($P < 0.01$) were present for the proportion of cows detected pregnant on d 49, the proportion of cows pregnant at the end of the breeding season, and days from the beginning of the breeding season to conception. A greater proportion ($P < 0.05$) of cyclic cattle in the AI treatment (88%, 104 of 118) had a viable fetus detected on d 49 of the breeding season compared with cyclic cattle in the NS treatment (74%, 88 of 119) and non-cyclic cattle in the AI (75%, 122 of 163) and NS treatments (77%, 120 of 156). A greater percentage ($P < 0.05$) of cyclic cattle in the AI treatment (94%, 111 of 118) were pregnant at the end of the breeding season compared with non-cyclic cattle in the AI treatment (84%, 136 of 162) whereas cyclic (88%, 105 of 119) and non-cyclic (89%, 140 of 157) cattle in the NS treatment were intermediate. Both cyclic (11.6 ± 1.4 d) and non-cyclic (14.5 ± 1.4 d) cattle in the AI treatment became pregnant earlier in the breeding season ($P < 0.05$) compared with cyclic (19.9 ± 1.4 d) and non-cyclic (17.9 ± 1.4 d) cattle in the NS treatment. Breeding systems for beef cattle that incorporated AI altered pregnancy rates and days to conception compared with natural service breeding systems.

Key Words: artificial insemination, estrous synchronization, natural service

32 Evaluation of the ability of grain distillers dried yeast to replace fish meal in the diets of juvenile rainbow trout *Oncorhynchus mykiss*.

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Grain distillers dried yeast (GDDY) is a single-cell protein obtained as a co-product during the production of fuel ethanol and may have potential as an alternative protein source for rainbow trout. The objective of the current study was to determine if GDDY could replace fish meal (FM) without negatively affecting growth performance and proximate composition of juvenile rainbow trout. A 2-phase approach was employed where a digestibility trial was first conducted to determine GDDY apparent digestibility coefficients (ADCs) for protein, lipid, energy, DM, and apparent availability coefficients (AACs) for P and amino acids. The second phase was to conduct a feeding trial where a control diet (42% digestible protein and 20% crude lipid with 25% FM) was compared with diets where FM digestible protein was replaced by GDDY at 7 different levels (25, 37.5, 50, 62.5, 75, 87.5, and 100%). All diets were formulated to provide equal amounts of available lysine, methionine, threonine and total P. Diets were fed twice daily to rainbow trout (initial weight 22.1g + 0.26) to apparent satiation in a 15°C recirculating system. There were 4 replicate tanks per diet (30 fish/tank) and diets were fed for 9 weeks. Bulk tank weights and feed intake (FI) were determined every 3 weeks. At conclusion of the feeding trial, 3 fish per tank were sampled for condition indices and proximate composition analyses. Grain distillers dried yeast ADCs for protein, DM, lipid, energy and AAC for P were quantified at 98, 65, 100, 70 and 81%, respectively. Feeding trial results showed that fish performance was not significantly different from the control diet at the 25% and 37.5% replacement levels. However, reduced growth ($P < 0.001$) and poorer feed conversion ($P < 0.001$) were observed when GDDY replaced more than 37.5% of dietary FM (11.2% GDDY inclusion). Feed intake, proximate composition and protein retention efficiency were not significantly affected by GDDY inclusion level. Apparent digestibility coefficients suggested that GDDY nutrients were highly digestible and FI measurements suggest no palatability issues; however, growth was reduced after extended feeding at higher inclusion levels.

Key Words: grain distillers dried yeast, alternative protein, rainbow trout

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

Two single nucleotide polymorphism (SNP) genotyping arrays, the Illumina High-Density Bovine BeadChip Array (BovineHD; 777,962 SNP) and the Affymetrix Axiom Genome-Wide BOS 1 Array (BOS1; 648,874 SNP), are available for bovine genomics analyses, such as quantitative trait loci (QTL) fine mapping and genomic selection. These genotyping arrays are of interest to researchers for their high marker density relative to other genotyping platforms. Differences in allele frequency distribution between arrays contributes to their efficacy for association studies as QTL may have rare alleles (low minor allele frequency, MAF), limiting the extent of linkage disequilibrium (LD) possible with intermediate MAF SNP. To evaluate MAF distribution differences between arrays in Holstein (HO) and Jersey (JE) breeds, we genotyped 16 DNA samples (10 HO, 6 JE) from UC Davis cows and their sires with both BovineHD and BOS1, and MAF distribution was determined within breed. A greater proportion of SNP had MAF equal to zero in BOS1 relative to BovineHD (HO: BOS1 45% vs. BovineHD 28%; JE: BOS1 55% vs. BovineHD 39%), which given the fewer number of total SNP in BOS1 resulted in fewer BOS1 SNP for all MAF. However, of polymorphic SNP, low to intermediate MAF SNP (MAF ≤ 0.20) were proportionally more highly represented in BOS1 (HO 45%; JE 42%) relative to BovineHD (HO 38%; JE 39%). An important issue in genotyping arrays is marker redundancy. SNP in complete LD have collinear effects, reducing the accuracy and stability of marker effect estimates when jointly analyzed. To evaluate if removal of redundant SNP altered the MAF distribution in BovineHD and BOS1, LD pruning was performed using SVS7. Using the LD threshold $r^2 \geq 0.99$, a greater proportion of polymorphic SNP were removed from BovineHD relative to BOS1 (HO: BovineHD 75% vs. BOS1 57%; JE: BovineHD 86% vs. BOS1 79%), yielding more informative SNP at nearly all MAF in BOS1 for HO (+18,775 SNP). The proportion of low MAF SNP in BOS1 (HO 37%; JE 32%) became similar to BovineHD (HO 34%; JE 31%), and the correlation between BovineHD and BOS1 MAF distributions rose in HO (0.58 to 0.95) but did not change in JE.

Key Words: genotyping, SNP, cattle

34 Comparing the lifetime productivity of beef females initially conceiving to, or sired by, artificial insemination or natural service. B. J. Bigler,* J. T. French, J. K. Ahola, J. C. Whittier, W. M. Frasier, G. E. Seidel, R. M. Enns, and R. K. Peel, *Colorado State University, Fort Collins.*

Artificial insemination and estrous synchronization can be valuable tools for the beef cattle industry due to the ability to increase productivity and reproductive efficiency. Therefore, the objectives of this study were to: 1) compare lifetime productivity between heifers that conceived to AI with those that conceived to natural service (NS) as a yearling, and 2) compare lifetime productivity between females that were the result of an AI mating with those that were the result of an NS mating. Calving and breeding records (n = 6,693) were utilized from 1,173 Angus females collected at 1 location from 1991 to 2010. The first objective classified heifers into 2 groups: conceived by AI or NS. The second objective categorized females into 4 dam groups, depending on whether they were conceived by an AI bred heifer (H-AI), an NS bred heifer (H-NS), an AI bred cow (C-AI), or an NS bred cow (C-NS). Cutoff dates were formulated to distinguish between AI and NS born calves by documenting the AI date and summing a 290-d gestation length. Economic significance was analyzed using weaning weights from all calves produced by each female while in the herd, along with price data collected from the nearest marketing center. Yearling heifers that conceived to AI were older and heavier ($P = 0.02$) at breeding than heifers that conceived by NS. When compared with heifers that were conceived by NS, females that conceived through AI had a greater ($P < 0.001$) average weaning weight, weaned more ($P < 0.001$) weight, and produced more ($P < 0.001$) total calves. Consequently, females that conceived to AI as yearlings yielded greater ($P < 0.001$) revenue throughout their lifetime in the cow herd than heifers that conceived to NS. There was a positive correlation between heifer age at breeding and lifetime productivity. These data suggest that if the majority of a beef cow herd calves within the first 30 d of the breeding season, producers can maximize the productivity and efficiency of each female, and as a result, increase total revenue per cow.

Key Words: artificial insemination, lifetime productivity, natural service

35 Identification of single nucleotide polymorphisms associated with feed efficiency in rams. R. R. Cockrum*[1], N. K. Pickering[2], R. M. Anderson[2], D. L. Hyndman[2], M. J. Bixley[2], K. G. Dodds[2], R. H. Stobart[1], J. C. McEwan[2], and K. M. Cammack[1], [1]*University of Wyoming, Laramie,* [2]*AgResearch Limited, Mosgiel, New Zealand.*

Residual feed intake (RFI) is a measure of efficiency that is time consuming, expensive, and labor intensive to obtain, making it an ideal trait for marker-assisted selection. The objectives of this research were to 1) identify single nucleotide polymorphisms (SNPs) and heritability associated with feed efficiency in sheep and 2) trace identified SNPs to the corresponding gene or genomic region. We hypothesized that regions of the genome corresponding to feed efficiency could be identified using the Ovine SNP50 BeadChip. Individual intake measurements were collected on rams from 2 separate ram tests (Dual Purpose Ram Test and Blackface Ram Test) at the University of Wyoming Ram Test (n = 328) from 2009 to 2011 using the GrowSafe System. Individual RFI (actual feed intake – predicted feed intake) values were generated. Blood was collected via the jugular and DNA was isolated. Single nucleotide polymorphisms in ram DNA were genotyped using the Ovine SNP50 BeadChip on the Illumina Infinium HD BeadChip Assay. Percentage loci scored per animal and locus, Hardy Weinberg deviations, animal information comparison, replicate sample reproducibility, and unusual allelic ratio analyses were conducted through Genome Studio and R for quality control analysis resulting in 50,896 SNPs used in the analysis. A genome wide association study (GWAS) analysis was conducted in R using the GenABEL package to identify SNPs using a polygenic model, $Y = \mu + G + e$, where μ is the intercept, G is the polygene, and e is the random residual, and estimate heritability. The SNP associated with *RXFP2* was used to confirm the accuracy of the polygenic model resulting in a high association ($P = 9.283^{-04}$) with the horn phenotype. Heritability for RFI was estimated as 0.14, which is similar to reports in cattle. Genome wide threshold ($P \leq 0.00025$) was obtained for 4 SNPs. Corresponding genes to identified SNPs were determined using the UCSC Genome Browser. Corresponding genes included zinc finger 1 (*Glis1*), interleukin 1 receptor accessory protein-like 1 (*IL1RAPL1*), and sex-determining region y – box 5 and 6 (*SOX5* and *SOX6*). Though 4 potential markers for RFI were identified, sample size must increase and markers must be validated for marker-assisted selection use.

Key Words: residual feed intake, sheep, single nucleotide polymorphism

36 Out-of-season reproductive performance of ewes synchronized to estrus with various 5-d protocols. C. G. Jackson*[1], T. L. Neville[1], V. R. G. Mercadante[2], K. M. Bischoff[2], G. C. Lamb[2], C. R. Dahlen[1], and R. R. Redden[1], *[1]North Dakota State University, Fargo, [2]North Florida Research and Education Center, University of Florida, Marianna.*

The objective of this experiment was to evaluate the reproductive performance of ewes after synchronization to estrus with progesterone (P_4) impregnated controlled internal drug release (CIDR) inserts in combination with GnRH and PG. Dorset and Katahdin ewes (n = 61 and 17; respectively) were assigned randomly during the anestrous period (April) to 1 of 4 treatments: 1) Untreated (U; n = 16); 2) CIDR (0.3 g P_4) inserts for 5 d (C; n = 21); 3) CIDR insert for 5 d and PG (dinoprost, 10 mg i.m.) at CIDR removal (P; n = 20); and 4) GnRH (gonadorelin, 0.02 mg i.m.) at CIDR insertion and PG at CIDR removal (G; n = 21). Rams equipped with marking harnesses were introduced at CIDR removal (d 0) and ewes were checked at 0800 h and 1700 h daily for breeding marks. Blood samples were collected via jugular venipuncture on d −12, −5, 0, 1, 2, 3, 4, 5, 8, 11, 14, 17, and 20 relative to CIDR removal and analyzed for serum concentrations of P_4 via RIA. Reproductive performance data were collected which included: days to estrus, days to lambing, percentage of ewes exhibiting estrus, pregnancy rate, lambing rate, and prolificacy. There was a treatment × time interaction ($P \leq 0.05$) for concentrations of P_4. Concentrations of P_4 were decreased ($P \leq 0.04$) in G compared with U on d 2. On d 14, C and P had greater ($P \leq 0.03$) concentrations of P_4 and G tended ($P = 0.06$) to have greater P_4 concentrations compared with U. In contrast, concentrations of P_4 on d 20 were greater ($P \leq 0.03$) in U compared with C. Days to estrus after CIDR removal, as indicated by breeding marks, were greater ($P \leq 0.02$) in U (6.5 ± 1.05) and P (5.90 ± 0.88) compared with G (2.98 ± 0.88). Pregnancy rate within 7 d post CIDR removal were similar ($P = 0.57$) for U, C, P, and G (30 ± 12.27, 30 ± 11.12, 35 ± 10.96, and 51 ± 10.78%; respectively). Similarly, no differences ($P \geq 0.32$) were detected for all remaining reproductive performance data. It appeared the 5 d CIDR coupled with GnRH and PG improved estrus synchronization; however, reproductive performance was not clearly improved by either of the 5 d CIDR protocols. These results warrant further research to determine the efficacy of industry-wide application of the 5 d CIDR in anestrous ewes.

Key Words: CIDR, ewe, synchronization

37 Effects of maternal fluoxetine dosage on lamb serum hormone concentrations and reproductive traits. P. L. Black,* D. M. Hallford, and T. T. Ross, *New Mexico State University, Las Cruces.*

Fluoxetine (human anti-depressant; selective serotonin reuptake inhibitor; FLX) depresses lactation in women and research has been conducted to evaluate sheep as a human lactation model. Fluoxetine has been shown to appear in the milk, yet little is known on how this drug will influence progeny. Our objective was to evaluate the effect of maternal FLX exposure on lamb growth and development. We utilized a completely randomized design with 18 mature Suffolk ewes (BW = 91 ± 12 kg; BCS = 2.0 ± 0.5). Treatments consisted of 0 (control) and 80 mg FLX; ewes were individually fed FLX using ground corn as the carrier at 0700 beginning on approximately d 126 of gestation and continued until 3 wk postpartum. The resulting 31 Suffolk-cross lambs were weighed at birth (birth weight = 4.6 ± 1.0 kg) and weaning (BW = 24.0 ± 3.2 kg; approximately 9 wk of age) and ADG was calculated. Blood samples were taken from lambs on d 1, 3, 5, 7, 14, 21, 28, 42, 56, and 66 and serum was analyzed for serum prolactin (PRL), IGF-I, and triiodothyronine (T_3) concentrations. Following weaning, ewe lambs were kept for subsequent evaluation. A total of 21 Suffolk-cross ewe lambs (BW = 44.7 ± 4.3 kg) were evaluated for age at puberty and pregnancy rate. No additional treatment was administered, as we only wanted to evaluate the effect of maternal FLX. Average daily gain from birth to weaning was similar ($P = 0.42$) between control and FLX-exposed lambs. Lambs exposed to maternal FLX had depressed PRL ($P = 0.01$), IGF-I ($P < 0.0001$), and T3 ($P = 0.04$) compared with controls. Age at first cycle was similar ($P = 0.53$) between FLX-exposed and control ewe lambs. Similarly, pregnancy rates were comparable ($P = 0.37$) between both control and FLX-exposed ewe lambs. Maternal supplementation of FLX reduced PRL, IGF-I, and T_3 serum concentrations in lambs, however this did not appear to have a negative effect on growth or reproductive performance.

Key Words: fluoxetine, growth, sheep

38 Digestibility of algal biofuel co-product in a forage diet. M. K. Beckman,* L. N. Tracey, N. Miller, K. Norman, K. Marchetti, E. J. Scholljegerdes, S. A. Soto-Navarro, C. L. Löest, and S. L. Lodge-Ivey, *New Mexico State University, Las Cruces.*

Co-product produced from extraction of oil from microalgae grown for biofuel production represents a novel feedstuff for ruminants. The objective of this study was to determine the influence of lipid extracted algae (LEA) on feed intake and diet digestibility when included in a forage diet. We hypothesized that an isonitrogenous addition of LEA to a forage diet would yield results similar to soybean meal (SBM). Fifteen crossbred wethers (43 ± 1.4 kg BW) fitted with ruminal and duodenal cannulas were used in a completely randomized design. Lambs were fed twice per day at 110% of previous 3 d DMI. Experimental diets included: 1) sorghum-sudan hay (CP 8.3%; NDF 52.79%, DM basis; HAY), 2) sorghum-sudan hay plus LEA (CP 13.6%; NDF 44.19% DM basis; ALGAE), and 3) sorghum-sudan hay plus SBM (CP 10.6%; NDF 51.24%, DM basis; SOY). Animals were adapted to treatments for 10 d followed by 5 d sample collection. Treatment did not influence OM intake ($P = 0.99$) or total tract OM and NDF digestibility ($P > 0.10$). Total tract CP digestibility was lowest for ALGAE while SOY and HAY did not differ (75.86 vs 84.88 and 82.12 ± 1.177%, respectively; $P < 0.01$). Ruminal pH, liquid dilution rate, and volume did not differ ($P > 0.10$) by treatment. Soybean meal increased ($P < 0.01$) ruminal ammonia by 57.4% and 56.0% compared with ALGAE and HAY, respectively. Total VFA production and molar proportion of butyrate did not differ ($P > 0.14$) by treatment. Acetate was highest for HAY, lowest for SOY, and ALGAE did not differ from HAY and SOY (74.11, 71.57, and 69.07 ± 1.245 mol/100 mol for HAY, ALGAE, and SOY, respectively; $P = 0.04$). Propionate was greatest for ALGAE which differed from HAY, while SOY was similar to ALGAE and HAY (14.80, 19.89, and 17.85 ± 1.233 mol/100 mol HAY, ALGAE, and SOY, respectively; $P = 0.04$). Acetate:propionate ratio was lowest ($P = 0.03$) for ALGAE. Adding ALGAE to a forage diet resulted in increases in propionate production while OM and NDF digestibility was comparable to SOY. However, ALGAE resulted in the lowest ruminal ammonia and total tract CP digestibility. These data imply that CP in LEA may not be as soluble as CP in SBM, therefore we reject our hypothesis.

Key Words: biofuels, sheep, digestibility

39 Effects of preovulatory estradiol concentration on embryo survival and pregnancy establishment in beef cows.

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The role of estradiol during the preovulatory period on embryo survival and pregnancy establishment has not been characterized in beef cows. We hypothesized that preovulatory estradiol is important for embryo survival and pregnancy establishment. To establish the importance of estradiol during the preovulatory period on embryo survival, ovariectomized multiparous cows (n = 26) received estradiol cypionate (ECP), estradiol benzoate (EB) or no treatment (CON) to mimic a preovulatory period. Prior to treatment, all cows received a progesterone-releasing device (CIDR) for 7 d, 25 mg injection of prostaglandin-F2α (PGF) at CIDR removal (d −2), and an injection of GnRH (100 µg; d 0) 2 d later to mimic the follicular phase. Utilizing a 3 × 3 Latin Square design, cows received either ECP 36 h before GnRH injection, EB 12 h before GnRH injection, or no estradiol (CON). Luteal phase progesterone was mimicked with 2× daily increasing progesterone injections from d 3 to 6 and use of CIDRs from d 7 to 29. On d 7 after GnRH injection, each cow received one embryo and a CIDR. Another CIDR was added 24 h following embryo transfer and every 6 d, the older of the 2 CIDRs was replaced with a new CIDR. Blood was collected every 4 h between d −2 and d 0 for characterization of serum estradiol profiles. Blood was collected on d −2, −1, 0, 3 to 7, 13, and 17 to 29 to characterize progesterone profiles. Serum estradiol profiles were different ($P < 0.001$) between treatments. Mean serum progesterone concentrations were decreased ($P = 0.05$) for EB and ECP treated cows compared with CON. Transrectal ultrasonography on d 29 indicated that 4% of CON, 29% of EB, and 21% of ECP treated cows were pregnant. Expression of interferon stimulated genes ISG15, Mx2, and Oas1 on d 19 indicated 66.0% of CON, 69.3% of EB, and 71.0% of ECP treated cows were pregnant. Thus, 62, 39.7, and 50% of pregnancies in CON, EB, and ECP treated cows, respectively were lost from d 19 to 29. Overall, results indicate greater embryonic survival and pregnancy establishment in cows exposed to estradiol in the preovulatory period.

Key Words: estradiol, embryo survival, pregnancy establishment

40 Individual mineral supplement intake by ewes swath grazing or confinement fed pea-barley forage.

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Sixty mature ewes (non-pregnant, nonlactating) were used in a completely randomized design to determine if feeding method of pea-barley forage (swath grazing or hay in confinement) had an effect on individual ewe mineral consumption. Thirty ewes were randomly allocated to 3 confinement pens and 30 ewes were randomly allocated to 3 grazing plots. Targhee ewes (65.4 ± 5.84 kg BW) were used in 2010. Rambouillet ewes (61.9 ± 6.28 kg BW) were used in 2011. The study was conducted during September 25-October 15, 2010 and September 6–19, 2011. Ewes had ad libitum access to food, water, and a mineral supplement containing 11–12.5% salt with 2% TiO_2 added as an external marker to estimate individual mineral intake. On d 1 of the data collection period, mineral/TiO_2 was weighed and placed in feeders in confinement pens and grazing plots. At the end of the collection period, remaining mineral was weighed and consumed mineral was recorded to provide an estimate of total mineral intake via disappearance. Forage intake was calculated using estimates of fecal output obtained by dosing gelatin capsules containing 2 g Cr_2O_3 every day for 14 d, and in vitro 48 h DM digestibility. Fecal grab samples were collected from each individual ewe for a period of 7 d and composited. Forage and mineral intakes were analyzed using individual ewe as the experimental unit. A year x treatment interaction ($P < 0.001$) existed for forage DMI and mineral DMI. Ewes in confinement consumed more forage than grazing ewes in 2010 (2.60 vs. 1.86 kg/d, respectively), but less than grazing ewes in 2011 (1.99 vs. 2.49 kg/d, respectively). Mean mineral intake was highest ($P < 0.001$) by grazing ewes in 2011 and 2010 (average 69 g/d), intermediate by ewes in confinement in 2010 (57 g/d), and lowest by ewes in confinement in 2011 (31 g/d). In this study, swath grazing ewes consumed more mineral than ewes in confinement, indicating that producers may want to provide a larger quantity of mineral to ewes swath grazing.

Key Words: mineral, confinement, swath

41 Effects of weaning age and winter development environment on heifer grazing distribution.

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The objective of this experiment was to determine if early weaning (approximately 125 d) vs. normal weaning (approximately 250 d) and wintering replacement heifers in drylot vs. rangeland affected heifer grazing distribution during the subsequent summer. Heifer calves from the 2009 and 2010 calf crop (n = 104 and 73, respectively) were allocated to the 2 weaning treatments and then stratified by age into the 2 winter development treatments. During the summer of yr 1 heifers were allocated to 2 pastures by winter treatment, and in yr 2 all 4 treatment combinations were allocated to separate pastures. A subset of heifers from each group were selected to wear global positioning system (GPS) collars (n = 2 and 5 in yr 1 and 2, respectively). Readings were taken from the GPS every 15 min in yr 1 and every 65 s in yr 2. The GPS coordinates were then analyzed relative to ecological sites,

water locations, fence locations, and temperature using Arc GIS (Esri, Redlands, CA). Winter treatment affected ($P < 0.05$) mean distance from fence lines, preference index (PI) for claypan and loamy sites in 2010, and distance from water in 2011. Day of sampling affected ($P < 0.05$) claypan and loamy site PI in 2010 and thin claypan site PI in 2011. Day of sampling interacted with winter treatment ($P < 0.05$) for distance from water in 2010, sand and thin claypan site PI in 2010 and thin claypan site PI in 2011, while day of sampling interacted with weaning treatment for distance from water in 2011. A winter by weaning treatment interaction affected ($P < 0.05$) thin claypan site PI in 2011. There was a 3-way interaction ($P < 0.05$) between weaning treatment, winter treatment and ambient temperate on the distance from water in both years and between weaning treatment, winter treatment and day of sampling on claypan and sand site PI in 2011. In conclusion, winter development influenced patterns of range utilization. Day-of-sampling interactions indicated that range heifers did not adjust preferences and thus were already adapted to the range environment, whereas drylot heifers adjusted preferences over time suggesting they re-learned how to utilize the range environment.

Key Words: heifer development, grazing distribution, weaning

42 Effects of distillers dried grains with solubles supplementation on grazing and subsequent feedlot performance of heifers grazing northern Great Plains rangelands.

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The objectives of this study were to evaluate the effects of distillers dried grains with solubles (DDGS) supplementation on animal performance while grazing northern Great Plains rangeland, as well as the effects of supplementation on subsequent feedlot performance and carcass characteristics. Eighty-two yearling heifers (319.5 ± 4.0 kg) were utilized in a completely random design to examine the outlined objectives. Heifers were stratified by BW and randomly assigned to 1 of 6 groups, with each group randomly assigned to 1 of 2 treatments: 1) no supplement and 2) DDGS supplemented at 0.6% BW. Stocking rates were 1AU/1.6 ha. Distillers dried grains with solubles were delivered daily and placed in plastic lined feed bunks. This study consisted of 2 portions a 74 d grazing phase and a 109 d finishing phase. Feedlot pens coincided with grazing pastures. All heifers received a common corn-based finishing ration for the duration of the 109 d finishing study. At the start of the grazing portion, initial BW was not different ($P > 0.09$). Final BW and ADG were greater for heifers supplemented DDGS ($P \leq 0.03$) during the grazing portion of this project. Heifers supplemented DDGS gained an additional 0.21 kg/d and came off pasture 11.21 kg heavier than heifers not receiving DDGS. No differences in animal performance were observed ($P \geq 0.13$) during the finishing phase. No differences in carcass characteristics were observed ($P \geq 0.23$). Although not statistically different, heifers receiving DDGS had greater marbling scores (Modest-514) compared with unsupplemented heifers (Small-470). Producers could benefit from this small increase in marbling scores; allowing the carcasses to qualify for certified programs possibly resulting in premium returns. Distillers dried grains with solubles improved average daily gain of yearling heifers grazing northern Great Plains rangeland with no adverse effects on feedlot performance or carcass characteristics.

Key Words: distillers dried grains with solubles, feedlot performance, yearling cattle

43 Effects of post-AI nutrition on reproductive and growth performance of yearling beef heifers.

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The objective of this study was to determine the effects of a change in nutritional plane during the 21 d immediately following artificial insemination, on growth performance and conception rates of yearling Angus heifers. This experiment was conducted at the University of Wyoming (Loc. 1) and Purdue University, IN (Loc. 2) using a total of 151 animals (n = 98 and 53 respectively). Prior to initiation, heifers were fed 0.68 kg/d between weaning (~7 mo of age) and breeding (~14 mo of age) to obtain a BW of approximately 65% of their mature weight by the beginning of the breeding season. Immediately following routine estrous synchronization and AI, heifers (BW = 931 ± 643.7 kg) were randomly assigned to 1 of 3 nutritional treatments for a 21 d nutritional study: 1) formulated to meet NRC (2000) requirements for heifers to gain approximately 0.68 kg/d (GAIN); 2) formulated to meet NRC (2000) nutrient requirements for maintenance only (MAINTAIN), and 3) formulated to provide 80% of the NRC, 2000 energy requirement for maintenance (LOSS). Two linear pre-planned orthogonal contrasts (Proc GLM; SAS Inst. Inc., Cary, NC) were used to compare effects of GAIN vs. others and MAINTAIN vs. LOSS. No treatment*location interaction ($P = 0.73$) was detected. Heifers fed the GAIN treatment had greater ($P = 0.04$) first-service conception rates (76.5%) when compared with the other 2 treatments (58.5%) overall. No differences were detected between MAINTAIN (56.2%) and LOSS (60.8%). As expected, ADG were greater ($P < 0.01$) for heifers fed the GAIN diet (0.78 kg/d) and greater ($P < 0.01$) for heifers on the MAINTAIN (0.06 kg/d) diet compared with heifers on LOSS treatment (−0.35 kg/d). These results suggest that even small changes in nutrition during the 21 d immediately after breeding can reduce conception rates. Data suggests that keeping heifers on a similar plane of nutrition before breeding and maintaining it through the first 21 d post-AI is beneficial.

Key Words: heifers, reproduction, nutrition

44 Dietary intake in a group of old mares.

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Dietary intake for 32 old (21.9 ± 0.65), non-pregnant, idle mares was tracked between February to July and was compared with the 2007 National Research Council predicted values for idle maintenance horses. Mares were maintained in stalls with access to ad libitum water and a salt block. Dietary intake was assessed weekly and changes were averaged. A mix diet of alfalfa and grass hay with commercial grain concentrates were weighed, fed twice a day, and any refusals were recorded. Caloric intake per kilogram of body weight was calculated by dividing the total calorie intake by the body weight (kg). Hay was analyzed for DE, CP, ADF, NDF, lignin, ethanol soluble carbohydrates (ESC), water soluble carbohydrates (WSC), starch, crude fat (CF), and minerals. Nutrient intake was analyzed by ANOVA and significant differences among months compared by least squares means analysis. Regressions were calculated between predicted and actual nutrient intake including BCS in the regression if significant. Overall, actual caloric intake was 13.8% higher than predicted caloric intake ($P < 0.0001$); more specifically, in the month of June, actual was higher than predicted by 21.6%. In addition, actual intake of CP, Ca, P, Mg, Zn, and Cu was higher in June than predicted intake of those same nutrients ($P < 0.0001$) in all other months. WSC and CF intake increased ($P = 0.03$; $P = 0.02$) from May (WSC = 6.7%; CF = 0.49%) to July (WSC = 7.6%; CF = 0.59%), occurred with the increase in DMI from May to June. Dietary caloric intake increased

by an average of 20% from May to July and BCS increased ($P < 0.05$) from 5.8 to 6.4; yet NCS ($P = 0.71$) and BW ($P = 0.99$) did not vary even though most of the time the mares were fed on average, 13.8% above DE requirements. No variation was found in CP, Ca, P, K, S, Zn, and Se ($P > 0.15$) intake. When BCS was included in regression between predicted and actual BW adjusted caloric intake, results were significant, but weak ($P < 0.001$; $r^2 = 0.17$). Regression between predicted and actual CP, Ca, P, were significant but weak and intake above required levels. Although previous research has indicated that nutrient intake is similar between old and young horses, in the current study, mares did not increase in BW or BCS when fed 10% above DE requirements.

Key Words: body condition score, water soluble carbohydrates, old horse

Animal Health I

45 Histological examination of the organs of the rats administered varying levels of *Vernonia amygdalina* leaves. A. H. Ekeocha,* P. C. Ekeocha, and T. Fasola, *University of Ibadan, Ibadan, Oyo, Nigeria.*

Histology of the liver, kidney and pancreas of rats administered with *Vernonia amygdalina* was examined. Thirty male Albino rats were divided into 6 groups of 5 rats each. Four groups with basal blood glucose levels of 88.0 ± 0.16, 89.2 ± 0.23, 85.2 ± 0.27, and 85.8 ± 0.25 mg/dL were injected with 10% alloxan in saline to make them diabetic (277.6 ± 6.55, 284.8 ± 3.80, 256.4 ± 1.39 and 265.6 ± 4.41 mg/dL fasting blood glucose (FBG) respectively). The 4 diabetic groups were then treated with different doses (g/kg of BW) of an aqueous extract of dried *Vernonia amygdalina* Leaves herein referred to as VaL. A fifth group (nondiabetic) was treated with 400mg VaL /kg BW. VaL was administered twice daily for 2wks using an oral canula. The sixth group (nondiabetic) received no VaL as a positive control. Blood was collected from the tail to determine blood glucose level on a glucometer. The FBG levels of the 6 albino rat groups were recorded every 2 d for 2 wk. At the end of wk 2, the rats were slaughtered and their liver, kidney and pancreas were examined histologically to ascertain if VaL was toxic to the organs or not. Data were analyzed using ANOVA (SAS, 1999). The plant extract was observed to have hypo-glycaemic effect on each group of diabetic rats as it reduces their fasting blood glucose (FBG) levels from 277.6 mg/dL to 142.2mg/dL (Group 1) 284.8 mg/dL to 102.0 mg/dL (Group 2), 256.4 mg/dL to 86.3 mg/dL (Group 3) and 265.6mg/dl to 82.1 mg/dL (Group 4) over a period of 2 wk. The fifth group consisting of noninduced rats was administered with 400 mg/kg of *Vernonia amygdalina* leaves for a period of 2 wk and the FBG level (91.4 to 81.6 mg/dL) was compared with that of the control group (87.1 to 86.9 mg/dL). The last group i.e the sixth group of rats used as control were only fed with feeds and given clean water only. Their FBG (86.9 mg/dL) were also checked every 2 d and compared with the FBG of the other groups from groups 1–5 (142.2, 102.0, 86.3, 82.1 and 81.6 mg/dL). The rats were sacrificed and their organs (liver, kidney and pancreas) of the experimental animals were examined histologically to ascertain if 400 mg/kg of the plant extract was toxic to the organs. The results show that the plant extract had no adverse effect when administered on normal rats except for a marked congestion of the mesenteric blood vessel. The extract reduced the level of damage to the kidney, liver and pancreas when administered on diabetic rats, which is an indication that the plant extracts of *Vernonia amygdalina* leaves has antidiabetic properties that slowly heals partly damaged organs but not packed up organs.

Table 1. Fasting blood sugar (mg/dL) of normal and induced-diabetic albino rats administered with varying doses of Vernonia amygdalina leaf extracts

Day	G1	G2	G3	G4	G5	G6	SEM
2	277.6^{a}	284.8^{a}	256.4^{b}	265.6^{b}	91.4^{c}	87.1^{c}	8
4	237.4^{a}	243.5^{a}	203.2^{b}	201.8^{b}	85.2^{c}	87.5^{c}	6
6	231.2^{a}	226.6^{a}	151.6^{b}	143.2^{b}	84.6^{c}	88.3^{c}	9
8	217.1^{a}	200.0^{a}	106.0^{b}	94.0^{c}	83.5^{c}	87.9^{c}	9
10	196.0^{a}	176.0^{a}	89.0^{b}	87.3^{b}	82.2^{b}	89.4^{b}	7
12	163.4^{a}	132.0^{b}	87.3^{c}	84.8^{c}	81.8^{c}	86.2^{c}	7
14	142.2^{a}	102.0^{b}	86.3^{c}	82.1^{c}	81.6^{c}	86.9^{c}	6

$^{a-c}$Means in the same row with different superscripts differ significantly ($P < 0.05$).

Key Words: *Vernonia amygdalina* leaves, organs, rat

46 Toxicological properties of liquid dishwashing detergent in Swiss albino mice. M. S. Gulay,* O. Yildiz Gulay, A. Ata, A. Demirtas, and S. Gungor, *Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Burdur, Turkiye.*

Detergent exposure can pose serious health risks to humans and animals. However, the effect of detergent exposure on animal health is yet to be studied. Thus, the aim of the current study was to investigate the toxicity of liquid dishwashing detergent on blood parameters and organ weights of male Swiss Albino mice. Fourty healthy male Swiss albino mice were randomly assigned to 5 groups of 8 animals each. Animals in TR1 served as control and received tap water while TR2, TR3, TR4 and TR5 received 0.1, 0.5, 1 and 5% v/v of the liquid detergent in tap water, respectively, as the only source of water. All treatments started right after weaning (3 wk of age) and continued for 60 d. Mice were kept in plastic cages under standard laboratory conditions. Food and water were provided ad libitum. At the end of the experiment, mice were kept under Sevorane anesthesia and blood samples were collected into Na-heparinized capillary tubes from the beating hearth. After blood collection, animals were sacrificed and internal organs were removed. Data were analyzed by one way ANOVA. Results of the current study indicate that water consumption among the groups did not differ ($P > 0.1$). There was no treatment effect on hematocrit, RBC, WBC, MCV, MCH, MCHC, total lymphocytes, monocytes, or basophils ($P > 0.1$). No effect of detergent treatment was detected on the weights of liver, kidney, spleen, lung, testis or brain ($P > 0.1$). However, total hemoglobin (TR1 = 15.2 ± 0.39, TR2 = 14.7 ± 0.35, TR3 = 14.4 ± 0.56, TR4 = 12.7 ± 0.54 and TR5 = 13.1 ± 0.40 g/dL; $P < 0.01$), plasma protein (TR1 = 6.88 ± 0.26, TR2 = 6.52 ± 0.13, TR3 = 6.71 ± 0.27, TR4 = 5.98 ± 0.11 and TR5 = 6.08 ± 0.31; g/dL $P < 0.05$), total neutrophils (TR1 = 0.83 ± 0.08, TR2 = 0.78 ± 0.13, TR3 = 0.91 ± 0.05, TR4 = 1.04 ± 0.10 and TR5 = 1.68 ± 0.41 x10^{3}; $P < 0.03$) and total eosinophils (TR1 = 0.071 ± 0.012, TR2 = 0.096 ± 0.024, TR3 = 0.082 ± 0.025, TR4 = 0.272 ± 0.092 and TR5 = 0.263 ± 0.083x10^{3}; $P < 0.03$) were affected adversely due to detergent treatment. In addition, serum alkaline phosphatase and aspartate aminotransferase levels were significantly elevated in TR4 and TR5 ($P < 0.05$). Thus, our results suggest that especially the higher doses used in the current study could be toxic and cause health risks to Swiss albino mice.

Key Words: detergent, toxicity, hematology

47 Isolation of lactobacillus strains with high adhesive ability to the intestinal epithelial cells. W. M. Zhang*[1], H. F. Wang[1,2], and J. X. Liu[1], [1]*Institute of Dairy Science, MOE Key Laboratory of Molecular Animal Nutrition, Zhejiang University, Hangzhou, China,* [2]*Department of Animal Science, College of Forestry and Biotechnology, Zhejiang A & F University, Hangzhou, China.*

This study was conducted to investigate the adhesive ability of lactobacillus and how the surface proteins of lactobacillus play a vital role in its adhering to the intestinal epithelia. Intestinal mucus and chyme were collected from a 20-d-old piglet. They were spread on de Man, Rogosa, Sharpe (MRS) agar plates for the selective culture. Agar plate was incubated at 37°C under anaerobic condition for 48 h, and the visible colonies were identified using microscope after stained by methylene blue. The selected colonies of lactobacillus were cultured anaerobically in MRS broth at 37°C. The partial 16s rRNA gene fragment of lactobacillus were then PCR amplified. The 16s rRNA sequences were deposited in GenBank, aligned with Clustal W. Phylogenetic analysis of these strains was performed using MEGA 3.0. The S-layer proteins were isolated with 5 M LiCl, and then analyzed by SDS-PAGE. Eighty-five strains of lactobacillus were obtained and classified into 1 *Lactobacillus johnsonii*, 54 *L. salivarius*, and 30 *L. reuteri* strains. Depending on the phylogenetic analysis of the pictures of the colonies, 40 strains were selected to adhere to caco-2 cells as model of intestinal epithelial cells. Five of 40 strains were found to have higher adhesive ability (4.9–15.9 cfu/cell) than the others ($P < 0.05$), including 4 *L. reuteri* strains and 1 *L. salivarius* strain. They were named as *L. reuteri* ZJ616 (accession number JN981858), *L. reuteri* ZJ617 (JN981859), *L. reuteri* ZJ621 (JN981863), *L. reuteri* ZJ623 (JN981865) and *L. salivarius* ZJ614 (JN981856), respectively. These 5 strains ($P < 0.05$) inhibited the *Escherichia coli* K88 and *Salmonella enteritidis* 50335, with *L. reuteri* ZJ621 indicating the higher inhibition to *S. enteritidis* 50335 than the others ($P < 0.05$). The molecular masses of s-layer proteins from these strains ranged from 34 to 75 kDa and differed from each other ($P < 0.05$). The ability for the strains without s-layer protein to inhibit the *S. enteritidis* 50335 was reduced, indicating that the S-layer protein plays an important role in inhibiting pathogens.

Key Words: *Lactobacillus*, adhesive ability, surface proteins

48 Effect of mycotoxins on the intestine: Analysis of the interaction between fusariotoxins.

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Most fungi are able to produce several mycotoxins simultaneously in separate feedstuffs, and considering it is a common practice to use multiple grain sources in animal diets, the risk to be exposed to several mycotoxins at the same time increases. Interactions between concomitantly occurring mycotoxins can be antagonistic, additive, or synergistic. The data on the in vivo combined toxic effects of mycotoxins are somewhat limited. Similarly, data with regard to the impact of these metabolites on intestinal functions and integrity have only gained significant interest over the last decade. Intestinal cells are the first cells to be exposed to mycotoxins, and mycotoxins specifically target high proteins turnover- and activated-cells, which are predominant in gut epithelium. We thus investigated the effect of Fusarium toxins in the gastrointestinal tract of piglets fed deoxynivalenol (DON) and fumonisins (FUMO), alone or in combination at low doses. Piglets received separate diets for 5 weeks: a control diet; a diet contaminated with either DON (3 mg/kg) or FUMO (6 mg/kg); or both toxins. Chronic ingestion of these contaminated diets induced morphological and histological changes, as shown by the atrophy and fusion of villi, the decreased villi height and cell proliferation, and by the reduced number of immune cells. Cytokines analysis (TNF-α, IL-1β, IFN-γ, IL-6, and IL-10) revealed an upregulation of their expression. In addition, ingestion of contaminated diets reduced the expression of the adherent and tight junction proteins, E-cadherin and occludin, respectively. Regarding the association of both mycotoxins, several types of interactions were observed depending on the parameters and intestinal segments assessed. In conclusion, further investigations are required to evaluate the impact of mycotoxins in intestine, especially for the multi-contamination. So far, our findings along with the current data reveal that mycotoxins may affect nutrient absorption, increase the nutrient requirement, predispose animals to infections by enteric pathogens, and lead to chronic intestinal inflammations.

Key Words: mycotoxin, intestine, co-contamination

49 Dietary supplementation of young broiler chickens with capsicum and turmeric oleoresin increases resistance to necrotic enteritis.

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The *Clostridium*-related poultry disease necrotic enteritis (NE) causes substantial economic losses on a global scale. In this study, a mixture of 2 plant-derived phytonutrients, capsicum oleoresin and turmeric oleoresin (XT), was evaluated for its effects on local and systemic immune responses using a co-infection model of experimental NE. Chickens were fed from hatch with a diet supplemented with XT, or with a non-supplemented control diet, and orally challenged with virulent *Eimeria maxima* oocyts at 18 d and *Clostridium perfringens* at 20 d of age. Parameters of protective immunity were (a) body weight gain, (b) gut lesions, (c) serum levels of *C. perfringens* α-toxin and NetB toxin, and (d) intestinal levels of proinflammatory cytokine/chemokine gene transcripts. Chickens fed the XT-supplemented diet had increased body weight gains and reduced gut lesion scores compared with birds given the non-supplemented diet. The XT-fed group also displayed decreased serum α-toxin and NetB toxin levels and reduced intestinal IL-8 and LITAF mRNA levels, but increased TNFSF15 mRNA levels, compared with non-supplemented controls. In conclusion, this study documents the molecular and cellular immune changes following phytonutrient dietary supplementation that are relevant to protective immunity against avian NE.

Key Words: phytonutrients, necrotic enteritis, protective immunity

50 The identification of candidate genes for BSE and the application to chronic wasting disease in mule deer.

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Previous work in our lab identified 64 regions throughout the bovine genome associated ($P < 0.05$) with classical BSE in European cattle. Bioinformatic analysis identified 89 candidate genes within the regions. Data from 10 different tissue mRNA sequence libraries and 2 whole genome sequences, created using next generation sequencing technology, was interrogated to identify structural variation in these candidate genes. Single nucleotide polymorphisms were identified in 87 of the 89 candidate genes and the identified polymorphisms were tested in 729 animals from 2 populations (193 controls and 225 case samples from paternal half sib families, and 14 control and 397 case samples from a second population). There were 31 markers identified as associated with BSE susceptibility ($P < 0.05$ and MAF >0.01) including 7 marker clusters on chromosomes 2, 10, 14, 17, and 20. The functions of the genes associated with significant markers include prion protein binding and proteasome structure and function as well as neurodegenerative disease in humans. A de novo assembly of the mule deer genome has been constructed and the candidate genes are being annotated to provide research targets in the gene pathways underlying prion disease progression, which will enhance our understanding of the disease.

Key Words: bovine spongiform, chronic wasting disease, genomics

51 Phosphorus utilization in broilers fed soybean and benniseed-based diets with and without microbial phytase supplementation. O. Adebiyi, A. Ologhobo, A. Omojola, O. Olusola, W. Muhammed, and M. Olumide*, *University of Ibadan, Ibadan, Nigeria.*

The effects of microbial phytase (Natuphos 500) supplementation of corn- soybean meal and benniseed meal based diets were studied with One hundred and sixty-eight (168) day- old Arbor Acre broiler chicken on the parameters of growth performance, hematology, carcass characteristics and phosphorus and calcium retention in tibia bone for 8 week. The chickens were within a weight range of 40–43 g at day old and allotted in a completely randomized design (CRD) to 6 dietary treatments with 7 broiler chickens per replicate having 4 replicates per treatment. Three levels of phytase (0, 300 and 600 FTU/kg diet) were added to the diets based on soybean meal and benniseed meal respectively. The diets contained 2972.00/ 3299.90 ME kcal/kg DM energy, 23.26/23.10% protein, 1.67/1.72% calcium and 0.85/ 0.87% phosphorus in the soybean meal and benniseed meal based diets respectively at the starter phase. At the finisher phase, the diets contained 3061.20/ 3363.44 ME kcal/kg DM energy, 21.02/ 21.09% protein, 1.52/ 1.57% calcium and 0.75/ 0.77% phosphorus in the soybean meal and benniseed meal based diets respectively. Body weight gains of 48.60 g/day and feed intake of 101.98 g/day were significantly ($P < 0.05$) increased by 300 FTU/kg phytase supplementation in benniseed meal diets when compared with the group without phytase supplementation (control group). Significant ($P < 0.05$) increases were also obtained for percentage retentions of nitrogen (N) 67.22, phosphorus (P) 45.58, ash 74.85, ether extract (EE) 65.43 and crude fiber (CF) 22 in the benniseed diet supplemented with 300FTU phytase. Phosphorus and calcium retentions in the tibia bone were not significantly ($P < 0.05$) affected by supplementation of soybean meal and benniseed meal based diets with microbial phytase supplementation. Likewise, the treatments also failed to induce any statistical effects on hematological parameters of broilers including the PCV, WBC, Hb and RBC respectively. There were however, significant ($P < 0.05$) differences in the magnitude of response of birds to the diets supplemented with phytase. Birds fed benniseed meal with 300 FTU/kg microbial phytase supplementation had the highest feed intake g/day (101.98), weight gain g/day (48.60) and phosphorus retention in tibia bone (24.29).

Key Words: phytase, phosphorus, tibia bone

52 Effects of tropical legume supplementation on parasite burden and health parameters in goats. M. A. Zarate*[1], J. C. Hamie[1], J. J. Romero[1], E. N. Muniz[2], Y. J. Jang[3], K. G. Arriola[1], O. C. Queiroz[1], and A. T. Adesogan[1], *[1]University of Florida, Gainesville, [2]Empresa Brasileira de Pesquisa Agropecuária, EMBRAPA, Aracajú, Sergipe, Brazil, [3]Gyeongsang National University, Jinju, South Korea.*

The objective of the experiment was to evaluate the effects of supplementing bahiagrass hay (BG; *Paspalum notatum*) with perennial peanut (PP; *Arachis glabrata*), soybean (SB; *Glycine max*), cowpea (CP; *Vigna unguiculata*) and lespedeza (LES; *Lespedeza cuneata*) on infection by *Haemonchus contortus* and *Eimeria* sp. in goats. Forty naturally infected male Kiko × Spanish, 8 mo old, kids (23.8 ± 5.2 kg) were blocked by weight, placed in 3 pens per treatment (each with 2 or 3 kids), and fed diets containing BG hay alone or BG hay supplemented with PP, SB, CP and LES at 50% of the diet. Body weight (BW) was measured on 2 consecutive days at the beginning and end of the 4 wk trial. On d 0 and every 7 d thereafter, blood packed cell volume (PCV), fecal egg counts (FEC) and BW were recorded. Data was analyzed as a randomized block design. The model included the effects of treatment, week and their interaction. The PDIFF statement of SAS with Tukey adjustment was used to evaluate means. Feeding PP, SB or LES hay ($P < 0.05$) reduced gastrointestinal nematode FEC compared with BG alone, but LES had the least values ($P < 0.01$). Goats fed LES had lower ($P < 0.01$) Eimeria FEC compared with BG alone and similar tendencies were evident for goats fed PP and SB ($P = 0.08$, $P = 0.06$). Legume supplementation increased PCV ($P < 0.05$) compared with feeding BG alone. Treatments did not affect BW or ADG. We conclude that feeding LES resulted in the greatest reduction in total FEC and it also increased PCV. Feeding PP and SB reduced total FEC to a lesser extent and also increased PCV but feeding cowpea only increased PCV.

Table 1. Effects of legume supplementation on gastrointestinal nematode and Eimeria fecal egg counts (NFEC, EFEC), Hematocrit (HEM), initial and final body weight (IBW, FBW), and average daily gain (ADG)

	Bahiagrass	Peanut	Soybean	Cowpea	Lespedeza	SEM
NFEC, epg	2773^{a}	2072^{bc}	1914^{b}	2641^{ac}	1147^{d}	161
EFEC, epg	2809^{a}	2162^{ab}	2197^{ab}	2700^{a}	1246^{b}	284
HEM, %	21.5^{a}	29.6^{b}	30.1^{bc}	26.4^{bc}	27.5^{c}	1.3
IBW, kg	24.9	25.1	23.5	24.4	24.7	3.3
FBW, kg	25.0	25.6	24.5	24.1	26.2	3.8
ADG, g/d	4.4	15.4	35.2	−9.2	51.6	22.2

$^{a–d}$Means within a row with different superscripts differ by $P < 0.05$.

Key Words: goat, parasite, legume

53 Carboxymethylation and antioxidant activity of exopolysaccharides. M. Huang,* T. F. Zhu, Z. Q. Lu, G. X. Wu, and Y. Z. Wang, *National Engineering Laboratory of Bio-Feed Safety and Pollution Prevention and Key Laboratory of Animal Nutrition and Feed Science of Ministry of Agriculture, Institute of Feed Science, Zhejiang University, Hangzhou, Zhejiang, China.*

Polysaccharides have been demonstrated to play an important antioxidant role as free radical scavengers, and chemical modification is one of the methods to improve their bioactivities. In our previous study, exopolysaccharides (EPS) produced by *Enterobacter cloacae* Z0206 were able to improve antioxidant function in rats, tilapia and Broilers. However, modification of EPS is necessary to improve their bioactivities. Therefore, to validate the possibility of enhancing the antioxidant activities of EPS through the carboxymethylated modification and screen out the optimum reaction conditions, carboxymethylated derivatives were prepared in aqueous alkaline medium using monochloroacetic acid (MCA) as etherifying agent according to the orthogonal test. Nine modification conditions were designed to study the effect of 3 parameters such as the reaction time, reaction temperature and ratio of NaOH to MCA on reaction yield and degree of substitution (DS), 9 carboxymethylated derivatives with different DS were obtained. The data were analyzed by general linear model ANOVA, differences between groups were considered statistically significant at the 5% ($P < 0.05$) level.The antioxidant activities were evaluated in vitro, by scavenging abilities on superoxide radical and hydroxyl radical. The results indicated that the extent of the impact of variables on DS followed the order: molar ratio of NaOH to MCA > reaction time > reaction temperature. With the increase of the reaction time and reaction temperature from 50°C to 60°C, DS of derivatives increased gradually. However, the DS decreased when the temperature up to 70°C. The carboxymethylated derivatives showed noticeable antioxidant activities compared with EPS, and carboxymethylated derivative with DS of 0.86 showed highest antioxidant activities. The optimum carboxymethylated conditions of EPS were the reaction time of 4 h, the reaction temperature of 60°C and the ratio of

NaOH to MCA of 2:1. This study provided a theoretical basis for the exploration of a potential antioxidant in feed additives or food industry.

Key Words: polysaccharides, carboxymethylation, antioxidant activity

54 Risk factors for switch in status from *Mycobacterium avium* ssp. *paratuberculosis* test positive to negative; data from the national Johne's disease control demonstration program. A. Kenyon*[1], S. Aly[1], and I. Gardner[2], [1]*Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California-Davis, Tulare,* [2]*Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California-Davis, Davis.*

The objective of this study was to identify the risk of a switch in status of cows tested by *Mycobacterium avium* ssp. *paratuberculosis* (MAP) antigen-based tests (Agtest) and antibody-based tests (Abtest). A switch in status was recorded when a cow that previously tested positive subsequently tests negative. Data from 65 demonstration herds nationwide were used to study the rate of switch in status from a positive to a negative test result. Study herds' dairy herd improvement records for the respective testing period was downloaded and verified for correctness before importing into the relational database. The data set was comprised of 144,150 dairy herd information association (DHIA) records and 245,063 Agtest and Abtest results including Biocor, Kinetics ELISA, HerdChek (Idexx), liquid culture Trek ESP, Bactec, culture on Herrold's egg yolk medium, MGIT and PCR. Matched DHIA records and results yielded 194,535 records that represent longitudinal data for all the cows tested as part of the national Johne's disease demonstration program and their DHIA records over spanning the time period from 1999 to 2010. In 11 years, a total of 48,434 cows were tested for MAP using at least a single test and a total of 4839 (10%) cows switched status at least once in their lifetime using any of the study tests. In comparison to first parity, as a cow's parity increased to 2, 3, and 4, its odds of switching serostatus using increased by 60, 30 and 50% (P value < 0.01). For every 100 d in milk increase in a cow's lactation, its odds of switching serostatus increased by 7% (P value 0.01). Cows were more likely to switch in status as they aged which could also be explained by repeated testing. In addition, cows were also more likely to switch in status as they progressed in their lactation regardless of parity.

Key Words: switch test results, Johne's, risk

55 Expressing an antimicrobial peptide cathelicidin-BF by fusion with SUMO in *Bacillus subtilis*. C. Luan,* Y. G. Xie, H. W. Zhang, and Y. Z. Wang, *Institute of Feed Science, Zhejiang University, National Engineering Laboratory of Biological Feed Safety and Pollution Prevention and Control, Key Laboratory of Animal Nutrition & Feed Science, Ministry of Agriculture, Hangzhou, Zhejiang Province, People's Republic of China.*

Cathelicidin-BF, an antimicrobial peptide purified from the snake venoms of *Bungarus fasciatus*, is an excellent alternative tool for clinical or agricultural antibiotics. The cathelicidin-BF efficiently killed bacteria and some fungal species, especially active against gram-negative bacteria. No hemolytic and cytotoxic activity was observed at the dose of up to 256 μg/mL. Most antimicrobial peptides were expressed in *Escherichia coli*. In this work, we developed a highly efficient expression system in *Bacillus subtilis* to allow for potential application of cathelicidin-BF. The cathelicidin-BF gene was fused with a small ubiquitin-like modifier (SUMO) gene and ligated into a *Escherichia coli*/*Bacillus subtilis* shuttle vector pHT43, generating pHT43-SUMO-CBF, which was subsequently transformed into *B. subtilis* strain WB800N. The fusion protein SUMO-CBF was secreted into the culture medium, and 60mg of recombinant fusion protein was purified from 1 L of culture supernatant by Ni-NTA chromatography. After the SUMO-CBF fusion protein was cleaved by the SUMO protease 1 at 4°C overnight, the cleaved sample was reapplied to a Ni-NTA resin. Finally, peptide yields of 8mg/l recombinant cathelicidin-BF were achieved. The recombinant cathelicidin-BF had similar antimicrobial activity to the synthetic cathelicidin-BF. These results may lead to a cost-effective way for the mass production of cathelicidin-BF in *B. subtilis*.

Key Words: antimicrobial peptide, *Bacillus subtilis*, expression

Breeding and Genetics Symposium: Systems Biology in Animal Breeding: Identifying relationships among markers, genes, and phenotypes

56 Building SNP-derived regulatory networks. A. Reverter,* *CSIRO Livestock Industries, Brisbane, Queensland, Australia.*

The advent of cheaply available high-throughput genetic and genomic techniques has equipped animal geneticists with an unprecedented ability to generate massive amounts of molecular data. As a result, large lists of genes differentially expressed in many experimental conditions of interests have been reported and, likewise, the association of an ever-growing number of DNA variants with phenotypes of importance is now a routine endeavor. While these studies have greatly improved our understanding of the genetic basis of complex phenotypes, they have also revealed the difficulty in explaining more than a fraction of the genetic variance. Inspired by this data rich - knowledge poor dichotomy, systems biology aims at the formal integration of seemingly disparate data sets allowing for a holistic view of the system and where the key properties emerge in a natural fashion. Herein, I present 2 examples of rigorous ways of integrating molecular data anchored in the power of gene network inference. The first example in concerned with the onset of puberty in cows bred in tropical regions of Australia. Using the results from genome-wide association studies across a range of phenotypes, we developed what we termed an association weight matrix to generate a gene network underlying cattle puberty. The network was mined for the minimal set of transcription factor genes whose predicted target spanned the majority of the topology of the entire network. The second example deals with piebald, a pigmentation phenotype in Merino sheep. Two networks were developed: a regulatory network and an epistatic one. The former is inferred based on promoter sequence analysis of differentially expressed genes. The epistatic network is build from 2-locus models among all pair wise associated polymorphisms. At the intersection between these 2 networks, we revealed a set of genes and gene-gene interactions of validated and de novo predicted relevance to the piebald phenotype. These new approaches render attractive a search for genetic mechanisms underlying phenotypes of importance in livestock species.

Key Words: systems biology, gene network

57 Networks and pathways to guide genomic selection. W. M. Snelling*[1], R. A. Cushman[1], J. W. Keele[1], C. Maltecca[2], M. G. Thomas[3], M. R. S. Fortes[4,5], and A. Reverter[4], *[1]USDA, ARS, US Meat Animal Research Center, Clay Center, NE, [2]Animal Science, North Carolina State University, Raleigh, [3]Animal Sciences, Colorado State University, Fort Collins, [4]Cooperative Research Center for Beef Genetic Technologies, CSIRO Livestock Industries, Brisbane, QLD, Australia, [5]The University of Queensland, School of Veterinary Medicine, Gatton, QLD, Australia.*

Many traits affecting profitability and sustainability of meat, milk and fiber production are polygenic, with no single gene having an overwhelming influence on observed variation. No knowledge of the specific genes controlling these traits has been needed to make dramatic improvement through selection. Gains have been made through phenotypic selection, enhanced by pedigree relationships and continually improved statistical methodology. Genomic selection, recently enabled by assays for dense SNP located throughout the genome, promises to increase selection accuracy and accelerate genetic improvement by emphasizing the SNP most strongly correlated to phenotype, although the genes and sequence variants affecting phenotype remain largely unknown. These genomic predictions theoretically rely on linkage disequilibrium (LD) between genotyped SNP and unknown functional variants, but familial linkage may increase effectiveness for predicting individuals related to those in the training data. Genomic selection with biologically relevant SNP genotypes should be less reliant on LD patterns shared by training and target populations, possibly allowing robust prediction across unrelated populations. While the specific variants causing polygenic variation may never be known with certainty, several tools and resources can be employed to identify those most likely to affect phenotype. Dense SNP associated with phenotype provide a one-dimensional approach to identify genes affecting specific traits, while associations with multiple traits allow defining networks of genes interacting to affect correlated traits. Such networks are especially compelling when corroborated by existing functional annotation and established molecular pathways. The SNP occurring within network genes, mined from public databases or derived from genome and transcriptome sequences, may be classified according to expected effects on gene products. Coupling evidence from livestock genotypes, phenotypes, gene expression and genomic variants with existing knowledge of gene functions and interactions may provide greater insight into the genes and genomic mechanisms affecting polygenic traits, and enable functional genomic selection for economically important traits. USDA is an equal opportunity provider and employer.

Key Words: genomic prediction, functional genomics, gene network

58 Causal graphical models in quantitative genetics and genomics settings. G. J. M. Rosa* and B. D. Valente, *University of Wisconsin, Madison.*

Phenotypic traits may relate to each other through complex causal relationship networks, which may transcend across transcriptome, proteome, metabolome, and endpoint phenotypes, such as economically important traits in livestock. Moreover, such systems of phenotypic interrelationships are often modulated by the joint action of genetic and environmental effects. For example, transcriptional levels may be affected by reproductive status or developmental stage, which in turn may be mediated by other physiological variables, with genetic polymorphisms and environmental components contributing to animal-to-animal variation. A probabilistic representation of such biological systems can be accomplished through causal graphical models, which allow expressing complex relationships between variables. Applying such models, however, involves a central task of inferring the causal structure underlying phenotypic networks, i.e., determining the subset of traits that directly affects each trait of interest. This challenge may be tackled by using algorithms that perform a data driven search for plausible causal network structures, based on some specific assumptions such as the causal sufficiency. In this context, quantitative genetics and genomics have been utilized either to relax the causal sufficiency assumption from removing polygenic pleiotropic effects or by using QTL information to aid in causal structure search and edge orienting. In this presentation we will discuss such applications to phenotype network studies, focusing on the use of genomic information to aid inferences. Additionally, we will provide examples of application of such methods, and discuss their potential benefits in animal sciences, such as optimal management decision and improvement of multiple traits in livestock.

Key Words: graphical models, causal inference, quantitative genetics

59 A systems biology definition for semen quality.

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We have shown that semen quality can be defined as the number of mobile sperm produced per male per day. Moreover, semen quality is subject to genetic selection when so defined. Sperm mobility is a quantitative trait in poultry, and male fertility is a function of sperm mobility phenotype. The term sperm mobility denotes sperm that move against resistance at body temperature. In other words, all mobile sperm are motile but not all motile sperm are mobile. Immobile sperm contain dysfunctional mitochondria. Such mitochondria are damaged before ejaculation. The ratio of mobile to immobile sperm within an ejaculate varies among roosters and is independent of age. We hypothesized that premature mitochondrial failure was due to sperm cell and reproductive tract attributes that interact to affect sperm in a stochastic manner. Our current work tested this hypothesis in terms of (1) reproductive tract throughput, as defined by the number of mobile sperm produced per gram testis per day, and (2) the testis transcriptome. Test subjects were roosters from 2 experimental lines of chickens developed at Oregon State University. Distinct sperm mobility phenotypes have been maintained between lines for more than a decade without inbreeding. Our experimental outcomes demonstrated that deferent duct transit time does indeed differ between lines. In this regard, it is noteworthy that this duct contains the bulk of a rooster's extragonadal sperm reserve. Whereas differential gene expression was first observed in terms of sperm cell glycolytic enzymes (downregulated in sperm from low line males), we have now observed differential gene expression between lines at the level of the testis transcriptome. Analyses based upon reads per kilobase of mRNA per million reads identified 3000 transcripts that were differentially expressed at 1.5-fold or more up or down ($P < 0.01$). Those genes were mapped to the original GWAS data to identify SNPs in mRNAs differentially expressed between lines. Three genes are now under investigation: ATP5a1, CKMT2, and ARMC2. We have 2 long-term goals: (1) to predict adult reproductive potential using DNA obtained from chicks, and (2) to improve fertility within pedigree lines of chickens through SNPlotype-based selection.

Key Words: fertility, sperm, transcriptome

60 A systems-genetics analysis of bovine skeletal muscle iron content.

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Regulation of cellular iron is critical in immune, mitochondrial, and erythrocyte function. Improper iron homeostasis results in disease both in the case of excessive iron (hemochromatosis) and when iron is deficient (anemia). Therefore, genetic regulation of iron is important to both human and animal health. Since beef is an excellent source of dietary iron, our objective was to investigate the genetic mechanisms responsible for variation in skeletal muscle iron content. To determine the genetic architecture of skeletal muscle iron content, we analyzed Illumina 54k bovine SNP genotypes ($n = 2259$) using a Bayes C genomic selection model in GenSel software. To investigate the transcriptional control of skeletal muscle iron content, we used RNA-seq to contrast mRNA levels in 5 high and 5 low ($n = 10$) total iron content Longissimus dorsi samples. Sequence tags were aligned to the UMD3 genome build using Cufflinks software and analyzed in R assuming a Poisson distribution accounting for fixed effects of iron, sex, age and contemporary group. False discovery rate was controlled using qvalues. GWAS results indicated that markers with the largest effect were located on chromosomes1, 7, 15, and 17. Markers on chromosomes 7 and 17 were near GDF15 and SMAD1 genes with known roles in human hemochromatosis. RNA-seq identified 3010 differentially expressed genes ($q < 0.05$). Pathway studio software was used to identify pathways including known regulators of iron homeostasis: BMP6 ($P < 6.38\text{E}^{-8}$), and STAT1 ($P < 1.3\ \text{E}^{-27}$). The SMAD3 pathway was identified as a potential novel regulator of iron homeostasis ($P < 3.07\text{E}^{-33}$). Additional pathway analyses and genome-wide re-sequencing are underway to identify novel iron regulatory mechanisms. Interestingly, our initial results indicate that many of the same genes involved in human hemochromatosis may also regulate bovine skeletal muscle total iron content.

Key Words: bovine skeletal muscle, genome-wide association study (GWAS), iron homeostasis

Companion Animals Symposium: Nutrition Special Needs—The relationship between novel ingredients, environment and gene expression

61 Alternative ingredients: Which have scientific merit? G. Aldrich,* *Pet Food & Ingredient Technology Inc., Topeka, KS.*

As pet foods continue to address market and health concerns, and as the volume of pet food around the world continues to grow, pressure to develop alternative ingredients and to expand existing ingredient reservoirs escalates. Alternative ingredients are considered for several reasons. These include perceived biomedical value to support the expanding need for novel proteins and starches for so-called hypoallergenic or elimination diets. Regulatory limitations on claims regarding food benefits beyond simple sustenance leaves marketing little latitude short of drawing attention to ingredients as primary points of competitive differentiation. Finally, as consumer perception of certain traditional ingredients becomes less accepting there is an increased demand for more unique, humanized, and less chemical or agricultural sounding elements. Regardless of rationale, utilization of non-traditional, novel, or experimental ingredients as alternatives necessitates the exploration of safety, efficacy and utility for pet diets. Some of this work has been accomplished for the targeted species (dogs and cats) and in some cases validation with model species such as rats and mice is available. However, many of these alternative ingredients are being utilized with little animal or food quality evaluations. Some of these alternative ingredients can be quite exotic, but most are more mainstream alternative ingredients being used with enough frequency that a closer look is warranted. This list includes such items as rabbit and duck meals for lamb and chicken meal, potato and pea protein concentrates for soybean and corn gluten meal, pea fiber for beet pulp, chia for flax, sweet potato and tapioca for grains, algal oil for fish oil, olive oil and coconut oil for soybean or canola oils, cod liver oil for vitamins A and D, and chicken cartilage for glucosamine to name a few. This presentation will review the relevant published information for the more popular alternative ingredients and identify which have scientific merit.

Key Words: petfood, dog, cat

62 Benefits of probiotic supplementation in stressful situations in companion animals. M. R. Lappin,* *Department of Clinical Sciences, Colorado State University, Fort Collins.*

There are many products in the veterinary market purported to contain probiotics that exert a beneficial effect on dogs or cats. In humans, results of studies vary dramatically which emphasizes that biological effects of individual probiotics will vary and that each probiotic should be rigorously evaluated in a controlled fashion to define the potential for clinical utility. In addition, the source of the probiotic should also be considered as the majority of veterinary products claiming to contain probiotics generally do not meet the label claim. It is known that many probiotics in the lactic acid bacteria group help balance the endogenous gastrointestinal microbiota and some can inhibit replication of pathogenic bacteria. It is also now known that some probiotics can beneficially influence innate and acquired immunity systemically by a variety of proposed mechanisms including inducing cytokine production, natural killer cell activity, and both specific and non-specific immunoglobulin production. Recently, our laboratory completed 2 studies showing the beneficial effect of a probiotic (FortiFlora; Nestlé Purina PetCare) on animals in stressful situations. Feline herpesvirus 1 (FHV-1) infection of cats causes chronic respiratory and ocular infections that can be reactivated by stress in a similar fashion to human herpesvirus associated cold sores. It was shown that cats supplemented daily with the probiotic developed less severe signs of FHV-1 associated illness during periods of stress when compared with the control group. Stress associated diarrhea is common in companion animals and is thought to result from changes in the gastrointestinal microbiota. When one cat room of an animal shelter was supplemented with the probiotic and the other room fed a placebo, it was shown that the proportions of housed cats with diarrhea of 2 d or greater was significantly lower in the treated group (20.7% versus 7.7%). In both of these stressful situations, it appears the use of the probiotic improved the health and wellbeing of the treated animals.

63 Dietary and environmental management of feline lower urinary tract disease (FLUTD). K. R. Kerr,* *University of Illinois, Urbana.*

Feline lower urinary tract disease (FLUTD) is a grouping of symptoms that affect the cat's lower urinary tract system and bladder; however, the clinical signs are rarely indicative of a particular disease. There are many conditions that can result in signs of FLUTD, including urolithiasis, cystitis, and urethral obstruction, but the vast majority of cases are idiopathic. Feline idiopathic cystitis (FIC) is seen in 50 to 65% of FLUTD cases. While cases of non-obstructive FLUTD are usually self-limiting, most cats have recurrence of clinical signs. Treatment is recommended to reduce recurrence because FIC is painful and distressing to the cat, can result in self-traumatization and behavioral changes. In cases that progress to obstructive disease, it could be fatal. The etiopathogenesis of FLUTD likely involves combinations of factors: locally present external factors within the urine, such as urine supersaturation, abnormalities in protective factors, or the presence of toxins and microorganisms; intrinsic abnormalities in the glycosaminoglycan (GAG) layer, the urothelium, or other urogenital morphology; and increased sensitivity or abnormal response to external or internal stimuli. Dietary impact and recommendations for decreasing recurrence of the most common types of urolithiasis based FLUTD have been available for many years. More recently, treatments that address additional contributing factors have arisen. The primary recommendations for FLUTD in general are to alleviate stress, and increase water intake. Multimodal environmental modification is one approach to alleviating stress that has been examined in regards to FLUTD. Supplemental GAGs are sometimes provided to potentially ameliorate abnormalities in the GAG layer. Until definitive cause for a FLUTD case can be identified and eliminated (if possible), environmental and dietary modifications will play a significant role in decreasing recurrence events.

Key Words: feline lower urinary tract disease (FLUTD)

64 Functional nutrition: Novel ingredients and new findings. I. S. Middelbos,* *Novus International Inc., St. Charles, MO.*

Human functional foods and beverages currently represent a multi-billion dollar market that is growing rapidly. These functional foods aim to deliver specific benefits beyond standard nutrition, based on the functional ingredients they contain. The continued premiumization of pet food, combined with the humanization of companion animals creates a strong drive to bring functional ingredients from the human market to pets. Indeed, many functional ingredients used in humans have application in companion animals. Two leading categories of functional ingredients for both humans and companion animals relate to joint health and digestive health. In many instances, manifestations of joint or digestive conditions include pain and below-normal functionality of the joint or the digestive tract. When joints are affected, often this leads to decreased mobility and reduced motivation for physical activity, which may in turn contribute to other conditions (e.g., obesity). Currently, several ingredients are under investigation for their potential to support healthy joints. Many of these are food ingredients or co-products that were not previously considered to have specific functionality. Examples include green-lipped mussel and hydrolyzed eggshell membrane and chicken collagen. Digestive conditions may be uncomfortable for the pet as well as the pet owner, because of the resulting symptoms (e.g., diarrhea and flatulence). Whereas dietary fiber has been a mainstay to support a healthy digestive tract, the science is currently evolving to help us understand how specific fiber fractions and structures may affect certain digestive health conditions. Moreover, the field of probiotics continues to evolve with ever more targeted strains to address conditions along the entire digestive tract. The common thread among all these conditions is the immunological component involved. The most successful ingredients appear to be those that are able to negotiate some moderation in immune response. The field of functional ingredients is growing rapidly and has much potential to improve functional nutrition of both man and companion animal, provided the regulatory frameworks allow for this potential to come to fruition.

Key Words: companion animals, functional ingredients, functional foods

65 Nutrigenomics: Using gene expression data to understand and manage pet obesity.

K. S. Swanson,* *University of Illinois, Urbana.*

Pet obesity is a major health problem, with an estimated 30 to 40% of dogs and cats considered as overweight or obese in the United States. Obesity is pleiotropic, resulting in altered adipose, liver, and skeletal muscle tissue function. These changes in tissue functionality lead to metabolic alterations (e.g., insulin resistance, hyperlipidemia), increase risk of chronic diseases, and decrease life span. Although obesity is well accepted as being unhealthy, the mechanisms by which the obese state leads to chronic disease are poorly understood. The use of transcriptomics, particularly whole genome microarrays and quantitative RT-PCR, has increased understanding of tissue biology and has begun to link mRNA changes to the physiological state. Companion animal biologists have applied these technologies to study adipose, skeletal muscle, and hepatic tissues of dogs and cats in many ways. Research has focused on lean vs. obese pets, pets rapidly gaining weight following spay/neuter or ad libitum feeding, pets undergoing weight loss, and obese pets fed specific dietary ingredients to improve metabolism or insulin sensitivity. The results of these studies and application to pet nutrition and management will be reviewed.

Key Words: pet obesity, transcriptomics, nutrition

Dairy Foods: Cheese and Products Processing

66 Influence of proteolysis and amino acid release on bitterness and texture of reduced-fat Cheddar cheese. M. W. Børsting[1], K. B. Qvist*[1], J. Vindeløv[1], F. K. Vogensen[2], and Y. Ardö[2], [1]*Chr. Hansen A/S, Hørsholm, Denmark,* [2]*Department of Food Science, Faculty of Life Sciences, University of Copenhagen, Copenhagen, Denmark.*

In spite of much research, it remains difficult to produce high quality reduced-fat Cheddar cheese. The objective of this study was to investigate the effects of 2 rennets, bovine (BC) and camel chymosin (CC), with different proteolytic activity, and 2 starter cultures with different ability to release amino acids on texture and flavor development. One starter (O) contained strains of *Streptococcus lactis* and *cremoris*; the other (OLb) additionally contained a proteolytic *Lactobacillus delbrueckii* strain. Cheeses with all 4 combinations of coagulants and cultures were produced in 4 replicates. During manufacture essentially identical acidification profiles were obtained, and cheeses were analyzed during 28 wk for composition of casein, peptides and free amino acids by capillary electrophoresis, LC-MS and HPLC, and for textural properties by uniaxial compression. Sensory evaluation of the ripened cheeses was made as well. BC cheeses showed more extensive hydrolysis of α_{S1}-CN, and of peptides derived from it than CC cheeses. BC cheeses also contained higher levels of the bitter peptide β-CN (f193–209) and obtained higher bitterness scores. In OLb cheeses, peptide degradation was extensive, and peptide profiles of BC and CC cheeses were similar after 28 wk, except for α_{s1}-CN (f1–9) and β-CN (f193–209). OLb increased the content of free amino acids ca. 3-fold over that obtained with O. After 28 wk CC cheeses had higher sensory hardness, stress at fracture and modulus of deformability than BC cheeses. OLb cheeses had higher stress but lower strain at fracture, and higher modulus of deformability than O cheeses. Overall, CC reduced problems with bitterness in reduced-fat Cheddar, compared with BC, but the associated increase in hardness was not compensated for by the addition of a proteolytic *Lactobacillus* strain.

Key Words: reduced-fat Cheddar, camel chymosin, *Lactobacillus*

67 Impact of sodium, potassium, magnesium, and calcium salt cations on pH, proteolysis and microbial populations during storage of Cheddar cheese. D. J. McMahon*[1], N. Farkye[2], L. V. Moyes[3], and C. J. Oberg[1,3], [1]*Western Dairy Center, Utah State University, Logan,* [2]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo,* [3]*Department of Microbiology, Weber State University, Ogden, UT.*

Sodium reduction in cheese can assist in reducing overall dietary Na intake, yet saltiness is an important aspect of cheese flavor. Our objective was to evaluate the effect of partial Na substitution on survival of lactic acid bacteria (LAB) and nonstarter LAB (NSLAB), pH and extent of proteolysis in full fat Cheddar cheese. Seven full fat Cheddar cheeses with molar salt contents equivalent to 1.7% (wt/wt) NaCl but with different ratios of Na, K, Ca and Mg cations were manufactured. Cheese made using 1.7% NaCl (C) served as a positive control while cheese made using 0.7% NaCl served as a negative control (LC). Cheeses were aged at 6°C for 9 mo. Total LAB, starter lactococci, and NSLAB were enumerated using selective media and varied incubation conditions. Proteolysis was monitored by gel electrophoresis and measuring water-soluble N (WSN). Cheese C had a mean composition of 35.0% moisture, 50.2% FDB, 26.0% protein, and 1.74% (±0.05%) salt. Other full salt cheeses had a similar composition, while the LC cheese had higher moisture, 37.3%, and a salt content of 0.68% (±0.04%). Mean water activity of full salt cheeses at 28 d was 0.956 while the LC cheese was 0.975. After salting there was a faster initial drop in cheese pH with K substitution and throughout storage the pH of cheese with 75% K substitution was lower than cheese C. There was no difference in residual casein levels or %WSN levels in the cheeses based on salt content with all cheeses increasing from ~5% WSN at d 1 to ~20% after 6 mo. Cheese C (~4.7% salt-in moisture) exhibited expected changes in bacteria microflora during storage with lactococci gradually decreasing from ~10^7 cfu/g after pressing to ~10^4 cfu/g after 4 mo, while the NSLAB gradually increased from < 10^3 cfu/g to ~10^5 cfu/g to become the dominant portion of total LAB after 4 mo. In cheese LC (~1.8% salt-in-moisture), the lactococci stayed at ~10^6 cfu/g through 6 mo of storage and remained the dominant LAB with NSLAB at ~10^5 cfu/g. With K substitution for Na, there was a trend for lactococci to remain dominant or be at similar levels as the NSLAB, especially when salt substitution also included 10% Mg or Ca.

Key Words: cheese, sodium, potassium

68 Impact of different types of emulsifiers on the reformability of grated cheese. C. Akbulut* and J. A. Lucey, *University of Wisconsin-Madison, Madison.*

Reforming the cheese has found several applications in dairy industry. Our objective was to determine the effect of different types of emulsifiers (EM) on the texture and rheological properties of low-fat and full-fat Cheddar cheese after reforming. Cheeses were ground using food processor and then pressed into plastic molds for 1 h using Carver food press. Eight different types of EM at 4% (w/w) level were added to grated cheeses before reforming. These types included anionic: citric acid esters of monoglycerides (CITREM), diacetyl tartaric acid esters of monoglycerides (DATEM), sodium stearoyl lactylate (SSL), zwitterionic: lecithin and non-ionic: distilled monoglycerides (DM), lactic acid esters of monoglycerides (LACTEM), acetic acid esters of monoglycerides (ACETEM) and sorbitan tristearate (STS). Control reformed cheeses were prepared for both low-fat and full-fat cheese made without any EM. Analyses were performed on cheese bases and reformed cheeses that had been stored for 2 wk at 4°C. Rheological properties of cheese were measured using small amplitude oscillatory test during heating from 5 to 85°C. Textural properties were tested with Texture Analyzer. Melt properties were tested using the UW-Melt-profiler. Use of SSL reduced the hardness of low-fat cheese and made it very sticky and soft. The use of CITREM, DATEM and STS resulted in firmer cheese texture. DATEM and SSL exhibited significantly lower loss tangent maximum during heating (less melt) as compared with control cheese. At low measurement temperatures, except for STS, non-ionic EM did not significantly alter the texture of full-fat cheese; however at high temperatures cheese with non-ionic EM differed from control and they had improved meltability. Use of non-ionic EM seemed to make the low-fat cheese more prone to fracture during compression except for the use of STS. It was concluded that the textural properties of the reformed cheese can be modified with the use of different types of EM. The texture and melting characteristics of the reformed cheese were dependent on charge, hydrophilic-lipophilic balance and molecular characteristics of the EM.

Key Words: cheese reforming, texture, emulsifiers

69 Phenotypic factors affecting cheese yield and whey losses from individual cows. C. Cipolat Gotet,* M. Penasa, A. Cecchinato, M. De Marchi, and G. Bittante, *Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Legnaro, Padova, Italy.*

The aims of this study were to assess sources of variation of several individual cheese yields obtained by using a micro-cheese making method. Traits were: [1] weight (g) of fresh curd (CY_{curd}) or curd total solids (CY_{solids}) or curd water (CY_{water}) divided by weight (g) of milk processed; [2] weight (g) of total solids (REC_{solids}) or fat (REC_{fat}) or protein ($REC_{protein}$) recovered in curd divided by weight (g) of constituent in milk. A total of 1,271 Brown Swiss cows from 85 herds were sampled. The cheese making procedure consisted of the heating of raw milk (1.5L), the acidification by the inoculation of a direct-to-vat starter of selected strains of *S. thermophilus*, the addition of calf rennet, the detection of coagulation time, 2 subsequent cuts of the curd, the rest of the curd, the pressing and the brining. Then, curd was weighed to calculate the aforementioned traits. Means (SD) for CY_{curd}, CY_{solids}, CY_{water}, REC_{solids}, REC_{fat} and $REC_{protein}$ were 0.150 (0.019), 0.072 (0.009), 0.078 (0.013), 0.521 (0.036), 0.899 (0.036) and 0.781 (0.024), respectively. The linear model considered effects of herd, vat, parity, days in milk and milk yield. The effect of days in milk was relevant for all traits: CY_{curd}, CY_{solids}, CY_{water} and REC_{solids} showed a decrease after parturition and an increase thereafter; REC_{fat} showed a decrease till mid lactation and a slow increase afterward, whereas an opposite trend was detected for $REC_{protein}$. Increasing parity decreased CY_{curd}, despite the inclusion of milk yield in the model, mainly because of a decrease of CY_{water} rather than as a consequence of the variation of CY_{solids}. The effect of milk yield was negative on CY_{curd} because of a decrease of CY_{solids}, and not of CY_{water}. Large differences were detected among herds suggesting differences in dairy management practices. The micro-cheese making method can be used to investigate variation in individual cheese yield and milk components recovery and for genetic purposes.

Key Words: individual cheese yield, whey losses, micro-cheese making

70 Sensory selection of an antimicrobial for use in string cheese. A. Lammert*[1], L. Collinsworth[1], N. Farkye[1], M. Arnold[1], A. Lathrop[2], and T. Taylor[2], [1]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo,* [2]*Department of Food Science and Nutrition, California Polytechnic State University, San Luis Obispo.*

Sodium has a significant role in the string cheese matrix such as flavor enhancement and inhibition of microbial growth. Recently, there have been government and industry initiatives to reduce the sodium content in a wide variety of foods by 25% within the next 5–10 years. String cheese, often marketed as a healthy snack, has 8% DV of sodium per stick. A lower sodium alternative would need to be safe to eat and taste good; therefore, the antimicrobial used to partially replace the role of salt should be effective against pathogens and have acceptable sensory qualities. The objective of this work was to find an antimicrobial, with demonstrated pathogen protection properties, that is sensory transparent. Three sensory tests were completed using 4 antimicrobials, with confirmed pathogen protection measured using a 5 pathogen cocktail and cheese agar, applied to commercial, unbrined string cheese: 1) A balanced reference duo-trio test was used to determine a difference with and without antimicrobial application (n = 38), 2) Twenty-two cheese consumers used a balanced, 9 point hedonic test to evaluate the overall acceptability, aroma, flavor, and after taste, and 3) A 2^2 design was used to determine the interaction of antimicrobial contact time (30 s and 3 min) and concentration (recommended concentration ± 50%). Differences were evaluated using a duplicated, balanced reference duo-trio test (n = 15). The results showed: 1) 3 potential antimicrobials could be sensory transparent and protect unbrined string cheese from potential pathogens, 2) consumers found no significant difference ($\alpha > 0.05$) for any of the antimicrobials tested for overall acceptability, flavor, or after taste; however, the aroma of 2 antimicrobials were found to be significantly different ($\alpha < 0.05$), and 3) the 3 min contact time and concentration + 50% was found to be significantly different($\alpha < 0.05$) than the rest of the combinations tested. The outcomes indicate that the perceived sensory aspects of unbrined string cheese may change based on the type or method used to apply the antimicrobial.

Key Words: lower sodium, antimicrobials, consumer testing

71 Microfiltration of skim milk and modified skim milk using a 0.1-μm ceramic uniform transmembrane pressure system at 50, 55, 60, and 65°C. E. E. Hurt,* M. Adams, and D. M. Barbano, *Cornell University, Department of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY.*

Our objective was to determine the effect of operating a microfiltration (MF) unit at temperatures up to 65°C on serum protein (SP) removal from skim milk (SM), with and without prior removal of low molecular weight (MW) soluble SM components by ultrafiltration (UF). SM was pasteurized (72°C, 16s) and split into 2 batches. The first batch was ultrafiltered to remove about 90% of the low MW soluble SM components. After UF, the UF retentate was diluted back to the protein concentration of SM. The diluted UF retentate (DUR) and unaltered SM were then microfiltered. The MF system was operated at a concentration factor of 3X and a flux of 54 kg/m^2 per h. After flushing the system with SM or DUR to remove water, the MF retentate and permeate were recycled to the feed tank. The MF system was run in recycle mode at 50, 55, 60 and 65°C for 1h at each temperature. Samples were taken of the retentate and permeate after each hour. The experiment was repeated 3 times. As temperature increased from 50 to 65°C the retentate recirculation pump frequency required to maintain a flow of 648L/min decreased from 59.0 to 57.7Hz ($P < 0.05$) for SM and from 58.6 to 57.3Hz ($P < 0.05$)for DUR indicating reduced pump energy requirements. No permeate pressure decreases indicative of fouling were seen, suggesting an increase in flux may be possible. Between 50 and 65°C there was a decrease in SP removal from 66.39 to 57.76% ($P < 0.05$) for SM and from 67.47 to 54.84%($P < 0.05$) for DUR. The decrease in SP removal was likely caused by heat denaturation of SP and interaction with casein. SP removal did not vary significantly between SM and DUR ($P > 0.05$). It may be possible to operate a MF system to remove SP from SM at temperatures above 50°C. The decrease in pumping costs and possible increase in flux has to be balanced with a decrease in SP removal as temperature increases. It does not appear that low MW soluble materials in SM such as lactose, NPN or calcium caused fouling that reduced SP removal at temperatures up to 65°C.

Key Words: microfiltration, serum protein removal, processing temperature

72 Leveraging existing processing lines for yogurt product innovation through the use of advanced texturizing systems. M. E. Yildiz,* S. Mutz-Darwell, M. Yurgec, A. Perez, and H. Simpson, *National Starch, Bridgewater, NJ.*

The objective of the current work was to test new ingredients to show that using ingredients with different functionalities, it is possible to formulate texturally very different products such as blended yogurt, Greek yogurt

and European set dessert using a common stirred yogurt lines. This will leverage existing capabilities, avoid investment in costly specialized equipment and capabilities and help dairy manufacturers produce variety of new products. In this study several texturally different products were made using Microthermix. Liquid ingredients were added to the Likwifier. Dry ingredients were slowly added while mixing at 500 rpm and hydrated for 30 min before processing in Microthermics. Preheating temperature range of between 140 to 150F and homogenizer pressure range between 50 to 250 bars were studied to find optimal conditions. Final heat and hold time was constant at 208F/6 min. Products made under optimal processing conditions were characterized using rheological and sensory analysis. Rheological methods included dynamic and steady tests whereas descriptive sensory analysis included characterization of several key fundamental texture attributes. In this presentation case studies on developing consumer preferred blended yogurts, producing Greek style yogurts without straining will be presented. For blended preferred yogurts, benchmark texture was quantified to have an elastic modulus (G') of 163 Pa and shear viscosity (Eta) of 6.6 Pa.s. Formulated yogurts had elastic modulus of 218 and shear Eta of 5.5. However, sensory analysis revealed that key attributes such as spoon indentation meltaway, thickness in the mouth and residual mouthcoating there were very similar. For Greek yogurt, commercial strained benchmark had G' of 2220 Pa and Eta of 13 Pa.s while formulated Greek yogurts had elastic modulus of 1535 Pa and Eta of 9.51 Pa.s. However, sensory analysis revealed that key attributes such as spoon indentation meltaway, thickness in the mouth and residual mouthcoating there were very similar. We conclude that it is possible to leverage existing stirred yogurt lines by only changing the key parameters for dairy unit operations to develop texturally very different products some of which are traditionally made with specialized equipment.

Key Words: dairy, processing, texturizers

73 Gravity separation of fat, somatic cells, and bacteria in raw and pasteurized milks.

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The objective of experiment 1 was to determine if the extent of gravity separation of milk fat, bacteria, and somatic cells is influenced by time and temperature of gravity separation or the level of contaminating bacteria present in the raw milk. The objective of experiment 2 was to determine if there was an effect of different temperatures of milk heat treatment on the gravity separation of milk fat, bacteria, and somatic cells. In raw milk, fat, bacteria, and somatic cells rose to the top of columns during gravity separation. About 50 to 80% of the fat and bacteria were present in the top 8% of the milk after gravity separation of raw milk. Gravity separation for 7 h at 12°C produced equivalent separation of fat, bacteria, and somatic cells as did separation for 22 h at 4°C. The completeness of gravity separation of fat was influenced by the level of bacteria in the milk before separation. Milk with high bacteria count had less (about 50 to 55%) gravity separation of fat than milk with low bacteria count (about 80%) in 22 h at 4°C. Gravity separation caused fat, bacteria, and somatic cells to rise to the top of columns for raw whole milk and HTST pasteurized (72.6°C, 25 s) whole milk. Pasteurization at >76.9°C for 25 s prevented all 3 components from rising, possibly due to denaturation of native bovine immunoglobulins that normally associate with fat, bacteria, and somatic cells during gravity separation. Gravity separation can be used to produce reduced fat milk with low bacteria and somatic cell counts, and may be a critical factor in the history of safe and unique traditional Italian hard cheeses produced from gravity separated raw milk. A better understanding of the mechanism of this natural process could lead to the development of new nonthermal thermal technologies to remove bacteria and spores from milk or other liquids.

Key Words: gravity separation, bacterial removal, somatic cell removal

74 Effect of PEF and UV and their combination on selected microorganisms and physico-chemical properties in whey.

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Pulsed electric field (PEF) and UV irradiation (UV) are emerging food processing technologies that could represent an alternative to conventional high-temperature short-time pasteurization (HTST) for whey preservation. This study looked into effects of both PEF and UV individually and combined for inactivation of *Listeria innocua* and *Zygosaccharomyces bailii* compared with HTST and change in whey qualitative aspects (pH, electrical conductivity, and color) was also investigated. Inoculated whey was PEF-processed at electric field strengths of up to 40 kV/cm, using treatment times up to 4937 µs, and resulting in energy densities up to 173 kJ/L, while UV was applied for treatment times of up to 7.7 s and dosages up to 229 mJ/mL. Thermal controls were obtained by pasteurizing whey at 72 and 90°C for respective holding times of 15 (HTST72) and 30 s (HTST90). *L. innocua* and *Z. bailii* loads in whey were reduced by up to 3.1 and 3.0 $\log_{10}$ cfu/mL, respectively, with PEF, whereas, UV inactivated up to 6.0 and 5.9 $\log_{10}$ cfu/mL, respectively ($P < 0.05$). With HTST higher *L. innocua* and Z. bailii inactivation of ≥ 8.9 and ≥ 7.8 $\log_{10}$ cfu/mL ($P < 0.05$) was obtained, correspondingly, at 72 and 90°C. However, PEF/UV proved to be comparably effective for bacteria and yeast inactivation of ≥ 8.8 and ≥ 7.9 $\log_{10}$ cfu/mL ($P \geq 0.05$) in whey, while lower reductions of up to 6.9 and 7.1 $\log_{10}$ cfu/mL of *L. innocua* and *Z. bailii* were obtained after UV/PEF ($P < 0.05$). For physico-chemical analysis whey was PEF/UV-treated at 2 selected processing intensity levels, low (PEF/UVL) and high (PEF/UVH), used during the microbial analysis. No significant differences were found in pH ($P \geq 0.05$) while colorimetry indicated HTST72 < PEF/UVH < PEF/UVL < HTST90 ($P < 0.05$). No significant differences in conductivity were obtained between HTST72 and PEF/UVL ($P < 0.05$) in contrast to HTST90 and PEF/UVH ($P \geq 0.05$). Findings showed comparable treatment efficacy with UV- and PEF-based hurdle technologies and HTST for contaminated whey. Overall similar or better product quality was obtained with PEF/UV compared with HTST, thus, indicating PEF/UV as effective non-thermal processing strategy for acid whey.

Key Words: UV irradiation, pulsed electric field (PEF), HTST

Forages and Pastures Symposium: Impact of Fungal-Endophytes on Pasture and Environmental Sustainability

75 Fungal endophytes: Forage friend or foe? C. Young,* *Noble Foundation, Ardmore, OK.*

The epichloae (sexual *Epichloë* and asexual *Neotyphodium* species) are endophytic fungi that systemically infect many cool season grasses, including the common forage grasses tall fescue and perennial ryegrass. The success of endophytes, such as *N. coenophialum* (tall fescue endophyte) and *N. lolii* (perennial ryegrass endophyte), within the host is due to a lifestyle strategy where the fungus systemically infects the aerial parts of the plant without causing disease and is subsequently transmitted in the seed where this association is maintained over successive generations. In modern monoculture-based agriculture, the presence of asexual *Neotyphodium* species has been shown to enhance persistence of the host plant by providing protection from biotic and abiotic stresses. Some known host fitness attributes provided by the endophyte arise from the production of bioactive alkaloids. Lolines and peramine provide beneficial anti-insect properties, while the ergot alkaloids and lolitrem B cause toxicity to grazing livestock that result in production losses. It is well documented that ergot alkaloids produced by the endophyte are the causative agent of fescue toxicosis that presents with numerous detrimental effects such as fescue foot, reproductive disorders, and reduced milk production and weight gains. Similarly, lolitrem B produced by some *N. lolii*-infected perennial ryegrass was found to cause ryegrass staggers. The genes required for the biosynthesis of each alkaloid have been cloned and characterized and this information can now be used to understand alkaloid diversity across the epichloae. To overcome endophyte-related toxicity problems, endophyte-free cultivars were established but despite the improvement in animal quality and production, pasture persistence significantly decreased. Inclusion of “livestock-friendly” endophytes in forage grasses is now considered important in forage grass breeding due to the beneficial properties they impart on the host. Cultivars with endophytes that ameliorate detrimental livestock effects yet retain host fitness benefits are now in use to overcome the problems of livestock toxicity.

Key Words: fescue toxicosis, endophyte, alkaloids

76 Impact of tall fescue—Fungal endophyte associations on sustainability of pastures under current and future environmental conditions. R. McCulley,* J. Iqbal, J. Siegrist, G. Brosi, and J. Nelson, *University of Kentucky, Lexington.*

Tall fescue (*Schedonorus arundinaceous*) is often infected with a fungal endophyte (*Neotyphodium coenophialum*) that, depending on the strain, is capable of producing alkaloids that can affect grazing animal health and pasture ecosystem structure and function. While the above-ground ecological effects of fescue symbiosis with the common toxic form of the endophyte have been well-documented, less is known about below-ground responses or effects of fescue symbiosis with other “novel” strains of *Neotyphodium*. Given that endophyte symbiosis confers abiotic stress tolerance to tall fescue and that the climate and atmosphere are changing, there is a need to understand how tall fescue, the endophyte symbiosis, and the production of toxic alkaloids will be affected by future climatic conditions. Here, we summarize results from 4 studies that explore these topics. Across a range of sites in the southeastern US, tall fescue stands infected with the common toxic strain of the endophyte consistently had greater soil organic carbon and nitrogen than adjacent endophyte-free stands, suggesting that endophyte infection has the potential to increase carbon sequestration in pastures of this region. In central Kentucky, stands of tall fescue infected with the novel endophyte ‘AR-542’ had higher soil-to-atmosphere fluxes of CO_2 and N_2O than adjacent stands of endophyte-free fescue or fescue infected with the common toxic or other novel endophyte ‘AR-584,’ illustrating that root and rhizosphere processes were influenced by endophyte genotype. In Tennessee, we found that 5 years of exposure to elevated atmospheric CO_2 concentrations promoted endophyte-infected tall fescue, but contrary to expectations, endophyte infection frequency did not change under drought conditions or with warming. In Kentucky, warming increased mortality of endophyte-infected vs. –free tillers, and in both experiments, warming significantly increased alkaloid concentrations in infected fescue. These studies demonstrate that endophyte infection is likely important for the sustainability of southeastern US tall fescue pastures both now and in the future.

Key Words: *Neotyphodium*, pasture ecosystems, biogeochemistry

77 Lessons from “down-under” in New Zealand and Australia: The critical role of endophyte in pasture quality and production. D. E. Hume,* *AgResearch, Palmerston North, New Zealand.*

The *Neotyphodium* fungal endophytes of ryegrass and tall fescue are essential for the survival and productivity of these grasses in a large proportion of the pastures in the moderate to high rainfall temperate zones of New Zealand and Australia. This is primarily due to the insect protection these endophytes impart to the grass plant through alkaloid production. This is most evident in New Zealand, with some endophyte strains protecting the grass plant from up to 5 different insect species. The most widespread strains of endophyte are toxic to grazing livestock, resulting in a dilemma for livestock farmers as to whether to choose endophyte-free or endophyte-infected grass seeds. This is of greatest concern for perennial and hybrid ryegrasses, as the market size for tall fescue is relatively small and the majority of tall fescue cultivars over the last century have been sold as endophyte-free. The main disadvantage for farmers is the animal toxic endophyte strains result in ill health of grazing livestock, primarily heat stress, ryegrass staggers (ryegrass only) and fescue foot (tall fescue only). While these symptoms are visually apparent, research has shown there are also reductions in liveweight gains, milk production, reproductive performance and immune function, and in sheep fecal soiling in the breach area resulting in increased fly strike. There are several options for dealing with advantages and disadvantages of endophyte in ryegrass. The most effective solution is the use of selected novel endophytes to manage pasture pests and animal productivity. Industry uptake of this technology has been rapid for the endophytes AR1 and AR37, with AR1 now the industry standard, with other strains also providing options. Greater use of the MaxP/MaxQ novel endophyte in tall fescue is likely to increase the use of this grass species as this endophyte is safe for sheep and cattle and improves grass production and persistence. Further novel endophyte developments are likely to present even more options for the farmer in the future.

Key Words: endophyte, quality, production

78 Phases of physiological adaptation to heat stress and fescue toxicosis.

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Consequences of consuming tall fescue (*Lolium arundinaceum*) infected with the endophyte *Neotyphodium coenophialum* are well known, along with the fact that simultaneous exposure to heat stress (HS) enhances the negative effect. Less information is available about adaptation to these stressors. Studies were performed using cattle in field and chamber environments to identify the components of physiological adaptation to HS and fescue toxicosis. Exposure of Angus cattle to HS in environmental chambers results in an increase in respiration rate (RR) that remains elevated and unchanged for up to 2 weeks of HS. In contrast, rectal temperature (Tre) exhibits a biphasic response, with an initial increase followed after a few days by a greater rise under constant cycling HS. Over the same period, the initial heat-induced rise in sweat rate decreases. Acclimation to HS over a month on pasture decreases both RR and core temperature responses to heat. In a separate study, Angus cattle were maintained on endophyte-infected (E+) and uninfected (E-) tall fescue pastures for 2 mo into mid-summer, then tested in environmental chambers, followed by return to identical pastures for another 2 mo (late-summer) and retesting after this time. Feed intake (FI) and sweat rate were depressed in E+ treated cattle exposed to HS in the chambers with no change from mid- to late-summer periods showing no signs of adaptation. In contrast, Tre of E+ animals exhibited a progressively greater HS response from mid- to late-summer periods with no biphasic pattern as in controls. However, this hyperthermia merged with controls after a few days of HS. Likewise, E+ animals displayed an increase in RR, which quickly returned to control level after several days of HS to suggest adaptation. Despite evidence of thermoregulatory adjustment to these stressors, some thermal responses characteristic of fescue toxicosis (i.e., skin temperature) still show increased sensitivity to a change in air temperature. These results demonstrate that thermoregulatory and non-thermoregulatory responses to the combined stressors of heat stress and fescue toxicosis exhibit different long-term patterns of change.

Key Words: bovine, acclimation, thermoregulation

79 Managing the fungal endophyte/forage symbiosis for optimum forage-animal production.

G. Aiken,* *USDA-ARS, FAPRU.*

Tall fescue (*Lolium arundinaceum* L.) is widely utilized for grazing in the eastern half of the USA. The grass is productive and persistent under low management, which is attributed to alkaloids produced by a fungal endophyte (*Neotyphodium coenophialum*) that infects most tall fescue plants. Unfortunately, the endophyte also produces ergot alkaloids that can induce fescue toxicosis in cattle. Symptoms of the malady include rough hair coat during the summer, elevated body temperature, labored respiration, and decreased serum prolactin. Ergot alkaloids bind biogenic amine receptors in peripheral vasculature that can reduce the animal's ability to dissipate body heat and make them vulnerable to severe heat stress at onset of high ambient temperature. Calf weight gain can be very low on toxic tall fescue, particularly in warm environments, which has limited the use of fescue for stocker production. Although the grass is primarily used for cow-calf production, calving percentages, milk yields, and weaning weights can be reduced on toxic endophyte-infected tall fescue. Further, there is concern of carry-over effects of ergot alkaloids on performance of calves consuming finishing rations in the feedyard. Management technologies have been developed that demonstrate potential in alleviating or mitigating the adverse effects of fescue toxicosis on cattle performance, physiology, and well being. Evaluations of these technologies will be reviewed and the advantages and disadvantages of each will be presented.

Key Words: tall fescue, ergot alkaloids, fescue toxicosis

Graduate Student Competition: ADSA Dairy Foods Division Oral Competition

80 Norbixin partitioning in full-fat and fat-free Cheddar cheese. T. J. Smith* and M. A. Drake, *North Carolina State University, Raleigh.*

Whey protein is an important commercial product for the dairy industry, and a large portion of it is manufactured from colored Cheddar cheese whey. The Cheddar cheese colorant, annatto, is also present in whey and must be removed by bleaching. A better understanding of the primary colorant in annatto, norbixin, is crucial to produce effective methods for its removal from liquid whey. The objective of this study was to determine norbixin partitioning in cheese and whey from full-fat and fat-free Cheddar cheese. Full-fat and fat-free Cheddar cheeses and wheys were manufactured from colored pasteurized milk in quadruplicate. Three different norbixin levels (7.5, 15, and 30 mL annatto/454 kg milk milk) were used for full-fat Cheddar cheese manufacture and one norbixin level was evaluated in fat-free Cheddar cheese (15 mL annatto/454 kg milk). Norbixin extractions were performed on the milk, the unseparated cheese whey, and the pressed cheese. Norbixin was extracted by solvent extraction and column purification and quantified by high performance liquid chromatography. An average of 9.0% of the norbixin added to the full-fat cheese milk was recovered in the whey and 80.3% was recovered in the cheese. In contrast, 1.2% of the norbixin added to skim milk was recovered in the skim milk cheese whey and 85.2% was recovered in the fat-free cheeses. Level of norbixin addition to cheese milk had no effect on norbixin recovery in cheese or whey ($P > 0.05$) but decreased fat content in cheese milk decreased norbixin content of cheese whey and increased norbixin concentration in the cheese ($P < 0.05$). These results suggest that either norbixin is able to more closely associate with casein when fat is not present or that casein matrix formation and final conformation of fat-free cheese differs from that of full-fat cheese such that a higher percentage of norbixin is entrapped.

Key Words: Cheddar cheese, annatto, norbixin

81 The effect of glucose and citric acid concentration on polymerization of lactose by twin-screw extrusion. A. J. Tremaine* and T. C. Schoenfuss, *University of Minnesota.*

The creation of value-added uses for lactose would benefit dairy processors and enhance whey utilization. Polymerization of lactose to produce oligosaccharides is a promising application. Sugars can be polymerized in the presence of heat and acid, and twin-screw extrusion is a process that could provide a continuous production method. The objective of this study was to investigate the effect of glucose seeding and citric acid levels on the yield of oligosaccharides from lactose. Formulas were blended with a ribbon blender and processed on a Buhler 44-mm twin-screw extruder without a die plate. A high shear profile screw was designed in pretrial experiments, and a feed rate of 15 kg/h and 4 barrel section temperatures of 230°C, 238°C, 238°C, and off, from inlet to outlet were chosen. Treatments included 3 glucose concentrations (0%, 10%, 20%) and 2 citric acid concentrations (1% and 2%), with the remainder of the formula consisting of lactose. Process (die temperature, motor torque and specific mechanical energy) and product responses (color, degree of polymerization (DP), soluble fiber) were measured. DP determined by HPLC indicated profiles were similar between treatments and ranged from DP 1 to DP 15 or higher. Quantification of fiber indicated 26–58% by weight of sample was low and high molecular weight soluble fiber. Citric acid positively affected oligosaccharide yield. These results indicate that oligosaccharides can be created with a continuous process. Further characterization of this product, as well as the development of clean up and concentration methods to remove mono- and disaccharides could lead to the production of a high-value soluble fiber from lactose.

Key Words: extrusion, lactose, oligosaccharides

82 Impact of bleaching on flavor and functional properties of 80% serum protein concentrate. R. E. Campbell*[1], M. Adams[2], D. M. Barbano[2], and M. A. Drake[1], [1]*North Carolina State University, Raleigh,* [2]*Cornell University, Ithaca, NY.*

Whey proteins that have been removed before the cheese making process are referred to as “native” whey proteins or milk serum proteins. Chemical bleaching of residual annatto has a detrimental effect on whey protein flavor and functional properties. Serum protein allows direct investigation of these effects without the confounding influence of cheesemaking parameters. The objective of this study was to characterize and compare the sensory and functional properties of 80% milk serum protein concentrate (SPC80) produced from bleached and unbleached microfiltered (MF) skim milk permeate with and without added annatto color. Colored and uncolored MF permeates were bleached with benzoyl peroxide (BP) or hydrogen peroxide (HP), ultrafiltered, diafiltered and spray-dried. SPC80 from unbleached colored and uncolored MF permeates were manufactured as controls. All treatments were manufactured in triplicate. Flavor and functional properties of SPC80 were evaluated by sensory and instrumental analyses. The HP bleached SPC80 was higher in lipid oxidation compounds than other bleached or unbleached SPC80, specifically hexanal, heptanal, nonanal, decanal, and 2,3 octadienone($P < 0.05$). Consistent with instrumental results, HP SPC80 were also higher in aroma intensity, cardboard and fatty flavors compared with other SPC80 ($P < 0.05$). The BP SPC80 had lower norbixin concentrations compared with SPC80 bleached with HP ($P < 0.05$). Functionality tests demonstrated that HP SPC80 had more soluble protein after 10 min of heating at 90°C at pH 4.6 and pH 7 than the no bleach and BP treatments regardless of additional color. SPC80 foams generated from bleached samples were more stable than those from unbleached samples ($P < 0.05$). SPC80 bleached with HP were lower in yield stress than other samples ($P < 0.05$). HP bleaching caused more lipid oxidation products and subsequent off flavors than BP bleaching. Bleaching also altered heat and foam stability and this effect was more pronounced with HP compared with BP. These results demonstrate that chemical bleaching alters flavor and functional properties of milk serum proteins. Optimized bleach concentrations and conditions should be determined for whey or chemical bleaching alternatives established.

Key Words: serum proteins, bleaching, functionality

83 Study of the heat-induced interaction pathway between whey protein and buttermilk components. M. Saffon*[1], R. Jiménez-Flores[2], M. Britten[3], and Y. Pouliot[1], [1]*STELA Dairy Research Center, Institute of Nutraceuticals and Functional Foods (INAF), Université Laval, Quebec City, QC, Canada,* [2]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo,* [3]*Food Research and Development Center (FRDC), Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada.*

Previous work showed that it was possible to form mixed aggregates by heating whey protein in the presence of buttermilk components. It was hypothesized that caseins and milk fat globule membrane proteins act as a nucleus in the process of whey protein aggregation. Buttermilk powders were obtained by spray drying after ultrafiltration (UF) and diafiltration (DF) of regular buttermilk and whey buttermilk. A portion of these powders was treated by supercritical fluid extraction (SFE) to remove non-polar lipids. Powders were mixed with UF/DF concentrated whey, and the mixtures were heated to 90°C for 5 min at pH 4.6. The dispersions were heated with or without thiol blocking N-ethylmaleimide (5 mM). The liberation of free –SH and the protein profiles were determined every 5 min respectively with the Ellman's reagent and one dimensional PAGE technique (SDS-PAGE) under non-reducing and reducing conditions. 3D images were taken at 100× with a confocal laser-scanning microscope. All experiments were performed in triplicate and the concentrations of free –SH in the mixtures were compared with control (whey) using T tests. Addition of buttermilk significantly decreased the liberation of free –SH during heating. SDS-PAGE gels under non-reducing conditions showed a decrease in native whey and buttermilk proteins during heating, and large aggregates were evident. These large aggregates were also found under reducing conditions and in the presence of N-Ethylmaleimide (NEM). Three-dimensional (3D) images confirmed the interaction between protein and fat globule membrane even in presence of NEM. Overall, our results suggest that the MFGM (either protein or phoshpolipids) could act as an initiator during the formation of mixed aggregates with whey proteins.

Key Words: heat-induced interaction, milk fat globule membrane, whey protein

84 Effect of milk processing on the anticarcinogenic capacity of the milk fat globule membrane.

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The milk fat globule membrane (MFGM), the surface-active material surrounding fat globules in milk, has been shown to have potential anticarcinogenic properties by inhibiting the proliferation of cancer cells through cytotoxic and apoptotic effects. Though the effect of milk processing on the MFGM functional properties is known, the effects over its bioactivity are still lacking. Objective of this work was to determine if processing (i.e., heat treatment) has an effect over the MFGM bioactivity. Two representative colon cancer cell models (HT-29 and Caco-2) were used to test the antiproliferative capacity of MFGM isolates obtained from raw and heat-treated milk. Raw MFGM material was obtained by washing the cream twice with endotoxin free water, subsequent freeze-thawing and ultracentrifugation. Bacterial contamination and lipopolysaccharide (LPS) presence was quantified and kept at minimum by collecting the milk with a catheter and working under sterile conditions. For the heat treated samples, raw milk was batch-treated at 80°C for 10 min (HT80), 74°C for 3 min (HT74) or 63°C for 30 min (HT63) and then the MFGM was extracted. Cell proliferation was studied by the BrdU colorimetric test. Results showed a similar dose-dependent DNA synthesis decrease in both cell lines exposed to 6.25–200 µg protein raw MFGM/mL, although Caco-2 cells seemed to be more resistant. The EC50 values were 111 and 88 µg protein MFGM/mL for Caco-2 and HT-29 cells, respectively. Ceramide (20 µM) used as positive control showed a similar effect, supporting the hypothesis of the sphingolipids as one of the possible compounds responsible for the bioactivity. When the heat treated samples where used, this bioactivity was significantly affected. The HT80 highest dose only produced a 10% reduction in cell proliferation while the lowest concentrations caused the opposite effect by incrementing cell DNA synthesis up to 35%. Similar trends, yet improved, were observed with the HT74 and HT63 fractions: 100 µg protein MFGM/mL caused a cell division decrease of 30 and 40% respectively. These results will be discussed in light of the physico-chemical changes occurring to the MFGM during heating, and they raise new questions related to which active components play a role in the antiproliferative effect observed with the colon cancer cell lines.

Key Words: MFGM, bioactivity, anticarcinogenic

85 Heat stability of micellar casein concentrate (MCC) as affected by temperature and pH.

A. Sauer* and C. I. Moraru, *Cornell University, Ithaca, NY.*

The increasing interest in using MCC obtained by membrane separation in manufacturing shelf-stable high protein products creates a need to understand the effect of sterilization treatments on the stability of this ingredient. The goals of this work were to: 1) elucidate the effects of pH and sterilization temperatures on the mineral distribution and dissociation of caseins; and 2) use the generated knowledge to develop solutions for stabilizing the MCC during sterilization treatments. MCC powders were reconstituted with water at 8% concentration, and the resulting dispersions were adjusted to pH values of 6.5–7.3. Subsequently, the 8% MCC samples were heated in an oilbath to 110°C to 150°C, in 10°C increments. The come-up time was identical for all heat treatments. The treated samples were evaluated for particle size, soluble minerals and casein dissociation. Measurement of soluble minerals and casein dissociation (by LC-MS/MS) were performed on supernatants obtained after ultracentrifuging the samples for 60 min at 100,000 × *g*. The study was conducted in triplicate and the data analyzed statistically. At pH 6.5 and 6.7, all heat treated samples were visibly aggregated or coagulated. At pH 6.9, higher temperatures lead to increased particle size, while at pH > 6.9 little or no changes were observed after heat treatment. Casein dissociation increased with increasing pH for all 4 caseins, at all temperatures, with dissociation of κ-CN and β-CN being most significant ($P \leq 0.05$). At higher pH, the levels of dissociated αs-CN decreased after heat treatment, suggesting aggregation of αs-CN due to the presence of calcium and lost protection by κ-CN. It was concluded that increased stability of MCC requires increasing the pH and lowering the processing temperature. MCCs were then submitted to sterilization after targeted modifications: increased pH and lower processing temperature, at equivalent lethality. A significant reduction ($P \leq 0.05$) in particle size was obtained and no coagulation or aggregation occurred after retorting or UHT. The generated knowledge will allow the effective stabilization of MCC in practical applications, such as the production of novel, shelf-stable protein beverages.

Key Words: micellar casein concentrate (MCC), sterilization, stability

86 Development of a model system to understand the mechanisms of instability and to predict the shelf-life of oil-in-water emulsions.

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Emulsion systems are generally very complex depending on the type and the amount of protein or surfactant present in the various emulsion phases; it is difficult to understand the mechanism of instability. The objective of this study was to design a simple model system to characterize the role of the proteins and surfactants present in the various phases of an emulsion and to probe the exact mechanisms of instability. Four possible oil-in-water model emulsion systems (pH 6.8 to 7.0) that represented potential interactions between protein-coated or surfactant-coated emulsion droplets and non-adsorbed proteins present in the continuous phase were designed. The model emulsions were prepared by 2 different methods: (a) by mixing stock emulsions [20% w/w oil-in-water emulsions stabilized by 1.0% w/w sodium caseinate (Na-CN) or Tween-20] with solutions of milk protein concentrate (MPC), whey protein concentrate (WPC) and hydrolyzate (WPH) to yield emulsions with a range of protein concentration and (b) by using Na-CN, WPC, and MPC as the sole source of emulsifier for a comparison study. Model emulsions were characterized for particle size, creaming stability, microstructure, rheology, and PAGE (PAGE). Depletion flocculation was observed in emulsions prepared with MPC when the protein concentration in the continuous phase was above 3% w/w and the oil droplets were stabilized primarily by either Na-CN or Tween-20. The state of aggregation and the polydispersity of non-adsorbed casein micelles in the continuous phase determined the extent of depletion flocculation and the shear flow behavior. The caseinate-stabilized droplets were incorporated in the heat-induced protein gel network in model emulsions containing excess non-adsorbed WPC, but Tween-20 stabilized droplets were repelled from the gel. PAGE analysis of various emulsion phases and the addition of EDTA to the systems confirmed competitive adsorption and surface displacement of caseins by whey proteins. The unique model systems approach improved our understanding of the influence of heat-induced ingredient interactions in the system and was success in describing the potential interparticle interactions, which can be used to improve the stability of protein-stabilized emulsions.

Key Words: milk protein, oil-in-water emulsion, instability

87 Shear stabilized micro-phase-separated dairy gels containing significant concentrations of β-glucan. N. Sharafbafi*[1], S. M. Tosh[2], and M. Corredig[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Agriculture and Agri-Food Canada, Guelph Food Research Center, Guelph, Ontario Canada.*

Incorporation of nutritionally significant concentrations of soluble fiber (β-glucan) into dairy food products is challenged by thermodynamic incompatibility between polysaccharide molecules and milk proteins. It was hypothesized that gelation of milk proteins under shear would increase the connectivity between the β-glucan phase separated domains, and result in dairy matrices for the delivery of nutritionally significant concentrations of dietary fiber. Rennet induced gelation was the method of choice as it possesses minimal effect on ionic condition of mixed systems. Different shear rates (50 and 100 s^{-1}), shearing times (17, 20, 25 min), and different concentrations of milk proteins (2.78, 5.57, and 8.36%, wt/wt) and β-glucan (0.2 and 0.4%, wt/wt) were tested, to evaluate possible differences in structure of the gels formed. The mixtures were continuously sheared (using rheometer) until approximately 80% of the caseino-macro-peptide was released. Shearing for a longer time resulted in an increase in the viscosity of the mixtures and breakage of the bonds formed between renneted casein micelles. At a constant shear rate and β-glucan concentration, increase in protein concentration significantly increased the stiffness of the gel. At constant protein concentration and low concentrations of β-glucan ($\leq$0.4%), an increase in shear rate reduced the time of gelation and the stiffness of the gel, while it resulted in a faster gelation time and higher gel modulus at higher concentrations of β-glucan ($\geq$0.4%; $P \leq 0.5$). Micro-structural analysis of gels after 2 h of renneting revealed high connectivity between the phase separated domains at high concentrations of milk proteins and β-glucan. At these concentrations, due to formation of bi-continuous structures upon mixing, increase in shear rate resulted in lower viscosity and formation of droplet like domains, which may have resulted in self supporting gels. It was concluded that controlling shear during gelation of milk proteins mixed with β-glucan makes it possible to create novel microstructures in dairy products that provide nutritionally significant ($\geq$0.3%, wt/wt) concentrations of soluble fiber.

Key Words: phase separation, shear, gelation

88 Streamlining the product development process: Use of the preferred attribute elicitation technique to extract key texture attributes influencing consumer liking of dairy yogurts. A. Grygorczyk*[1], M. Corredig[1], I. Lesschaeve[2], and L. Duizer[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Vineland Research and Innovation Centre, Vineland Station, ON, Canada.*

Understanding the key attributes affecting consumer liking is very important for guiding the product development process. While conventional profiling methods employing trained panelists provide a detailed description of products, they cannot generate insight into importance of attributes as they do not engage consumers. The method examined in this study is a novel method, which we will refer to as preferred attribute elicitation (PAE). The method derives important attributes by asking a panel of consumers to agree to a set of attributes which stand out most to them, to rank them according to importance and then to rate the products based on those attributes. As this a novel technique there is a need to examine the method further to understand its strengths and weaknesses, as well as its place among sensory methodologies. The principal components plots generated by the PAE approach and conventional profiling were compared using multiple factor analysis and the RV coefficient. The results for texture characterization of yogurts were found to be highly correlated between the 2 methods (RV coefficient = 0.877). The PAE method was repeated in 4 sessions and a comparison of sessions employing the same set of products generated significant RV coefficients, indicating that the approach generated reproducible data for this set of products. The results confirmed the importance of texture to consumer liking and found that runny texture and gritty mouthfeel detracted from liking. Nearly all attributes generated by consumers explained a significant portion of the variability in the study, indicating that consumers were capable of characterizing products in a meaningful way. It is expected that the method would be most useful in the early stages of product development when only a general product characterization is required and a detailed description may generate confusion.

Key Words: yogurt, rapid profiling, texture

Graduate Student Competition: ADSA Production Division Graduate Paper Competition–PhD Students

89 Hyperprolactinemia during late gestation increases milk yield from primiparous gilts and piglet growth. M. K. VanKlompenberg,* R. Manjarin, H. F. McMicking, and R. C. Hovey, *University of California, Davis.*

A major limitation for piglet growth and survival is maternal milk yield that is dependent on maximal mammary growth and optimal lactogenesis. Several lines of evidence point to prolactin (PRL) as being crucial for these processes in pigs, where a critical period during late gestation has been defined as being PRL-dependent. We hypothesized that administering a dopamine antagonist to induce hyperprolactinemia in primiparous gilts during late gestation would increase mammary growth, subsequent milk yield and piglet growth. A total of 19 Yorkshire/Hampshire gilts were assigned to receive either vehicle (VEH, n = 9) or domperidone (DOM, n = 10) twice daily from gestation (G) d90 to 110. Serial blood sampling during the treatment period and lactation, and subsequent radioimmunoassay confirmed that serum PRL levels were increased in treated animals at G91 ($P < 0.001$). Data were analyzed using a linear mixed model and *t*-test comparisons. Mammary gland biopsies were performed on d90, 100 and 110 of gestation and d 2 and 21 of lactation (L) to analyze various aspects of mammary gland growth. Piglets raised by DOM dams were 21% heavier than controls (4279 ± 341.0 g and 3533 ± 348.1 g, respectively; $P < 0.05$) at weaning (L21), having significantly greater average daily gains between L8 to 14 (234.7 ± 18.7 g/d, 195.0 ± 19.1 g/d; $P < 0.05$), and L15 to 21 (258.7 ± 18.7 g/d, 206.3 ± 19.1 g/d; $P < 0.01$). Milk production was measured using the weigh-suckle-weigh method on L2, 7, 14 and 21. Similar to piglet gain, milk production rate by DOM dams compared with controls was greater on L14 (30.7 ± 3.3 mL/h, 24.9 ± 3.3 mL/h; $P < 0.05$), and L21 (35.3 ± 3.3 mL/h, 26.9 ± 3.3 mL/h; $P < 0.01$). Taken together, these data indicate that pharmacologically induced hyperprolactinemia in primiparous gilts during late gestation leads to increased milk yield during established lactation that enhances piglet growth.

Key Words: mammary gland, milk production, prolactin

90 Photoperiod treatment during lactation alters organ weights but does not affect litter weight gain in mice. P. A. Bentley* and T. B. McFadden, *University of Alberta, Edmonton, Alberta, Canada.*

Manipulation of photoperiod is a well established method of enhancing milk production in dairy cows. Cows exposed to either short day photoperiod during the dry period or to long day photoperiod during lactation produce more milk. Photoperiod treatment is known to alter hormonal signaling and affect systemic immunity, both of which could be related to the milk yield response; however, definitive understanding of the underlying physiological mechanisms is lacking. The objectives were to determine the effects of different photoperiods on milk yield and weights of organs related to metabolic support of lactation or immune function in mice. Mice (n = 6 for each trt × time) were exposed to normal day length (12L:12D) during gestation and were then randomly allocated to long day (16L:8D), short day (8L:16D), or normal day length treatments from parturition through 15 d of lactation. Milk yield was estimated from litter weight gain and organs were weighed immediately after mice were euthanized. Data were analyzed using Proc GLM to test significance of main effects and interaction of photoperiod and time. Photoperiod had no effect on litter weight or litter weight gain/d. The main effect of photoperiod on dam weight was significant ($P < 0.03$), and dams on long day photoperiod weighed more ($P < 0.001$) on d 5 of lactation than those on short days. There was also an overall effect of photoperiod treatment on weight of dam's liver, normalized to body weight ($P < 0.01$), and d 15 liver weight was greater for dams on long days than on normal or short days ($P < 0.01$). Spleen weight was affected ($P < 0.02$) by photoperiod treatment, being greater in mice exposed to long days ($P < 0.01$). These data demonstrate that exposure of lactating mice to different photoperiods elicited physiological changes but did not affect milk yield. Increased weight of body, liver, and spleen of dams suggests that photoperiod may affect metabolic and immune function in mice, perhaps through mechanisms similar to those affecting mammary and immune function in dairy cows. Understanding of responses to photoperiod treatment in mice may help identify mechanisms of action in dairy cows.

Key Words: photoperiod, lactation, immune

91 Serotonin (5-HT) affects glucose metabolism in transition rats. J. Laporta,* T. L. Peters, K. E. Merriman, and L. L. Hernandez, *University of Wisconsin, Madison.*

The role of 5-HT in regulating processes such as milk synthesis and secretion have been defined. 5-HT has also been implicated in liver glucose homeostasis. 5-HT is synthesized in a 2-step reaction from the amino acid L-tryptophan (L-TRP). The rate-limiting step is catalyzed by tryptophan hydroxylase (TPH1) isoform to form 5-hydroxytryptophan (5-HTP), the immediate precursor to 5-HT. To explore 5-HT's role in glucose homeostasis during the transition period (9 d pre and postpartum) we fed 45 rats (n = 15 per-treatment) 3 diets: control (CON), 5HTP (0.2% total diet) and L-TRP (1.35% total diet) to increase endogenous 5-HT production. We measured daily milk yield (MY) and collected milk samples on d 1, 5 and 9 of lactation to measure lactose concentrations. We collected serum and plasma on d 20 of gestation and d 9 of lactation to measure circulating 5-HT and glucose levels. Total RNA was isolated from liver and mammary gland tissue and mRNAs for growth hormone receptor (GHR), pyruvate carboxylase (PC), phosphoenol pyruvate carboxykinase-1 (PEPCK1) in liver, and for glucose transporter-1 (GLUT1), PC and GHR in mammary gland were quantified by quantitative real time PCR. The 5-HTP and L-TRP treatments effectively increased serum 5-HT over time ($P < 0.001$), with a greater increase seen in the 5-HTP cohort. MY was the same among all cohorts, until d 8 and 9, in which it increased in L-TRP animals ($P < 0.05$). There were no significant differences in milk lactose levels between treatments ($P > 0.05$). Plasma glucose concentrations decreased from d 20 of gestation to d 9 of lactation in all cohorts, but more markedly in the L-TRP ($P < 0.001$). Liver GHR mRNA expression was decreased in both treatment cohorts ($P < 0.05$) while PC mRNA was increased only in the 5-HTP cohort ($P < 0.01$), however there were no significant changes in the mammary gland. Liver PEPCK1 was not affected while GLUT1 mRNA was greater in the mammary gland of both treatment groups when compared with CON group ($P < 0.05$). Feeding 5-HTP during the transition period increases 5-HT synthesis and appears to affect glucose homeostasis, and negatively affects GH's effects in the liver.

Key Words: 5-HT, liver, glucose

92 Inflammatory pathways contribute to the metabolic adaptations to lactation in dairy cattle.

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Inflammation has been proposed as a contributor to metabolic disorders in transition dairy cows. The purpose of this experiment was to determine if a non-steroidal anti-inflammatory drug, sodium salicylate (SS), alters metabolism of transition dairy cows. At calving, 78 cows (n = 39 primiparous [1P]; n = 24 2nd lactation [2P]; n = 15 ≥ 3 lactations [3P]) were alternately assigned to either control (CON) or SS treatment for 7 d and remained on study until 21 d postpartum. SS treatment was administered via individual water bowls at a concentration of 1.68 g/L, delivering a mean of 123.3 ± 5.5 g SS/d during the 7 d of treatment. Blood samples were collected weekly and liver biopsies were collected on d 4 and 21 postpartum. Data were analyzed using mixed models with repeated measures over time and significance was declared at $P < 0.05$ and interactions were investigated at $P < 0.15$. There were no overall treatment effects on daily intake of water or DM, and SS treatment resulted in plasma salicylate concentrations of 34.4 ± 15.0 μg/mL on d 7. Liver TNFα mRNA abundance was decreased by SS on d 4 (28% reduction). Plasma glucose concentration was decreased by SS on d 7, especially in 2P and 3P cows (51.7 vs. 40.7 ± 3.1 mg/dL); 3P cows treated with SS had a 49% reduction in glucose-6-phosphatase mRNA on d 4 and a 81% reduction (d 21) in mRNA abundance of CREBH, a positive regulator of gluconeogenesis induced by inflammatory pathways. Plasma BHBA concentration was elevated in SS cows on d 14 and 21 (977 vs. 749 ± 56 μM), and plasma NEFA was elevated in SS cows on d 21 (525 vs. 377 ± 36 μM). SS treatment significantly increased liver triglyceride content on d 4 (29% increase) but by d 21 concentrations were similar across treatments. Because the most dramatic responses were observed in 3P cows, plasma samples from this block were analyzed for 14 eicosanoids. An index comprised of 11 pro-inflammatory eicosanoids showed no differences on d 7, but were significantly elevated for SS on d 14 (150% increase). Therefore, responses to SS after d 7 may have been due to altered metabolic programming or to post-SS increases in inflammatory signals. In summary, SS suppressed liver inflammation but decreased plasma glucose, increased plasma ketones, and contributed to liver triglyceride accumulation. These findings suggest that interrupting inflammation during the first week after parturition alters the metabolic adaptations to lactation.

Key Words: transition, inflammation, liver metabolism

93 Metabolism of butyrate infused in the rumen or abomasum of lactating dairy cows.

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This research was to investigate the effects on plasma metabolites and rumen measures when butyrate was infused into the rumen or abomasum of lactating cows. Jugular catheters were inserted into 5 ruminally fistulated Holstein cows (94.2 ± 23.3 DIM; 717 ± 45 kg BW) in a 5 × 5 Latin square with 3-d periods. Cows were infused for 24 h with one of 5 treatments: water (CON), 1 g/kg BW of butyrate infused into either the abomasum (A1) or rumen (R1), or 2 g/kg BW of butyrate infused into either the abomasum (A2) or rumen (R2). Sodium butyrate was the source of butyrate and NaCl was added to the CON, A1, and R1 treatments to provide equal amounts of sodium as the 2 g treatments. Flanges were inserted into the abomasum to allow infusion to the abomasum and peristaltic pumps provided continuous infusion of all treatments. Serial blood samples were collected at −2, −1, 0, 0.5, 1, 2, 3, 4, 6, 8, 12, 18, and 24 h relative to starting dosing. Rumen fluid samples were collected at −2, −1, 0, 1, 2, 4, 6, 8, 12, 18, and 24 h relative to starting dosing. Area under the curve (AUC) was calculated using the pre-dosing values as a baseline. Average DMI and average production measures were not affected by treatment ($P < 0.05$). Plasma glucose (73.0, 67.2, 65.3, 69.6, and 62.1 mg/dl), plasma β-OHB (β-hydroxybutyrate) (615, 965, 1454, 676, and 1235 mM), and plasma butyrate (0.08, 0.09, 0.11, 0.10, and 0.15 mM) for the CON, R1, R2, A1 and A2 treatments were affected by butyrate addition and treatment dose ($P < 0.05$). The site of dosing affected ($P < 0.05$) plasma butyrate. Rumen butyrate (9.0, 15.3, 22.1, 9.4, and 9.7 mM) for the CON, R1, R2, A1 and A2 treatments respectively were affected by treatment, dosage, site of infusion, and interaction of site and dosage ($P < 0.05$). The AUC (44, −105, −342, −119, and −338 mg/dL • h) and the height of the largest peak for plasma glucose (−7.3, −12.2, −24.4, −12.8, and −25.6 mg/dL) and the AUC for rumen pH (−12.22, −8.15, −4.95, −10.60, and −6.58 pH • h) for CON, R1, R2, A1, and A2 were affected ($P < 0.05$) by butyrate addition and dose. Results demonstrate that butyrate infused into the rumen or abomasum decreases plasma glucose and increases plasma β-OHB.

Key Words: butyrate, infusion, ketone

94 Effect of breed on the metabolic profile in transition Holstein and Jersey dairy cows.

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Significant advances in productivity have resulted due to genetic selection of Holstein and Jersey dairy cattle, as well as enhanced nutritional management. The objective of this study was to determine whether differences exist between the metabolic profile of Holstein and Jersey cows during the periparturient or transition period. Blood samples were collected from Holstein (n = 3658) and Jersey (n = 1699) cows within the transition period via coccygeal vessel venipuncture in nonheparinized vacuum tubes at morning feeding on 8 commercial dairies of each breed. Following centrifugation, samples were stored frozen (−20°C) in duplicate before laboratory analysis for calcium (Ca), phosphorus (P), magnesium (Mg), albumin, urea, glucose, cholesterol, sodium (Na), potassium (K), chloride (Cl), and nonesterified fatty acids (NEFA). Feed samples were collected on the day of sampling. Herd records were reviewed to identify data points from cows experiencing dystocia, retained placenta, displaced abomasum, twin births, stillbirths and cows being dry <30d or >80d and data were analyzed using multiple regression. The effect of breed was significant ($P < 0.001$) for all measured parameters exclusive of Na and cholesterol. Further, sampling week relative to calving was shown ($P < 0.001$) to affect P, Mg, Na, K, Cl, NEFA, glucose, and cholesterol, while number of lactations affected ($P < 0.05$) Ca, P, albumin, urea, glucose, cholesterol, and NEFA levels. Animal health is a factor in profile levels as animals experiencing one or more of the previously stated health incidences displayed differences ($P < 0.05$) in Ca, Mg, albumin, urea, cholesterol, K, and Cl but no difference in NEFA or glucose levels. These results suggest greater focus is necessary for the individual breeds if utilizing the metabolic profile as a diagnostic tool.

Key Words: dairy cow, metabolic profile, transition period

95 Effects of corn silage hybrids and quality of alfalfa hay on nitrogen metabolism and ruminal fermentation of early lactating dairy cows.

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This experiment was conducted to determine the effects of corn silage (CS) hybrids and quality of alfalfa hay (AH) in high forage dairy diets on N metabolism and ruminal fermentation by early lactating dairy cows. Eight multiparous Holstein cows were used in a duplicated 4 × 4 Latin square experiment with a 2 × 2 factorial arrangement of treatments. The 8 cows (average days in milk = 23 ± 11.2) were surgically fitted with ruminal cannula, and the 2 squares were conducted simultaneously. Within square, cows were randomly assigned to a sequence of 4 diets during each of the 4 21-d periods (14 d of treatment adaptation and 7 d of data collection and sampling); conventional CS (CCS) or brown midrib CS (BMRCS) was combined with low quality AH (LQAH: 46.4% NDF and 18.7% CP) or high quality AH (HQAH: 37.4% NDF and 21.8% CP) to form 4 treatments: CCS with LQAH, CCS with HQAH, BMRCS with LQAH, and BMRCS with HQAH. Diets were isonitrogenous across treatments averaging 15.8% CP. Intake of DM did not differ because of CS hybrids and AH quality. While feeding BMRCS-based diets decreased urinary N output by 32% ($P < 0.01$), it did not affect fecal N output. Feeding HQAH decreased urinary N output by 18% ($P = 0.01$), but increased fecal N output by 14.5% ($P = 0.01$). Nitrogen efficiency (milk N (g/d)/intake N (g/d)) was similar across treatments. Ruminal ammonia-N concentration was lower for cows fed BMRCS-based diets than those fed CCS-based diets ($P = 0.02$), but was not affected by quality of AH. Feeding BMRCS-based diets decreased MUN concentration and yield by 23% ($P < 0.01$), whereas feeding HQAH decreased MUN concentration and yield by 15% ($P < 0.02$). Total VFA concentration increased with HQAH ($P = 0.02$), but was not influenced by CS hybrids. Milk yield did not differ due to CS hybrids, but it tended to decrease ($P = 0.08$) by feeding HQAH. Significantly decreased MUN by feeding BMRCS or HQAH suggests improved whole-body N utilization efficiency.

Key Words: brown midrib corn silage, alfalfa hay, nitrogen efficiency

96 Effects of partial replacement of dietary starch from barley or corn with lactose on the performance of dairy cows.

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Sugars are more rapidly fermented in the rumen than starch, and replacing dietary starch with sucrose in corn/alfalfa silage-based diets has been reported to improve milk production in dairy cows. Few studies have used lactose as a partial replacement of starch from barley or corn, which differ in their rates and extents of ruminal fermentation. The objective of this study was to determine the effects of replacing barley or corn starch with lactose (as dried whey permeate; DWP) on DMI, milk yield and composition, ruminal pH, and blood metabolites. Eight lactating dairy cows were used in a replicated 4 × 4 Latin square design with 28-d periods (18 d of dietary adaptation and 10 d of measurements) and a 2 × 2 factorial arrangement of dietary treatments. Four cows in one Latin square were ruminally-cannulated for the measurement of ruminal fermentation characteristics. The treatment factors were source of starch (barley vs. corn) and dietary inclusion level of DWP (0 vs. 6%, DM basis) as a partial replacement for starch. Diets were isonitrogenous (18% CP) and contained 3% (low) or 8% (high) sugar. The starch content of the low sugar diets was 24% compared with 20% for the high sugar diets. Dry matter intake, milk composition, milk and milk component yields, and blood glucose and β-hydroxybutyrate concentrations did not differ ($P > 0.05$) with diet. The daily mean and maximum pH were similar ($P > 0.05$) across diets. However, minimum pH tended to be lower ($P = 0.07$) when feeding barley compared with corn. The duration (h/d) that ruminal pH was below pH 5.8 also tended to be shorter ($P = 0.06$) whereas the area (pH × min/d) that pH was below pH 5.8 was smaller ($P = 0.04$) on the corn diet compared with the barley diet (47 vs. 111). Cows fed 6% DWP had lower ruminal ammonia ($P = 0.04$; 11.2 vs. 14.0 mg/dL) and milk urea nitrogen concentrations ($P < 0.01$; 16.5 vs. 17.8 mg/dL) and tended to have lower blood urea nitrogen ($P = 0.07$) compared with those fed 0% DWP. In conclusion, partially replacing corn or barley starch with DWP improved N efficiency, but had no effect on production and ruminal pH in dairy cows.

Key Words: lactation performance, lactose, starch

97 In search of privacy: Dairy cow preference for an isolated calving area.

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When dairy cows are housed in semi-natural environments, they distance themselves from the herd to calve. Indoor-housed cows have limited ability to isolate from the herd, as many are housed in group pens or in individual pens located in high traffic areas. The aim of this study was to assess whether indoor-housed cows would seek isolation to calve if given a choice, and if this choice was influenced by the time of day and the number of cows in the pen. Seventy-two Holstein dairy cows (50 multiparous; 22 primiparous) were paired by calving date. At 6.6 ± 3.0d before calving, each pair entered one of 4 maternity pens. Each pen included an “open” sawdust pack (2.4 × 7.3m) and an “enclosed” sawdust pack (2.4 × 6m); the enclosed pack was surrounded by 2.4m high plywood walls on 3 sides, the fourth side had a 2.4m opening that allowed cows to freely enter or exit the enclosure. Once the first cow of a pair calved she was removed; the second cow remained single-housed in the pen until she calved. We used video to assess the time and area where calving took place. The probability that pair- and single-housed cows would calve in the open or enclosed pack, and during the ‘day’ (08:00 to 21:00 h) or ‘night’ (21:00 to 08:00 h), was assessed using Chi-Square tests. We noted no differences between primiparous and multiparous cows, so tests were done using a combined data set. Pair-housed cows were more likely to calve in the open pack, whereas single-housed cows were more likely to calve in the enclosed pack (Chi-Square = 4.5; $P = 0.03$). Choice of calving area was contingent on the time of day for single-housed cows (Chi-Square = 7.5; $P = 0.01$) but not for pair-housed (Chi-Square = 0.2; $P = 0.67$). Single-housed cows that calved at night were more likely to calve in the open, but cows that calved during the day were more likely to be in the enclosed area. Results suggest that isolation-seeking at calving is contingent on time of day and the number of cows in the pen.

Key Words: transition, housing, maternity

98 II. Identifying within-herd risk factors affecting reproductive performance of lactating dairy cows under field conditions. S. Bas*[1], R. L. Nebel[2], and G. M. Schuenemann[1], *[1]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [2]Select Sires Inc., Plain City, OH.*

Many factors influence the reproductive performance of dairy herds, thus, profitability. Successful identification of factors affecting pregnancy rate (PR) at herd level can be challenging due to their multi-factorial nature. The objective was to assess the effectiveness of an interactive dairy herd index (DI) to aid in decision making about reproductive management of dairy cows. Data from one dairy herd, previously assisted to improve PR, was used to validate the DI. Risk factors [stillbirth, retained fetal membranes (RFM), metritis, mastitis, lameness, body condition score (BCS), estrus detection (ED), conception risk (CR), labor-cow ratio, and stocking density] were assessed according to their contribution weights (CW) on PR. Data from previous studies were used to estimate the CW using linear regression. Additionally, risk factors (one yr before and after intervention) were compared with desired reference values to obtain the relative difference for individual DI by components and ranking of risk factors. According to the DI, stocking density, metritis, lameness, and stillbirth were the top 4 risk factors explaining PR before intervention. These risk factors were in agreement with findings collected during the herd walk-through. Recommendations were close-up pen for dry cows; 85% stocking density for close-up and fresh cows; comprehensive training (calving management and hoof trimming) to dairy personnel; and no changes were made on nutrition and reproductive management. After intervention, the relative difference (change of risk factor values) was improved for stillbirth (45%), lameness (46%), metritis (33%), stocking density (13%), and mastitis (13%). No changes were observed for RFM (0%), BCS (0%), and labor-cow ratio (0%) while the relative differences for ED (3%) and CR (6%) were decreased after intervention. Dairymen, consultants, and veterinarians often trouble-shoot poor PR in dairy herds and this process requires constant monitoring and comprehensive assessment of several events. Risk factors affecting PR varies from farm-to-farm and blanket recommendations often fail when applied to many herds. This DI may assist decision makers to focus on real within-herd risk factors accounting for the effect of management.

Key Words: index, pregnancy, dairy cow

99 Efficacy of a combination butaphosphan and cyanocobalamin product and insulin for ketosis treatment. J. L. Gordon*[1], S. J. LeBlanc[1], L. Neuder[2], T. H. Herdt[2], D. F. Kelton[1], and T. F. Duffield[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Michigan State University, East Lansing.*

Ketosis is a common transition disease in dairy cattle and can be challenging to treat. The objective of this study was to determine the efficacy of a combination butaphosphan and cyanocobalamin product (B+C; Catosal, Bayer) and insulin on ketosis cure rates and β-hydroxybutyrate (BHBA) concentrations. A double blind randomized clinical trial was performed in 16 herds in Ontario and 1 herd in Michigan from May to September 2011. All cows were tested for BHBA twice, at 3–9 and 10–16 d in milk (DIM) using the Precision Xtra meter (Abbott Laboratories). Cows that tested ≥ 1.2 mmol/L were considered to have ketosis. A total of 629 animals were enrolled and all received 300 g propylene glycol orally for 3 d. Animals were randomly allocated to receive additional treatment in a 2 × 2 factorial design with 199 cows receiving 200 IU (2 mL) insulin glargine (IG; Lantus, Sanofi-Aventis,) and 25 mL saline subcutaneously (SQ), 115 cows receiving 25 mL B+C and 2 mL saline SQ, 108 cows receiving 25 mL B+C and 200 IU IG, and 207 cows receiving both placebos. B+C or corresponding placebo was given for 3 d total. BHBA was measured at 7 and 14 d after treatment. An animal was categorized as a cure if d 7 BHBA was < 1.2 mmol/L. Logistic regression was used to determine the effect of treatment on cure rates and linear regression was used to examine the effect on d 7 post-treatment BHBA controlling for farm, lactation, and enrollment BHBA. Due a temporarily unavailability of B+C, only the 371 cows from Michigan were used for this analysis. All cows were used to analyze the effects of insulin. B+C tended to increase cure rates (OR = 1.5, 95% CI: 0.99–2.29, $P = 0.08$) and decrease d 7 post-treatment BHBA (−0.19 mmol/L, $P = 0.07$). Insulin was not significantly associated with cure (OR = 0.98, $P = 0.93$) or 7-d post-treatment BHBA (−0.07 mmol/L, $P = 0.91$). There was no interaction between B+C and IG. These results suggest that B+C treatment given with oral PG may improve ketosis cure rates, while IG is not helpful.

Key Words: ketosis treatment, insulin, cyanocobalamin

100 Ecology of subclinical ketosis in transition dairy cattle. J. A. A. McArt*[1], D. V. Nydam[1], and G. R. Oetzel[2], *[1]Cornell University, Department of Population Medicine and Diagnostic Science, Ithaca, NY, [2]School of Veterinary Medicine, University of Wisconsin, Madison.*

The purpose was to describe the ecology of subclinical ketosis (SCK) in dairy cows in early lactation and to determine the effect of: 1) presence of SCK, 2) d in milk (DIM) at onset of SCK, and 3) blood β-hydroxybutyrate (BHBA) concentration at onset of SCK on development of displaced abomasum (DA) and removal from herd in the first 30 DIM, conception to first service, d to conception within 150 DIM, and early lactation milk yield. Cows from 4 free-stall dairy herds were each tested 6 times for SCK from 3 to 16 DIM using the Precision Xtra meter. SCK was defined as a BHBA concentration of 1.2 to 2.9 mmol/L. Mixed effects multivariable Poisson regression was used to assess DA, removal from herd, and conception to first service. Semiparametric proportional hazards models were used to evaluate d to conception, and repeated measures ANOVA was used to evaluate milk yield in the first 30 DIM. A total of 741 of 1,717 (43.2%) eligible cows had a least one BHBA test of 1.2 to 2.9 mmol/L. Peak incidence of SCK occurred at 5 DIM when 22.3% of cows had their first SCK positive test. Peak prevalence of SCK occurred at 5 DIM when 28.9% of cows had a SCK positive test. Median time from first positive SCK test until BHBA test <1.2 mmol/L was 5 d. Cows first testing SCK positive from 3 to 5 DIM were 6.1 times more likely (95% confidence interval (CI) = 2.3 to 16.0) to develop a DA than cows first testing SCK positive at 6 DIM or later. Cows first testing SCK positive from 3 to 7 DIM were 4.5 times more likely (95% CI = 1.7 to 11.7) to be removed from the herd, 0.7 times as likely (95% CI = 0.6 to 0.8) to conceive to first service, and made 2.2 kg less milk per day for the first 30 DIM than cows first testing SCK positive at 8 DIM or later. Each 0.1 mmol/L increase in BHBA at first SCK positive test raised the risk of developing a DA by a factor of 1.1 (95% CI = 1.0 to 1.2), raised the risk of removal from herd by a factor of 1.4 (95% CI = 1.1 to 1.8), and was associated with a decrease in milk production by 0.5 kg per day for the first 30 DIM. These results show that time of onset and BHBA concentration of first SCK positive test are important indicators of individual cow performance.

Key Words: ketosis, incidence, prevalence

Graduate Student Competition: ADSA/ASAS Northeast Graduate Paper Competition

101 Metabolomic profiling of the liver in developing chicken embryos and post-hatch chicks reveals unique metabolic differences. Q. Hu,* U. Agarwal, and B. J. Bequette, *University of Maryland, College Park.*

The emerging new field of metabolomics aides in the identification and characterization of global metabolite patterns of organs and tissues. In this study, a metabolomic profiling approach was employed to investigate differences in metabolism in the liver of chicken embryos from 2 egg sizes and from broiler breeders of different maternal ages. Whole livers were collected on embryonic (e) d 17 and 20, and on post-hatch d 1 (n = 9–10) from embryos and chicks derived from broiler breeders of different ages (32 wk vs 51 wk, 63.2 ± 1.2 g) and from 2 sizes of eggs laid by 45 wk old breeders (55.8 ± 1.2 g vs 67.7 ± 1.1 g). Livers were lyophilized to dryness and freezer-milled, and the metabolites were extracted before chemical derivatization. Metabolites were separated by gas chromatography and under full scan mode complete ion spectra were recorded by mass spectrometry. Data files were converted using Agilent data analysis software and processed with the XCMS online server. Compound identification was determined by searching against the NIST 2008 library. Principal component analysis was employed to visualize the metabolite differences between 2 groups at 3 developmental stages. The results showed that embryos on both e17 and e20 from 32 wk old breeders clustered separately from 51 wk old breeders. However, this was not observed for embryos from small vs large eggs at these developmental stages. Concentrations of 6 metabolites from e17 livers differed ($P < 0.05$) between 32 wk and 51 wk old breeder eggs, 13 metabolites differed on e20 and 5 metabolites differed on post-hatch d 1. Metabolite categories included amino acids, carbohydrates, fatty acids and cholesterol esters. Comparison of small and large egg sizes revealed that 14 metabolites differed ($P < 0.05$) on e17, 13 metabolites differed on e20 and 6 metabolites differed on post-hatch d 1. In conclusion, these results reflect that the liver metabolisms of embryos during later development are distinct due to breeder age and egg size. Together, this study is the first assessment of global metabolism of developing embryo livers and our data provides the framework for further metabolic pathway analysis.

Key Words: chicken embryo, liver, metabolomic profiling

102 Effect of resveratrol supplementation on glycemic response in moderately exercised geldings. J. L. Zambito*[1], H. S. Spooner[1], and R. Hoffman[2], [1]*West Virginia University, Morgantown,* [2]*Middle Tennessee State University, Murfreesboro.*

Resveratrol is known to exert numerous health benefits including improved glycemic response. Resveratrol is present in equine supplements, yet no research exists in an athletic horse model. This study tested the hypothesis that resveratrol supplementation would improve glucose tolerance and insulin sensitivity in the athletic horse. Six mature geldings were assigned to 3 groups in a Latin Square design. Horses either received no supplementation (control, C) or one of 2 doses of trans-resveratrol (Equithrive, Lawless, KY); low (L, 2.5g) or high (H, 5g) daily for 14-d. Horses were exercised 3x weekly for 60 min. Body weight (BW) was collected on d0 and d14 of each period. A frequently sampled intravenous glucose tolerance test (FSIGT) was conducted on d10. Samples were analyzed for plasma insulin (INS) and glucose (GLU). Area under the curve (AUC) for INS and GLU was calculated via the trapezoidal method. Glucose effectiveness (Sg), insulin sensitivity (Si), acute insulin response to glucose (AIRg) and disposition index (DI) were calculated using minimal model software. Data were analyzed using ProcGLM in SAS 9.1, and further separated by Tukey's test. Contrasts were conducted to examine differences between C and treatment (T, both low and high). Minimal model analysis of FSIGT, along with AUC INS and GLU showed no effect of resveratrol supplementation (Table 1). In conclusion, resveratrol supplementation in the moderately exercised horse did not improve glycemic response, which may already be optimized in this model. These findings indicate a need to further evaluate resveratrol in other equine models, including a more in-depth assessment in the athletic horse.

Table 1. Glucose and insulin parameters in exercising horses supplemented with resveratrol

	Treatment			*P*-value	
	Control	Low	High	Treatment	Control
Sg (min^{-1})	0.030 ± 0.003	0.032 ± 0.004	0.035 ± 0.003	0.56	0.43
Si (L*mU^{-1} *min^{-1} *10^{-4})	5.93 ± 1.77	7.83 ± 2.33	8.70 ± 1.77	0.59	0.38
AIRg (mU* min*L^{-1})	304 ± 21	333 ± 28	272 ± 21	0.34	0.96
DI	2092 ± 647	2204 ± 857	2440 ± 648	0.93	0.80
AUC GLU (mg/dL*min)	20433 ± 1241	19302 ± 1241	19506 ± 1241	0.80	0.54
AUC INS (mIU/L*min)	7057 ± 992	6666 ± 992	6213 ± 992	0.84	0.64

Key Words: horse, exercise, resveratrol

103 Effects of intrauterine growth retardation due to poor maternal nutrition on bone formation in sheep. S. Neupane*[1], M. L. Hoffman[1], M. A. Rokosa[1], E. R. Ackell[1], D. M. Kaelin[1], S. A. Zinn[1], T. D. Crenshaw[2], and K. E. Govoni[1], [1]*Department of Animal Science, University of Connecticut, Storrs,* [2]*Department of Animal Science, University of Wisconsin, Madison.*

Intrauterine growth retardation (IUGR), often due to poor maternal nutrition, leads to either slow growth or reduced fetal size. Specifically, IUGR impairs muscle and bone development, and leads to increased adipose tissue development. We hypothesized that poor maternal nutrition would impair bone formation in offspring by reducing the differentiation of bone marrow stromal cells (BMSC) into osteoblasts. A total of 24 ewes were fed a diet of 60% (R; n = 8), 100% (C; n = 8), or 120% (O; n = 8) of NRC requirements beginning at d 85 of gestation. Lambs were euthanized at birth (n = 3/treatment) and 3 mo of age (n = 3 to 5/treatment). Femurs (F) and tibia (T) were collected at birth and 3 mo and BMSC were collected at birth. Bone mineral content (BMC) and bone mineral density (BMD) were measured on excised bones by dual-energy x-ray absorptiometry. To determine if IUGR affects ability of BMSC to differentiate into osteoblasts, BMSC were cultured in differentiation media (α-MEM plus β-glycerophosphate, dexamethasone and ascorbic acid) for 21 d and stained with alizarin red to determine mineralization. As reported, BW were reduced in R lambs by 16% at birth and 3 mo ($P \leq 0.05$) compared with C. At birth, maternal diets tended ($P = 0.19$) to affect bone area (22.6 ± 2.7, 20.6 ± 3.4, and 26.0 ± 1.3 cm^2; C, R and O, respectively); however, significant treatment effects were not observed for F BMC or BMD ($P \geq 0.29$). An effect of treatment was not observed for T variables at birth ($P \geq 0.29$). At 3 mo, bone area of the T tended ($P = 0.10$) to be reduced in R and O groups compared with C (53.8 ± 0.7, 50.8 ± 1.5, 50.7 ± 0.6 cm^2; C, R, and O, respectively). Compared with C, significant differences in BMC and BMD were not detected for F or T at 3 mo ($P \geq 0.51$). Cell culture experiments did not demonstrate a significant difference in alizarin red staining between treatment groups ($P \geq 0.6$). In conclusion, poor maternal nutrition reduces bone area in offspring with effects persisting during early postnatal development.

Key Words: bone, bone marrow stromal cells, intrauterine growth retardation

104 Hypoxia stimulates GLUT1 expression in bovine mammary epithelial cells.

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Expression of glucose transporters in bovine mammary gland increases a few to several hundred-fold from late pregnancy to early lactation and this increase is not mediated by lactogenic hormones. Hypoxia has been shown to increase glucose transporter 1 (GLUT1) expression in many cell types. Deletion of hypoxia-inducible factor HIF-1α, a key signaling factor which mediates hypoxia effects, in mouse mammary gland results in impaired mammary differentiation and failure in lactation. Therefore, we hypothesized that hypoxia mediates the upregulation of GLUT expression in bovine mammary gland during the transition period. To test our hypothesis, Mac-T bovine mammary epithelial cells and bovine primary mammary epithelial cells were treated with 2% of O_2. GLUT1 mRNA increased 2.2-, 2.8-, and 2.9-fold in Mac-T cells and 5.1-, 8.3-, and 4.2-fold in primary cells after 3, 12, and 24 h hypoxia treatment, respectively ($P < 0.01$). However, GLUT8 mRNA decreased by 42% and 30% in Mac-T cells and 50% and 51% in primary cells after 12 and 24 h hypoxia treatment ($P < 0.01$). Then Mac-T cells were treated with 2, 5, and 10% of O_2 for 12h. GLUT1 mRNA increased 2.4- and 1.8-fold ($P < 0.05$) in cells treated with 2% and 5% of O_2 respectively, and 10% O_2 had no effect. In addition, Mac-T cells and primary cells were treated with 2% of O_2 for 24 h and then incubated with 200 µM of 2-NBDG, a glucose analog with fluorescent group, for 15 min. Glucose uptake was measured by flow cytometry and results showed that hypoxia increased glucose uptake 2.1 fold in Mac-T cells and 2.8 fold in primary cells ($P < 0.05$). Furthermore, when Mac-T cells were transfected with HIF-1α siRNA for 6 h and then treated with 2% of O_2 for 12 h, the upregulation of GLUT1 by hypoxia was abolished, indicating that hypoxia regulates GLUT1 expression through HIF-1α in bovine mammary epithelial cells. Our studies suggest that hypoxia, associated with high levels of oxygen consumption in mammary development and lactogenesis, may be at least partially responsible for increasing GLUT1 expression and glucose uptake through transcription factor HIF-1α in bovine mammary epithelial cells during the transition period.

Key Words: hypoxia, glucose transporter, mammary gland

105 Poor maternal nutrition reduced body weights and circulating concentrations of IGF-I and IGFBP-3 in lambs.

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Intrauterine growth retardation (IUGR) may be the result of poor maternal nutrition, and can influence the somatotropic axis and the growth potential of offspring. To determine the effects of nutritional status during gestation on growth and serum concentrations of IGF-I and IGFBP-3 in lambs, 24 (21 Dorsets, 3 Shropshires) ewes were assigned (balanced for breed, parity and age) to 1 of 3 diets; control (C; 100% NRC, n = 8), restricted (R; 60% NRC, n = 8), or overfed (O; 120% NRC, n = 8). Treatment started at d 85 ± 5 of gestation. Nine lambs (3/treatment) were slaughter within 24 h of birth (d 1) and 15 lambs (3 to 5/treatment) were fed a control diet consisting of milk replacer (fed at 1.7%/BW), creep feed and hay for 3 mo and then euthanized. Body weights were taken on d 1 and every 2 to 4 d until slaughter. Crown rump (CRL) measurements were taken weekly, and heart girth (HG) measurements were taken at d 1 and slaughter. Blood samples (10 mL) were collected on d 1 and every 7 d until slaughter. Concentrations of IGF-I and IGFBP were determined by RIA and ligand blot, respectively. At birth, lambs from R ewes (4.15 ± 0.3 kg) were lighter than C (5.3 ± 0.3 kg) and O (5.1 ± 0.3 kg) lambs ($P = 0.01$). At 3 mo, lambs from R ewes (31.0 ± 1.3 kg) tended to be lighter ($P = 0.06$) than C (35.2 ± 1.3 kg) and O (33.5 ± 1.7 kg) lambs. However, we did not observe an effect of maternal diet on CRL at birth ($P = 0.67$) or 3 mo of age ($P = 0.29$). At birth, heart weight ($P = 0.06$) and HG ($P < 0.01$) were less in R (30.2 ± 3.2 g and 36.9 ± 0.8 cm, respectively) than C (36.3 ± 3.2 g and 40.7 ± 0.8 cm, respectively) and O (43.8 ± 3.2 g and 40.4 ± 0.8 cm, respectively) lambs, but not at 3 mo of age ($P = 0.60$, $P = 0.17$). Average serum IGF-I was decreased ($P = 0.04$) in R (158 ± 36 ng/mL) compared with C (308 ± 37 ng/mL) and O (227 ± 40 ng/mL) lambs. Average concentrations of IGFBP-3 were decreased ($P = 0.05$) in R (1,032 ± 135 AU) and O (1,014 ± 148 AU) compared with C (1,438 ± 135 AU). We did not observe a treatment effect on circulating IGFBP-2 ($P = 0.63$). In conclusion, poor maternal nutrition may inhibit fetal growth by reducing circulating concentrations of IGF-I and IGFBP-3.

Key Words: intrauterine growth retardation, IGF, IGFBP

106 Effect of rumen-protected amino acid supplementation of a protein-deficient diet on performance of lactating dairy cows.

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The objective of this experiment was to evaluate the effect of supplementing a metabolizable protein (MP)-deficient diet with rumen-protected (RP) Lys, Met, and specifically His on dairy cow performance. The experiment was conducted for 12 wk with 48 Holstein cows (75 ± 5.6 DIM). Following a 2-wk covariate period, cows were blocked by DIM and milk yield and randomly assigned to one of 4 diets, based on corn silage and alfalfa haylage: control, MP-adequate diet (AP; MP balance: +9 g/d); MP-deficient diet (DP; MP balance: −317 g/d); DP supplemented with RPLys (AminoShure-L) and RPMet (Mepron; DP-LM); and DP-LM supplemented with RPHis (DP-LMH). Analyzed CP content of the AP and DP diets was 15.7 and 13.6%. Apparent total tract digestibility of all nutrients, plasma urea-N, and urinary-N excretion were decreased ($P < 0.001$) by the DP diets compared with AP. Milk N secretion as a proportion of N intake was greater (34.6 vs. 29.4%, $P = 0.001$) for the DP diets compared with AP. Compared with AP, DMI tended to be lower ($P = 0.06$) for DP, but was similar for DP-LM and DP-LMH (24.5, 23.0, 23.7, and 24.3 kg/d, respectively). Milk yield was decreased ($P = 0.004$) by DP (35.2 kg/d), but was similar to AP (38.8 kg/d) for the DP-LM and DP-LMH diets (36.9 and 38.5 kg/d, respectively), following the trend in DMI. Milk fat and true protein

content did not differ among treatments. Milk protein yield followed the trend in milk yield response ($P = 0.002$; 1.13, 1.01, 1.10, and 1.14 kg/d, respectively). Plasma essential AA, Lys, and His were lower ($P < 0.03$) for DP compared with AP. Compared with AP, plasma Met concentration was higher ($P < 0.001$) for DP-LM and DP-LMH and that of His was similar for DP-LMH. In conclusion, MP-deficiency, approximately 15% below NRC (2001) requirements, decreased DMI and milk yield in dairy cows. Supplementation of the DP diet with RPLys and RPMet diminished the difference in milk yield compared with AP and addition of RPHis eliminated it. This study suggests that His is likely a limiting AA in dairy cows fed MP-deficient diets.

Key Words: metabolizable protein, rumen-protected histidine, dairy cow

107 Effects of lasalocid and pulse-dosed chlortetracycline on health, growth, and thyroxine concentrations of prepubertal dairy heifers.

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The effects of feeding chlortetracycline (CTC) and lasalocid (L) and the combination were studied using 40, 12 wk old Holstein heifers (108 ± 12 kg) in a randomized complete block design utilizing a 2 × 2 factorial arrangement of treatments. Heifers were blocked by birth date to 1 of 4 treatments: 1) carrier (30 g; C); 2) L + carrier (1 mg/kg BW; L); 3) CTC+ carrier (22 mg/kg BW; CTC); 4) L + CTC + carrier (CTCL). Heifers on CTC/CTCL were given their respective treatment during wk 1–4, 6, and 10 and within these weeks given treatment Monday— Friday and carrier only on weekends. Heifers were individually fed a total mixed ration (TMR) with treatments top-dressed at 1200 h daily. Heifer DMI was monitored and adjusted according to individual intakes. Skeletal measurements were taken weekly and blood samples obtained every Monday, Wednesday, and Friday. Blood samples were analyzed for thyroxine concentration via radial immunoassay. Heifers supplemented with L (L, CTCL) had lower DMI ($P = 0.05$), ADG ($P = 0.02$), overall BW gain ($P = 0.03$), overall wither gain ($P = 0.04$), and overall girth gain ($P = 0.09$) compared with heifers not fed L (C, CTC). Overall BW ($P = 0.04$) and body length ($P = 0.02$) gains and ADG ($P = 0.10$) were greater in CTC heifers (CTC, CTCL). Interactions occurred for: feed efficiency ($P = 0.03$), overall hip height ($P = 0.03$), and wither height ($P < 0.01$) gains and daily hip height gains ($P = 0.08$) were greater in C and CTCL heifers compared with CTC and L heifers. There was no effect on serum thyroxine concentrations. Supplementation with L did not increase growth. Supplementation with CTC improved growth for some skeletal measurements. The combination of CTC and L was more effective than either L or CTC fed individually. Supplementing CTC and L to growing heifers under conditions of stress may be of benefit.

Key Words: heifer, lasalocid, chlortetracycline

108 Effect of post-ruminal supplementation of phytonutrients on immune response, blood cell counts, and blood chemistry in lactating dairy cows.

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The objective of this experiment was to investigate the effects of post-ruminal supplementation of phytonutrients on immune response, blood cell counts and blood chemistry in lactating dairy cows. Eight ruminally-cannulated Holstein cows (232 ± 34.1 d in milk) were used in a replicated 4 × 4 Latin square design trial with 23-d periods. Treatments were: (1) control (CON), (2) 2 g/d curcuma oleoresin (CU), (3) 2 g/d garlic extract (GE), and (4) 2 g/d capsicum oleoresin (CA). The phytonutrients were dissolved in ethanol solution and pulse-dosed into the abomasum of the cows once daily, 2 h after feeding for 9 d during each experimental period. Control cows received ethanol solution only. Compared with CON, CU, GE, and CA increased ($P = 0.01$) concentration of cluster of differentiation-antigen-4-positive cells ($CD4^+$; 11.9 vs. 20.3, 18.4, and 17.8%, respectively). Treatments had no effect on $\gamma\delta^+$ and $CD8^+$ cells, interleukin-6, tumor necrosis factor-α and interferon-γ cytokines, and T-cell proliferation ($P = 0.34$ to 1.00). Monocyte counts were lowered ($P = 0.04$) by CU and GE compared with CON (0.26, 0.26 and 0.33 × 10^3/μL, respectively). Relative to CON, CA increased ($P = 0.04$) lymphocytes as proportion of the total white blood cells (WBC; 39.3 and 41.8%, respectively). Lymphocyte counts tended to be decreased ($P = 0.10$) by GE compared with CON (3.43 and 3.77 × 10^3/μL, respectively). Cows treated with GE and CA had lower ($P = 0.03$) mean platelet volume than CON cows (6.51, 6.56, and 6.91 fL, respectively). Blood glucose, BUN, and creatinine concentrations were not different among treatments ($P = 0.39$ to 0.47). In conclusion, post-ruminal supplementation of phytonutrients had no effect on $\gamma\delta^+$ cells, $CD8^+$ cells, cytokine concentrations, T-cell proliferation, and blood chemistry, but all treatments significantly enhanced $CD4^+$ cells, CU and GE reduced monocytes, and CA increased lymphocyte proportion of WBC in dairy cows.

Key Words: phytonutrients, immune response, dairy cow

Growth and Development

109 Zfp423 promotes adipogenic differentiation of bovine stromal vascular cells. Y. Huang*[1], A. Das[1,2], Q. Yang[1,2], M.-J. Zhu[1,2], and M. Du[1,2], *[1]Department of Animal Science, University of Wyoming, Laramie, [2]Department of Animal Sciences, Washington State University, Pullman.*

Intramuscular fat or marbling is critical for the palatability of beef. Intramuscular fat mainly locates inside perimysial connective tissue. In mice, very recent studies show that adipocytes and fibroblasts share a common pool of progenitor cells, with Zinc finger protein 423 (Zfp423) as a key initiator of adipogenic differentiation, while fibrogenesis is promoted by transforming growth factor-β (TGF-β) signaling pathway. To evaluate the role of Zfp423 in intramuscular adipogenesis and marbling in beef cattle, we sampled Sternocleidomastoid muscle for separation of stromal vascular cells (SVC). These cells were immortalized with pCI neo-hEST2 which carries a telomerase and individual clones were selected by G418, an aminoglycoside antibiotic. A total of 288 clones (3 X 96 well plates) were isolated and induced adipogenic differentiation, and their adipogenic potential was assessed by the formation of adipocytes with Oil-Red-O staining. Three clones with the highest and lowest adipogenic potential were selected for further analyses. The expression of Zfp423 was much higher (307.4 ± 61.9%, $P < 0.01$) in high adipogenic cells, while TGF-β was higher (156.1 ± 48.7%, $P < 0.05$) in low adipogenic cells. Following adipogenic differentiation, the expression of peroxisome proliferator-activated receptor γ (PPARγ) and CCAAT/Enhancer Binding Protein α (C/EBPα) were higher (239.4 ± 84.1% and 310.7 ± 138.4%, respectively, $P < 0.05$) in high adipogenic cells. Transfecting a plasmid overexpressing Zfp423 in both stromal vascular cells and cloned low adipogenic cells dramatically increased their adipogenic differentiation, accompanied with the inhibition of TGF-β expression. In conclusion, data show that Zfp423 is a critical regulator of adipogenesis in stromal vascular cells, and Zfp423 may provide a molecular target for enhancing intramuscular adipogenesis and marbling in beef cattle.

Key Words: adipogenesis, muscle, beef cattle

110 Agouti signaling protein abundance in cattle—Relationship with fat deposition. E. Albrecht*[1], K. Komolka[1], H. Sauerwein[2], T. Gotoh[3], and S. Maak[1], *[1]Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, [2]University Bonn, Bonn, Germany, [3]Kyushu University, Kuju-cho, Oita, Japan.*

The agouti signaling protein (ASIP), originally known for its role in melanogenesis, has been related to obesity in mice and humans. The potentially crucial role in adipocyte development, elucidated in cell culture models, makes it a tempting candidate for economically relevant, fat related traits in farm animals. The objective of our study was to characterize the protein abundance of ASIP in different adipose tissues, in skeletal muscle, and in blood of cattle differing in fat deposition. Japanese Black (JB; n = 6) and Holstein (HS; n = 5) steers were fed a high energy diet to maximize intramuscular fat (IMF) deposition, resulting in 34.3% (±1.7) and 20.4% (±2.5) IMF content in longissimus muscle (LM) for JB and HS, respectively, when harvested at 26 mo of age. Protein extract from subcutaneous, visceral, perirenal, intra- and intermuscular fat, and LM were investigated by Western blotting with a bovine-specific ASIP antibody. Blood plasma samples were also investigated by Western blotting after albumin removal. By immunohistochemistry, ASIP was localized in different cell types of adipose tissues, including adipocytes, and also in skeletal muscle tissue, but never in muscle fibers. In addition to the expected cytosolic signal, a putative nuclear localization of ASIP was observed. The protein abundance was highly variable among animals, and did not show a clear relationship with fat related traits like depot weights or fat cell size. Between breeds, the protein was similarly abundant within fat depots and did not reflect the earlier described ASIP mRNA overexpression in JB compared with HS. However, we detected higher ($P < 0.05$) ASIP levels in blood plasma of JB (normalized to albumin) than in HS (1.13 ± 0.08 vs. 0.89 ± 0.09, respectively), which were paralleled by higher ($P < 0.05$) leptin concentrations in JB (18.9 ng/ml ± 3.1) vs. HS (12.6 ng/ml ± 4.1). Our results provide evidence for a widespread expression of ASIP in bovine adipose tissues at the protein level and for the first time for the secretion and circulation of this protein in the blood of cattle, suggesting a potential endocrine function.

Key Words: ASIP, adipose tissue, blood

111 Blood glucose and acylated ghrelin in response to duration of maternal undernutrition during gestation in twin sheep pregnancies. M. E. Field,* R. V. Anthony, M. D. Vetters, C. Flörcke, T. E. Engle, S. L. Archibeque, and H. Han, *Colorado State University, Fort Collins.*

The experimental objective was to determine the effect of duration of maternal undernutrition during gestation in twin pregnancies on maternal and lamb blood parameters. Multiparous Western white face ewes were fed 100% (Control; n = 8), or 50% of their nutrient requirements from 28 to 78 d gestational age (dGA) and readjusted to 100% beginning at 79 dGA (50–100; n = 10), or 50% from 28 to term (50–50; n = 9). Lambs were birthed naturally, weaned at 10 wk postpartum (wPP) and harvested at 18 wPP. Data were analyzed by preplanned orthogonal contrasts: Control vs. 50–100 and 50–50 and 50–100 vs. 50–50. At 49 and 77 dGA GLU was greater ($P < 0.05$) in Control vs. 50–100 and 50–50 ewes; the same trend ($P < 0.10$) occurred at 63 dGA. At 105, 112, 126, and 147 dGA GLU was greater ($P < 0.05$) in 50–100 vs. 50–50 ewes. At 2 wPP ewe GLU was greater ($P = 0.03$) in 50–100 (3.60 ± 0.17 mM) and 50–50 (3.29 ± 0.17mM) than Control (2.99 ± 0.16 mM). Ewe aGRL was greater ($P = 0.02$) in 50–100 (237 ± 32 pg/mL) and 50–50 (239 ± 38 pg/mL) vs. Control (136 ± 32 pg/mL) at 140 dGA and at 4 wPP the same pattern was observed (50–100, 388 ± 38 pg/mL; 50–50, 326 ± 45 pg/mL; Control, 184 ± 38 pg/mL). Lamb GLU was reduced ($P = 0.02$) in 50–100 (4.12 ± 0.09 mM) vs. 50–50 (4.52 ± 0.09 mM) at 14 wPP. Lamb aGRL was greater ($P = 0.06$) in 50–100 (141 ± 47 pg/ml) and 50–50 (184 ± 48 pg/ml) vs. Control (59 ± 37 pg/ml) at 2 wPP, but did not differ at 16 wPP. Elevated post-weaning glucose in 50–50 lambs may indicate increased insulin resistance in these lambs. Early nutrient restriction resulted in elevated aGRL, even following realimentation, which persisted into the postpartum period, suggesting potential long-lasting programming of maternal appetite control during early- to mid-gestation as a result of dietary restriction. 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: maternal undernutrition, ghrelin, sheep

112 Delaying a bovine viral diarrhea vaccine and growth implant with metaphylaxis affects performance, but not health of feedlot heifers.

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Stress and low nutrient intake of newly received feedlot calves may limit efficacy of both a bovine viral diarrhea (BVD) vaccine and growth implant at initial processing. Use of chlortetracycline (CTC) when delaying an initial vaccine and implant may be beneficial. This 56-d study evaluated effects of timing (TIME) of a BVD vaccine and growth implant with or without CTC on health and performance of 312 heifers (184 ± 0.7 kg BW). Initial processing of heifers included treatment with tulathromycin and vaccination for bovine respiratory disease. Heifers were sorted into 24 pens, which were randomly assigned to 4 treatments. Treatments (2 × 2 factorial) were growth implant (Synovex-C; Fort Dodge Animal Health) and BVD vaccination (Bovi-Shield Gold BVD; Pfizer Animal Health) of calves on d 1 (INITIAL) or d 28 (DELAYED) after arrival with (+CTC) or without (-CTC) 3 5-d pulse-doses of CTC (Aureomycin; Alpharma Animal Health) in their diets. Diets were based on a complete feed (RAMP; Cargill) and ground corn delivered twice daily. Performance and health were analyzed using MIXED and GLIMMIX procedures of SAS, respectively. A TIME × CTC interaction ($P = 0.06$) occurred for DMI; DMI was lower for DELAYED than INITIAL when heifers received -CTC, but DMI was not different between DELAYED and INITIAL when heifers received +CTC. No TIME × CTC interactions ($P \geq 0.21$) occurred for BW, ADG, or G:F. Timing of BVD vaccine and implant did not affect ($P = 0.18$) BW of heifers on d 28, but BW were lower ($P = 0.04$) for DELAYED than INITIAL heifers on d 56. From d 29 to 56, ADG was lower ($P = 0.02$) and G:F tended to be lower ($P = 0.07$) for DELAYED than INITIAL heifers. Delaying the BVD vaccine and implant also tended to lower ($P = 0.09$) ADG from d 0 to 56, but did not affect ($P = 0.27$) G:F. On d 28, BW of +CTC heifers tended to be lower ($P = 0.06$) than -CTC heifers, but CTC did not affect ($P \geq 0.21$) d-56 BW, ADG, or G:F. Morbidity and mortality during the 56 d were not affected ($P \geq 0.17$) by treatments. Delaying the initial BVD vaccine and growth implant with or without CTC may not improve animal health, and may have negative implications on performance of newly received feedlot heifers.

Key Words: vaccine, implant, heifer

113 The effects of intrauterine growth retardation (IUGR) due to poor maternal nutrition on adipose tissue development and metabolic status in sheep.

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Poor maternal nutrition negatively affects growth and development of the fetus as well as postnatal metabolism. We hypothesized that intrauterine growth retardation (IUGR) due to poor maternal nutrition would increase adiposity and negatively affect metabolism. Ewes pregnant with twins (n = 24) were fed 100% (CON), 60% (RES) or 120% (OVER) of NRC requirements beginning at d 85 of gestation. Offspring were euthanized within 24 h of birth (d 1; n = 3/treatment) or at 3 mo of age (n = 3 to 5/treatment) at which point blood samples and renal adipose tissues were collected. Animals maintained until 3 mo were removed from the ewe and fed a control diet of milk replacer and 18% creep feed. Circulating concentrations of leptin, insulin and glucose were determined by quantitative ELISA. Total cholesterol (TC) and triglycerides (TG) were determined by enzymatic analysis. Gene expression was determined by real time-reverse transcriptase (RT)-PCR. Data were analyzed using ANOVA with significance considered as $P \leq 0.05$. As reported, BW were reduced by 16% in RES lambs at d 1 and 3 mo ($P \leq 0.05$) compared with CON. A significant effect of treatment was not observed for concentrations of insulin or glucose ($P \geq 0.30$) or mRNA expression of markers for adipogenesis, *PPARγ* and *C/EBPα*, at d 1 or 3 mo ($P \geq 0.60$). However, at d 1, concentrations of leptin tended to be 34% and 61% greater in RES and OVER, respectively (1.28 ± 0.16, 1.72 ± 0.12, 2.07 ± 0.40 mg/dL; CON, RES, OVER, respectively; $P \leq 0.12$). At 3 mo, concentrations of leptin tended to be 25% and 31% greater in RES and OVER, respectively (0.91 ± 0.16, 1.14 ± 0.11, 1.27 ± 0.08; CON, RES, OVER, respectively; $P \leq 0.13$). A similar trend was observed in *leptin* mRNA expression with a 2.60 ± 0.70-fold increase in OVER at 3 mo ($P \leq 0.13$). At d 1, we did not observe a significant effect of treatment on TC (39.52 ± 3.09, 47.3 ± 4.27, 46.70 ± 2.44; CON, RES, OVER respectively; $P \leq 0.22$). At 3 mo, TG were 45% greater in OVER compared with CON ($P = 0.07$). In conclusion, these data suggest that poor maternal nutrition during gestation alters markers of adipogenesis and metabolism of lipids during early postnatal growth.

Key Words: intrauterine growth retardation, adipose tissue, leptin

114 Maternal nutrition of beef cattle on pasture mediates long-term consequences for offspring primarily through effects on growth early in life.

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Long-term consequences of dam nutrition on offspring, beyond those due to variation in early-life growth, were studied. Hereford cows were mated in consecutive years to Piedmontese or Wagyu sires. When confirmed pregnant, treatments (low or high pasture quality and availability) were applied to cows (n = 513) until parturition and(or) weaning. At weaning (7mo), 4 early-life growth groups (gestation-preweaning: Low-Low, Low-High, High-Low and High-High) of offspring (n = 240) were selected within steer and heifer cohorts for further study, resulting in multi-modal distributions of offspring growth to birth and weaning. A stage stepwise regression procedure (final exclusion parameter, $P > 0.05$) examined covariates including birth (BW) and weaning (WW) weight, age at measurement (A), and effects of nutrition during pregnancy (P) and lactation (L), calf sex (S), year (Y), sire breed (G), and first order interactions of factors and with covariates. BW was affected by P; WW by L and P, over and above differences due to BW. For feedlot entry (26mo), exit (30mo) and carcass (CW) weights, there were significant linear effects of BW and WW plus effects of G, S and Y, but no effects of P or L beyond those due to differences in BW and WW. Average differences of 6kg in BW of calves due to P and 55kg in WW due to L both translated into differences of ~20kg in CW, 11–12kg in retail yield and 6kg of fat trim at 30mo, but did not affect beef tenderness or marbling. When adjusted to a constant CW, heavier WW cattle had more fat trim and less retail yield. There were few interactions, however at the same CW there was a significant G x P interaction for rib eye area: Piedmontese-sired, Low 95.7 vs. High 88.4cm^2; Wagyu-sired, both groups 85.7cm^2. Feedlot feed intake (n = 142) was affected by BW and WW but not when corrected for weight at start of the intake test. FCR was affected by WW and L, and whether dams were lactating in early pregnancy. Maternal nutrition did not affect RFI. Overall, there were few long-term influences of maternal nutrition on offspring beyond those related to early-life growth within our pasture-based system. Optimal maternal nutrition that maximizes capacity to re-breed has greater economic effect than longer-term consequences of maternal nutrition on offspring.

Table 1. Effects on productivity

	Mean	BW	WW	P	P	L	L	Model
		Slope/ kg	Slope/ kg	Low	High	Low	High	R^2%;terms[1]
BW, kg	33.7	NA[2]	NA	29.8	35.8*	NA	NA	33.2; P G S
WW, kg	188.8	2.26*	NA	179.1	190.6#	158.3	211.5*	62.5; L BW A S P
CW, kg	382	2.58*	0.38*	ns	ns	ns	ns	67.5; BW Y WW G
US marble score	446	ns	ns	ns	ns	ns	ns	40.8; G S
Rib eye area,[3] cm²	89.7	ns	ns	See text		ns	ns	48.8; CW Y P G
Retail yield,[3] kg	249.1	ns	−0.08*	ns	ns	ns	ns	95.2; CW G WW
LD shear force, kg	4.05	ns	ns	ns	ns	ns	ns	14.0; Y S

[1] See text.

[2] Not applicable.

[3] Constant CW.

*$P < 0.001$; #$P < 0.01$; NS $P > 0.05$.

Key Words: birth weight, fetal programming, nutrition

115 Lean tissue accretion and the efficiency of energy and protein retention are enhanced by intermittent bolus compared to continuous feeding.

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Feed remains the largest non-fixed input cost in animal production systems, and dietary interventions aimed at enhancing the efficiency of nutrient utilization may provide new avenues for improving profitability. To determine the effect of feeding modality on growth and lean tissue accretion, neonatal pigs (n = 6/treatment, 6-d-old) were fed the same diet in equivalent amounts continuously (CON) or intermittently (INT; meal every 4 h) for 21 d. Body composition was measured by dual x-ray absorptiometry (DXA) before and 18 d following the initiation of feeding, and fractional rate of protein synthesis was measured using the flooding dose method. Fractional protein synthesis rates, and plasma glucose and insulin were determined on the last day of feeding. Weight gain was greater ($P < 0.05$) for INT than for CON pigs and resulted in heavier body weights from 9 d of feeding onwards . Total lean tissue mass and spine length were greater ($P < 0.05$) in INT than CON pigs. Glucose and arterial insulin levels were greater ($P < 0.05$) for INT pigs after the meal than for CON pigs. Compared with the CON group, muscle protein synthesis was 40% higher in longissimus dorsi, and 34% higher in gastrocnemius and soleus ($P < 0.05$) of INT pigs. Longissimus dorsi and soleus muscles were 56 and 35% heavier ($P < 0.05$) in INT than CON pigs. Protein synthesis was 22 and 48% higher ($P < 0.05$) in liver and ileum of INT compared with CON pigs. Liver, jejunum and ileum weights were 72, 40, and 35% higher ($P < 0.05$) in pigs receiving the INT compared with the CON treatment. Intermittent feeding resulted in improved ($P < 0.05$) feed conversion efficiency (5.1 vs. 7.2 kg milk/kg body weight gain) compared with continuous feeding. In addition, the efficiency of protein and energy retentions were both enhanced ($P < 0.05$) by 30 and 44% with intermittent compared with continuous feeding. These results indicate that intermittent feeding, as compared with continuous feeding, upregulates protein synthesis resulting in an improved efficiency of protein and energy retention, greater lean tissue accretion, and enhanced growth in the neonate. Supported by NIH AR444474 and USDA/ARS 6250-51000-055.

Key Words: protein synthesis, body composition, insulin

116 Tripalmitolein infusion in finished lambs.

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Palmitoleic acid (C16:1 *cis*-9) has been proposed to function as a lipokine, regulating lipogenesis and desaturation in murine liver. Previously, our bovine adipocyte cultures provide evidence that palmitoleic acid decreases lipogenesis and desaturation. Our objective was to determine if palmitoleic acid functions similarly in ruminant animals where the primary site of lipogenesis is adipose tissue. Eight Southdown lambs approximately 13 mo of age were assigned to 1 of 2 treatment groups [tripalmitin (control) or tripalmitolein (lipokine)] in a completely randomized design. Both jugular veins were cannulated; one was used to infuse 4 μM triglyceride treatment at 9 μmol*kg BW^{-1} per d over a 4 d period and the other was used to sample blood throughout the study and every 30 min for 9.5 h before slaughter. On the last day of infusion, 0.7 mmol 1-^{13}C18:0 was administered 8 h before slaughter. Lambs were sacrificed 96 h after infusion began. Serum was analyzed for fatty acid composition and enrichment. Dorsal and sternal subcutaneous adipose tissues and liver were flash frozen for gene expression and fatty acid analysis. Lipogenic genes of interest were *fatty acid synthase* (*FASN*) and *stearoyl-CoA desaturase* (*SCD1*). There was a main effect of depot on fatty acid composition and gene expression. In the liver, C16:0, C16:1 *cis*-9, C18:1 *cis*-9, were decreased ($P < 0.05$) and C18:2 n-6 was increased ($P < 0.05$) compared with adipose tissue depots. The desaturation ratios (C16:1/C16:0 and C18:1 *cis*-9/C18:0) were highest in sternal adipose tissue compared with dorsal and liver tissues. Expression of *FASN* and *SCD1* was reduced ($P < 0.05$ and $P = 0.07$, respectively) in sternal adipose tissue compared with dorsal subcutaneous fat. In addition, FASN was downregulated ($P < 0.05$) in lipokine compared with control lambs. Enrichment of serum C18:0 and C18:1 *cis*-9, detectable at 90 min following stable isotope injection, indicates a reduction in desaturase activity. The fractional synthetic rate and tracer:tracee ratio of C18:1 *cis*-9 from C18:0 was greater over time ($P < 0.05$) in control compared with lipokine lambs. Therefore, intravenous tripalmitolein infusion alters on fatty acid biosynthesis in lambs.

Key Words: palmitoleic acid, lamb, desaturation

117 Nutritional milieu of preadipocytes determines the differentiating capabilities of bovine primary stromal vascular cultures.

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Objectives were to determine the effect of nutritional milieu of preadipocytes on adipogenesis and adipose lipid metabolism in bovine adipocytes. Bovine primary stromal vascular cultures were isolated from intermuscular fat of Angus x Hereford steers (508 kg BW,n = 3 per treatment) fed alfalfa/soybeans with (LC) or without (L) corn grain supplementation (0.75% BW) for 105 d. Preadipocytes were differentiated (D0) in differentiation media [DMEM containing 10% fetal calf serum, 2.5 μg/mL insulin, 0.25 μ*M* DEX, 1 μ*M* rosiglitazone, 0.5 m*M* IBMX, and 10 m*M* acetate] for 2 d and from D2 to D12 without DEX and IBMX. From D2 to D12, cells were treated with (0 or 100 μ*M*) of linoleic acid (C18:2). Cells were harvested on D-2, D0, D2, D4, D6 and D12 for gene expression by RT-qPCR and on D6 for fatty acid (FA) analysis by GLC. Cell viability of pre-differentiated cells was assayed using Cell Counting Kit-8. The adipocyte cell sizing was done using Cell Scepter. Glycerol-3-phosphate dehydrogenase (GPDH) activity was assayed to determine adipocyte differentiation. The treatment effects were analyzed by Proc Mixed of SAS 9.2 with steer as experimental unit. The average diameter of preadipocytes and differentiated adipocytes ($P < 0.05$) were larger in LC (16.25 ± 0.48 μm and 18.08 ± 0.37 μm) compared with those of L (15.58 ± 0.43 μm and 16.95 ± 0.32 μm). However, the preadipocytes from L proliferated faster ($P < 0.05$) than those from LC . The GPDH activity (nmol/mg protein per min), an indicator of adipocyte differentiation was higher ($P < 0.01$) in adipocytes from L (4.32 ± 0.50) compared with LC (0.51 ± 0.5). Also, the expression of genes associated with adipocyte differentiation: *fatty acid binding protein 4*, *GPDH*, *peroxisome proliferator-activated receptor gamma*, *CCAAT/enhancer binding protein α* (*C/EBPα*), and *stearoyl-CoA desaturase 1*, were higher ($P < 0.05$) in L compared with LC . Whereas the total FA content or the FA composition (except C18:1c9, $P < 0.05$) did not differ between un-supplemented L and LC, C18:2 supplementation showed higher ($P < 0.05$) content of total FA, C16:0, C16:1, C18:0, C18:1 and C18:2 in L compared with LC. The results showed that the nutritional milieu determines the differentiating capabilities of bovine primary stromal vascular cultures.

Key Words: adipocytes, fatty acids, adipogenesis

118 Effects of feeding different forage sources on rumen fermentation and gastrointestinal tract development in young calves.

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It has been previously demonstrated that offering chopped forage to young calves increases ADG and feed intake. However, the mechanism involved in improving calf performance is not clear. Fifteen Holstein calves (BW = 43.6 ± 4.37 kg) were randomly assigned to one of the 3 dietary treatments (n = 5) to determine the effects of feeding different forages sources on rumen fermentation and gastrointestinal tract (GIT) development. Treatments consisted on a pelleted starter concentrate (20% CP, 21% NDF) offered alone (CTR), with alfalfa hay (ALF), or with oats hay (OAT) in separate buckets. Calves received 2 L of milk replacer (MR) at 12.5% DM twice daily until 49 d of age. From 50 to 56 d of age, calves received 2 L/d of MR at 12.5% and were weaned at 57 d of age. Starter, forage, and MR intake were recorded daily and BW weekly. A rumen sample was taken by an oral tube weekly to determine rumen pH and VFA concentrations. Three weeks after weaning, animals were harvested and each anatomical part of the GIT was dissected and weighed. Data were analyzed with a mixed-effects model with repeated measures, except for harvest data that had no repeated measures. Animals in OAT treatment tended ($P = 0.10$) to eat more starter concentrate than the other treatments after weaning (2612 vs 1990 ± 270.8 g/d, respectively), and ALF animals ate more ($P = 0.05$) forage than OAT animals (147 vs 47 ± 31.0 g/d, respectively). Rumen pH was lower ($P < 0.01$) in CTR compared with OAT and ALF calves (5.5 vs 6.2 ± 0.16, respectively). Furthermore, acetate proportion in the rumen tended to be greater ($P = 0.10$) in ALF than in CTR and OAT treatments (51.8 vs 46.4 ± 1.91% respectively), and butyrate proportion was numerically ($P = 0.12$) lower in ALF compared with the others 2 treatments (9.9 vs 14.7 ± 1.77%, respectively). Total GIT weight expressed as a percentage of BW tended ($P = 0.07$) to be greater in ALF compared with the other 2 treatments (22.4 vs 20.1 ± 0.75%, respectively). In conclusion, feeding forages to young calves increases rumen pH, although the rumen fermentation profile differs depending on the forage source.

Key Words: calves, forage, gastrointestinal development

International Animal Agriculture Symposium: Increasing Undergraduate and Graduate Student Training in International Animal Agriculture

119 What type of employee will international agribusiness companies be seeking? K. A. Jacques* and K. A. Dawson, *Alltech Center for Animal Nutrigenomics & Applied Animal Nutrition, Nicholasville, KY.*

The globalization of agricultural markets and resources has driven up the importance of having a broad-based understanding of the rate-limiting steps that govern food production. Employers look to hire people who command an overall knowledge of an increasingly complex food chain, from production to consumption. The market importance of consumer demands has risen in response to the growth of living standards in emerging nations and worldwide food safety concerns. These considerations are re-shaping the industry and mandate that the ag industry employees of the future be capable of presenting their message across cultures. Moreover, with the rapid emergence of industry-changing biotechnologies, such as nutrigenomics, it is increasingly essential that prospective employees have the communication skills to enable them to explain sophisticated science to a diverse audience. These job demands have important implications for undergraduate and graduate programs in agriculture. Course plans must encourage students to build a wide knowledge base of the economic and cultural, as well as the scientific factors, that drive the industry's future. Today's animal science graduate, for example, comes best equipped with cross training beyond the traditional single species/sector focus and an understanding of the issues that affect the value chain at each stage between farm and consumer. The ability to look beyond a regional or species-based focus is of special value to international companies that typically work in multiple aspects of grain and animal protein production. Partnerships between industry and academia that provide students internship experience will be of increasing value to both employers and students.

Key Words: globalization, education, agribusiness

120 The role of animal scientists in assuring food security in developing countries. J. Turk,* *U.S. Agency for International Development, Washington, DC.*

The objectives of this presentation are to 1) highlight the values of livestock in economic growth and human nutritional security in developing countries; 2) relate how animal scientists are important to this security; 3) describe what skills are required to work in the field; and 4) introduce the international donor livestock community, i.e., the multilateral institutions, bilateral organizations, government agencies such as the European Union and BRIC governments, private foundations (e.g., Rockefeller Foundation, Bill and Melinda Gates Foundation), and non-government organizations (NGOs). The global livestock sector employs 1.3 billion people directly or indirectly. Approximately 70% of households living on less than US$1 per day are fully or partially dependent on livestock for their livelihoods. The largest single sector of agricultural economies, it accounts for up to 50% of agricultural GDPs in most developing and transition countries. As a repository for rural capital livestock provide often more than 10%. For poor households, livestock are key to managing risk, protecting savings, and offering insurance against drought or crop failure. Livestock represent diversified values—social, environmental, economic and nutritional—but not all can be measured in hard numbers or equated across cultures and ecosystems. Although livestock′s economic value is usually regarded as the primary benefit, nutritional value of animal source foods is one of the most difficult to assess. Traditional diets often lack critical micronutrients essential for children′s physical and cognitive development. Improving livestock production and health throughout the value chain requires the knowledge to address major challenges. These include: low animal productivity; disease transmission; weak or non-existent national policies regarding disease control; weak service delivery caused by lack of trained providers; lack of inputs and supplies; inability of producers to pay for services; lack of production, health and market information; and impacts of climate change on all production systems. This paper relates how animal scientists are important to the international livestock community and food security.

Key Words: livestock production, food security, developing countries

121 Implementing new technologies in developing countries: Intellectual property, patent laws, and technology transfer agreements. K. Krafka,* *Kemin Industries Inc., Des Moines, IA.*

As new graduates seek and secure employment in animal agriculture and work in a more global economy, there is an emerging need for today′s scientific professionals to become more familiar with a basic recognition of intellectual property. Those professionals who are proficient in operating with knowledge of intellectual property issues will become more poised to contribute to new product development. The objective of this abstract is to increase both awareness and understanding of intellectual property, including trade secrets, patents, patent laws, registrations and technology transfer agreements, as they may relate to the use of innovative technology on a more global basis. Intellectual property is often misunderstood and consequently overlooked as part of technology transfers from one geography to another. Certain rights are inferred with patents, and those may or may not be applicable across different geographies. Patent terms or lengths may also vary among world geographies. A case study will be presented using an example novel product developed in one geography that is desired for transfer and use in a secondary geography. Intellectual property rights, freedom to operate strategies and licensing options will be discussed. The use of patents as a core strategy and revenue stream for both universities and industry will be explained. The case study will demonstrate how a successful technology transfer can be approached and properly executed on a timely basis. In conclusion, careful management of roles and responsibilities as they relate to intellectual property may result in an increased ability to conduct business in multiple geographies, enhanced research and manufacturing partnerships and most importantly, full utilization of cutting-edge technologies to further improvements and maximize value in livestock and poultry production globally.

Key Words: intellectual property, patents, technology transfer

122 A theme-based approach in smallholder dairy training through a partnership between Malawi and Scotland. M. G. G. Chagunda*[1], T. N. Gondwe[2], and D. J. Roberts[1], *[1]Scottish Agricultural College, Edinburgh, UK, [2]Bunda College of Agriculture, Lilongwe, Malawi.*

Over the past decade the Malawian agrarian policy has been shifting from what was predominantly tobacco based industry into other enterprises. The Department of Animal Health and Livestock Development

(DAHLD) has identified dairy farming as its flagship due to its potential to substantially contribute to sustainable household income, food and nutritional security. However, acute staff shortages and inadequate expertise within DAHLD and other non-governmental organizations has been a major challenge (Mtukuso, 2006, CISANET, 2006). Capacity building and skill development are needed for adequate human capital to complement technical interventions (World Bank, 2009). The national livestock policy and DAHLD strategic plan (DAHLD 2004, 2006) identified the following 6 specific issues in the area of dairy in Malawi. These are, a) inadequate availability of improved breeding stock and inefficient insemination program b) high cost of veterinary drugs and health care c) feed and nutritional problems d) low levels of husbandry e) inadequate production and marketing infrastructure and f) milk keeping quality. Since 2008, Scottish Agricultural College and Bunda College of the University of Malawi have been working on a theme-based program for smallholder dairy training with the 6 specific issues turned into training themes. Each theme is dealt with at different levels reflecting the trainees' prior knowledge, function and commonality of practice. Each training session is delivered by the appropriate resource person, for example, trainers, facilitators and innovators depending on need. Scientists and development workers are sent on either top-up courses or graduate programs and hence integrate training into the sustainable smallholder dairy development initiative. Courses are obtained either locally in Malawi or through sandwich programs in Scotland. Currently, 586 farmers, 28 lead farmers, 43 extension workers, 6 postgraduates, and 16 senior staff have been trained. Through this initiative, a practical diploma course in dairy science has been established in Malawi. A hop-on hop-off program for life-long learning is envisaged in the future.

Key Words: training, partnership, smallholder dairy

123 Preparing students for a changing world: Employer prioritized attributes from international engagement. L. J. Unruh Snyder,* J. M. Fernandez, and M. A. Russell, *Purdue University, West Lafayette, IN.*

As educators, we want to brace students for a changing world to address the needs for our global society. As agriculture students complete their baccalaureate degrees to enter the workforce, we anticipate they will embrace this with a skill set to overcome challenges and to be successful with their new careers. In 2009, the NRC highlighted the need for a new focus in the undergraduate agricultural education experience, and Purdue's College of Agriculture's strategic goal stated that every undergraduate student graduating will participate in at least one transformational learning experience—study abroad, undergraduate research, or internship, etc. Studies have shown that through international engagement students have a deeper understanding and respect of global issues, cultures, stronger intercultural communication skills, increased ability to problem solve more effectively (Table 1). These set of transformational skills are highly prized by future employees. In 2011, APLU and UIC reported that international experiences consistently rank the lowest for preparing students to enter the workforce; however, study abroad literature demonstrates positive effect on learning. The disconnect needs to be brought to the attention of the educators and students on how to articulate these experiences to gain the employers attention. Thus, there is a need to help students report self-efficacy based on these experiences affecting their career development. Preparing students for leadership in animal sciences through exemplary teaching, and learning experiences helps to set the stage for their career advancement.

Table 1. A three-year study comparison of cultural awareness in Costa Rica (Pre-Test N = 43; Post-Test N = 43; Six-Month N =25)

Statement	Pre-test (M, SD)	Post-test (M, SD)	Six month (M, SD)
As a student studying agriculture, it is important for me to understand issues related to international agriculture	4.79 (0.47)	4.60 (0.70)	4.40 (0.96)
Participating in this program will/has enhance(d) my cultural awareness	4.65 (0.53)	4.42 (0.82)	4.12 (1.01)

Note: * < 0.05 and denotes a significant difference between the signified mean and that on the pre-test.

Key Words: international, education, employment

124 In-country partnering needed for successful international service learning. P. Ebner*[1], H. Oliver[2], and M. Russell[1], [1]*Department of Animal Sciences, Purdue University,* [2]*Department of Food Science, Purdue University.*

Service learning is a form of experiential learning that integrates community service by the students with the skill development and learning of course content through that service. Purdue Animal Sciences now offers an "Animals & Food Security" undergraduate-level service learning course that take place each year in 2 international settings (Romania and Haiti). In each course, students are introduced to Extension methodologies, communication strategies and resource management by working directly with food animal producers in the respective countries. Integral to service learning is the identification and development of community partners. An ideal community partner relationship is cooperative, producing equitable benefits for both parties. The success of both service learning courses offered by Purdue Animal Sciences has relied heavily on fostering close and functional relationships with their community partners and similar models are used by each course to identify such partners. A total of 72 Purdue students and 28 host-university students have participated in this community- and student-development course. In each case, Purdue partners with a host-country university (Banat University of Veterinary Medicine and Agricultural Sciences in Romania and the University of Antenor Firmin in Haiti). Working directly with host country universities offers connections to students, shared educational and human capital development, and the capacity to incorporate research components into the service learning courses. Likewise, each course partners with Heifer International, a non-governmental organization devoted to global hunger and food security issues. These partnerships offer connections to local farmers and farmer groups and the ability to integrate into a successful development model and use it as an educational tool. Taken together, these partnerships ensure not only the successes and sustainability of the actual working projects, but the continued functionality of courses themselves. We will elaborate on the values and challenges of working with local partners to make the experience educational for the students and of definite benefit to the host community.

Key Words: international, service-learning, extension

Lactation Biology I

125 Serotonin (5-HT) regulates calcium mobilization at the onset of lactation in rats. J. LaPorta, T. L. Peters, K. E. Merriman, and L. L. Hernandez,* *University of Wisconsin, Madison.*

Serotonin is a known homeostastic regulator of lactation and was recently demonstrated to be a regulator of bone turnover. Circulating calcium (Ca^{2+}) is known to decrease at the onset of lactation, and often results in milk fever in dairy cattle. Serotonin is synthesized in a 2-step reaction from the amino acid L-tryptophan (L-TRP). The rate-limiting step is catalyzed by tryptophan hydroxylase (TPH1) isoform to form 5-hydroxytryptophan (5-HTP). To explore 5-HT's role on Ca^{2+} homeostasis in the transition period (10 d pre and postpartum) rats were fed 3 diets (n = 15 per treatment): control (CON), 5-HTP (0.2% total diet) and L-TRP (1.35% total diet) to increase endogenous 5-HT production. Milk samples were collected on d 1, 5 and 9 of lactation to measure Ca^{2+} concentrations. Serum and plasma samples were obtained on d 20 of gestation and d 9 of lactation to measure circulating 5-HT, Ca^{2+} and parathyroid hormone-related protein (PTHrP) levels. Total mRNA was isolated from mammary gland tissue from d 9 lactating animals and analyzed for PTHrP, TPH1, plasma membrane Ca^{2+} ATPases 1 and 2 (PMCA1, 2), sodium- Ca^{2+} exchanger 1 (NCX1), secretory Ca^{2+} ATPase 1 and 2 (SPCA1, 2), and sarco(endo)plasmic reticulum Ca^{2+} ATPase 2 (SERCA2). The 5-HTP and L-TRP treatments effectively increased serum 5-HT over time ($P < 0.001$), with a greater increase seen in the 5-HTP cohort. Plasma PTHrP was significantly increased ($P < 0.05$) on d 9 of lactation in the 5-HTP cohort. There was a significant increase of milk Ca^{2+} in the 5-HTP and L-TRP cohorts ($P < 0.05$), and decreased serum Ca^{2+} on d 9 lactation in the L-TRP group ($P < 0.05$). The mRNAs for PTHrP, TPH1, NCX1, PMCA2, SPCA2, and SERCA2 were increased in the mammary glands of the 5-HTP cohort ($P < 0.05$) and in the L-TRP cohort, except for PMCA2 and PTHrP ($P < 0.05$). The SPCA1 mRNA was decreased in both the 5-HTP and L-TRP cohorts ($P < 0.05$). These results suggest that feeding 5-HTP increases PTHrP induction in the plasma and mammary glands of transition rats, and increases Ca^{2+} transport within the mammary gland. It is possible that the L-TRP cohort could be working through a different mechanism to increase Ca^{2+} transport.

Key Words: 5-hydroxytryptophan (5-HT), Ca^{2+}, parathyroid hormone-related protein (PTHrP)

126 Genes and functions associated with photoperiodic effects on the mammary gland. T. B. McFadden*[1] and E. H. Wall[2], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada,* [2]*Department of Medicine, University of Vermont, Burlington.*

Pubertal heifers exposed to short day photoperiod during induction of lactation produced more milk in the ensuing lactation than heifers exposed to long day photoperiod, but the mechanisms behind this effect are unknown. To gain insight into potential mechanisms, we used microarray analysis to identify genes differentially expressed in mammary gland of heifers hormonally induced into lactation while exposed to different photoperiods. Holstein heifers (n = 6/treatment; 14 mo old) were assigned to long day (LD; 16 h light:8 h dark), or short day (SD; 8 h light:16 h dark) photoperiod and fed melengesterol acetate for 14 d to synchronize estrous. Heifers were then treated with estrogen and progesterone (E + P; 0.1 and 0.25 mg/kg per d) for 7 d to induce lactation. Mammary tissue was obtained by biopsy at 0, 5, and 10 d relative to initial E+P injections, and Affymetrix GeneChip Bovine Arrays were used to measure gene expression. Ingenuity Pathway Analysis was used to determine functions enriched by differentially expressed genes. Mammary expression of 187 genes was influenced by photoperiod ($P < 0.05$). Enriched functions included cellular assembly and organization, cell morphology, and molecular transport. Those functions are consistent with differences in mammary gland differentiation and activity, which could support the higher milk yield of heifers exposed to SD. Hormonal induction of lactation elicited differential expression over time of 4540 genes ($P < 0.05$), assigned to functional categories including cell cycle, cell death, and protein synthesis, which correspond with the marked development and activation of the mammary gland in preparation for lactation. There was a significant treatment by time interaction such that the temporal pattern of expression of 598 genes differed between LD and SD heifers ($P < 0.05$). Similar to the main effects, enriched functions included cellular development, organ morphology, and lipid metabolism. We conclude that exposure to SD during hormonal induction of lactation markedly influences gene expression in the mammary gland. The genes and functions identified represent potential mechanisms by which photoperiod alters mammary function.

Key Words: gene expression, mammary gland, photoperiod

127 Effect of ovariectomy on milk yield and mammary gland activity in lactating cow. L. Yart*[1,2], F. Dessauge[1,2], L. Finot[1,2], S. Wiart[1,2], A. Mottin[1,2], A. Eveno[1,2], P. G. Marnet[2,1], and V. Lollivier[2,1], [1]*INRA, UMR1348 Pegase, Saint-Gilles, France,* [2]*Agrocampus Ouest, UMR1348 Pegase, Rennes, France.*

Milk yield (MY) in dairy cows is highly dependent on both mammary tissue remodeling and mammary epithelial cell activity during lactation. Previous studies on lactating cows suggested that ovarian steroids (estradiol and progesterone) have a negative effect on MY after the peak of lactation. However, little is known about the effects of ovarian steroids on mammary tissue. The aims of this study were to investigate the effect of ovariectomy on MY and on mammary gland remodeling and molecular activity in lactating cows. Fourteen multiparous Holstein cows were either ovariectomized (Ovx, n = 7) or sham-operated (Sham, n = 7) around 60 d in milk. Cows were milked twice daily during 12 mo; MY was recorded daily throughout the study and milk samples were harvested weekly to follow the milk composition. Mammary tissue samples were collected at 1.5 mo in milk (2 weeks before ovariectomy) and at 4, 8 and 12 mo of lactation to perform molecular analysis on the mammary tissue. Ovariectomy at the time of lactation peak improved MY in the end of lactation (+ 17.1% on mo 8 ($P < 0.1$) and + 60.8% on mo 12 of lactation ($P < 0.1$) for Ovx cows in comparison with Sham cows) without significantly modifying milk composition. Ovariectomy also reduced somatic cell release in milk as of mo 8 of lactation. Moreover, zymography performed on milk samples revealed that mammary tissue remodeling (MMP2 activity) was reduced in Ovx cows. Molecular analysis performed on mammary tissue samples showed that mammary cell apoptosis (Bax transcript level) was reduced by 22.2% ($P < 0.05$) in the Ovx group in an advanced stage of lactation. The Western blot quantification of lactoferrin protein showed that lactoferrin increased over time in both Ovx and Sham cows, but it was reduced by ovariectomy on mo 8 (- 27.4%, $P < 0.1$) and 12 (- 53.3%, $P < 0.1$) of lactation. Taken together these suggest that ovariectomy could delay mammary gland involution.

Key Words: ovariectomy, mammary gland, involution

128 Effect of cooling during the dry period on neutrophil gene expression after *Streptococcus uberis* infection. I. M. Thompson,* S. Tao, K. C. Jeong, W. W. Thatcher, and G. E. Dahl, *University of Florida.*

Heat stress in the dry period affects immune status of dairy cows in lactation. We hypothesized that cooling during the dry period improves immune response to postpartum intramammary infection (IMI) to environmental pathogens such as *Streptococcus uberis*. Cows were dried off 46 d before expected calving and assigned to cooling (CL, n = 15) or heat stress (HT, n = 15). CL cows were housed with sprinklers, fans and shade, whereas the HT group had only shade. All cows were cooled postpartum. Rectal temperature (RT) and respiration rate (RR) were recorded during the dry period. From −46 to 42 d relative to calving, DMI, milk yield and composition were recorded daily, and both BW and BCS weekly. *S. uberis* IMI was induced at 5 d postpartum in a subset of cows (CL, n = 5; HT, n = 5). Blood was collected at 0, 12, 18, 24 and 36 h after IMI. Hematology was performed, and neutrophils isolated for RNA extraction. Neutrophil genes (*TLR2*, *IL1-β*, *IL6*, *IL8*, *IL10*, and *TNFα*) were assessed by real time RT-PCR. Relative to HT, CL cows had lower RT and RR ($P < 0.01$). CL cows also consumed more feed ($P < 0.01$) prepartum but not postpartum, gained more ($P < 0.01$) BW prepartum but lost more ($P = 0.05$) BW in lactation, had higher ($P = 0.01$) BCS score prepartum and a lower ($P < 0.10$) BCS postpartum. During 15 wks of lactation, CL produced more milk (38.8 > 33.6 kg/d; $P < 0.07$) but did not affect milk composition. CL cows had greater ($P = 0.05$) white blood cell count and more ($P = 0.09$) neutrophils than HT during IMI. From 0 to 36 h post IMI, *TNFα* mRNA expression decreased ($P = 0.02$) while *IL6* ($P = 0.02$) and *IL8* ($P < 0.01$) mRNA expression increased in both treatments. Additionally, CL cows had lower ($P = 0.04$) *IL10* mRNA expression at 18 h post IMI. *TLR2* mRNA expression decreased ($P = 0.05$) over time in both treatments. However, CL cows had greater ($P = 0.02$) overall *TLR2* mRNA expression than HT. No differences were detected for mRNA expression of *IL1-β*, *IL6*, *IL8*, and *TNFα*. Cooling cows during the dry period alters immune function and neutrophil response to IMI.

Key Words: heat stress, neutrophils gene expression, intramammary infection

129 Short-term increases in milking frequency and a higher plane of nutrition did not increase total milk production in pasture-based dairy cows during an extended lactation. A. G. Rius,* C. V. C. Phyn, J. K. Kay, and J. R. Roche, *DairyNZ, Hamilton, New Zealand.*

Extended lactations (EL) of > 600 DIM could benefit seasonal, pasture-based dairy systems by improving animal welfare and reducing breeding-related costs; however, lower milk yields on an annualized basis limits farmer adoption. This study determined if temporary increases in milking frequency (MF) and nutrition increased milk production during an EL. Non-pregnant, multiparous Holstein-Friesian cows (333 DIM, n = 120) were randomly allocated to one of 4 treatments (n = 30 cows) for 68 d in a 2 × 2 factorial arrangement which included 2 MF and 2 diets. Treatments were cows i) milked twice daily (2×) and fed pasture only (PAS), ii) milked 2× and fed pasture plus 6 kg DM/d of concentrate (CON), iii) milked thrice daily (3×) and fed PAS, and iv) milked 3× and fed CON. Cows were offered a generous pasture allowance (23 kg DM/d) throughout and milked 2× post-treatment. Statistical analyses were conducted on milk production and body weight (BW) during treatments and an 84-d carry-over period. There were no interactions between MF and diet for each trait in either period and treatments did not affect lactation length (DIM = 570). During treatment, cows milked 3× had increased yields of milk (13.3 vs. 12.0 kg/d; $P < 0.003$) and lactose (0.602 vs. 0.565 kg/d; $P < 0.05$), but not energy-corrected milk (14.7 vs. 14.1 kg/d; $P > 0.18$), relative to 2×. Cows fed CON increased yields of milk (13.1 vs. 12.1 kg/d; $P < 0.01$), protein (0.545 vs. 0.503 kg/d; $P < 0.02$), and lactose (0.612 vs. 0.554 kg/d; $P < 0.002$), and tended to increase energy-corrected milk (14.8 vs. 14.0 kg/d; $P = 0.08$), relative to PAS. Diet and MF did not affect production during the carry-over period or cumulative production from d 1 of treatment to dry-off. Cows fed CON gained more BW (544 vs. 523 kg; $P < 0.001$) and the difference remained for 5 weeks post-treatment. In conclusion, short-term 3× milking and CON increased milk production but these responses did not carry-over to improve total EL yields. Imposing treatments longer than 68 d could increase subsequent production responses but this remains to be tested.

Key Words: extended lactation, dairy cows

130 Transcriptome analysis of blood in heat-stressed dairy goats. A. A. K. Salama*[1], S. Hamzaoui[1], B. Badaoui[2], A. Zidi[3], and G. Caja[1], *[1]Grup de Recerca en Remugants (G2R), Universitat AutÃ³noma de Barcelona, Bellaterra, Barcelona, Spain, [2]Integrative Biology Group, Parco Tecnologico Padano-CERSA, Lodi, Italy, [3]Centre de Recerca en Agrigenomica (CRAG), Bellaterra, Barcelona, Spain.*

With the aim of studying the effects of environmental heat stress on global gene expression, 8 Murciano-Granadina dairy goats (43.3 ± 1.6 kg BW; 81 ± 3 DIM), kept in metabolic cages and allocated in 2 balanced groups, were randomly assigned to 2 climatic treatments according to a crossover design (35-d periods). Treatments were (temperature, °C; humidity, %; THI, Thorn heat index):1) thermal neutral (TN, 15 to 20°C and 35 to 45%; THI = 59 to 64), and 2) heat stress (HS, 12 h/d at 37°C and 45%, and 12 h/d at 30°C and 45%, THI = 86 and 77, respectively). Feed intake and milk yield were recorded daily. Blood samples were collected at d 35 of the second period for microarray analysis (n = 3/treatment). Blood RNA was extracted immediately after collection using RiboPure-Blood Kit (Ambion, Life Technologies, Madrid, Spain). The extracted RNA had an integrity number = 8.6 ± 0.2. Affymetrix GeneChip Bovine Genome designed to monitor expression of approximately 23,000 transcripts was used. The signal intensity of globin genes was low and did not affect the detection of gene expression. The arrays were normalized using the robust multi-array average method. After filtration and normalization, 4,259 genes were included in the analysis. We used the Ingenuity Pathways Analysis (IPA) software to examine biological changes related to heat stress. Feed intake (1.75 vs. 2.47 kg DM/d) and milk yield (1.53 vs. 1.68 L/d) were lower ($P < 0.01$) in HS than in TN goats. We identified 39 and 74 genes whose expression was up- and downregulated, respectively, by HS ($P < 0.05$). These genes were mainly related to biological processes and, to a lower extent, to molecular functions and cellular components. Moreover, IPA analysis detected important pathways related to cell proliferation and death, free radical scavenging, inflammatory response, lipid metabolism, and glycolysis/gluconeogenesis. Transcription regulators affected by HS were: SATB1 (global chromatin organizer) and PPARD (might be related to insulin resistance). In conclusion, chronic HS produced a stress response that was detectable in blood. The HS elicited changes in gene expression related to transcriptional regulation and metabolic processes.

Key Words: heat stress, gene expression, microarray

131 Effects of high feeding level on caprine mammary gland development and milk yield potential. J. M. Aubry[1,2], L. Finot[1,2], L. Yart[1,2], S. Wiart[1,2], E. Siroux[1], M. Chorho[1], J. Lassalas[1], and F. Dessauge*[1,2], [1]*INRA, UMR1348 Pegase, Saint-Gilles, France,* [2]*Agrocampus Ouest, UMR1348 Pegase, Rennes, France.*

The correlation between growth rate during rearing and the subsequent milk yield potential has been extensively studied in dairy cattle and sheep. Many studies highlighted that high feeding level before puberty negatively affected mammary development, but such results are scarce in dairy goats. Present study aimed then to investigate the effect of high feeding level from rearing to kidding on caprine mammary gland development and milk yield potential. A total of 52 Alpine dairy goats were submitted to 2 feeding levels ($n = 26$ per treatment). From weaning (17 kg, 60 d of age) to kidding (50 kg, 12 mo of age), they received either a controlled standard diet according to commercial recommendations (BD, 92 UFL - 17 MAT) or an ad libitum diet (HD, 85 UFL - 17 MAT). Goats weighed twice monthly and were milked twice daily. Milk yield (MY) and composition were recorded twice a week. At mid-gestation, 6 goats of each group were slaughtered and mammary glands were collected. Mammary glands were weighed and dissected for molecular analysis. DNA mammary concentration analysis was measured and used to estimate the total number of mammary cells. Expression of proteins involved in mammogenesis was evaluated on mammary tissue by real-time qPCR, Western Blotting and immunohistochemical staining (ER α, PCNA, MMPs). Before weaning, average daily gain (ADG) were similar between the 2 groups of animals (230 g/d). From weaning to 4 mo of age and from 4 mo of age to conception, HD goats grew faster than BD goats: 180 and 154 g/d vs. 128 and 127 g/d, respectively. At mid-gestation, HD goats had a well developed mammary gland. At slaughter, mammary glands from HD goats already presented a well organized mammary ductal network with the presence of milk. During lactation one, they had a higher milk yield than BD goats (2.92 kg/d vs. 2.73 kg/d on average, $P < 0.05$) during first 2 mo of lactation. Reproduction performance was not affected. In conclusion, high feeding level from weaning to first kidding does not affect mammogenesis and milk yield potential in dairy goats.

Key Words: mammary gland, feeding level, goats

Nonruminant Nutrition: Minerals and Vitamins

132 Determination of endogenous intestinal losses of Ca and digestibility of Ca in canola meal fed to growing pigs. J. C. Gonzalez-Vega*[1], C. L. Walk[2], and H. H. Stein[1], [1]*University of Illinois, Urbana,* [2]*AB Vista, Marlborough, UK.*

An experiment was conducted to test the hypothesis that endogenous Ca is lost from the gastrointestinal tract of growing pigs. The objective was to determine the apparent total tract digestibility (ATTD) and the true total tract digestibility (TTTD) of Ca in canola meal without and with added microbial phytase. Retention of Ca from canola meal was also determined. Forty 8 growing barrows (average initial BW: 16.72 ± 2.52 kg) were allotted to a randomized design with 8 dietary treatments and 6 pigs per treatment. Diets were based on sucrose, cornstarch, potato protein isolate, corn gluten meal, and canola meal. Diets were formulated to contain 0.08, 0.16, 0.24, or 0.32% Ca from canola meal, respectively. All diets were formulated with 0 or 1,500 units per kilogram of microbial phytase (Quantum, AB Vista, Marlborough, UK) and contained 0.32% digestible P. Feces and urine samples were collected from d 6 to d 11. Results indicate that feed intake, Ca intake, P intake, and P excretion increased ($P < 0.05$) by increasing the level of Ca in the diets. The ATTD of Ca and Ca retention increased ($P < 0.05$) if dietary Ca increased and also if phytase was added to the diets. The TTTD of Ca increased ($P < 0.01$) if phytase was used, but was not affected by the level of Ca in the diets. Total endogenous losses of Ca were determined using the regression procedure. Regression analyses indicated that apparent total tract digested Ca increased (linear, $P < 0.05$) as dietary Ca intake increased. The estimated total endogenous loss of Ca was 0.160 and 0.189 mg/kg DMI for canola meal without and with microbial phytase, respectively, and these values were not different. In conclusion, endogenous Ca is lost from the gastrointestinal tract of growing pigs, and values for TTTD of Ca are, therefore, different from values for ATTD of Ca. Values for ATTD of Ca are influenced by the level of dietary Ca, but that is not the case for values for TTTD of Ca. Microbial phytase increases the digestibility of Ca in canola meal, but does not influence the endogenous loses of Ca.

Key Words: calcium, endogenous losses, pigs

133 The effect of supplemental vitamin D_3 as an oral dose or in early nursery pig diets on pig growth performance and serum $25(OH)D_3$ concentrations. J. R. Flohr*[1], M. D. Tokach[1], S. S. Dritz[1], S. C. Henry[2], M. L. Potter[2], N. S. Shelton[1], L. L. Greiner[3], J. Connor[3], R. D. Goodband[1], J. L. Nelssen[1], and J. M. DeRouchey[1], [1]*Kansas State University, Manhattan,* [2]*Abilene Animal Hospital, Abilene, KS,* [3]*Innovative Swine Solutions, Carthage, IL.*

A total of 400 barrows from 80 litters (PIC 1050, initially 7 d of age) were used in a 38 d study in a 2 × 2 factorial to determine the effects of vitamin D_3 supplementation from either a single oral dose or from high levels of vitamin D_3 in early nursery diets on pig performance and serum $25(OH)D_3$. On d 7 after birth, matched pairs of pigs within litters were randomly allotted to 1 of 2 oral dosages (none or 40,000 IU vitamin D_3) in a RCBD. Pigs were weighed at d 7 and weaning (d 21). Following weaning, a subset of 300 barrows were used from d 21 to 45 to determine the effects of the previously administered oral vitamin D_3 and 2 levels of dietary vitamin D_3 (1,378 or 13,780 IU/kg; 0.80% Ca and 0.63% available P) from weaning to d 31 on pig growth and serum $25(OH)D_3$. A common diet containing 1,378 IU/kg of vitamin D_3 (0.70% Ca and 0.47% available P) was fed from 31 to 45 d of age. Barrows were allotted to pens based on their respective vitamin D_3 dose with pens randomly allotted to dietary treatments. There were no dose × diet interactions ($P > 0.09$). Serum $25(OH)D_3$ was increased ($P < 0.01$) on d 21 and tended to be increased on d 31 by dosing pigs with vitamin D_3 before weaning. On d 31, serum concentrations increased with increasing dietary vitamin D_3 levels ($P < 0.01$). Weaning weight was not influenced ($P > 0.17$; dosed 5.26 kg vs. undosed 5.18 kg) by the oral dose of vitamin D_3. Supplementing vitamin D_3 by either dose or diet did not influence ($P > 0.23$) nursery performance. In conclusion, supplementing vitamin D_3 either orally or in the nursery diet increased serum $25(OH)D_3$, but did not influence nursery pig growth performance.

Table 1.

Dosage:	No vitamin D_3		40,000 IU D_3			*P*-value		
Phase 1 Diet:	1,378 IU	13,780 IU	1,378 IU	13,780 IU	SEM	Dose × diet Interaction	Dosage Effect	Diet Effect
Item								
$25(OH)D_3$, ng/mL								
weaning	7.8	7.9	26.8	21.6	2.6	0.30	<0.01	0.32
d 31	21.3	33.5	28.6	35.6	2.6	0.33	0.08	<0.01
d 45	10.1	14.3	15.6	13.7	2.6	0.25	0.35	0.66
Nursery performance								
ADG, g	311	306	305	308	8	0.59	0.83	0.92
ADFI, g	386	378	380	388	9	0.28	0.83	0.99
G:F	0.80	0.81	0.80	0.79	0.01	0.65	0.57	0.84

Key Words: nursery pig, vitamin D, $25(OH)D_3$

134 Carbohydrase and phytase complex improves performance and bone mineralization of pigs fed wheat-soybean base diet. P. Cozannet[1], R. Gerritsen[2], R. Maillard[1], E. Devillard*[1], and A. Preynat[1], [1]*Adisseo France SAS, CERN, Malicorne, France,* [2]*Schothorst Feed Research, Lelystad, Netherlands.*

The trial was carried out to investigate the effects of a multi-enzyme (enz) complex containing carbohydrases (from *Penicillium funiculosum*) and 6-phytase (from *Schizosaccharomyces pombe*) on performance and bone mineralization of growing-finishing pigs fed a wheat-soybean meal diet. Gilts [360; Talent × (GYz × Finnish Landrace)]; 7 wk; 25 kg BW) were assigned to 1 of 3 treatments according a randomized block design with 12 replicates (10 gilts/pen) for 100 d. The positive control (PC) diet was a standard diet, formulated to meet the requirement of all nutrients during growing and finishing period (NE = 8.92/8.95 MJ/kg and lys dig = 0.98/0.56 g/MJ NE, respectively), while the negative control (NC) diet was formulated with reductions in energy (0.42 MJ NE/kg), available phosphorus (av P; 0.10%) and calcium (Ca; 0.08%). NC diet was supplemented or not with Rovabio Max (1,100 endo-β-1,4-xylanase visco units, 100 endo-1,3(4)-β-glucanase units and 500 Phytase units /kg of feed; 50 g/ton of feed). Animal feed intake and BW were recorded at the end of each period. Front left meta-carpi of one pig per pen were collected for bone ash percentage (BAP) measurement at the end of the experiment. Results were analyzed in Genstat (ANOVA) and means compared using LSD test. During the 5 weeks growing period, no treatment effect was observed. During finishing period, ADFI was not affected by treatments ($P = 0.29$).Gilts had higher ADG (887 vs. 818

g/day; $P < 0.05$) when they received PC compared with NC whereas enz addition in NC diet partly restored ADG to PC level (857 vs. 887 g/day; $P < 0.05$). FCR was similar for PC and NC + enz with values lower than NC (2.45 vs. 2.58; $P = 0.01$). Considering overall period, pig fed NC diet were 2.6 ($P < 0.05$) and 4.6 ($P < 0.005$) kg lighter than pig fed NC + enz and PC diet, respectively. Moreover, as expected, BAP was negatively affected by mineral depletion (53 vs. 56%; $P < 0.05$) and fully compensated by enz addition as suggested by no difference between PC and NC + enz ($P > 0.05$). These results demonstrate the efficiency of enz complex to balance av P, Ca and NE depletion on wheat-based diet.

Key Words: pig, carbohydrase, phytase

135 Modulation of phosphorus digestive utilization in weanling pigs: influence of dietary calcium and phytase on gastro-intestinal digesta pH and mineral solubility. A. Narcy[1], M. P. Létourneau-Montminy*[2], E. Bouzouagh[1], N. Même[1], M. Magnin[3], and J. Y. Dourmad[4], *[1]INRA, UR83 Recherches Avicoles, Nouzilly, France, [2]Agriculture et Agroalimentaire Canada, Sherbrooke, QC, Canada, [3]BNA-NA, Chateau-Gontier, France, [4]INRA-Agrocampus Ouest, UMR 1348, Saint Gilles, France.*

The study was conducted to evaluate the impact of dietary calcium (Ca) concentration, added in the form of calcium carbonate (CaCO3), on phosphorus (P) digestibility and gastro-intestinal digesta pH and soluble mineral concentration in weanling pigs fed diets with or without microbial phytase. A 3 × 2 factorial arrangement was used with maize-soybean meal based diets formulated to contain combinations of 3 concentrations of Ca: 0.50, 0.75 and 1.00% with or without the addition of 1000 FTU of microbial phytase/kg. After a 5-d adaptation period under a standard diet, 40 male weanling pigs were blocked by weight and allotted to one of the 6 dietary treatments in a 29 d experiment. The addition of microbial phytase improved ($P < 0.001$, +20.1 points) P digestibility regardless of dietary Ca concentration. In addition, P digestibility was linearly decreased ($P < 0.001$, −4.30 points) when increasing dietary Ca. Dietary Ca concentration and microbial phytase did not affect the pH of the different digestive compartments. Nevertheless, the pH of the different segments followed an increasing proximo-distal gradient (segment, $P < 0.001$): 4.69, 5.62, 6.66 and 7.10 pH units respectively for the stomach, the duodenum, the jejunum and the ileum. A negative quadratic relation was observed between the gastric pH and the proportion of soluble inorganic P (iP) and Ca. In the same segment, phytase improved the solubility of iP depending on dietary Ca concentration (Ca x phytase, $P < 0{,}001$). Indeed, the addition of microbial phytase increased the proportion of soluble iP (% total P) by 20.2, 9.30 and 8.90 points in diets containing 0.50, 0.75 and 1.00% of dietary Ca respectively. The present results suggest that the increase of dietary Ca concentration may affect the solubility of phytates in the stomach reducing in this way their hydrolysis by phytase. Nevertheless, this step did not appear to be limiting regarding the enzyme efficacy in ameliorating P digestibility.

Key Words: phosphorus, calcium, pig

136 Phosphorus utilization in finishing broiler chickens: Effect of dietary calcium and microbial phytase. X. Rousseau*[1,2], M. P. Letourneau-Montminy[3], M. Magnin[1], N. Même[2], Y. Nys[2], and A. Narcy[2], *[1]BNA NA, Château-Gontier, France, [2]INRA UR83 Recherches avicoles, Nouzilly, France, [3]Agriculture and Agri-Food Canada, Lennoxville, Québec, Canada.*

The optimization of phosphorus (P) utilization is crucial to ensure poultry production sustainability. This is particularly the case in finishing broilers (21 to 38 d of age) considering that about 70% of the overall feed intake occurs during the last phase, which also leads to high P excretion, approximately 50% of the P intake being lost in the environment. Response to dietary P in broilers chickens were shown to be dependent on a balance between dietary Ca and P including also P released by microbial phytase. This experiment was carried out to evaluate the response of 144 finishing broilers, reared in individual cages, to 12 dietary treatments differing in dietary Ca (0.37; 0.57; 0.77%), non-Phytate P (nPP; 0.18 or 0.32%) and microbial phytase (0 or 500 FTU/kg). Growth performances, P and Ca retention and bone mineralization were determined. Dietary treatments had no significant effect on ADG, ADFI and FCR. Tibia ash deposition decreased with reduction in dietary Ca at the highest nPP, but improved with reduction in dietary Ca at the lowest nPP (Ca × nPP; $P = 0.035$). Birds fed P-deficient diets used P more efficiently for tibia ash deposition if dietary Ca was sufficient (Ca × nPP; $P < 0.001$). Birds response to microbial phytase was greater with lower level of nPP in terms of P retention and tibia ash content (nPP × phytase; $P = 0.009$ and $P = 0.021$ respectively). Birds could have developed regulative process to cope with P and/or Ca deficiency. Nevertheless, a balanced supply between Ca and P must be considered to ensure optimal utilization of these minerals especially for bone mineralization.

Key Words: phosphorus, calcium, finishing broiler

137 The effect of dietary levels of copper and zinc on rate and efficiency of growth by rainbow trout. E. S. Read*[1], W. M. Sealey[2], F. T. Barrows[3], M. K. Petersen[4], and J. A. Paterson[1], *[1]Montana State University, Bozeman, [2]US Fish and Wildlife Service, Bozeman, MT, [3]US Department of Agriculture, Agriculture Research Service, Bozeman, MT, [4]US Department of Agriculture, Agriculture Research Service, Miles City, MT.*

The objectives of this factorial experiment were to determine if interactions existed between dietary Cu and Zn levels on rate and efficiency of growth and whole body element retention in growing trout. After 6 wk of feeding a diet deficient in Cu (9.4 ppm) and Zn (37.7 ppm), 600 fish (avg wt of 40 g) were randomly assigned to diets with supplementary $CuSO_4$ or $ZnSO_4$ added to provide diets with 0 or 10 ppm added Cu and 0, 30, 300 or 1500 ppm added Zn. There were 25 fish per tank with 3 replications per diet. Diets were formulated to contain 40% CP from soybean meal and corn protein concentrate and 20% crude lipid. Fish were fed experimental diets for 12 wk. The main effects of dietary Cu level, Zn level and the potential interaction on growth and mineral retention were tested. After 6 and 12 wk, 3–5 fish from each tank were sacrificed to determine liver and whole body concentrations of Cu and Zn. Cataracts were observed at 12 wks in 69% of fish fed the Cu and Zn deficient diet compared with an average of 0.01% for all other treatments. Dietary Zn ($P = 0.002$) but not dietary Cu ($P = 0.263$) increased 12 wk weight gain. An interaction ($P = 0.008$) between dietary Cu and Zn was observed for 12 wk weight gain. Slowest gains (19 g/d) were for the Cu and Zn deficient diet and fastest gains (45 g/d) were in the 10 ppm Cu and 1500 ppm Zn diet. Dietary Zn ($P = 0.001$) but not dietary Cu ($P = 0.996$) increased 12 wk whole body Zn levels. Dietary Cu ($P = 0.094$) or Zn ($P = 0.095$) did not alter whole body Cu levels and no interactions were observed ($P = 0.806$). Results of this study indicate rainbow trout fed plant-based diets require Zn supplementation to obtain sufficient growth. Level of supplemented Cu did not improve weight gain. However, the level of Zn did improve weight gain, at the higher levels (300 and 1500 ppm) of Zn. The highest levels of Zn supplementation did not impair Cu uptake in rainbow trout. Diets without additional

Cu or Zn caused increased incidence of cataracts compared with diets with added Cu and Zn.

Key Words: copper, zinc, rainbow trout

138 Varied sources of conjugated linoleic acid (CLA) does not alter bone mineral density (BMD), bone mineral content (BMC), or body fat content in postmenopausal ovariectomized rats. K. M. Kanosky,* Z. D. Callahan, M. A. Brown, C. S. Perkins, E. A. Benavides, D. H. Keisler, and B. R. Wiegand, *University of Missouri, Columbia.*

Altering dietary fat source has been shown to change the fatty acid profile in non-ruminant animals; subsequently changing downstream metabolic events such as bone remodeling, which is influenced by inflammatory prostaglandin E2 (PGE2). Excess production of PGE2 is linked to osteoporosis and associated with postmenopausal bone loss. One potential anti-inflammatory agent is conjugated linoleic acid (CLA). Previous studies have reported that CLA feeding in rats resulted in decreased PGE2 production, thus improving bone mineral density (BMD). The objective of this study was to determine if body fat content, specific organ weights, bone mineral content (BMC) and BMD were altered if aged, ovariectomized female rats were fed varied sources of CLA. All procedures were performed according to University of Missouri Animal Care and Use Committee Approved Protocol. Retired breeder (365 ± 28 d of age and 4.5 ± 0.5 parity), Sprague Dawley, female rats (n = 86) were randomly assigned to ovariectomy (OVX) or sham (SHAM) surgeries. Rats were fed 4% soy oil (CON) for 14 d. For an additional 70 d, within surgery groups, rats were randomly allotted to dietary treatments: CON, 0.6% CLA + 3% soy oil (CLA), 0.6% CLA from cheddar cheese powder + 3% soy oil (CC), or 0.3% CLA + 0.3% CLA from cheddar cheese powder + 3% soy oil (CCCLA). Feed intake and body weight were measured weekly. Dual-energy x-ray absorptiometry (DEXA) scans were performed to measure body fat content and bone composition before dietary treatments and post-mortem. At the end of the feeding period rats were sacrificed, blood was collected, and livers, thigh muscles, peritoneal fat, femurs, and tibias were removed and weighed. There were no significant effects of treatment on bone mineral content (BMC, g), bone mineral density (BMD, g/cm^2), or body fat content (%). Compared with SHAM, rats that were OVX had lower BMD ($P < 0.01$) and femur weights ($P < 0.01$), therefore resulting in less dense bones. However, fat content ($P < 0.001$), ADG ($P < 0.0001$), and ADFI ($P < 0.05$) increased in OVX rats. Unlike growing finishing pigs, 0.6% CLA inclusion in rat diets may not be enough CLA for this enhanced anti-inflammatory response. In conclusion, we were able to make an appropriate postmenopausal rat model that exhibited a decrease in BMD, which may be beneficial in future osteoporosis research.

Key Words: linoleic acid, rats, bone

139 Effects of selenium-enriched exopolysaccharide produced by *Enterobacter cloacae* Z0206 on growth performance, immunity and antioxidant activities in broiler chickens. Z. Q. Lu,* Y. M. Wang, M. Huang, and Y. Z. Wang, *Institute of Feed Science, Zhejiang University, National Engineering Laboratory of Bio-feed Safety and Pollution Prevention, Key Laboratory of Animal Nutrition and Feed science of Ministry of Agriculture, Hangzhou, Zhejiang Province, China.*

Enterobacter cloacae Z0206 (*E. cloacae* Z0206), a recently discovered bacterial strain, could produce huge amount of exopolysaccharides. Our previous studies found that *E. cloacae* Z0206 could accumulate selenium (Se) in the form of Se-enriched exopolysaccharide (Se-ECZ-EPS) efficiently in medium enriched with selenium. Se-ECZ-EPS contained 535.7 mg/kg Se and has been proven to possess immunostimulatory function in mice. However, little was known about the bioactive activities of Se-ECZ-EPS in chickens. Thus the present study was conducted to investigate the effects of Se-ECZ-EPS on growth performance, serum cytokine concentrations and antioxidant enzyme activities in broiler chickens. Two hundred forty Avian broiler chickens were allocated randomly into 5 groups with 4 replicates in each group and 12 chickens in each replicate. Control group was fed with basal diet containing 0.15 mg/kg Se (Na_2SeO_3), and the another 4 groups were fed with diets supplemented with Se-ECZ-EPS at the level of 280 mg/kg (0.15 mg/kg Se), 560 mg/kg (0.30 mg/kg Se), 840 mg/kg (0.45 mg/kg Se) and 1120 mg/kg (0.60 mg/kg Se), respectively. The results showed that average daily gain and feed conversion ratio in 840 and 1120 mg/kg groups were significantly enhanced from 0 to 42 d compared with the control group ($P < 0.05$). And the serum concentrations of TNF-α, IFN-γ, IL-2 and IL-6 showed positive responses in 1120 mg/kg group ($P < 0.05$). Furthermore, administration of Se-ECZ-EPS at the level of 560, 840 and 1120 mg/kg significantly increased activities of glutathione peroxidase and superoxide dismutase, and decreased malondialdehyde production ($P < 0.05$). These results implicated that Se-ECZ-EPS can improve the growth performance, and enhance immune and antioxidant functions by stimulating secretion of cytokine and improving antioxidant enzyme activities in broilers.

Key Words: exopolysaccharide, immunity, broiler

Ruminant Nutrition: Beef Production I

140 Effects of metabolic imprinting on growth performance and gene expression of early-weaned beef heifers.

P. Moriel*[1], V. Mercadante[2], A. D. Aguiar[1], S. E. Johnson[2], M. J. Hersom[2], J. M. B. Vendramini[1], and J. D. Arthington[1], [1]*Range Cattle Research and Education Center, University of Florida, Ona, FL,* [2]*University of Florida, Gainesville.*

The study evaluated the effects of calf management system after early-weaning (EW) on performance and liver gene expression of beef heifers. On d 0, Brahman × British heifers (n = 40; BW = 83 ± 10 kg; age = 69 ± 9 d) were stratified by age and BW, and randomly assigned to a control treatment that was normally weaned (NW) on d 177, or 1 of 3 EW treatments, (1) EW and grazed on ryegrass pastures for 67 d then on bahiagrass pastures until NW (Ryegrass), (2) EW and fed a high-concentrate diet in drylot until NW (Drylot), or (3) EW and metabolically imprinted by feeding a high-concentrate diet for 94 d then grazed on bahiagrass pastures until NW (MI). Heifers were assigned to 1 of 2 pens per treatment. On d 177, heifers were grouped by treatment and grazed on bahiagrass pastures until the start of breeding season (d 335). Heifers on pastures were supplemented at 1.0% BW until NW and 1.5% BW from NW to d 335. On d 177 and 335, Ryegrass heifers were lightest ($P < 0.01$) and Drytlot heifers heaviest ($P < 0.001$) compared with all other treatments and Control and MI heifer BW did not differ ($P \geq 0.64$; BW = 212 and 300, 178 and 264, 216 and 302, and 261 and 333 for Control, Ryegrass, MI, and Drylot on d 177 and 335, respectively; SEM = 7.8). On d 94, liver GHR-1A mRNA was greatest ($P < 0.01$) for Control, but similar ($P = 0.64$) among the other treatments, whereas liver IGF-1 mRNA was least ($P = 0.004$) for Ryegrass, but similar ($P > 0.90$) among the other treatments. On d 177, liver GHR-1A was greater for Control and Drylot ($P < 0.03$) than Ryegrass and MI, whereas liver IGF-1 mRNA was greatest for Drylot than all other treatments and greater ($P < 0.07$) for Control than Ryegrass and MI. On d 260, liver GHR-1A mRNA was least ($P < 0.08$) for Ryegrass, whereas liver IGF-1 was greater ($P < 0.04$) for Drylot compared with Ryegrass. Thus, heifer management systems following EW result in significant differences on BW at NW and at the start of breeding season. These impacts appear to affect liver gene mRNA expression, which may persist despite placing heifers on a same plane of nutrition.

Key Words: beef steers, high-concentrate, metabolic imprinting

141 Effects of metabolic imprinting on growth performance of early-weaned beef steers.

P. Moriel*[1], V. Mercadante[2], A. D. Aguiar[1], S. E. Johnson[2], M. J. Hersom[2], J. M. B. Vendramini[1], and J. D. Arthington[1], [1]*Range Cattle Research and Education Center, University of Florida, Ona,* [2]*University of Florida, Gainesville.*

This study evaluated the effects of calf management system after early weaning (EW) on performance of beef steers. On d 0, Brahman × British steers (n = 40; BW = 90 ± 12 kg; age = 72 ± 14 d) were stratified by age and BW, and randomly assigned to a normally-weaned treatment (NW; d 177) or 1 of 3 EW treatments, (1) EW and grazed on ryegrass pastures for 67 d then on bahiagrass pastures until feedlot entry (d 260; Ryegrass), (2) EW and fed a high-concentrate diet in drylot until d 260 (Drylot), or (3) EW and metabolically imprinted by feeding a high-concentrate diet for 94 d then grazed on bahiagrass pastures until d 260 (MI). Within each treatment, steers were assigned to 1 of 2 pens. Concentrate was limit fed at 1% of BW from d 177 to 260, 7 to 260 and 94 to 260 for NW, Ryegrass and MI steers, respectively. Shrunk BW was measured at normal weaning and feedlot entry. Carcass ultrasound was measured on d 260. At normal weaning, Drylot steers were heavier ($P = 0.006$; SEM = 16) than all other treatments, and Control and Ryegrass steers had similar BW (215 and 196 kg, respectively; $P = 0.14$; SEM = 13), but were lighter ($P < 0.04$) than MI steers (243 ± 13 kg). Similarly, at the time of feedlot entry (d 260), Drylot steers were heavier (359 ± 16 kg; $P = 0.0002$) than all other treatments, and Control and Ryegrass steers had similar BW (228 and 230 kg, respectively; $P = 0.94$; SEM = 16), but were lighter ($P < 0.01$) than MI steers (277 ± 16 kg). On d 260, back fat thickness was similar ($P > 0.35$; largest SEM = 0.01) among Control, Ryegrass and MI steers (0.14, 0.14 and 0.15 cm, respectively), but was less ($P < 0.0001$) than Drylot steers (0.18 cm). Area of LM was least (30.4 cm^2; $P < 0.09$; largest SEM = 1.33) for Ryegrass steers, similar ($P = 0.20$) between MI (32.0 cm^2) and Control (30.4 cm^2) steers, and the greatest ($P < 0.001$) for Drylot steers (41.6 cm^2). Thus, feeding a high-concentrate diet to EW steers for at least 94 d (Drylot and MI) increased BW at the time of NW and at feedlot entry compared with calves weaned at a normal age or early-weaned and grazed on pasture with 1% concentrate supplement.

Key Words: beef steers, high-concentrate, metabolic imprinting

142 Correlation of feed intake and efficiency with small intestinal angiogenic factor and receptor expression in finishing cattle born to dams fed varying levels of nutrients during early to mid-gestation.

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We hypothesized that gestational nutrition would affect calf feed intake and efficiency as well as small intestinal development, and that feed intake and efficiency would be correlated with small intestinal measures. Multiparous beef cows (n = 36) were fed 1 of 3 diets from d 45 to 185 of gestation: a control (CON) diet of grass hay and supplement to meet NRC recommendations, a nutrient restricted (NR) diet providing 70% of CON NE_m, or an NR diet with a ruminally undegradable protein (NRP) supplement to provide similar essential AA as CON. Individual feed intake of calves was measured with the GrowSafe System during finishing. At slaughter (552 ± 10.2 kg BW), the jejunum was sampled for real time RT-PCR analysis of angiogenic factors (vascular endothelial growth factor [*VEGF*], VEGF receptor-1 [*FLT1*], VEGF receptor-2 [*KDR*], endothelial nitric oxide synthase 3 [*NOS3*] and soluble guanylate cyclase [*GUCY1B3*; nitric oxide receptor]). Data were analyzed as a mixed model with calf sex as block. It was previously reported that maternal nutrition affected calf small intestinal length, but not other measures of intestinal growth, intake, or feed efficiency. Jejunal *GUCY1B3* mRNA expression was affected by maternal nutrition ($P = 0.03$), where calves born to NRP dams had greater ($P < 0.03$) *GUCY1B3* than CON and NR (4.59 vs. 2.85 and 2.56 ± 0.54 relative mRNA expression). There was no effect ($P \geq 0.34$) of maternal nutrition on *VEGF*, *FLT1*, *KDR*, or *NOS3* expression. Feed intake was positively correlated with jejunal mRNA expression of *KDR* ($r = 0.37$; $P = 0.05$) and *NOS3* ($r = 0.35$; $P = 0.06$) and tended to be negatively correlated with *VEGF* ($r = -0.30$; $P = 0.11$). Residual feed intake and G:F were not correlated ($P \geq 0.20$) with angiogenic factor mRNA expression. Results indicate that offspring intestinal gene expression may be affected by gestational nutrition even when apparent tissue growth is unchanged. Additionally, changes in intestinal expression of *VEGF* and *NOS3* systems are associated with feed intake and may alter intestinal vasculature.

Key Words: feed efficiency, gestation, small intestine

143 Reproductive and productive responses to suckling-restriction treatments and flushing in primiparous grazing beef cows.

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The objectives of this experiment were to analyze the reproductive and productive responses to suckling management treatments and flushing in primiparous grazing beef cows. During 3 years, 153 primiparous anestrous cows were assigned randomly to 4 treatments in a 2 × 2 factorial arrangement of suckling management treatments and flushing. Suckling management treatments started at 61 ± 10 d postpartum and consisted of applying nose plates to calves for 12 d (i.e., TS treatment) or 5 d of isolation of the cow-calf pair followed by applying nose plates to calves for 7 d as calves were reunited with their mothers (i.e., IS treatment). Nutritional treatments (flushing vs. control) started at the beginning of the breeding season immediately after the suckling management treatments were finished (73 ± 10 d postpartum) with cows being offered or no 2 kg/day of whole-rice middling for 22 d. Weather, pasture quantity and quality, calving date, and cow body condition score BCS were recorded every 20 d from calving until definitive weaning (140 ± 10 d postpartum). Calf weight was recorded at birth, at 73 d of age, and at definitive weaning. Duration of postpartum anestrus (PPA) and probability of cyclicity were estimated by plasma progesterone concentrations analyzed in weekly samples. Pregnant cows were determined by ultrasound at 45 d after bull introduction (early pregnancy; EP) and at the end of the breeding period (total pregnancy; TP). The year affected BCS at calving and changes in BCS (ΔBCS), which were indicative of forage availability and weather conditions. Increased cow BCS at calving decreased PPA (b = −41 d; $P < 0.0001$) and in interaction with ΔBCS increased EP ($P < 0.008$) and TP ($P < 0.003$). No interaction was found between suckling and flushing. Isolated suckling (IS) reduced PPA by 11 d when compared with TS ($P < 0.004$). Flushing increased EP by 40%, which was also affected by BCS at calving and was greater in cows that gained, than maintained or lost BCS. We conclude that flushing was a low cost and environmentally tool that was useful in improving pregnancy rates of primiparous beef cows with “suboptimal” body condition (lower than 4.5) at calving and grazing native pasture.

Key Words: body condition score, primiparous beef cows, suckling and flushing

144 Use of an injectable mineral in beef cattle: Mineral status.

O. N. Genther* and S. L. Hansen, *Iowa State University, Ames.*

The objective of this study was to examine the effect of trace mineral (TM) status and response to mineral injection in beef cattle. Forty steers were stratified by weight (323 ± 14.8 kg) and assigned to treatments for an 84 d depletion period: 1) a corn silage-based diet supplemented with Cu, Mn, Se and Zn at NRC recommendations (CON), or 2) CON diet without supplemental Cu, Mn, Se or Zn, plus Fe and Mo as dietary TM antagonists (DEF). Liver Cu and Se concentrations in DEF steers were lower than CON steers before injection ($P < 0.05$) indicating mild deficiencies of these TM. To mimic shipping stress steers were shipped for 20 h on d −3 and received back on d −1. On d 0 an equal number of steers from both dietary treatments were injected with sterilized saline (SAL) or Multimin®90 (MM; containing 15, 40, 10 and 5 mg/mL of Cu, Zn, Mn and Se, respectively) at a dose of 1 mL/68 kg BW. Steers were fed a common finishing diet supplemented with Cu, Mn, Se and Zn at NRC recommendations for the 90 d repletion period. Blood samples were taken on d 0, 1, and blood and liver biopsy samples were collected on d 8, 15, 29, 57, and 85 post-injection. Data were analyzed as repeated measures. Red blood cell lysate (RBCL) Mn superoxide dismutase activity was higher in MM steers ($P = 0.02$), suggesting incorporation of injectable TM into a biological process. Diet or injection did not affect RBCL glutathione peroxidase activity ($P > 0.20$), but plasma Se in MM steers was elevated through d 15 ($P < 0.05$). For liver Se there was an interaction between diet, injection and day where the magnitude of the increase was greater in CON vs. DEF ($P = 0.02$), suggesting that TM from injection were utilized rather than stored in DEF steers. Liver Se and Cu ($P < 0.05$) were elevated through at least d 30 by TM injection. Liver Zn was slightly higher in DEF steers vs. CON ($P < 0.01$) and TM injection tended ($P < 0.10$) to increase Zn liver concentration on d 8 and 15 regardless of previous diet. Interestingly, by d 57 liver TM were higher in DEF steers ($P < 0.05$) suggesting differential TM utilization between CON and DEF steers. Overall, TM from an injectable mineral were utilized differently between TM adequate and mildly deficient steers.

Key Words: cattle, trace minerals

145 Use of an injectable mineral in beef cattle: Growth and carcass characteristics.

O. N. Genther* and S. L. Hansen, *Iowa State University, Ames.*

Trace minerals (TM) are vital for growth in cattle. To examine the effect of TM status and mineral injection on performance in beef cattle, 40 steers were used in a growing and finishing study. Steers were stratified by weight (323 ± 14.8 kg) and assigned to one of 2 treatments for an 84 d depletion period: 1) a corn silage-based diet supplemented with Cu, Mn, Se and Zn at NRC recommendations (CON), or 2) CON diet without supplemental Cu, Mn, Se or Zn, and supplemented with Fe and Mo as dietary TM antagonists (DEF) to induce mild deficiencies. To mimic shipping stress steers were shipped for 20 h on d 88 and were received back on d 89. On d 91 an equal number of steers from both dietary treatments were injected with sterilized saline (SAL) or Multimin 90 (MM; containing 15, 40, 10 and 5 mg/mL of Cu, Zn, Mn and Se, respectively) at a dose of 1 mL/68 kg BW. Steers were fed a common finishing diet supplemented with Cu, Mn, Se and Zn at NRC recommendations for the 90 d repletion period. Steers were harvested 94 d post-injection and carcass data were collected. During the depletion period diet did not affect ADG ($P = 0.72$). During shipping, DEF steers tended to lose more weight per day than CON steers ($P = 0.06$) and had lower DMI after shipping ($P < 0.05$), suggesting that TM status is important in the stress response. During the repletion period ADG of DEF-MM steers was greater ($P = 0.02$) compared with DEF-SAL, and was not different ($P = 0.91$) among CON-MM and CON-SAL steers. There was no effect of diet or injection on HCW or dressing percentage ($P > 0.20$). Within the CON group TM injection decreased yield grade ($P = 0.03$) but did not affect yield grade of DEF steers ($P > 0.20$). MM steers had larger rib eye area ($P = 0.04$) regardless of previous diet. Interestingly, both diet and injection affected marbling scores (MS), where CON steers had greater MS than DEF steers ($P = 0.01$), and MM steers had greater MS than SAL steers ($P = 0.04$). These results indicate that TM are essential for marbling development, during both the growing and finishing phases. Overall, an injectable mineral improved rib eye area and MS regardless of TM status, and improved growth of mildly TM deficient steers.

Key Words: cattle, trace minerals

146 Effects of restricted versus conventional dietary adaptation over periods of 9 and 14 days on feedlot performance and carcass traits of Nellore cattle. R. S. Barducci[1], M. D. B. Arrigoni[1], C. L. Martins[1], D. D. Millen*[2], L. M. N. Sarti[1], M. C. S. Franzói[1], L. C. Vieira Júnior[1], T. L. de Jesus[1], T. C. Putarov[1], M. T. Cesar[1], A. S. Pereira[1], E. T. Macedo[1], A. Perdigão[1], F. A. Ribeiro[1], A. L. N. Rigueiro[2], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, 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 (STEP) over periods of 9-d and 14-d on overall feedlot performance and carcass traits. The experiment was designed as a completely randomized block with a 2 × 2 factorial arrangement, replicated 6 times (5 bullocks/pen), in which 120 22-mo-old yearling Nellore bulls (361.3 ± 30.2 kg) were fed in 24 pens for 84-d according to the treatments: STEP for 9-d and 14-d, REST for 9-d and 14-d. The STEP program consisted of ad libitum feeding of 3 adaptation diets over periods of 9-d or 14-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 9-d or 14-d. No significant ($P > 0.05$) days main effect was observed for any of feedlot performance and carcass characteristics variables evaluated. No significant ($P > 0.05$) protocol main effect was observed for final BW, ADG in kg (STEP = 1.71, REST = 1.73; 9-d = 1.74, 14-d = 1.70) and total weight gain (STEP = 143.29, REST = 145.79; 9-d = 146.04, 14-d = 143.05) from 0-d to 84-d. However, significant ($P < 0.05$) protocol main effect was observed for DMI in kg from 0-d to 28-d (STEP = 9.67, REST = 9.01); DMI in % of BW from 0-d to 28-d (STEP = 2.52, REST = 2.36), and from 0-d to 56-d (STEP = 2.58, REST = 2.47); G:F ratio from 0-d to 84-d (STEP = 0.157, REST = 0.165); and cost to gain 1 kg of BW from 0-d to 84-d (STEP = $3.77, REST = $3.59). With respect to carcass traits, no significant ($P > 0.05$) protocols and days main effects were observed for kidney-pelvic fat in kg, HCW, and dressing %. Animals in REST protocol were more efficient than those in STEP protocol. The adaptation in 9-d did not negatively impact the overall feedlot performance and carcass traits of Nellore cattle. Grant provided by São Paulo Research Foundation (FAPESP), São Paulo, Brazil.

Key Words: adaptation, feedlot, Nellore

147 Effect of dietary energy density and control of meal size on growth performance, eating pattern, and carcass and meat quality in Holstein steers fed high-concentrate rations. S. Marti*[1], M. Pérez-Juan[2], A. Aris[1], A. Bach[3,1], and M. Devant[1], *[1]IRTA-Ruminant Production, Animal Nutrition, Management, and Welfare Research Group, Torre Marimon, Caldes de Montbui, Barcelona, Spain, [2]IRTA-Monells, Girona, Spain, [3]ICREA, Barcelona, Spain.*

A total of 121 steers (116 ± 3.7 kg of BW and 97 ± 2.4 d of age) were used to study the effect of dietary energy density and meal size limitation on intake and growth, hormones associated with the regulation of nutrient intake, and carcass and meat quality. Steers were randomly allocated to 3 treatments: a concentrate of moderate energy density (CTR, 3.16 Mcal of ME/kg, 6.1% EE) fed ad libitum with no control on meal size, a concentrate of high energy density (HE, 3.36 Mcal of ME/kg, 8.3% EE) fed ad libitum with no control on meal size, and a HE concentrate offered ad libitum but limited to a maximum meal size of 0.7 kg (HELM), with no total daily concentrate intake limit. Live BW was recorded every 14 d and concentrate consumption and eating pattern were recorded daily with a computerized concentrate feeder. At d 163, blood samples were collected to determine leptin, ghrelin, GLP-1, CCK, glucose and insulin serum concentrations After slaughter, the 9-10-11th rib section was removed to estimate separable bone, lean and fat. Muscle pH and color, WBSF and i.m. fat were analyzed in the LM. Data were analyzed using a mixed-effects model including diet as a main effect. Steers in the HELM had a less ($P < 0.01$) final BW and ADG than CTR and HE steers. Concentrate intake was greater ($P < 0.001$) in CTR steers (6.6 ± 0.1 kg/d) than in HE steers(5.7 ± 0.1 kg/d), and HELM (5.1 ± 0.1 kg/d) ate less than in CTR and HE steers. However HE and HELM steers were more efficient ($P < 0.01$) than CTR steers. Mean daily meals and eating rate were less ($P < 0.05$) in HE and HELM than in CTR steers. Serum concentrations of GLP-1, CCK and insulin were lower ($P = 0.05$) in HELM than CTR and HE steers; also leptin and glucose concentration tended to be less ($P = 0.10$ and $P = 0.08$, respectively) in HELM steers, indicating different satiety levels among treatments. Carcass conformation and HCW were less ($P < 0.05$) in HELM steers than in CTR. No differences were observed in carcass fat cover and i.m. content among treatments. In conclusion, HELM steers reduced total energy intake and performance, however, fat deposition was not affected.

Key Words: beef, hormones, meal size

148 Dataset-specific dry matter intake prediction equation determination for growing calves. M. F. Wilken,* L. L. Berger, G. E. Erickson, M. K. Nielsen, M. L. Spangler, and S. D. Kachman, *University of Nebraska-Lincoln, Lincoln.*

Four years of data collected at the University of Illinois-Urbana were utilized to create a data set-specific model for dry matter intake (OBSm). Previous analysis (Wilken et al., 2011) showed significant inaccuracies between observed intakes and that of 3 intake prediction equations (NRC, 1996; Galyean et al., 2009; Owens et al., 2002) leading to the objective of effectively determining a data set-specific intake prediction model. Individual intakes of calf-fed steers were measured over the feeding period by use of GrowSafe feeding system (GrowSafe Systems Ltd.). While 13 diets were fed over the 4 yr collected, varying in diet NE_m (dNE_m) values, only 3 diets (n = 481) were utilized in the analysis to add minimal dNE_m variation and greater statistical power without being statistically different in energy composition. Treatments were 1) 75% corn and 15% corn silage; 2) 50% corn, 25% dry distillers grains plus solubles, and 15% corn silage; and 3) 40% modified corn distillers grains plus solubles, 35% soyhulls, and 15% corn silage. All diets contained a 10% fine ground corn-based supplement. Because the NRC model for intake {NRCm; $\text{DMI} = \text{SBW}^{0.75} \times [0.1493\ (\text{dNE}_\text{m}) - 0.0460\ (\text{dNE}_\text{m}^2) - 0.0196]$} is the most widely used and verified prediction equation, the current analysis utilized metabolic body weight and dNE_m as parameters for analysis also. Feedstuff NE_m values were obtained from the NRC (1996) and used to calculate dNE_m for analysis in both the NRCm and OBSm. After fitting different models, OBSm was determined to be $\text{DMI} = \text{SBW}^{0.75} \times [23.3078\ (\text{dNE}_\text{m}) - 5.6287\ (\text{dNE}_\text{m}^2) - 24.0203]$. With OBSm defined, this data set-specific model was then compared with that of NRCm. Difference between OBSm and NRCm were significant ($P < 0.01$). The NRCm was determined to overestimate intake which coincides with previous research. These findings allow us to conclude that, while the NRCm is currently the standard equation for dry matter intake prediction, more accurate prediction equations are warranted and can be developed.

Key Words: dry matter intake, feedlot cattle, prediction equation

149 The use of biometric measures to assess body fat composition of F1 Nellore × Angus bulls and steers. M. A. Fonseca*[1,2], L. O. Tedeschi[2], S. C. Valadares Filho[1], H. J. Fernandes[3], N. F. De Paula[1,2], M. G. Machado[1], F. A. C. Villadiego[1], and J. M. Silva Junior[4], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]Texas A&M University, College Station, Texas, United States, [3]Universidade Estadual do Mato Grosso do Sul, Aquidauana, Mato Grosso do Sul, Brazil, [4]Universidade Federal Rural de Pernambuco, Garanhuns, Pernambuco, Brazil.*

This study was conducted to assess the body fat composition using biometric measures (BM) and postmortem measurements of 40 F1 Nellore x Angus bulls (B) and steers (S). The animals were 12.5 ± 0.51 mo old, with a shrunk BW (SBW) of 233.03 ± 23.47 and 238 ± 24.58 kg for B and S, respectively. Animals were fed 60% corn silage and 40% concentrate. The trial was design with at 2 × 3 factorial arrangement of treatments (2 genders and 3 slaughter weights). The Animals were slaughtered at the beginning of the trial (4B and 4S), and when the group reached an average BW of 380 (6B and 5S), 440 (6B and 5S), and 500 kg (5B and 5S). Before the slaughter, each animal was lead through a squeeze chute where BM were taken, including hook bone width (HBW), pin bone width (PBW), abdomen width (AW), body length (BL), rump height (RH), height at withers (HW), pelvic girdle length (PGL), rib depth (RD), girth circumference (GC), rump depth (RuD), body diagonal length (BDL), and thorax width (TW). Additionally, the postmortem measurements were collected, including subcutaneous fat (SF), internal fat (InF), intermuscular fat (ImF), carcass physical fat (CF), empty body physical fat (EBF), fat thickness at the 12th rib (FT), and 9 – 11th rib section fat (HHF). The equations were developed using a stepwise procedure to select the variables with the best goodness-of-fit and the least root mean square error (RMSE). Due to differences ($P < 0.05$) in gender the following equations were developed: EBF (kg) = 0.2769 × SBW - 1.0138 × RD ($r^2 = 0.994$ and RMSE = 3.93) for steers, EBF (kg) = −55.0900 + 0.0873 × SBW + 0.0446 × PBW −1.1608 × PGL + 0.3524 × TW + 0.4296 × BDL ($r^2 = 0.992$ and RMSE = 1.28) for bulls, CF (kg) = - 19.2136 - 0.1027 × SBW ($r^2 = 0.924$ and RMSE = 3.09 kg) for steers, and CF (kg) = 26.7893 + 0.1232 × SBW - 1.3067 × PGL ($r^2 = 0.921$ and RMSE = 2.37) for bulls. The main BM observed which affected the CF and EBF in this database were RD for S, and PBW, GC, TW, BDL and PGL for B.

Key Words: carcass fat estimation, empty body fat estimation, modeling

150 Evaluation of volatile fatty acid stoichiometries and methane predictions for high grain fed beef cattle within a mechanistic digestion model. J. L. Ellis*[1,2], J. Dijkstra[2], A. Bannink[3], E. Kebreab[4], S. Archibeque[5], and J. France[1], *[1]Centre for Nutrition Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [2]Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands, [3]Wageningen UR Livestock Research, Lelystad, the Netherlands, [4]Department of Animal Science, University of California-Davis, Davis, [5]Animal Sciences, Colorado State University, Fort Collins.*

Mechanistic modeling can provide insight into dietary strategies aimed at reducing CH_4 emissions from ruminants, but requires appropriate representation of aspects of underlying rumen fermentation and digestion. Proper prediction of the production of volatile fatty acids (VFA) is central to accurate CH_4 prediction within these models. Previous analysis showed the Dijkstra model to perform poorly in terms of CH_4 predictions on beef cattle data, while it performed well on dairy cow data. The purpose of this study was therefore to evaluate prediction of CH4 emissions from high grain fed beef cattle data using the Dijkstra model with pH-independent and pH-dependent VFA stoichometries, as well as with a new VFA stoichiometry which adjusts for the use of monensin, to see if prediction improvements could be made. Also, several improvements were made to the model to adapt it for typical high-grain beef cattle and their diets. Adaptations included new equations to predict fluid volume and fractional rate of passage of fluid and solids in the rumen and the hindgut, as adjustment to the kinetics of fiber fermentation in the hindgut and changes to the recycling of urea to the rumen. The evaluation database consisted of 98 individual datapoints from 6 studies of high grain fed beef cattle where the average CH_4 (MJ/d) was 5.6 ± 2.19, bodyweight was 425 ± 68.7 kg, DMI was 7.8 ± 1.93 kg/d and roughage % was 11.8 ± 5.62. Root mean square prediction error for CH_4 (MJ/d) prediction was reduced from 49.3% for the pH-independent stoichiometry to 47.2% with the pH-dependent stoichiometry, and was further reduced to 44.0% when monensin stoichiometry was included. While the majority of error was from random sources, all VFA stoichiometries tended to over-predict low observed CH_4 (MJ/d) values for the beef cattle database. Results indicate that progress to-date has made incremental improvements in predictions, but that further work is still required.

Key Words: feedlot beef, modelling, methane

151 Supplemental vitamin C alleviates negative effects of high sulfur diets on beef quality. D. J. Pogge,* S. M. Lonergan, and S. L. Hansen, *Iowa State University, Ames.*

High S (HS) diets may contribute to antemortem oxidative stress in cattle, hindering live performance and expressing residual effects on meat quality. The objective of this study was to examine the effects of a supplemental rumen-protected vitamin C (VC) on meat quality of cattle receiving varying concentrations of dietary S. Angus type steers (n = 120) were blocked by initial BW (355 ± 23 kg) and assigned to treatments including: 1) low S corn diet (LS; 0.18% S), 2) LS + VC, 3) medium S (MS), 40% DDGS diet (0.32% S), 4) MS + VC, 5) HS (0.56% S), MS + sodium sulfate, and 6) HS + VC. An average of 10.3 g supplemental VC$\cdot h^{-1} \cdot d^{-1}$ was consumed. A rib steak, collected from each carcass after a 24 h chill, was stored at −20°C and homogenized before analysis. Data were analyzed on a pen mean basis (n = 5 pens per treatment). By design, increasing dietary S linearly increased ($P < 0.01$) g of S consumed. Increasing dietary S resulted in steaks with a lesser ($P < 0.01$) percent lipid. The proportion of the catalytic subunit of μ-calpain present as the unautolyzed 80 kDa band was increased ($P < 0.05$) as dietary S increased. The abundance of the unautolyzed μ-calpain band tended to decrease ($P < 0.10$) in the HS + VC treatment compared with HS. Addition of VC, regardless of dietary S, tended to increase ($P < 0.10$) the proportion of the catalytic subunit present as the 76 kDa autolysis product of the protease μ-calpain, but was specifically increased ($P < 0.05$) in the MS + VC and HS + VC treatments. This suggests that VC provided a reducing environment that allowed activation of the calpains. Increasing dietary S decreased ($P < 0.05$) troponin-T degradation and protein carbonylation ($P < 0.01$), while added VC, regardless of dietary S, decreased ($P < 0.05$) protein carbonylation. TBARS values were greater ($P < 0.05$) in VC treatments, which may relate to a tendency ($P < 0.10$) for increased Fe content in steaks from VC cattle. In conclusion, supplemental VC appears to negate the negative effects of HS on oxidation of the protease μ-calpain and muscle protein degradation. This may translate to an enhancement in meat quality and potential increases in tenderness of the final meat product.

Key Words: cattle, meat quality, vitamin C

Ruminant Nutrition: Dairy Production I

152 Liver gene expression patterns can explain accumulation of lipid in the liver during the transition period. H. R. Khazanehei,* P. Eck, A. Regassa, D. O. Krause, and J. C. Plaizier, *University of Manitoba, Winnipeg, MB, Canada.*

The effects of 2 dry-period managements of dairy cows on the expression of genes related to lipid metabolism in the liver were compared. Twenty-four multiparous cows were paired based on expected calving date, and randomly assigned to treatment within each pair. Treatments were a 60-d dry period (60 d) with separate far-off and close-up diets and a 40-d dry period (40 d) with only close-up diet. The 60-d dry period was divided into a 39-d far-off and a 21-d close-up period. The far-off diet contained 1.28 Mcal/kg net energy for lactation (NEL), 14.7% of crude protein (CP), and 50% of neutral detergent fiber (NDF) on a DM basis. The close-up diet contained 1.43 Mcal/kg NEL, 14.6% of CP, and 38% of NDF. A common diet was fed to all cows after calving, which contained 1.69 Mcal/kg, 17.6% of CP, and 31% of NDF. Liver biopsies were obtained at wk −3, 1 and 4 relative to parturition. Differential gene expression was assessed by Affymetrix microarray analysis and data were normalized through RMA algorithm and then statistically analyzed using FlexArray 1.6.1. An FDR-adjusted P-value lower than or equal to 0.1 and a fold-change greater than 2 were considered as a cut-off point to indicate significant up- or downregulation of genes. Gene networks were assembled using Ingenuity Pathway Analysis. A parallel study showed that lipid accumulation in the liver was greater at wk 1 than and wk −3 and wk 4, and at wk 1, this accumulation was greater for the 40 d than for the 60 d treatment. There was no difference in gene expression between the treaments across the sampling days. Genes involved in lipid accumulation and triacylglycerol synthesis in the liver were upregulated at wk 1. Also mitochondrial fatty acids transporters aiding β-oxidation were upregulated, and genes involved in hydroxylation of fatty acids aiding β-oxidation were downregulated at wk 1. Gene expression at wk 4 was similar as at wk −3. The changes in lipid deposition during the transition period are reflected in changes in the expression of genes related to lipid metabolism in the liver, but the difference between the 40 d and 60 d treatments is not.

Table 1. Comparison of expression of genes involved in liver lipid metabolism between week 3 before and week 1 after calving

	Fold-change +1/-3	
Genes	40-d treatment	60-d treatment
Beta-oxidation		
PPARGC1	1.03‡	1.03†
CPT1B	2.26‡	2.51‡
SLC22A5	1.27‡	1.27‡
Fatty acid hydroxylation		
CYP2C9	−2.01‡	−1.25‡
CYP2E1	−1.43‡	-
CYP2U1	−1.26‡	−1.11‡
Lipid accumulation		
PLIN2	1.47†	1.39†
ELOVL5	1.08‡	1.15‡
ACSL1	1.21‡	1.17‡
GHR	−1.12‡	−1.08‡
APOA1	2.83‡	2.54‡

†$P < 0.1$, ‡$P < 0.05$.

Key Words: dry period, gene expression, lipid metabolism

153 Effects of nutrition, ketosis, and inflammation on hepatokine and nuclear receptor expression in liver of peripartal Holstein dairy cows. H. Akbar,* J. M. Khan, D. B. Carlson, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

In rodents, fibroblast growth factors 21 (FGF21) has emerged as a metabolic regulator produced by liver in response to different physiological conditions that regulate glucose and lipid metabolism. Its upregulation induces glucose uptake in adipose tissue and skeletal muscle; whereas in liver it increases hepatic fatty acid oxidation, reduces triacylglycerol accumulation, and stimulates ketogenesis. The regulatory mechanism and action of FGF21 in ruminants remain unclear. We sought to investigate the mRNA expression of FGF21, FGF receptors, the hepatokine ANGPTL4, and genes involved in regulation of fatty acid oxidation (CPT1A, PPARA) under different nutritional conditions including early postpartal ketosis (KET), peripartal dietary L-carnitine supplementation (CAR), and prepartal level of dietary energy. We also examined hepatic FGF21 in response to intramammary lipopolysaccharide (LPS) challenge at 7 d postpartum. In CAR liver biopsies were harvested at d 2 and d 10 postpartum in cows assigned to control (n = 5), 100 g CAR/d (C100, n = 5), and 200 g CAR/d (C200, n = 4). In KET, liver biopsies were obtained at d 14 postpartum from control (n = 7) and feed-restricted induced ketotic (n = 7) cows. In the LPS study, cows (n = 6/treatment) were fed during the dry period either moderate-energy (M) or control energy (S) and received 0 (M:N, S:N) or 200 Î1/4g LPS (M:Y, S:Y) at 7 d postpartum. Liver biopsies were harvested at d 7 and d 14 postpartum. Expression of FGF21 was analyzed via RT-PCR. There was an interaction effect ($P < 0.05$) of CAR for FGF21 expression due primarily to lower expression at d 10 with C100 and C200 vs. control. The opposite effect was observed for ANGPTL4 expression (a hepatokine) at d 2 which was greater with C100 and C200 vs. control. Subsequently, a marked decrease by d 10 was observed with C200 at which point ANGPTL4 was lower than C100 and controls. The significant interaction ($P < 0.05$) for PPARA expression was due to a marked increase at d 10 with C100. A similar response to C100 was observed for CPT1A and KLB expression. Ketosis induced the expression of FGF21 ($P < 0.05$), KLB ($P < 0.05$) and FGFR1 ($P = 0.08$); whereas, no effect was observed for the expression of FGFR2 and KL. In the LPS study, expression of FGF21 was induced ($P < 0.05$) with both M:Y and S:Y at d 7 but the response was more marked with S. By 14 d expression decreased markedly with S:N but remained nearly unchanged with other treatments. Prepartal M led to greater ($P = 0.06$) overall ANGPTL4 postpartum. Overall, results indicate that in transition cows both L-carnitine and inflammatory challenge regulate FGF21 expression likely through their effects on fatty acid oxidation and ketogenesis, i.e., L-carnitine enhances and inflammation inhibits both processes. Ketosis could upregulate the expression of FGF21 likely via incoming nonesterified fatty acids and potentially via PPARα. However, the role of PPAR α on FGF21 activation remains unclear because of the inverse response observed with C100.

Key Words: metabolism, transition cow

154 Effects of a moderate-energy diet during the close-up dry period on immunometabolic indices in peripartal dairy cows. J. S. Osorio*[1], E. Trevisi[2], P. Ji[1], J. K. Drackley[1], G. Bertoni[2], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Universita Cattolica del Sacro Cuore, Piacenza, Italy.*

The peripartal period is characterized by marked changes in hormonal, metabolic, and immune/stress-like conditions all of which may contribute to regulating dry matter intake (DMI) and the supply of nutrients to mammary gland. Twenty 3 multiparous Holstein cows were fed a control diet (CE, n = 10; 1.24 Mcal/kg DM; high-straw) during the entire dry period (ca. 50 d) or were switched to a moderate-energy (ME, n = 13; 1.47 Mcal/kg DM) diet during the last 21 d prepartum through calving. All cows were fed a common lactation diet (1.67 Mcal/kg DM postpartum). Blood samples were collected at −21, −10, 7, 14, and 21 DIM for profiling of 21 markers of liver function, metabolism, oxidative stress, and inflammation. Concentration of cholesterol (CHOL) and the negative acute-phase protein albumin (ALB) decreased (time $P < 0.05$) through calving but CHOL increased markedly between 7 and 21 DIM regardless of treatment. Paraoxonase concentration through calving followed a similar pattern (time $P < 0.01$) as CHOL and ALB; however, concentration remained unchanged from 7 to 21 DIM. Glutamic-oxaloacetic transaminase (GOT) and bilirubin (BIL) concentration increased (time $P < 0.01$) from −21 to 7 DIM regardless of treatment after which it decreased. Concentration of gamma-glutamyl transpeptidase (GGT) tended (treatment × time $P = 0.11$) to differ due to greater concentration with ME after 7 DIM. The concentration of haptoglobin, an inflammation marker, increased (time $P < 0.01$) between −21 and −10 DIM after which it remained stable through 7 DIM and decreased gradually by 21 DIM regardless of treatment. In contrast, concentration of ceruloplasmin, another inflammatory marker, increased (time $P < 0.01$) linearly between −21 and 14 DIM regardless of treatment. The concentration of reactive-oxygen metabolites (ROM; diet $P = 0.08$) and urea (diet $P = 0.07$) was greater overall with CE. For ROM, differences between diets were evident at 7 and 14 DIM. The marked increase in haptoglobin at 7 DIM with CE agrees with that of ROM and ceruloplasmin. Overall, preliminary data provide some evidence that plane of dietary energy during the close-up dry period alters immunometabolism.

Key Words: inflammation, nutrition, metabolism

155 Integrating control by gene expression in adipose tissue into a mechanistic, dynamic model of metabolism to investigate the biological basis for variation in genetics of feed conversion efficiency in lactating dairy cattle. S. Shields* and J. McNamara, *Washington State University, Pullman.*

Variation in efficiency of feed is a multiple function of metabolic flux in visceral, muscle, and adipose tissues. These processes are affected by genotype, phenotype, and intake, and are under control of hormonal and neural systems. To help identify 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. Our present objective was to integrate changes in gene transcription in adipose tissue into control elements in the model. Data were collected from 2nd to 4th parity cows (n = 120) in the first 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. 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). Visceral and lean body energy use were the 2 major contributors ($P < 0.05$) to variation in milk production efficiency. Expression of several genes coding for metabolic enzymes in adipose tissue measured by transcriptomic arrays were related to efficiency of milk production. The amount of gene transcripts that control lipolysis including the ADRB2 and LIPE, accounted for 10 to 15% of variation in efficiency ($P < 0.02$). Transcripts of genes controlling lipogenesis, including SREBP, TSHSP14, LPL, and ACACA accounted for 15 to 18% of the variation in efficiency ($P < 0.05$). 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: systems biology, transcriptomics, metabolic model

156 Dietary manipulation of crude protein and starch content affects energy balance in early lactation dairy cows. S. J. Whelan*[1,3], F. J. Mulligan[2], V. Gath[2], B. Flynn[3], and K. M. Pierce[1], *[1]School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland, [2]School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland, [3]University College Dublin Lyons Research Farm, Newcastle, Dublin, Ireland.*

During early lactation, high levels of milk production and low dry matter intake result in a state of negative energy balance (NEB) and a metabolic status that can be detrimental to the health and longevity of the dairy cow. Reducing dietary CP and providing glucogenic nutrients have been shown to alter energy balance (EB) and metabolic status when employed as separate dietary strategies. However, simultaneous employment of these strategies has yet to be reported. This experiment investigated whether or not offering diets low in CP and high in starch (LP-HS) can reduce NEB and improve the metabolic status of the early lactation dairy cow compared with a higher CP low starch diet (HP-LS). Ten Holstein Friesian dairy cows were assigned to each dietary treatment in a randomized block design. Diets were isoenergetic (1.79 Mcal NE/ kg DM) and formulated to contain 119 and 275 g/kg DM of CP and starch respectively (LP-HS); or 146 and 57 g/kg DM of CP and starch respectively (HP-LS). The experiment was conducted from d 0 to 63 of lactation. Energy balance was calculated daily and blood samples harvested weekly for metabolite analyses; data were then analyzed using Proc Mixed of SAS. Intake of DM (17.4 ± 0.5 kg/ d, $P = 0.25$) and energy (31.6 ± 1.02 Mcal NE/ d, $P = 0.22$) were not affected by diet. The HP-LS group had a higher milk yield (31.6 vs. 29.2 ± 0.6 kg/ d, $P < 0.01$) versus the LP-HS group. However, the LP-HS group had a more positive EB (2.2 vs. −0.7 ± 1.02 Mcal NE/ d, $P = 0.02$) when compared with the HP-LS group. Blood glucose (3.2 ± 0.1 mmol/ L, $P = 0.36$) was not affected by diet. However, blood urea N (3.5 vs. 1.8 ± 0.2 mmol/ L, $P < 0.01$) was higher, while β hydroxy butyric acid (0.7 vs. 0.8 ± 0.1 mmol/ L, $P = 0.03$) was lower for the HP-LS group compared with the LP-HS group. These data suggest that limiting milk production through offering a low CP, high starch diet reduces both the degree of and length of NEB in early lactation dairy cows. Such strategies may be useful in reducing production diseases associated with severe NEB on dairy farms.

Key Words: dairy cows, early lactation, energy balance

157 Colostrum yield by multiparous cows is positively correlated with prepartum body fat mobilization. N. Litherland,* W. Weich, D. Lobao, and Z. Sawall, *University of Minnesota, St. Paul.*

One hundred and 20 Holstein and Holstein-cross multiparous dairy cows from 2 studies in 2010 and 2011 were used in a correlation analysis to determine if prepartum nutrition, metabolism, and management factors affect colostrum yield (CY). Cows were fed moderate-energy high-forage diets containing corn silage, wheat straw, alfalfa hay, ground corn, and molasses and protein supplements. Prepartum diets averaged 14.5% CP, 40.5% NDF, 1.5 Mcal NEL/kg DM, 16.8% starch, 6.0% sugar, 2.0% fat. Cows averaged 42.7 ± 8.1 d dry, 13.6 ± 0.9 kg DMI/d, 3.1 ± 1.1 lactations and postpartum 305ME = 10,516 ± 2,203 kg. All cows were from the St Paul Dairy Research Unit and were managed similarly. Colostrum yield was not significantly affected by treatment or by study. Samples were collected and analyzed using the same techniques for both studies. Data were pooled and subjected to Pearson Correlation analysis in SAS. Correlation coefficients and P-values were calculated among CY, parity, days dry, calf birth weight, average prepartum DMI, crude protein intake (CPI), neutral detergent fiber intake (NDFI), sugar intake (SI), starch intake (STI), mature equivalent 305 milk yield (305 ME), pre- and postpartum serum NEFA concentration, and pre- and postpartum liver triglyceride concentration. Colostrum yield averaged 7.9 ± 4.2 kg with a minimum yield of 0.91 kg and maximum yield of 21.6 kg. Twenty-six percent of cows produced <5.0 kg colostrum. Colostrum yield tended to be correlated ($r = 0.19$; $P = 0.06$) with calf birth weight. Colostrum yield was positively correlated with serum NEFA 7 d prepartum ($r = 0.40$; $P < 0.05$), serum NEFA 1 d postpartum ($r = 0.53$; $P < 0.05$), serum NEFA 7 d postpartum ($r = 0.29$; $P < 0.05$), serum NEFA 14 d postpartum ($r = 0.19$; $P < 0.05$). Colostrum yield was positively correlated with liver triglyceride concentration 7 d postpartum ($r = 0.28$; $P < 0.05$) and 14 d postpartum ($r = 0.24$; $P < 0.05$). Prepartum nutrient intake; DMI, CPI, NDFI, SI, and STI were not significantly correlated with CY. Colostrum yield was not significantly correlated with 305ME ($r = 0.07$; $P = 0.6$).

Key Words: colostrum yield, NEFA, transition cow

158 A starch-binding agent decreases the in vitro rate of fermentation of wheat.

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The rapid rumen fermentation of the starch in wheat can result in sub acute ruminal acidosis (SARA) with resultant inhibition of rumen function and loss of milk production in dairy cattle. The aim of the present study was to investigate the effect of a starch binding agent (Bioprotect, RealisticAgri, Ironbridge, UK) on the rate of in vitro gas production. The active ingredient in Bioprotect is a stable non-volatile organic salt that complexes with the hydroxyl groups of starch at neutral or slightly acidic conditions (pH 6 to 7), as observed in the rumen. These complexes decompose under more acidic (pH 2 to 3) conditions as in the abomasum and duodenum, making the starch available for enzymatic digestion. Wheat and maize were ground and passed through a 1 mm sieve. A subsample of the ground wheat was treated with Bioprotect (8 mL/kg). Samples (1.0 g) of the grain ($n = 6$ for each grain) were added to serum flasks containing buffered rumen fluid obtained from lactating dairy cows. The flasks were purged with carbon dioxide and maintained in a shaking water bath at 39°C. Gas production was monitored every 5 min for 48 h using the ANKOM wireless in vitro gas production system. Gas production was modeled using a Gompetz equation to determine the rate and maximum amount of gas production (Rmax) and the rate constant (β). The Rmax was slightly higher for the control wheat than the treated wheat and the maize (134 vs 129 and 130 mL/g for wheat, treated wheat and maize, $P = 0.05$). The β was greater for the control wheat than the treated wheat, which in turn was greater than for maize (0.267 vs 0.207 and 0.173 min^{-1}, $P < 0.001$). These data demonstrate that wheat is fermented faster than maize and that Bioprotect can slow the fermentation of wheat. If more starch can pass through the rumen without being fermented it may reduce the incidence of SARA and allow for greater post-ruminal enzymatic digestion of starch.

Key Words: wheat, fermentation, starch

159 Effects of intrajugular glucose infusion and dietary protein concentration on feed intake, milk yield and metabolic responses of postpartum cows.

W. E. Brown* and M. S. Allen, *Michigan State University, East Lansing.*

Effects of glucose infusion on feed intake, milk production, and metabolic responses of postpartum cows fed a low or high protein diet were evaluated utilizing a randomized complete block design with a 2 × 2 factorial arrangement of treatments. Twenty-four multiparous Holstein cows were blocked by BCS and 305-ME milk production, and randomly assigned at calving to one of 4 treatments. Treatments were continuous intrajugular infusion of glucose (GLU, 1 kg/d as 4 L/d of 25% w/v dextrose) or isotonic saline (SAL, 4 L of 0.9% sodium chloride), and diets containing 13.9% (LP) or 18.4% (HP) crude protein. Treatments were initiated at the first scheduled feeding following parturition and lasted 12 d. Data for DMI was collected daily, blood was collected every 2 d, milk yield was collected at each milking, and milk samples were obtained on d 4, 8, and 12. Data were analyzed by ANOVA, with repeated measures when applicable. The GLU infusion reduced cumulative DMI for HP (164.0 vs. 196.5 kg) but not LP (194.2 vs. 189.7 kg) compared with SAL (interaction $P = 0.04$) and tended (interaction $P = 0.12$) to reduce daily DMI for HP (13.6 vs. 16.4 kg/d) but not LP (16.4 vs. 15.9 kg/d). The GLU infusion did not affect cumulative milk yield for HP (441.6 vs. 437.8 kg) but increased milk yield for LP (469.1 vs. 395.0 kg) compared with SAL (interaction $P = 0.02$). The HP treatment tended to increase loss of body condition from 0.65 to 0.82 BCS units/12 d ($P = 0.06$) compared with LP. Consistent with this, HP increased plasma concentrations of NEFA (1184 vs. 895 μEq/L, $P = 0.01$) and BHBA (13.0 vs. 9.5 mg/dL, $P = 0.03$), milk fat concentration (5.71 vs. 4.72%, $P < 0.01$) and yield (2.14 vs. 1.78 kg/d, $P < 0.01$) and 3.5% fat-corrected milk (50.9 vs. 45.1 kg, $P = 0.02$) compared with LP. Greater dietary protein concentration increased milk fat concentration and yield by mobilization of lipid reserves resulting in greater FCM yield. Furthermore, dietary protein concentration interacted with glucose supply to affect feed intake, milk yield and metabolic responses of postpartum cows.

Key Words: transition cow, glucose infusion, dietary protein

160 Effects of feeding moderate-energy high-forage diets with reduced DCAD for 21 or 42 days prepartum on mineral homeostasis and postpartum performance by multiparous dairy cows.

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Objectives were to determine 1) if lowing DCAD is beneficial for cows fed moderate-energy high-fiber (MEHF) diets, 2) if feeding a low DCAD MEHF diet for 21 or 42d prepartum affects postpartum performance and mineral homeostasis differentially. Holstein and Holstein-cross cows were randomly assigned to one of 3 treatments ($n = 20$) 42d before expected calving date. Treatments included: 1) CON, DCAD = +12 mEq/ 100 g DM, 2) 21-ND, DCAD = +12/-16 mEq/ 100 g DM, 3) 42-ND, DCAD = −16 mEq/ 100 g DM, with treatments containing 38.6% corn silage, 22.8% wheat straw, 17.6% protein mix, 12.1% alfalfa, 6.0% molasses supplement and 2.9% ground corn on a DM basis. Prepartum diets were similar in nutrient composition, averaging 17.0% CP, 42.0% NDF and 1.5 Mcal/kg DM. High and low DCAD diets were created using 2 isonitrogenous protein mixes: 1) 97.5% soybean meal and 2) 52.8% Bio-Chlor®, 45.8% soybean meal. CON was fed high DCAD prepartum for 42d. 21-ND received high DCAD for the first 21d of the dry period, then switched to low DCAD until calving. 42-ND received low DCAD for 42d prepartum. After calving cows received a common lactation diet (16.6% CP, 31.6% NDF, 1.7 Mcal/kg DM). Urine pH for 21-ND and 42-ND were lower ($P < 0.01$) compared with CON, demonstrating effectiveness of low DCAD.

Pre- and postpartum data were analyzed separately using Mixed models in SAS with repeated measures. Pre- and postpartum DMI was similar among treatments. Milk yield by 21-ND and 42-ND were higher ($P < 0.05$) than CON on wk 2 and 3 and tended ($P < 0.10$) to be greater on wk 1. Serum ionized Ca was similar among treatments. 21-ND and 42-ND had higher ($P < 0.05$) total serum Ca compared with CON at 72h postpartum, and tended ($P < 0.10$) to be higher at 12h postpartum. Biopsies of liver on d −14, 7 and 14 relative to calving had similar contents of triglyceride and glycogen among treatments. Serum concentration of NEFA increased after calving but were similar among treatments. These data suggest low DCAD in MEHF diets during a 21 or 42d transition period had positive effects on postpartum total Ca and milk yield.

Key Words: blood Ca, negative DCAD, transition cow

161 Comparison of methane prediction for pasture fed dairy cows using a simulation model (Molly) incorporating revised VFA stoichiometry and microbial pools. J. McNamara*[1], P. Buekes[2], P. Gregorini[2], M. Hanigan[3], and G. Waghorn[2], *[1]Washington State University, Pullman, [2]Dairy New Zealand, Hamilton, New Zealand, [3]Virginia Tech University, Blacksburg.*

This study compared the outcomes of 3 versions of DairyNZ's metabolic model, Molly, with 2 different VFA stoichiometry constructs, to describe ruminal VFA pattern and methane (CH4) production (g/d). The models outputs were validated using 30 observations from 30 dairy cattle (82 DIM, 17 kg milk/d) fed fresh cut ryegrass (DMI 12.3 kg DM) in respiration chambers. The model versions were DairyNZ Molly4 (similar to Baldwin, 1995); Molly84, which includes updated ruminal fiber digestive parameters and animal hormonal parameters (Hanigan et al., J. Dairy Sci.); and Molly85, a revised version of Molly84 with new digestive and rumen parameters. The original forage diet VFA construct was compared with a new VFA stoichiometry based on a more recent and larger set of data, including lactate and valerate production and, amylytic, cellulytic bacteria, as well as protozoal pools. Average observed CH4 production was 266 (SD 30) (g/d). Mean predicted values for CH4 production were 287 and 258 (g/d) for Molly4 without and with the new VFA construct, respectively. Molly84 predicted 295 and 288 (g CH4/d) with and without the new VFA construct ($P > 0.5$) respectively. Molly85 predicted the same CH4 production (276 g CH4 /d) with or without the new VFA construct. The incorporation of the new VFA construct did not consistently reduce the mean relative prediction error (RPE %) across the versions of Molly evaluated in the present study. The improvements in the Molly versions from 4, 84 to 85 resulted in a decrease in RPE from 8.6, 8.3 to 4.3%, ($P < 0.05$) respectively. The majority of the root mean square prediction error was apportioned to random bias, e.g., 43, 71 and 70% in Molly4, 84 and 85, respectively. The slope bias was 2% in all cases. It is concluded that DairyNZ present version (Molly85) has the capability to predict CH4 production of pasture fed dairy cows with acceptable accuracy.

Key Words: metabolic cow model, methane prediction, VFA

162 Effects of dry period management and time relative to calving on the expression of genes involved in carbohydrate metabolism in the liver. H. R. Khazanehei,* P. Eck, A. Regassa, D. O. Krause, and J. C. Plaizier, *University of Manitoba, Winnipeg, MB, Canada.*

The effects of a 60-d dry period with far-off and close-up diets and a 40-d dry period during which only a close-up diet was fed on the expression of genes involved in carbohydrate metabolism were compared. Twenty-four multiparous cows were paired based on expected calving date, and randomly assigned to treatment within each pair. Treatments were a 60-d dry period (60 d) with separate far-off and close-up diets and a 40-d dry period (40 d) with only close-up diet. The 60-d dry period was divided into a 39-d far-off and a 21-d close-up period. The far-off diet contained 1.28 Mcal/kg net energy for lactation (NEL), 14.7% of crude protein (CP), and 50% of neutral detergent fiber (NDF) on a DM basis. The close-up diet contained 1.43 Mcal/kg NEL, 14.6% of CP, and 38% of NDF. A common diet was fed to all cows after calving, which contained 1.69 Mcal/kg, 17.6% of CP, and 31% of NDF. Liver biopsies were obtained at wk −3, 1 and 4 relative to parturition. Differential gene expression was assessed by affymetrix microarray analysis and data was normalized through RMA algorithm and then statistically analyzed by EB (Wright; Simon) method using FlexArray 1.6.1. An FDR-adjusted P-value lower than or equal to 0.1 and a fold-change greater than 2 were considered as a cut-off point to indicate significant up- or downregulation of genes. Gene networks were assembled using Ingenuity Pathway Analysis. The results showed that in both treatments at wk +1 compared with wk −3, relative to parturition, genes that are involved in glycogenesis downregulated and genes that were involved in gluconeogenesis upregulated. Glucose-6-phosphatase, catalytic subunit, expressed only in 40-d treatment and serine dehydratase expressed only in 60-d treatment. In the 40-d treatment, at wk 4 compared with wk 1, pyruvate carboxylase, which is involved in gluconeogenesis, was downregulated and the PPP1R3C transcript, encoding protein phosphatase 1 regulatory subunit 3C, which is involved in glycogenesis, was upregulated. However, there was no change in gene expression between wk 1 and wk 4 in the 60-d treatment. In conclusion, at the first week after parturition gene expression shows that gluconeogenesis was greater than glycogenesis in both treatments. However, after 4 weeks, cows on the 40 d treatment showed signs of enhanced recovery to normal carbohydrate metabolism in the liver compared with cows on the 60 d treatment.

Table 1. Effects of dry period length on liver gene expression in regard to carbohydrate metabolism

		Fold-change wk +1/-3		Fold-change wk +4/+1	
Genes	Name	40-day trt	60-day trt	40-day trt	60-day trt
Gluconeogenesis					
G6PC	Glucose-6-phosphatase	1.04	-	-	-
PC	Pyruvate carboxylase	2.4	1.73	−1.59	-
SDS	Serine dehydratase	-	1.51	-	-
PPARGC1A	Proxisome proliferator-activated receptor gamma	1.03	1.03	-	-
Glycogenesis					
PPP1R3C	Protein phosphatase 1, subunit 3C	−2.03	−1.61	1.25	-
PPP1R3B	Protein phosphatase 1, subunit 3B	−1.70	−1.34	-	-
IGF1	Insulin-like growth factor 1	−1.71	−2.06	-	-

Key Words: dry period, gene expression, carbohydrate metabolism

Ruminant Nutrition I

163 Silage process affects chemical composition and digestion site in high moisture sorghum grain. M. Torterolo[1], A. Curbelo[2], C. Cajarville[2], J. L. Repetto[1], and M. Aguerre*[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.*

The aim of this work was to evaluate the effect of silage process on chemical composition and DM digestion site in high moisture sorghum grain. Commercial paddocks of sorghum grain ($n = 25$) were harvested as high moisture grain. A sample was immediately frozen and another sample was ensiled in 1 L drums. For silage production, sorghum grain was compacted with a manual press, and the drum was hermetically sealed. After 60 d silages drums were opened. Chemical composition, rumen and intestinal DM digestibility and in vitro digestibility were determined. For rumen and intestinal digestibility, 3 Holstein steers equipped with ruminal and duodenal cannulas and fed a diet composed by 2 parts of forage and one part of sorghum grain were used. In vitro digestibility was determined after 48 h of incubation in a DAISY fermenter. The effect of silage process on the variables studied was analyzed with the mixed procedure of SAS. While crude protein and condensed tannins contents decreased 4 and 35%, respectively, by silage process ($P \leq 0.028$), in vitro digestibility tended to increase by silage process ($P = 0.062$) (Table 1). Although silage process did not affect total digestibility, it improved rumen degradability by 14% ($P < 0.001$) and reduced intestine digestibility by 20% ($P < 0.001$; Table 1). In conclusion, silage process produced decreases in CP and condensed tannins contents and improved in vitro digestibility. Although total digestibility was not affected, silage process produced changes in the site of digestion.

Table 1. Chemical composition, in vitro digestibility, rumen degradability, intestine and total digestibility of high moisture sorghum before (no silage) and after (silage) silage

	No Silage	Silage	SEM	*P*-value
Moisture (%)	26.2	26.5	1.92	0.298
Composition (% of DM)				
OM	98.9	98.9	0.07	0.947
Ash	1.02	1.03	0.07	0.947
NDF	9.76	9.53	0.33	0.461
CP	7.87	7.56	0.22	0.028
Condensed Tannins	0.66	0.43	0.08	0.004
In vitro rumen digestibility (%)	93.7	94.6	0.56	0.062
Digestibility (%)				
Ruminal	51.4	58.5	1.68	<0.001
Intestinal	32.0	25.4	2.17	<0.001
Total	83.4	83.8	1.07	0.744

Key Words: high moisture grain silage, intestinal digestion, rumen degradation

164 Effect of corn residue removal on cattle performance and subsequent grain yield. A. L. McGee,* J. L. Harding, T. J. Klopfenstein, S. J. van Donk, and L. A. Stalker, *University of Nebraska, Lincoln.*

A 53 ha, center pivot irrigated, corn field near Brule, Nebraska, was utilized to evaluate the effects of residue removal by grazing and baling on subsequent residue quality, grain yield, and cow performance. The field was divided into 8, 6.6 ha paddocks with 4 treatments that have been maintained for 4 yr: heavy stocking (0.8 AUM/ha), light stocking (0.4 AUM/ha), baled, and no residue removal. Pre-grazing residue was collected from 10 randomly located 0.5 X 0.5 M quadrats in each paddock and sorted into 7 plant part categories. Cattle were weighed and body condition scored before and after grazing each year. There was 16.4 kg (DM) of residue per 21.8 kg (DM) grain yield of which 5.8 kg was the bottom 2/3 of the stem, 3.4 kg was leaf, 2.7 kg was cob, 2.2 kg was leaf sheath, 1.4 kg was husk, 0.6 kg was top 1/3 of the stem, and 0.3 kg was shank which did not differ among treatments ($P \geq 0.23$). Assuming cattle eat only the leaf, leaf sheath, husk and shank, there was 7.2 kg of forage /21.8 kg grain yield after harvest. In vitro organic matter disappearance was similar among treatments ($P \geq 0.37$) and ranged from 67.6% in the husk to 36.8% in the bottom 2/3 of the stem; with the top 1/3 of the stem (43.9%), leaf (51.1%), leaf sheath (50.3%), cob (46.2%), and shank (42.9%) intermediate. Corn yields reflecting the effect of multiple years of treatment application are not different (10.7, 10.0, 10.4, 10.4 Mg/ha for high stocking, low stocking, baling and control, respectively; $P = 0.31$). Final BW was 33 kg greater ($P = 0.005$) and final BCS was 0.3 greater ($P = 0.003$) for cows assigned to the light stocking rate treatment compared with cows assigned to the heavy stocking rate treatment. Stocking rate affected cow performance but residue removal has not affected corn grain yield after 3 yr of data collection.

Key Words: corn residue quality, grazing corn residue, beef cattle

165 Effects of restricted versus conventional dietary adaptation over periods of 9 and 14 days on rumen papillae of feedlot Nellore cattle. T. V. B. Carrara[2], D. D. Millen*[2], M. D. B. Arrigoni[1], C. L. Martins[1], R. S. Barducci[1], F. T. V. Pereira[2], L. M. N. Sarti[1], M. C. S. Franzói[1], D. D. Estevam[2], L. L. Cursino[2], P. L. P. Fontes[1], R. D. L. Pacheco[1], R. A. Rizzieri[1], C. F. da Costa[1], L. D. F. Miranda[1], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil.*

This study 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 (STEP) 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 22-mo-old yearling Nellore bulls (361.3 ± 30.2 kg) were fed in 24 pens for 84-d according to the treatments: STEP for 14-d and 21-d, REST for 14-d and 21-d. The STEP 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 490 kg of BW. At harvest a 1-cm^2 fragment of each rumen was collected from cranial 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. RASA in cm^2 was calculated as follows: $1 + (NOP*MPA) - (NOP*0.002)$. Animals in REST protocol had larger ($P < 0.05$) MPA (0.59 vs. 0.52) than those in STEP protocol. Significant (P

< 0.05) interactions were observed between days and harvesting dates, and protocols and harvesting dates. Animals adapted for 9-d had reduced RASA after adaptation than: 1) after finishing (19.5 vs. 33.2), and 2) animals adapted for 14-d after adaptation (19.5 vs. 26.4). Animals in STEP protocol had reduced RASA after adaptation (20.8 vs. 25.1), but no differences were detected after finishing when compared with animals in REST protocol (33.6 vs. 31.8). The REST protocol and 14-d of adaptation led to greater RASA than STEP protocol and 9-d, respectively, which could indicate lesser extent of rumen lesions. Grant provided by São Paulo Research Foundation (FAPESP), São Paulo, Brazil.

Key Words: papillae, zebu

166 Fatty acid composition of backfat, intermuscular, KPH and tail fat depot sites of Angus cross steers finished on grass or high grain diets. G. Acetoze*[1] and H. A. Rossow[2], [1]*Department of Animal Science, University of California, Davis,* [2]*Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California- Davis, Tulare.*

Fatty acid profiles of backfat, intermuscular fat, KPH and tail fat depots from 15-mo old steers (n = 18) finished on a grass diet at Yolo Land and Livestock Cattle Company were compared with those finished on a grain diet at UC Davis feedlot (n = 14). Grass finished steers grazed on average 10-mo on ryegrass and white clover irrigated pasture (CP = 15.1% and ME = 2.58 Mcal/kg DM). Grain finished steers were fed an 80% corn diet (DM basis) (CP = 11.5% and ME = 2.83 Mcal/kg DM), for 4-mo. Grass finished fat depots contained higher percentages of C6:0, C12:0, C14:0, C16:0 and C20:0 while grain finished had higher percentages of C18:0 and C18:3 ($P < 0.01$) (Table 1). Percentages of C18:1 *trans*9, C18:2 *cis*9 *cis*12 and C18:2 *trans*9 *trans*12 were higher in grass finished steers than grain ($P < 0.01$) (Table 1). C18:0 content was higher in the KPH region (20.7%) compared with outer fat depots such as backfat, intermuscular and tail (16.5%, 19.7% and 14.8%, respectively, ($P < 0.05$) while C18:1 *cis*9 content was lower in the KPH region (29.8%) as compared with outer fat depots such as backfat, intermuscular and tail (46.5%, 39.9% and 48.7%, respectively, ($P < 0.05$). In conclusion, percent inner fat depots were higher in saturated fatty acids compared with outer fat depots. No interaction was found between diet and fat depots. Finishing cattle on grass provided fat with higher percentages of conjugated linoleic acid (CLA).

Table 1. Percentages of fatty acids (FA, g FA/100g FA) of grain and grass finished steers

Fatty Acid	Grain ± SE	Grass ± SE	*P*-value
C6:0	1.3 ± 0.3	2.4 ± 0.4	0.008
C10:0	1.7 ± 0.1	1.5 ± 0.2	0.401
C12:0	0.7 ± 0.1	0.9 ± 0.1	0.003
C14:0	2.4 ± 0.3	3.9 ± 0.55	0.001
C16:0	10.8 ± 2.0	19.1 ± 2.6	0.002
C18:0	22.4 ± 1.1	15.4 ± 1.4	< 0.0001
C18:1 c9	44.0 ± 2.6	39.1 ± 3.5	0.162
C18:2 c9c12	1.3 ± 0.1	2.1 ± 0.1	< 0.0001
C18:1 t9	2.2 ± 0.4	3.8 ± 0.5	0.004
C18:2 t9 t12	0.1 ± 0.1	0.4 ± 0.1	< 0.0001
C18:3	2.1 ± 0.1	1.1 ± 0.4	0.008
C20:0	0.2 ± 0.1	0.4 ± 0.1	< 0.0001

Key Words: beef cattle, fat depot sites, fatty acid profile

167 Replacing corn and soybean meal in lactating dairy cow diets with field peas (*pisum sativum*) on milk production and nitrogen utilization. J. J. Albrecht,* K. F. Kalscheur, A. R. Hippen, D. J. Schingoethe, and D. P. Casper, *South Dakota State University, Brookings.*

Sixteen lactating Holstein cows were used in a multiple 4 × 4 Latin square design with 28 d periods to evaluate replacing corn and soybean meal (SBM) with field peas (FP) on milk production and N utilization. Cows were 122 ± 47 DIM, producing 35.4 ± 6.7 kg of milk, and weighed 645 ± 82 kg at the start of the study. All diets contained 37.5% corn silage, 12.5% alfalfa hay, and a 50% concentrate mix. Diets were formulated to replace corn and SBM with FP at 0 (FP0), 12 (FP12), 24 (FP24) and 36% (FP36) (DM basis) of the diet. Milk and DMI data were collected the last 2 wk of each period and milk composition samples were collected on d 17, 18, 24 and 25. No changes in body weight or BCS were observed. With increasing inclusion rate of FP in the diet DMI, milk yield, protein %, fat yield, protein yield, and ECM all linearly ($P \leq 0.03$) decreased while MUN linearly ($P < 0.01$) increased (Table 1). Feed efficiency (ECM/DMI) responded quadratically ($P < 0.01$) to increased inclusion of FP. In the milk, total antioxidant capacity (TAC; 238, 240, 263, and 252 µmol/L FeSO47H2O) tended ($P = 0.10$) and NPN (0.166, 0.168, 0.170, and 0.175%) linearly increased ($P = 0.03$) with the inclusion of FP. True protein (2.91, 2.85, 2.74, and 2.68%), casein (2.33, 2.29, 2.17, and 2.15%), and whey protein (0.57, 0.55, 0.56, and 0.53%) decreased linearly ($P \leq 0.01$) with the inclusion of FP. These results show that replacing corn and SBM with FP at 24% of the diet or greater negatively affects the percentage and yield of milk protein. A deficiency of methionine could have possibly occurred due to the low Met content of FP.

Table 1.

Item	FP0	FP12	FP24	FP36	SEM	*P*-value[1]
DMI, kg/d	24.2a	24.6a	23.5a	21.8b	0.75	L
Milk, kg/d	37.0a	35.4ab	33.8b	33.0b	1.00	L
Fat, %	3.53	3.57	3.58	3.69	0.14	NS
Protein, %	3.06a	3.02a	2.89b	2.84b	0.06	L
MUN, mg/dL	11.6a	12.2ab	13.2bc	14.0c	0.33	L
Fat, kg/d	1.29	1.25	1.21	1.22	0.05	L
Protein, kg/d	1.13a	1.07a	0.97b	0.93b	0.03	L
ECM, kg/d	36.9a	35.5ab	33.7b	33.3b	1.02	L
ECM, kg/DMI kg	1.54	1.46	1.43	1.55	0.04	Q

[a–c] Different letters significant ($P < 0.05$).

[1] L = linear treatment effect ($P < 0.05$); Q = quadratic treatment effect; NS = no significant treatment effect.

Key Words: field peas, milk production, protein

168 Milk production response to increasing net energy intake in dairy cows. A meta-analysis. C. Jensen*[1,2], M. R. Weisbjerg[1], and S. Østergaard[1], [1]*Department of Animal Science, Aarhus University, Denmark,* [2]*Knowledge Centre of Agriculture, Skejby, Denmark.*

The objective of the study was to estimate the effect of increasing net energy intake (NEL) on milk production in dairy cows in early lactation. A new model for economical optimization of the feeding level of dairy cows is to be developed. Previous models are outdated due to higher yield capacity of cows and a new Nordic feed evaluation system, NorFor. This requires development of production functions on milk responses to increased NEL. A data set from recent feeding trials in Norway, Sweden and Denmark were gathered. Prerequisites of data

were that cows were fed ad libitum, planned ration energy density was independent of recorded milk yield, and different energy levels were planned within trials. The data set included treatment means from 66 primiparous groups (primi) and 68 multiparous groups (multi). Cows averaged 69 DIM during trials. Average milk yield was 27 kg ECM for primi and 33 kg ECM for multi. Range of NEL in data set was from 75 to 154 MJ/day for primi and from 95 to 169 MJ/day for multi. Data were analyzed using nlme of R. A mixed effects model regression analysis with random regression of trials was used to model milk production (kg ECM/day). The preliminary models included independent variables for NEL, NEL^2, NDF per NEL, amino acids absorbed in small intestine per NEL and breed. All analyzed ration characteristics were estimated by NorFor. For multiparous cows a significant decreasing marginal milk response (kg ECM per MJ NEL) ($P < 0.001$) was estimated as: 0.919 - 0.00502 × NEL. In the data set the marginal ECM response to NEL for multi decreases from 0.442 to 0.071 with mean at 0.236. For primiparous cows a decreasing marginal milk response to NEL (kg ECM per MJ NEL) was estimated as: 0.454 - 0.00204 × NEL, however the decrease was not significant ($P = 0.1$). In the data set the marginal ECM response to NEL for primi decreases from 0.301 to 0.140 with mean at 0.218. In either of the models there were no interactions between the independent variables. The significant diminishing return of ECM to increasing NEL found in this meta-analysis emphasizes the importance of economic optimization of the energy level for high producing dairy cows.

Key Words: dairy cows, modelling, production response

ADSA-SAD Undergraduate Competition: Dairy Foods

169 Nutritive value of bovine milk as compared with alternative dairy-free beverages. S. M. Smith* and J. M. Bewley, *University of Kentucky, Lexington.*

In recent years, many dairy-free alternative beverages have been developed and marketed to replace traditional bovine milk. Consumers now have a large variety of alternative dairy-free beverages substitutes to choose from in the grocery store. This emerging market represents a considerable and formidable competitive threat to the dairy industry. With many of these alternative beverages branded as "milk," confusion and frustration prevails in the dairy industry and among consumers. The dairy industry must grapple with questions as to why consumers are choosing these alternative beverages. Per-capita consumption of bovine milk decreased from 24.3 gallons per person in 1994 to 20.8 gallons in 2008. Meanwhile, the alternative beverage industry is growing at a fast pace, with almond beverage sales increasing by 79% in 2011 alone. Bovine milk contains essential nutrients in suitable quantities for human consumption and milk promotes growth and bone strength in children. Bovine milk is a wonderful source of protein, calcium, fat, carbohydrates, as well as sodium and potassium. Some consumers have a negative opinion of bovine milk without any clinical or epidemiological evidence. These negative claims include that saturated milk fat is unhealthy and that bovine milk causes cancer. Moral or ethical controversies about milk also exist with regard to animal care and well-being. Health food beverage alternatives available on the market today include coconut, rice, and soy, each of which have different nutritive properties (i.e., vitamin D, Ccalcium, carbohydrates, and potassium). Nutritional deficiencies have been documented in toddlers as a result of being fed these alternative beverages instead of bovine milk. The parents of children most often are well-educated and conscientious, while providing regular medical care. Growing children who avoided bovine milk had smaller stature and poor bone health. Some of these children even developed diseases such as rickets or kwashiorkor. Additional education and research is needed to reflect the importance of bovine milk in human diets.

Key Words: human nutrition, alternative dairy beverages

170 Milk and cognitive abilities: Can dairy products work to improve your memory? N. L. Leckie* and C. L. Widener, *Clemson University, Clemson, SC.*

With an aging population it becomes important to research and discover possible preventative measures for geriatric diseases, such as the loss in cognitive function. This loss in function affects not only the elderly, but their family and caregivers as well. It is a frustrating and progressive disease that has a negative effect on the individual's quality of life along with an increase in their health care costs. The disease of dementia, particularly of Alzheimer's, is not well understood and the physical, physiological and psychological changes that are caused by these diseases are still being researched. Recent research has shown a surprising and encouraging correlation between daily consumption of dairy products and scoring on a cognitive test, with the highest dairy consumers having the highest scores. Even on the low-end of the consumption spectrum, consumers who ate or drank a dairy product 2 to 4 times per week performed better than those who only ate a dairy product once a week. Taking it a step further, those who drank skim or low-fat milk performed better than those who drank whole milk. Now this correlation between dairy consumption and cognitive function can partially be attributed to the fact that the most frequent dairy consumers also indicated that they ate the most healthfully overall. However even after factoring out risk factors for cardiovascular disease, sex, demographic, lifestyle and dietary factors the relationship between cognitive function and dairy intake remained, suggesting that some factors specific to milk must directly correlate to brain function. Obviously more research needs to be conducted to determine the specific link between dairy and cognitive function, however this new information is promising for both the consumers and the dairy industry.

Key Words: memory, dairy foods, cognition

171 Milk production and pasteurization: Two opposing viewpoints. M. Sprague* and E. L. Karcher, *Department of Animal Science, Michigan State University, East Lansing.*

In the early 1900s a case was made for enforced sanitation of milk and milk products. Diseases, such as typhoid fever, tuberculosis, scarlet fever, and diphtheria, were widespread, and out of these issues, 2 schools of thought emerged. One advocated for the pasteurization of milk, while another for ensuring the cleanliness of the product throughout the whole process as a way to prevent contamination, resulting in a "Certified Milk" product. Because of costs associated, the Certified Milk movement eventually disintegrated. Today a similar type of debate continues between the proponents of pasteurized milk and those of raw milk. Although there are states where the sale of raw milk on farm or in retail stores is legal, there are many states that allow raw milk sales under some circumstances. Several states ban the sale of raw milk, but have legalized "herd shares" or have no laws prohibiting the sale of "herd shares," which allows consumers to pay to own a portion of an animal. The FDA states that raw milk is not a safe product for consumption. However, several unsupported claims have been made stating that raw milk prevents disease, is more nutritious, and better tasting. Research has shown that raw milk does not have any significant nutritional advantages, so the question remains, why risk public health? Enforcing standards on raw milk, like the certified program, would not guarantee the health of consumers. Whether at a state or a national level, the best approach for the entire population should be taken into account. Pathogens, such as *Salmonella*, *Escherichia coli*, and *Listeria*, make drinking raw milk, especially among at risk populations, a dangerous and unnecessary risk. Due to these safety issues of consuming raw milk, bans should be put into place on the retail or on-site sale of raw milk. Alternative options for those who wish to consume raw milk may be pasteurization but not homogenization of milk products. In addition more emphasis on consumer education about the pasteurization process is crucial if these types of raw milk bans were put in place.

Key Words: raw milk, pasteurization

172 The effects of flavored milk in the cafeteria. S. M. Vignes* and C. C. Williams, *Louisiana State University, Baton Rouge.*

In the United States obesity has drastically increased over the past several years. The 2007–2008 National Health and Examination Survey (NHANES) states about one-third of adults are obese. Also, about 17% of children between the ages of 2 and 19 are obese. These staggering statistics have left people searching for answers to improve the weight of Americans. One proposed answer affects the dairy foods industry because the USDA is putting forth a new rule regarding milk requirements in the school cafeteria. The new rule requires schools to serve 8 ounces of milk with lunch and breakfast. The stipulation though is that it must be low-fat or fat-free white milk or fat-free flavored milk. This rule has led some schools to consider pulling flavored milk from the menu entirely. Requiring the flavored milk to be fat free will deter some because the product will not be as satiable. The business from the chocolate milk (the most popular flavored milk) will in turn be shifted to alternative drinks such as juices or soft drinks which have more sugar and less health benefits. The fear that flavored milk is contributing to childhood obesity is misguided though. Chocolate milk contains 2–4 teaspoons of sugar which is about half of drinks that would essentially replace it. Also the benefits of flavored milk greatly outweigh the bad. Milk provides essential nutrients for a healthy body such as: calcium, phosphorous, proteins, and vitamins. A little extra sugar and fat is completely overshadowed by the benefits of continuing to serve flavored milk in the cafeteria due to the beneficial constituents of milk.

Key Words: flavored milk, school lunches, obesity

173 Importance of texturants in dairy products.

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Although most consumers recognize the importance of flavor, many do not realize the important role texture plays in determining food preferences. Poor texture can be a deal breaker, no matter how good the flavor. Different ingredients can have a significant effect on a product's texture. Texturants have a variety of functions and play an important role in the formation of dairy foods. They can assist with stability, nutritional value, and provide lower cost ingredients. Texturants function by interacting with proteins, fats, and carbohydrates. They set up a stable structure within the product to allow for easier processing and more consistency over the product's life. Commercially available texturants come in a variety of forms with specific applications, usage level and functionality. They can work together or independently to change the properties of a specific item. For example, gelatin ingredients have many functions in manufacturing dairy products. They help with the freeze-thaw stability of ice cream by changing the nature of ice crystals and also offer stability to casein in yogurt and cheeses. Acacia gum assists in mouthfeel, stability, and added fiber. Guar gum is a hydrocolloid that can influence viscosity and enhance creamy textures in ice cream and other dairy foods. Inulin and some citrus based texturants can help reduce fat in many products without adversely affecting their sensory appeal. Processors will continue to develop products where texturants will replace more expensive and high calorie ingredients while maintaining flavor. Food scientists will discover new synergies among existing ingredients and develop additional texturants. These will provide the framework for healthier products and will allow companies to expand their market share while maintaining cost effectiveness. The continued evolution of texturant technology will benefit consumers and manufacturers through improved dairy products in the marketplace.

Key Words: texturants, dairy product texture

174 Production of functional probiotic and prebiotic dairy foods.

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As people strive to lead healthy lives, more emphasis is being placed on the link between consumption of food and potential health benefits. The addition of live microorganisms to select dairy products is one way to meet this demand. Probiotics are live microorganisms that may provide health benefits when consumed including inhibition of bacterial pathogens and anti-carcinogenic effects. A symbiotic relationship with prebiotics exists; prebiotics are non-digestible food ingredients that stimulate the growth of the probiotic. In order for beneficial effects to be realized, consumption must be around 10^6 to 10^9 viable cells per day. Viability of the probiotic is affected by storage of the fortified product. These products are typically stored in plastic containers, which are highly oxygen permeable. Probiotics require low oxygen levels, creating storage challenges. The use of oxygen-removing steps or addition of oxygen-absorbing compounds are alternatives under consideration. Another factor for consideration is the appeal of the product to the consumer. Studies conducted with the addition of *Lactobacillus casei* and inulin, serving as probiotics and prebiotics, respectively, at levels of 3% inulin, found that health benefits were ensured and sensory characteristics were not altered. Consuming dairy products fortified with probiotics and prebiotics can lead to beneficial effects on intestinal microorganisms and overall health benefits.

Key Words: probiotics, prebiotics

Physiology and Endocrinology: Estrous Cycle Manipulation–Dairy

175 Ovulatory responses to withdrawal of progesterone feedback during the early and late luteal phase. G. E. Mann*[1] and R. S. Robinson[2], *[1]University of Nottingham, School of Biosciences, Division of Animal Sciences, Sutton Bonington Campus, Loughborough, UK, [2]University of Nottingham, School of Veterinary Medecine and Science, Sutton Bonington Campus, Loughborough, UK.*

Synchronization protocols aim to optimize timing of ovulation following removal of the inhibitory action of progesterone on the final stages of ovulatory follicle development. This study investigated the effects of blocking progesterone action during different stages of the luteal phase on endocrine and ovulatory responses in cyclic ewes. Ewes (n = 4 per group) were treated during the Early (d 3–5) or Late (d 12–14) luteal phase with progesterone antagonist (100 mg i.m. 2 × daily; onapristone ZK98299, Schering AG) or Control vehicle and slaughtered on d 17 to determine ovarian morphology. Hormone changes were analyzed by ANOVA for repeated measured and ovulation rate by ANOVA. Early treatment resulted in increased ($P < 0.01$) plasma LH within 6h (Control 1.8 ± 0.3; Treated 5.7 ± 0.3 ng/mL), with LH then rising to surge like levels within 25.5 ± 5.1 h (range 12–36 h). Following Late treatment, an initial modest ($P < 0.1$) increase in LH (Control 0.9 ± 0.1; Treated 2.0 ± 0.4 ng/mL) was followed by surge-like levels 51.0 ± 3.9 h after the start of treatment (range 42–60 h). During Late treatment plasma estradiol (Treated 2.0 ± 0.1, Control 1.2 ± 0.1 pg/mL; $P < 0.001$) and progesterone (Treated 3.3 ± 0.2, Control 2.1 ± 0.2 ng/mL; $P < 0.01$) were elevated. In contrast, Early treatment was not associated with any increase in either hormone. In Control ewes ovulation rate was 2.0 ± 0.0. In the Late group there were 2.0 ± 0.0 mature corpora lutea and 1.5 ± 0.3 accessory corpora lutea (total 3.5 ± 0.3) per ewe. In the Early group it was not possible to clearly differentiate between the original and accessory corpora lutea but the total number (5.3 ± 0.5) was higher ($P < 0.05$) than that seen in the Late group. Blocking progesterone feedback during the early luteal phase resulted in a more rapid induction of an LH surge and higher rate of accessory ovulation than treatment later in the luteal phase. This differential response of the endogenous reproductive architecture, presumably reflecting differences in both follicle populations and hypothalamic-pituitary responsiveness at the time of treatment, is often overlooked in the development of ovulatory synchronization programs.

Key Words: progesterone, ovulation, LH surge

176 Estrus behavior and fertility responses in lactating grazing dairy cows after a timed AI program using estradiol cypionate. M. N. Correa*[1], M. E. Lima[1], C. C. Brauner[1], A. R. T. Krause[1], E. G. Xavier[2], E. Schmitt[1], A. Schneider[1], and F. A. B. Del Pino[1], *[1]Universidade Federal de Pelotas, NUPEEC, Pelotas, RS, Brazil, [2]Granjas 4 Irmaos S/A, Rio Grande, RS, Brazil.*

The objective of this study was to determine the estrus behavior influence during an estrus synchronization program (Heatsynch) on fertility responses in lactating grazing dairy cows. Four hundred and 70 primiparous (n = 229) and multiparous (n = 241) Holstein cows were enrolled in a artificial synchronization program consisting of a controlled internal drug-releasing (CIDR) containing 1.9 g of progesterone, either a new one or previously used once (7 d), plus 25 µg i.m. injection on d 0 (85 + 6 DIM) and all cows were given 25 mg $PGF_{2\alpha}$ i.m. upon CIDR removal 7 d later (d 7) followed by an injection of 1 mg of estradiol cypionate (ECP) i.m. at d 8. Cows were then observed for signs of estrus for at least 2 h (twice daily at 7:00 and 18:00) for 3 d following CIDR removal. Those cows detected in estrus were inseminated 12 h later. Based on the detection of estrus, cows were divided into 3 groups: estrus behavior before TAI (Estrus AI) and inseminated 48–60 h after CIDR insert removal (n = 143); estrus behavior at the TAI (Estrus TAI) (n = 127); and no estrus detection and timed inseminated (TAI) 72 h after CIDR removal (n = 200). A single technician was responsible for the estrus detection and inseminations. Pregnancy status was determined by ultrasonography at 30 to 35 d and 60 to 65 d after AI. Data were analyzed by the LOGISTIC procedure of SAS. Estrus behavior had effect on fertility responses ($P < 0.01$), where both groups that showed estrus (Estrus AI and Estrus TAI) had greater pregnancy rates than the TAI group at 30–35 d (45.5 vs 46.5 vs 28.5), and 60–65 d (36.4 vs 35.4 vs 15.5). Pregnancy losses also were affected ($P < 0.01$) by the estrus behavior (20.0 vs 23.7 vs 45.6), respectively for Estrus AI, Estrus TAI and TAI groups. There was a correlation ($P = 0.02$) among fertility responses and parity, where primiparous cows had better results than multiparous cows. Estrus behavior was similar ($P > 0.05$) among primiparous and multiparous cows. Estrus behavior during a Heatsynch program is beneficial to improve reproductive performance in lactating grazing dairy cows.

Key Words: estradiol cypionate (ECP), timed AI, pregnancy

177 Effect of reusing CIDRs on estrus behavior and fertility responses in a Heatsynch protocol of grazing dairy cows. C. C. Brauner*[1], M. E. Lima[1], A. R. T. Krause[1], E. G. Xavier[2], A. Schneider[1], E. Schmitt[1], F. A. B. Del Pino[1], and M. N. Correa[1], *[1]Universidade Federal de Pelotas, NUPEEC, Pelotas, RS, Brazil, [2]Granjas 4 Irmaos S/A, Rio Grande, RS, Brazil.*

The objective of this study was to determine the effect of reusing intravaginal progesterone inserts (CIDR) on estrus behavior and fertility responses of grazing dairy cows in a Heatsynch protocol. Three hundred and 90 5 primiparous (n = 183) and multiparous (n = 212) Holstein cows were enrolled in a Heatsynch program consisting of a CIDR containing 1.9 g of progesterone, either a new one or previously used once (7d use), plus 25 µg GnRH i.m. injection on d 0 (82 + 6 DIM) and all cows were given 25 mg $PGF_{2\alpha}$ Â ± i.m. upon CIDR removal 7 d later (d 7) followed by an injection of 1 mg of estradiol cypionate (ECP) i.m. at d 8. Used CIDRs had been thoroughly rinsed with a mild disinfectant solution, air-dried, and stored in a dry, enclosed container after first use. Cows were then observed for signs of estrus (twice daily at 7:00 and 18:00) for 3 d following CIDR removal. Cows observed in estrus were inseminated 12 h later. Based on the detection of estrus, cows were divided into 3 groups: estrus behavior before TAI (Estrus AI) and inseminated 48–60 h after CIDR insert removal (n = 115); estrus at the TAI (Estrus TAI) (n = 98); and no estrus detection and timed inseminated (TAI) 72 h after CIDR removal (n = 152). A single technician was responsible for the estrus detection and inseminations. Pregnancy status was determined by ultrasonography at 30 to 35 d and 60 to 65 d after AI. Data were analyzed by the LOGISTIC procedure of SAS. There were no difference ($P > 0.05$) among CIDR uses on pregnancy at 30–35 d (38.6% vs 40.1%); and 60–65 d (24.7% vs 30.0%) and pregnancy losses (36.1% vs 25.3%), respectively for CIDR use 1 and 2. We could not find any difference ($P > 0.05$) of estrus behavior and CIDR uses, as well as across cows parity. However, percentage of pregnancy losses in the primiparous group was great ($P = 0.04$) for the first CIDR use than the second one (42.3 vs 21.1). In conclusion, estrus behavior and fertility responses in a heatsynch protocol of grazing dairy cows are not affected by CIDR uses. Primiparous cows seems to have greater pregnancy losses (up to 65 d) when first CIDR was used.

Key Words: estradiol cypionate (ECP), timed AI, reproduction

178 Effect of intrauterine administration of GnRH on LH secretion in lactating dairy cows.

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The objective of this study was to evaluate the release of LH following the intrauterine (i.u.) administration of GnRH (Gonadorelin) in lactating dairy cattle. Cows (n = 22) were presynchronized with 2 injections of PGF2α given 14 d apart (starting at 26 ± 3 DIM) followed by Ovsynch [OV; d −9 GnRH, d −2 PGF2α, d 0 GnRH (h 0)] 12 d later. Ovarian structures were recorded and blood samples were collected on d −9 and d −2. Only cows presenting a CL ≥ 15 mm and at least one follicle ≥ 10 mm in diameter at the initial GnRH were used in the study (n = 13). 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 = 4) received 2 mL i.m. of sterile water, 2) intramuscular group (IM; n = 4) received 100 µg i.m. of GnRH, and 3) intrauterine group (IU; n = 5) received 200 µg i.u. of GnRH with the addition of glycerol (7% v/v). Blood samples for determination of LH serum concentrations were collected at h −0.5, 0, 0.5, 1, 1.5, 2, 3, 4 and 5. Ovulation was determined 48 h after the second GnRH of OV (d 0) by transrectal ultrasonography. Progesterone and LH data were analyzed using mixed procedures of SAS. Serum progesterone concentrations at h 0 did not differ ($P > 0.05$) between groups. The area under the curve for LH was greater for ($P < 0.05$) IM cows compared with IU or CON cows. Most of the cows ovulated by 48 h relative to d 0 in IM (4/4) and IU (3/5) groups compared with CON cows (0/4). Although IU administration of GnRH resulted in lower serum concentrations of LH than IM group, more IU cows ovulated by h 48 compared with CON. These findings support our previous findings, and further, suggests that i.u. administration may be an alternative route of delivery for GnRH to synchronize ovulation in estrous synchronization programs.

Key Words: intrauterine GnRH, LH, dairy cow

Graduate Student Competition: ADSA Southern Section (Graduate)

179 Volatile fatty acids and biohydrogenation intermediates in continuous cultures are returned to normal by addition of potassium carbonate but not by potassium chloride. P. H. Morris*[1], J. G. Andrae[1], J. K. Bernard[2], E. Block[3], and T. C. Jenkins[1], [1]*Clemson University, Clemson, SC,* [2]*University of Georgia, Tifton,* [3]*Arm & Hammer Animal Nutrition, Princeton, NJ.*

In previous work, an increase in milk fat percentage has been reported when lactating cattle were fed $K_2CO_3 \cdot 1.5\ H_2O$, and addition of K_2CO_3 to continuous cultures of ruminal microorganisms partially or totally returned volatile fatty acid (VFA) and biohydrogenation patterns back to normal. The objective of this study was to determine if shifts in conjugated linoleic acids (CLA) and VFA observed previously with K_2CO_3 were also caused by addition of KCl. Six dual-flow continuous fermenters were fed 60 g/d of 1:1 forage (dehydrated alfalfa pellets) to concentrate mix in 2 equal portions at 0800 and 1600 h. The study was conducted as a randomized complete block design consisting of 4 blocks (4 10d periods) and 6 treatments. Treatments consisted of the following additions to the control diet; 1) 0% fat and 0% K 2) 0% fat and 3% K from K_2CO_3 3) 0% fat and 3% K from KCl 4) 3% soybean oil and 0% K 5) 3% soybean oil and 3% K from K_2CO_3, and 6) 3% soybean oil and 3% K from KCl. Addition of K_2CO_3 but not KCl increased ($P < 0.05$) pH, although average daily pH values for all treatments were maintained between 6.1 and 6.5. Supplemental fat increased ($P < 0.05$) production rates (mg/d) of trans-10 18:1 and *trans*-10, *cis*-12 CLA, and decreased ($P < 0.05$) acetate:propionate. Addition of K_2CO_3 increased ($P < 0.05$) cis-9, trans-11 CLA outflow from 7.3 to 16.0 mg/d and increased ($P < 0.05$) *trans*-11 C18:1 outflow from 130.8 to 272.3 mg/d, but *trans*-10 C18:1 decreased ($P < 0.05$) from 221.2 to 143.6 mg/d. No effect on CLA or trans monene outflows were observed with the addition of KCl. *Trans*-10, *cis*-12 CLA outflow was not affected by addition of either K2CO3 or KCL. The addition of K_2CO_3 increased ($P < 0.05$) acetate:propionate at 4 h after feeding from 1.77 to 2.06 in the 0% fat diets and from 1.54 to 1.86 in the 3% fat diets. No changes in VFA were seen when KCl was added. The results of this experiment show that disturbances of VFA and biohydrogenation patterns induced by high fat were alleviated by addition of 3% K as K_2CO_3 as previously observed, but were not alleviated by the same dose of K from KCl.

Key Words: conjugated linoleic acid, biohydrogenation, potassium

180 Dietary L-arginine supplementation effects on growth and health parameters in neonatal Holstein bull calves. A. N. Vanderlick*[1], G. A. Holub[1], and W. T. Bissett[2], [1]*AgriLife Research Texas A&M University, College Station,* [2]*College of Veterinary Medicine, Texas A&M University, College Station.*

The purpose of this study was to determine if calves fed 4 L of arginine supplemented milk replacer daily differed in growth and health parameters as compared with calves supplemented with alanine in heat stress conditions. Previous studies performed in piglets and calves showed increased body weight gains when supplementation of arginine was provided. Calves were supplemented with 0.484 g/d of arginine or 0.818 g/d of alanine (isonitrogenous control). Holstein bull calves (n = 30) < 2 d of age were assigned to a trial based on initial body weight, physical health score, and total serum protein levels. The study was conducted for 56 d from July 24 to September 17, 2011. Fecal scores (FS) of 1 to 4 (1 = hard, firm, 2 = soft, firm, 3 = no form, and 4 = watery) were recorded daily to monitor scouring. Calves with a FS of 4 were considered to have diarrhea requiring treatment. Respiration rates and rectal temperatures (RT) were recorded at 0600 and 1800 to monitor respiratory challenges while rectal temperatures were used to monitor febrile events. If RT was greater than 39.17°C calves were treated for fever. Calves provided arginine supplementation had a higher frequency of treatments for fever (0.957 treatments/d vs 0.03133 treatments/d, $P = < 0.0007$) than calves given alanine for the duration of the study; however, rectal temperatures in the AM or PM did not differ significantly for the 2 treatments. All growth parameters including body weight, hip height, hip width, wither height, heart girth, and cannon bone length were not significantly different for treatment by week, nor for the duration of the trial. Other health parameters including AM and PM respiration rates, fecal score, respiratory treatment, or scour treatment did not differ significantly for treatment by week, nor for the duration of the trial.

Key Words: arginine, calves, health

181 Changes in cortisol levels with alternating access to rotating cow brushes. R. A. Black*[1], M. R. P. Elmore[2], D. L. Ray[1], A. B. Klingenfus[3], B. L. Klingenfus[3], J. D. Clark[1], and J. M. Bewley[1], [1]*University of Kentucky, Lexington,* [2]*University of Illinois, Urbana,* [3]*Harvest Home Dairy, Crestwood, KY.*

Rotating cow brushes are an environmental enrichment device for dairy cows that may satisfy grooming behavior needs. The objective of this study was to quantify changes in cortisol with alternating access to rotating cow brushes. Twenty lactating (2 groups of 10) Holstein cows were provided alternating access to a rotating cow brush (Lely Luna, Maasluis, the Netherlands) in a crossover experiment at the University of Kentucky Coldstream Dairy. Addition or removal of the brush occurred on d 0, 10, 20, 30, 40, and 50. Blood samples were collected on study days −1, 1, 5, 9, 11, 15, 19, 21, 25, 29, 31, 35, 39, 41, 45, 49, 51, 55, and 59 to establish an immediate change, short-term change, and a baseline for the alternating brush access. Samples were collected between 0800 and 0900h in the freestall, feedbunk, or holding pen with minimal added stress. Locomotion scores (Sprecher, 1997; 1 = normal, 5 = severely lame) were evaluated by the lead author. The MIXED procedure of SAS (Cary, NC) was used to assess the effect of sample day, brush access (with or without), group (1 or 2), locomotion score, and their interactions on cortisol level. Cortisol levels were normalized using a natural log-transformation. All interactions were tested using backward elimination ($P < 0.05$). No difference ($P > 0.05$) in cortisol between group 1 (0.32 ± 0.10 μg/mL) and group 2 (0.40 ± 0.10 μg/mL) was observed. Cortisol was not altered by changing brush access (0.40 ± 0.10 vs. 0.32 ± 0.09 μg/mL with and without brush access, respectively, $P > 0.05$). Cortisol was lower in group 1 (0.24 ± 0.13 μg/mL) than in group 2 (0.43 ± 0.13 μg/mL) when access to the brush was restricted; however, no difference in cortisol was observed when brush access was permitted (0.44 ± 0.14 μg/mL vs. 0.37 ± 0.14 μg/mL, $P > 0.05$). A brush access × group interaction was observed ($P < 0.05$) with higher cortisol for group 1 (0.24 ± 0.13 μg/mL) than group 2 (0.43 ± 0.13 μg/mL) when brush use was restricted and no differences in cortisol when brush use was permitted (0.44 ± 0.14 and 0.37 ± 0.13 μg/mL for groups 1 and 2, respectively). Other behavioral and physiological effects of rotating cow brush use should be examined.

Key Words: rotating cow brush, cortisol, stress

ADSA-SAD Undergraduate Competition: Dairy Production

182 Glucose transporter and hypoxia-associated gene expression in the mammary gland of transition dairy cattle. C. N. Niewiadomski,* S. A. Mattmiller, and E. L. Karcher, *Michigan State University, East Lansing.*

Glucose is an important energy substrate needed by transition dairy cows postpartum to support the onset of lactation. The prioritization and regulation of glucose uptake is accomplished in part by shifts in cellular glucose transport molecules (GLUTs) within the mammary gland (Zhao and Keating, 2007). These shifts have been demonstrated in rat (Abdul et. al., 1996), mouse, bovine mammary epithelial cells (Zhao and Keating, 2007), and in bovine mammary endothelial cells (BMECs), which are responsible for transport of glucose from the blood. Additionally, increased metabolic activity of the lactating mammary gland causes a decrease in oxygen, a physiologic state referred to as hypoxia, which can also affect the mammary vasculature and potentially glucose utilization. While Zhao et al. (1996) described GLUT expression on epithelial cells, Mattmiller et al. (2010) evaluated for the first time, expression, localization, and functionality of GLUTs and hypoxic associated-genes over the transition period in bovine mammary endothelium. Significant shifts were observed in gene expression of the GLUTs and some of the hypoxia-associated genes evaluated. GLUT1, 3 and 4 were detected on cultured BMECs and shown to be functional. A better understanding of glucose uptake at the endothelial level could prove to be critical to improve glucose absorption and utilization in the mammary gland.

Key Words: GLUT, hypoxia, endothelium

183 Challenges and inconsistencies associated with goat somatic cell counts. K. M. Wolf* and J. M. Bewley, *University of Kentucky, Lexington.*

Goat somatic cell counts (SCC) are considerably higher than cow SCC, which presents a troubling issue for dairy goat producers. Most states have adjusted SCC regulations for goats to allow for this discrepancy. However, because high SCC are typically an indication of an intramammary infection caused by bacteria, elevated goat SCC still present challenges. An increased understanding of the factors affecting SCC and physiological differences between does and cows is needed. Nonpathogenic factors known to contribute to SCC in both species include stage of lactation, animal age, and milking frequency. Goats have several unique characteristics that contribute to elevated SCC. First, unlike cows, most does are seasonal breeders, with estrus occurring only a few months each year. Second, over 65% of the goat population produces antibodies for the caprine arthritis encephalitis (CAE) virus. A primary symptom of CAE is the presence of interstitial mastitis. Additionally, production of antibodies may be correlated with higher SCC, regardless of the presence of an actual infection. A 1997 study involving 1,799 goats from 66 herds demonstrated that first-lactation CAE-negative does had higher SCC than first-lactation CAE-positive does. SCC for CAE-positive does increased significantly through subsequent lactations, and SCC for CAE-negative does did not increase. Another significant difference between goats and cows is in the actual mammary gland physiology. In goats, milk is produced via apocrine secretion. In this type of secretion, a cytoplasmic fragment of the secreting cell is released with the milk fat. Each cell fragment may contribute to a higher SCC with certain cell counting methods. To contrast this, cow milk production occurs by alveolar merocrine secretion, which does not contribute to SCC. Thus, increased goat SCC is caused by goat-specific characteristics not necessarily associated with intramammary infections caused by bacteria. While goat dairy operators should still try to minimize SCC and clinical mastitis, physiological differences may necessitate different standards for goat SCC.

Key Words: goat, somatic cell counts

184 On-farm culturing as a new management practice. A. Patch,* D. Winston, I. Mullarky, and C. Petersson-Wolfe, *Virginia Tech, Blacksburg.*

On-farm culturing (OFC) of milk, an increasingly popular management technology, uses microbiological cultures to identify mastitis-causing pathogens present in a dairy herd. Pathogen identification is usually completed within 24 to 28 h of sampling. Researchers evaluated 2 types of OFC, the University of Minnesota Tri-plate and the 3M Petrifilm; the practicality of materials needed, as well as sensitivity, specificity, and ability to interpret results was examined. This experiment evaluated the ability of 3M petrifilm to correctly identify *Staphylococcus aureus*, with the addition of the Staph express disk (STX disk) to verify the presence of the pathogen. The University of Minnesota Tri-plate was used to identify *Streptococcus* spp. and *S. aureus*. The sensitivity and specificity of the Tri-plate for the classification of *S. aureus* were 97.9% and 81.8%, respectively. The classification of *Streptococcus* spp. using the Tri-plate yielded a sensitivity and specificity of 92.6% and 89.5%, respectively. The addition of the STX disk on the Petrifilm improved the specificity of *S. aureus* detection from 76.1% to 93.1%. In contrast the sensitivity was 97.4% without the use of the STX disk and 92.1% with the addition of the STX disk. Based on the high sensitivity and specificity values of the Petrifilm system with the STX disk and the Tri-plate system to identify *S. aureus* and the Tri-plate system to identify *Streptococcus* spp. both systems are appropriate tools to identify common gram-positive mastitis-causing pathogens in milk. Using OFC to identify cows with mastitis caused by *S. aureus* and *Streptococcus* spp. may lead to decreased use of antibiotics.

Key Words: culturing, mastitis, pathogen

185 New approaches to combat milk fat depression. J. M. Risser* and D. R. Olver, *Pennsylvania State University, University Park.*

Diet-induced milk fat depression (MFD) has been observed for well over a century. MFD is characterized by a drastic decrease in milk fat yield with little to no change in milk production or other milk components. MFD often results from diets supplemented with high levels of oil, especially those derived from plants or fish, or those containing highly fermentable feeds. According to a study at Michigan State University, highly fermentable diets may decrease intake and fiber digestibility and lead to synthesis of bioactive trans fatty acids in the rumen that are known to reduce milk fat synthesis. However, highly fermentable diets are important to maximize energy intake and milk production. With rising input costs, dairy producers require new ways to maximize milk production while ensuring high yield of components. Recent developments have pointed to modifiers of the rumen environment to combat MFD even when feeding rapidly fermentable and high concentrate diets. One example of a rumen modifying additive is yeast culture. Michigan

State researchers found that yeast culture supplementation may assist in the prevention of MFD when transitioning to a diet containing highly fermentable starch. Yeast cultures are responsible for stabilizing rumen fermentation during diet shifts by increasing the population of lactate-utilizing microorganisms, thus maintaining an environment for normal fermentation. In addition to yeast culture supplementation, dietary molasses also has a role as a rumen modifier. Through research at Kansas State, molasses has been shown to change fatty acid biohydrogenation pathways in the rumen, and reduce the synthesis of bioactive fatty acids that cause MFD. These additives, among other rumen modifiers, can lead to more efficient dairy cows by stabilizing rumen fermentation while simultaneously increasing profit for the producer.

Key Words: milk fat depression, rumen modifiers

186 Monitoring the composition of waste milk fed to dairy calves. E. L. Stayduhar,* K. D. Stevens, M. L. Eastridge, and K. M. Daniels, *The Ohio State University, Columbus.*

Profitability of dairy farms is influenced by several characteristics, one of which is calf management. The growth and health of replacement animals influences their future milk yield. With the increasing size of dairy farms and the aim to reduce costs of raising heifers, many farms are opting to pasteurize waste milk for feeding to calves. With this shift from feeding milk replacer to pasteurized waste milk, the cost of pasteurizers has decreased. However, when using this feeding practice, the producer needs to know the composition of the milk being fed. The proportion of milk from fresh cows and cows treated for mastitis (often lower in solids than from healthy cows) will affect the composition of the waste milk. Adequate concentrations of fat and protein (or total solids) in the milk is vital for sound health and expected growth rates for the calves. Simple tests, such as pH and ethanol coagulation, can be easily used, but they only indicate whether or not the waste milk has spoiled. Other on-farm measurements are needed that are more reflective of milk composition. Total solids in milk can be determined using a Brix refractometer, with the Brix readings being converted to total solids using reported equations. In addition, these refractometers are inexpensive and the readings are very rapid. On-farm analytical instruments are available today for measuring the fat, protein, and other solids in milk (e.g., LactiCheck; Page and Pedersen International Ltd., Hopkinton, MA). These instruments require routine calibration, but standards for the calibration are readily available and the calibration steps are simple. Although these instruments are much more expensive than refractometers, they provide more information than just total solids and they can be used to monitor the composition of milk from individual cows (e.g., milk fat concentration for ketosis risk) and the bulk tank. Using the methods described to measure total solids or fat and protein concentrations allows the producer to fortify waste milk with the appropriate amount of milk replacer to increase total solids to the desired level. Continued improvement in on-farm measurement of the composition of waste milk fed to calves will improve calf performance and increase farm profitability.

Key Words: waste milk, calves, milk composition

187 Early pregnancy detection methods in reproductive management. C. E. Burke* and C. C. Williams, *Louisiana State University, Baton Rouge.*

In the cattle industry, pregnancy diagnosis is an important tool in measuring the success of reproductive management. A cow that remains open longer than desired will ultimately cost the producer, whether it is money spent on synchronization and breeding materials or simply the cost to keep her in the herd. To reduce economic losses, producers rely on early pregnancy detection to better manage the reproductive efficiency of the herd. Today many producers use synchronization programs to aid in the breeding process. The hormone prostaglandin is given to an animal to regress its corpus luteum (CL) and cause her to cycle, setting her up for breeding. When a cow is pregnant her CL will remain throughout her pregnancy, preventing her from cycling. One of the many disadvantages of not knowing pregnancy status is mistakenly causing the cow to abort by treating her with prostaglandins as if she were open. The 2 most common methods of pregnancy detection are rectal palpation and ultrasonography, both of which are very invasive procedures. Although these methods are used extensively throughout the industry, there is a new method providing a friendly, cost effective way to detect early pregnancy. Blood pregnancy tests such as BioPRYN simply test for pregnancy specific protein B in the blood rather than relying on invasive practices. BioPRYN uses ELISA technology that requires only a sample of blood from the cow under question. At a price of less than $3 per test, BioPRYN is a cost effective alternative that does not require a trained technician. With labs throughout the United States and internationally, a producer can send in samples and have their results within 27 h of assay setup. Cows must be 90 d postpartum and 30 d post breeding to get an accurate reading. BioPRYN offers up to 95% specificity on pregnant cows and 99% sensitivity on open cows. Blood testing for pregnancy is the next step in improving the reproductive management systems in cattle herds. The earlier a pregnant or open status can be confirmed, the sooner the producer can take the necessary steps to safely and properly manage his herd.

Key Words: pregnancy detection, reproductive management, blood test

188 Anaerobic digestion and the benefits to dairy farmers. S. K. Luther,* A. C. Wilkie, and M. E. Sowerby, *University of Florida, Gainesville.*

Anaerobic digestion has the potential to be a large part of the solution for shrinking our fossil fuel consumption. Anaerobic digestion is a biological process that turns waste into fuel and resources. It is essentially the breakdown of organic materials using a mixed consortium of bacteria in the absence of oxygen. Anaerobic digestion is a full circle process that captures the remaining energy in feedstocks that are currently considered waste and gives back usable goods. On the farm, anaerobic digestion has the ability to produce combustible methane gas and efficient fertilizer. The methane produced is collected and when used eliminates the carbon dioxide that would have been released from the fossil fuels that the methane can replace. With all the hype over going "green," farmers need to be doing all they can to improve their public image and conserve the environment for future growers. As businessmen, dairy farmers can turn their digester output into renewable biofuel, carbon credits, and fertilizer. Anaerobic digestion is a very effective waste management practice on farms that already have manure collection systems in place. It helps to reduce odors normally associated with spray fields and lower pathogen levels in the animal manure that is digested. Anaerobic digestion inactivates "weed" seeds and conserves nutrients, making the liquid effluent a valuable biofertilizer. Dairy farmers must consider herd size, current waste management methods, and possible farm expansion when choosing and sizing a digester. There are 4 main types of digesters, which are each suitable for different manure management methods. For example, one type of digester was specifically designed for the flushing systems used in dairy freestall barns. Anaerobic digestion is a technology that will further contribute to our sustainability efforts while improving the relationship between agriculturalists and consumers. The process captures the energy in feedstocks that are currently considered waste and delivers usable goods.

Key Words: anaerobic digestion, manure management, digester designs

189 Supplemental melatonin: A potential strategy for maintaining mammary health in dairy cattle.

M. M. Palmer,* D. N. Williams, and J. L. Fain, *Clemson University, Clemson, SC.*

Increased somatic cell count (SCC), associated with mastitic infections in dairy cattle can have detrimental effects on animal welfare, reproduction, milk quality and overall milk production. Novel investigations have established melatonin as a potential potent regulator of SCC in dairy cattle. Seasonal response patterns in estrous cycles of small ruminants led to the increased use of melatonin implants to regulate incidences of anestrus during periods of increased day length. Consequently, producers noticed a reduction in SCC in both sheep and goats. Previous work indicates that melatonin acts to protect cells and tissues against damage caused by oxidation. During the inflammatory reaction associated with mastitis, there is damage that occurs to the mammary epithelium. The somatic cell composition changes from a majority macrophage concentration to increasing levels of polymorphonuclear neutrophils (PMN) moving from the blood stream to congregate in the mammary gland during times of infection. These PMNs then engulf the invading pathogen through phagocytosis. During this process, the neutrophils release reactive oxygen species (ROS) which defend against invading pathogens but also trigger epithelial cell damage. Melatonin has demonstrated abilities to scavenge hydroxyl radical, a noted ROS. Serving in an antioxidant capacity, melatonin may be used to supplement the animal's endogenous mechanisms, allowing for faster rate of recovery with reduced total tissue damage. With potential decrease in legal limit SCC, faster recovery rates from mastitis could decrease bulk tank SCC. An even larger impact may be the potential for melatonin to abrogate decreased milk production associated with increased SCC through reduction in tissue damage. Continuous investigation of melatonin and other antioxidents may allow for more insight into their role in maintaining mammary health.

Key Words: melatonin, mastitis, dairy

ADSA Southern Section Symposium: Meeting the Nutrient Requirements of Dairy Cattle During Heat Stress

190 Heat stress in young dairy calves. C. C. Williams,* *Louisiana State University AgCenter, Baton Rouge.*

The initial 2 mo of a calf's life directly influence the quality and condition of its future growth and development. During this period, stress is detrimental to the proper growth of the calf. One common type of stress of particular concern to southern dairy producers is heat stress. Heat stress occurs when any combination of environmental factors causes the relative temperature of the environment to be greater than the calf's thermoneutral zone. In the southern United States, heat stress is particularly common due to uncontrollable environmental factors such as the temperature-humidity index (THI). As a result of an elevated THI, the calf's respiration, internal temperature, and water intake will increase, and dry matter intake, average daily gain, fecal score, and feed efficiency will decrease. These homeostatic alterations disrupt calf development and prohibit the achievement of full production potential. In addition, heat stress can cause a variety of problems on a molecular level. Heat stress causes the adrenal gland to produce the steroid cortisol; in high enough quantities, cortisol can render a calf incapable of absorbing important immunoglobulins through its cellular membranes. Heat stress can also lead to dehydration, which can cause blood urea nitrogen levels to rise. This is a direct result of poor renal function. Dehydration and poor renal function, left uncorrected, are associated with a high mortality rate among calves less than 2 mo old. Limited research has been conducted to determine the effect of heat stress in neonatal calf health and performance. However, studies that been conducted indicate that providing supplemental shade to calves housed in hutches can reduce the severity of heat stress.

Key Words: heat stress, dairy calves

191 Managing heat stress in dairy heifers. R. E. James* and S. Neal, *Department of Dairy Science, Virginia Tech, Blacksburg.*

Limited research indicates that heat stress affects dairy heifers through depressions in ration dry matter intake, nutrient utilization, reproductive function and colostrum production although not to the same degree as milking animals. Given this relationship, the recently weaned heifer, the breeding age heifer and close springing heifer will benefit most from reductions in heat stress. Weaned heifers are especially susceptible to reduced intake as they are adjusting to dry feed and group housing systems. Italian workers found that exposure of 10-mo-old heifers to a THI of > 84 resulted in depressed intake and increased water intake and rectal temperature. However, they also noted that heifers adjusted to longer term heat stress. Virginia Tech researchers found that the influence of temperature on intake was relatively minor as heifers delayed consumption of the diet until the cooler hours of the evening. The breeding age heifer expresses impaired growth and function of the dominant follicle when exposed to 33°C at 50% relative humidity as compared with 21°C at 60% relative humidity. Smaller follicles were associated with decreased serum estradiol concentrations, delayed luteolysis and impaired reproductive success. During the prepartum period, exposure of gravid heifers to a THI of 82 as compared with one of 65 resulted in lower concentrations of IgG, IgA, total protein, lactalbumin, fat and lactose in the colostrum. Management should focus on the critical ages noted. First priority should be given to provision of adequate supplies of water. Water intake is highly correlated with feed intake and is especially important during heat stress. Research is not available to estimate the economic return from use of cooling fans and sprinkler systems. Given the critical influence of reproductive function on timely calving and the production of IgG rich colostrum, facilities featuring use of fans, high and open side walls and open ridge vents will facilitate animal cooling for these animals. Finally, it is apparent that increasing nutrient density of the ration will maintain nutrient intake during heat stress.

Key Words: heifers, heat, stress

192 Impact of management on feeding dairy cows in heat stress. G. Bethard,* *Dairy Records Management Systems, Raleigh, NC.*

Most modern and productive dairy cows experience heat stress of some kind throughout the year. Heat stress degrades short-term financial performance, largely through the direct loss of milk production and milk components. Milk volume declines are obvious and noticeable; less noticeable and potentially more costly are milk component and quality premium losses. Other short-term losses include herd health issues and associated herd losses. Long-term costs are escalated by poor reproductive performance. Much of the economic cost is directly related to the decline in dry matter intake and change in feeding behavior. Lower dry matter intake can lead to lower milk production and body condition loss; altered feeding behavior can lead to slug feeding and perceived rumen health issues. Much is known about the physiological consequences of heat stress. Much less is known about nutritional approaches to alleviate these consequences. Nutritional strategies implemented in the field include altering mineral levels, cation-anion balance, buffering capacity, or fiber digestibility. None are widely accepted in the field, and implementation of strategies differs by region. Management at the dairy typically provides the best opportunity to prevent the decline in dry matter intake. Heat abatement strategies are obvious and recognized widely in the dairy industry. Cow comfort, over-crowding, and cow resting time also have an effect and heightened during periods of heat stress. Preserving and managing forages to extend bunk life and managing feedbunks is crucial to minimizing the declines in dry matter intake.

Key Words: heat stress, dairy, feeding

193 Lactating cows and changes in dry matter intake during heat stress. J. W. West,* *University of Georgia, Tifton.*

Exposure of high yielding dairy cows to elevated ambient temperature and relative humidity impairs the cow's ability to dissipate body heat, leading to increased internal heat load. The mechanisms to dissipate excess body heat (conduction, convection, radiation, and evaporation) are compromised by hot, humid conditions, leading to physiologic and metabolic responses that reduce DMI and milk yield. Declining DMI during thermal stress may be a protective mechanism to limit metabolic heat and is credited with a concomitant reduction in milk yield. Work indicates that reduced DM and nutrient intake is only partially responsible for declining milk yield and that hormonal shifts alter energy metabolism, further reducing yield. Slower rate of passage in the digestive tract occurs in hot weather and can limit intake, though nutrient digestibility may improve. Subclinical acidosis often limits DMI because of very high energy diets fed in an attempt to maintain energy intake at a time when blood buffering is reduced by hyperventilation. The reduced DMI that occurs during heat stress is a complex response to environmental stressors and the steps to ameliorate the impact are multifaceted. Most important is to reduce exposure to radiant energy by shading and to enhance body heat transfer to the environment via cooling. Greater air movement with fans and addition of water in the form of sprinklers or misters are keys to enhancing evaporative cooling for the cow. Once environmental modifications are in place, dietary adjustments to enhance DM or nutrient intake can be implemented. Dietary buffers and rumen modifiers including yeast culture and fungal additives stabilize the rumen environment and may reduce body temperature. Attention to forage quality and particle size is crucial during hot weather and caution should be used when dietary fiber is reduced in the pursuit of greater dietary nutrient density. Continued genetic selection for greater DMI and milk yield presents challenges for the manager who must balance the exceptional metabolic potential of the modern dairy cow with the need to eliminate excess metabolic heat produced in a challenging climatic environment.

Key Words: dairy, heat stress, DMI

194 Use of fat and other feed additives in heat-stressed cattle.

L. H. Baumgard*[1], A. Nayeri[1], M. V. Sanz-Fernandez[1], J. S. Johnson[1], D. B. Snider[1], D. P. Bu[2], and R. P. Rhoads[3], [1]*Iowa State University, Ames,* [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agriculture Sciences, Beijing, China,* [3]*Virginia Polytechnic Institute and State University, Blacksburg.*

Heat stress (HS) negatively affects parameters associated with profitable milk production. Implementing HS-abatement strategies (barn construction, fans, evaporative cooling, etc.) is crucial to minimize fiscal losses and quantitatively more important at maintaining milk production than potential nutritional changes. However, the effects of nutritional management are not trivial and are key components to efficient production and optimal cow-health during the summer months. Obviously the most vital nutrient to consider is water (water intake can more than double during HS) and ensuring adequate access to clean, fresh water is critical. HS reduces rumen pH and thus nutritional approaches aimed at maintaining rumen health are important. Potassium requirements increase during HS as ruminants utilize potassium to sweat, therefore a dietary potassium based rumen buffer may have dual benefits. A widely held dogma is that supplementing dietary fat is an effective tactic during HS stemming from theoretical calculations indicating that the heat increment of feeding is much lower for lipids (especially compared with roughages). HS markedly alters post-absorptive metabolism and this is, in part, characterized by increased systemic glucose utilization so dietary strategies aimed at safely increasing gluconeogenic precursors (i.e., monensin) are suggested. HS causes “leaky gut” in a variety of species and although not described in ruminants, we suspect it plays a key role in the etiology of HS-induced poor performance and mortality in dairy cows. Consequently, dietary strategies aimed at strengthening intestinal integrity (rehydration therapies, betaine, zinc, etc.) show promise and need to be thoroughly evaluated. It is unknown whether protein or energy requirements (and this is especially true for maintenance costs) increase or decrease during HS, but this is of practical and economic importance to the dairy industry. Surprisingly, our understanding of nutrient requirements during HS is woefully insufficient, and this makes formulating nutritional strategies to mitigate summer-induced low production difficult.

Key Words: heat stress, nutrition, dietary fat

195 Feeding dairy cattle in a grazing system during heat stress.

J. K. Bernard,* *University of Georgia, Tifton.*

Dairy cattle in a grazing system are negatively affected by heat stress resulting in decreased DMI and milk yield and elevated core body temperature. The physiological and metabolic responses to heat stress that contribute to reduced DMI and milk yield will be discussed by others in this symposium. For grazing dairy cattle, heat stress alters grazing behavior as cows seek shade during the day and tend to graze more at night and early morning, reducing nutrient intake. Forage quality also tends to decline in response to heat stress, resulting in higher NDF concentrations and lower digestibility further reducing energy intake. Concurrently, maintenance requirements increase during heat stress because of panting and greater time standing as cows attempt to reduce body temperature. Diets must be adjusted to compensate for reduced DMI to meet higher maintenance requirements and maintain milk yield. Effective strategies include feeding additional energy concentrates, high quality forage, or a partial TMR to maintain DMI and nutrient intake. Provision of shade and soaking plus supplemental high quality forage are reported to maintain milk yield through improved DMI while reducing core body temperature. Supplemental energy may be provided by concentrates or fat. The quantity of starch should be limited to avoid subclinical acidosis and the quantity of supplemental fat should be limited to avoid decreased fiber digestibility or reduced DMI. Dietary buffers to provide additional Na, K, and Mg should be increased to replenish losses incurred through increased panting and sweating and provide additional buffering capacity in the rumen. In addition to dietary changes, water consumption increases in response to heat stress and provisions must be made to provide adequate water.

Key Words: heat stress, grazing, feeding

ADSA-SAD Undergraduate Competition: Original Research

196 Monitoring the incidence of ketosis in fresh cows using milk composition, urine ketones, and milk ketones. K. D. Stevens,* E. L. Stayduhar, M. L. Eastridge, and K. M. Daniels, *The Ohio State University, Columbus.*

Fresh cows have a high risk for ketosis within the first 30 DIM due to low DM intake and the rapid mobilization of fat after parturition. Early detection of ketosis, including subclinical ketosis, can allow for earlier intervention and minimize the loss of milk production. Detection of ketosis is commonly done in the field with measuring ketones in urine or milk, but concentration of fat in milk also may be useful for detection of ketosis. A 700-cow Holstein farm in Ohio was used for collecting samples at 7 and 14 DIM (n = 204 cows). Composite milk samples were collected using a BouMatic (Madison, WI) in-line sampler and right-front (RF) quarter strip samples were collected. Both samples were analyzed for milk components at the farm using a LactiCheck (LIC; Page and Pedersen International Ltd., Hopkinton, MA), with weekly calibration using samples from Eastern Laboratory Services (Medina, OH). Composite milk samples also were sent to DHI Cooperative, Inc. (Columbus, OH) for analysis of milk components. Keto-Test strips (Elanco, Greenfield, IN) were used to measure ketones (β-hydroxybutyrate) in milk stripped from the RF quarter, and urine ketones (acetoacetate) were measured with KetoStix (Bayer Healthcare LLC, Monheim, Germany). The average fat concentration from LIC composite samples was 5.36 ± 2.05% and 5.15 ± 1.90% from DHI, with the RF strippings having a lower milk fat (3.17 ± 1.88%). Average milk ketone concentration was 0.55 ± 0.98 mg/dL, and urine ketone concentration was 4.41 ± 15.4 mg/dL; however, the incidence of clinical ketosis was relatively low in the herd (3.4% based on urine ketones ≥40 mg/dl or 6.9% based on milk ketones ≥2.0 mg/dL). The correlation coefficient for LIC and DHI composites was 0.70 ($P < 0.0001$), and the correlations between the composites and the RF samples were similar for both methods of analysis (0.30; $P < 0.0001$). The correlation of the RF milk fat percentage and the milk and urine ketones also was similar (0.22; $P < 0.001$). The changes in milk fat concentrations from 7 to 14 DIM were similar for LIC and DHI composites and the RF samples (−0.63, −0.88, and −0.77, respectively). Monitoring milk fat concentration of individual cows holds promise for the diagnosis of ketosis, and it appears that either composite samples or strippings can be used to establish a baseline from which to identify cows with elevated milk fat concentrations.

Key Words: ketosis, urine ketones, milk ketones

197 Effect of a liquid acid footbath solution containing a cationic surfactant on digital dermatitis in dairy cattle. T. A. Reiter*[1], B. A. Beavers[2], F. R. Moreira[3], K. J. McQueery[1], C. L. Wood[1], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]Beavers Hoofcare Service LLC, Lebanon, KY, [3]GEA Farm Technologies, Naperville, IL.*

Dairy producers use many different footbath solutions for control of digital dermatitis (DD); however, many of these compounds have adverse effects on cows, handlers, or the environment. The objective of this research, consisting of 3 studies, was to examine the effects of a liquid acid footbath solution containing a cationic surfactant (PediCuRx Prevent A (PED), GEA Farm Technologies, Naperville, IL) on digital dermatitis size (DDS) and pain (DDP). For each study, treatment cows were exposed to a 2% PED solution 3X per wk. The same observer evaluated DDS and DDP scores using 0 to 3 scales with 0 assigned to hooves with no DD. For DDS, scores were assigned as follows: 0 = no DD; 1 = <20 mm DD; 2 = ~20 mm DD; and 3 = >20 mm DD. The pain caused by wart presence was determined by the cow's reaction to either water or finger pressure on the hoof. For DDP, scores were assigned as follows: 0 = no pain; 1 = minimal pain; 2 = moderate pain; and 3 = severe pain. Study 1 included 53 cows in a commercial dairy that were exposed to PED in a footbath for 4 mo. Study 2 included 250 cows in 2 commercial dairy farms in a 4-mo experiment comparing PED to a 10% copper sulfate (CS) solution. Study 3 was conducted at the University of Kentucky Coldstream Dairy with 53 cows assigned for 4 mo to either a PED treatment or a 5% CS control. The MIXED procedure of SAS® (Cary, NC) was used to assess factors affecting DDS and DDP. In study 1, mean responses for DDS and DDP were higher ($P < 0.05$) before starting the study (0.37 and 0.39 for DDS and DDP, respectively) than for the 3 test months after the study started (December: 0.12 and 0.10; January: 0.09 and 0.08; February: 0.00 and 0.00 for DDS and DDP, respectively). In study 2, mean responses for DDS and DDP were not different ($P < 0.05$) during PED periods and CS periods (PED: 0.42 and 0.40; CS: 0.40 and 0.39 for DDS and DDP, respectively). In study 3, mean responses for DDS and DDP were not different ($P < 0.05$) between treatments (PED: 0.28 and 0.28; CS: 0.21 and 0.25 for DDS and DDP, respectively). Control of DD was similar for PED and CS footbath solutions.

Key Words: digital dermatitis, footbath

198 Establishment of antibiotic resistance genes in the gut of pre-weaned dairy calves. L. Woloohojian,* E. Hurley, P. Ray, B. Willing, H. Littier, A. Pruden, and K. Knowlton, *Virginia Tech, Blacksburg.*

Antibiotic resistance genes (ARG) are caused by mutations found on specific genes that enable bacteria to survive exposure to antibiotics. ARG are readily transferred horizontally and longitudinally. While ARG have been found in the gut and feces of pre-weaned calves little data are available on the succession of ARG in the early weeks. The objective was to observe the establishment of ARG in fecal bacteria of dairy calves from birth to weaning. Six heifer calves were fed a medicated milk replacer (28% CP, 20% fat, containing neomycin sulfate and oxytetracycline hydrochloride each fed at 10 mg/calf/d) and free choice water and calf starter (22% CP) until weaning at d 42. Fecal grab samples were collected using sterile gloves on d 1, 3, 5, 7, 14, 21, 28, 35 and 42 of age. Colostrum, drinking water, milk replacer, and grain samples were collected to assess possible sources of inoculation with ARG-carrying bacteria. All samples were immediately frozen (−20°C) until DNA extraction. Quantitative polymerase chain reaction was performed to quantify 16S rRNA genes and *tet*W and *sul*1 ARG encoding resistance to tetracyclines and sulfonamides, respectively. Changes in absolute and relative abundance of the ARG over time were analyzed using PROC GLIMMIX procedure in SAS. Both genes were present in the feces of 1-d old calves and the abundance of 16S rRNA (log gene copies/g wet feces) did not change during the 42 d of the study. Similarly, relative abundance of *tet*W and *sul*1 (gene copies/16S rRNA) remained constant over the study period. This study provides new insight into the colonization of calf gut flora with ARGs in the early weeks.

Key Words: antibiotic resistance gene, feces, dairy calf

199 Effects of supplementing propionibacteria in lactation dairy diets on ruminal fermentation in continuous cultures. K. A. Dolecheck*[1], J. M. Vera[1], A. J. Young[1], A. H. Smith[2], V. Fellner[3], and J.-S. Eun[1], [1]*Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan,* [2]*Danisco USA Inc., Waukesha, WI,* [3]*Department of Animal Science, North Carolina State University, Raleigh.*

The aim of the present study was to assess characteristics of in vitro ruminal fermentation when mixed cultures were offered lactation dairy diets supplemented with the direct-fed microorganism, *Propionibacterium* P63 in continuous cultures. The design of the experiment was a 2 × 2 factorial with 4 replications. Diets based on corn silage and alfalfa hay as the forage sources were formulated; high forage (HF) or low forage (LF) diet with a forage-to-concentrate ratio of 60:40 or 40:60 (DM basis), respectively, was combined without or with P63 to form 4 treatments: HF without P63, HF with P63, LF without P63, and LF with P63. Approximately 700 mL of the strained ruminal fluid obtained from 2 lactating dairy cows was inoculated into each of 4 fermentors with a continuous dual-flow system. The cultures were allowed 6 d of adaptation to the treatments followed by 3 d of sampling and data collection. Feed totaling 40.0 g of DM was added to each fermentor daily in equal portions delivered at 0700 and 1900 h. The P63 treatments received 7×10^8 cfu of P63/fermentor/feeding. Data were analyzed with a model that included the effects of level of forage in the diet (high vs. low forage), P63 (without vs. with P63), and the interaction between level of forage and P63. Supplementing P63 decreased culture pH ($P = 0.05$) in the LF diet, but not in the HF diet. Feeding the LF diet increased total VFA concentration compared with the HF diet ($P = 0.01$), and supplementing P63 increased total VFA concentration regardless of level of forage in the diet ($P < 0.01$). Molar concentrations and proportions of acetate and propionate did not differ in response to supplementing P63 in the HF and the LF diet. However, molar concentration and proportion of butyrate increased due to P63 supplementation ($P < 0.05$) only in the LF diet, resulting in interactions between level of forage and P63 supplementation ($P < 0.08$). Overall results in this in vitro study indicate that P63 supplementation enhanced ruminal fermentation by increasing VFA production, but its effects on continuous culture fermentation differed between the HF and the LF diet.

Key Words: propionibacteria, ruminal fermentation, continuous cultures

200 Effect of calf starter form and milk source on growth and intake of dairy calves. S. A. McCullough,* T. S. Dennis, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

A combination of texturized calf starter and milk replacer are commonly used feeds for dairy calves, but alternative feeds may offer improved growth and development. The objective of this study was to determine the effects of different forms of calf starter and sources of milk on growth, dry matter intake, and feed efficiency of dairy calves on a commercial dairy. In this randomized complete block design with a 2 × 2 factorial arrangement of treatments, 120 Holstein heifers (BW = 39.6 ± 5.4 kg) were blocked in groups of 4 by hutch type and birth date. Heifers were assigned to either pasteurized whole milk (WM) or milk replacer (MR) and either texturized (T) or pelleted (P) starter. The MR fed was 24% CP and 18% fat. Samples of WM were collected at each feeding and analyzed for total solids, protein and fat. Calves were allowed ad libitum access to starter and received 3.8 L/d of milk for 14 d, 6.7 L/d from d 15 to 21, and 7.6 L/d from d 22 to 56. Calves were weaned on d 63. Calves were weighed at birth and measured every 2 wk for BW, hip and withers height, body length, and heart girth circumference (HGC) for 10 wk. Feed and refusal samples were collected weekly and starter intake was measured every 2 wk. Data were analyzed as repeated measures using the Proc Mixed procedure of SAS. Heifers fed WM were 4.3 kg heavier at wk 10 than heifers fed MR ($P < 0.01$). Heifers fed WM also had greater ADG than heifers fed MR (0.76 and 0.70 kg/d, respectively; $P < 0.01$). Additionally, heifers fed WM and T or MR and T had greater ADG than heifers fed MR and P (0.76, 0.72, and 0.68 kg/d, respectively; $P < 0.01$). Dry matter intake of starter did not differ between milk or starter source, resulting in heifers fed WM having improved feed:gain compared with heifers fed MR (0.65 and 0.78 kg/kg, respectively; $P < 0.05$). Heifers fed WM and P were taller at the hip than heifers fed MR and P ($P < 0.05$). Withers height and HGC were greater ($P < 0.04$) and hip height tended ($P < 0.09$) to be greater for heifers fed WM compared with MR. However, skeletal measurements were similar between starter sources. Feeding heifers WM as compared with MR resulted in improved body weight and ADG.

Key Words: calf starter, dairy calf, milk

201 Effect of a mannanoligosaccharide (Bio-Mos) on health and growth of Holstein and Jersey calves. L. R. Such,* G. D. Hobgood, B. A. Hopkins, and S. Davidson, *North Carolina State University, Raleigh.*

Forty-two neonatal Holstein (n = 24) and Jersey (n = 18) calves were used to examine the effects of adding Bio-Mos, a mannanoligosaccharide, to the milk, on health and growth. Calves were assigned at birth to treatments in a completely randomized block design: 1). Seven grams of Bio-Mos or 2). 0 g of Bio-Mos (control) added to the whole milk diet. Calves were fed colostrum after birth and housed in individual calf hutches through 63 d. Starter mix was fed from d 1 through 56. Data that included repeated measures were analyzed using the mixed procedure (PROC MIXED) of SAS, and data that included one value per calf, such as ADG and feed efficiency (FE), were analyzed using the general linear models procedure (PROC GLM) of SAS. There were no differences in body weight, average daily gain, starter DMI, hip height, hip width, wither height or FE between calves fed Bio-Mos and control calves ($P > 0.05$). Preweaned Holstein calves had greater ADG (0.71 kg/d) and starter DMI (0.67 kg/d) than Jersey calves (0.46 kg/d and 0.41 kg/d, respectively), but there were no differences ($P = 0.26$) in FE between the breeds (1.2 kg/kg in Holstein vs. 1.5 kg/kg in Jersey). Feeding 7 g/d Bio-Mos in the milk did not improve growth or health of pre-weaned Holstein and Jersey calves.

Key Words: calf, Holstein, Jersey

202 Predicting early life illness in Holstein heifer calves. C. A. Bellmund,* K. C. McRoberts, and D. J. R. Cherney, *Cornell University, Ithaca, NY.*

Practical technological tools such as infrared surface temperature and calf feeder intake reports may predict early life health problems in Holstein heifer calves. Early prediction of illnesses including bovine virus diarrhea virus (BVDV) and bovine respiratory disease can allow effective treatment and preventative individual isolation. Calves (n = 50) born between April and July 2011 were selected at birth from the dairy herd at Cornell University's Teaching and Research Dairy Unit, and tracked the first 30 d. Non-invasive infrared surface temperatures were recorded daily using a Fluke 561 hand-held infrared thermometer at 3 locations: cheek, ribs, and rump. Hair color was also noted at these locations. Core temperatures were measured weekly using a digital rectal thermometer. Drinking speed and intake rate of milk replacer were recorded using an automatic feeder. Daily air temperature and relative humidity readings were taken at calf housing locations. Calf illness was assessed based on observation of either BVDV or bovine respiratory disease and coded into multiple parameters including daily calf illness and severity. Nominal logistic model development was undertaken using JMP Pro 9.0.2. Parameters significantly predicting daily illness status included: observation date, core temperature, cheek surface temperature, and intake rate, Coefficient of determination was low (<0.15) for all models and goodness of fit was poor. Hair color recorded at surface temperature locations appeared to be higher for black-haired calves than white-haired calves, especially under sunny, high air temperature conditions. Infrared thermometry, core temperature and intake rate can be used to predict calf illness status; however, efficacy of prediction is poor and its utility as a management tool is minimal. Additional environmental and epidemiological factors not considered in this study are likely contributing more to calf disease status than those recorded. Calves observed in this study will continue to be tracked for age at first calving, milk yield, and lifetime productivity, which could be influenced by early life health status.

Key Words: calf health, illness prediction, bovine virus diarrhea virus

203 Who's listening? The preferred means of communication for Tennessee dairy producers.

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The dairy industry encompasses a wide range of individuals, from those involved with on-farm production to allied professionals in diverse settings, and requires efficient and effective communication to disseminate information. The objective of this study was to investigate how Tennessee dairy producers currently receive information, how they prefer to receive new knowledge, and how they communicate with their employees. To address this objective, 452 written surveys (with an online option) consisting of 28 questions were mailed to dairy farms with a current grade A milk permit as of September 2011. Survey responses were quantified using the FREQ procedure in SAS. Unanswered questions were treated as missing data. There was a 30% response rate, with 130 responses returned by mail and 4 responses online. Tennessee dairy producers primarily use non-electronic forms of communication, indicating they sometimes or often rely on personal experience (97%), veterinarians (97%), and magazines (94%) to acquire new information. The internet was the least utilized with only 56% of respondents using this resource sometimes or often versus 44% that never use it. This trend was continued in their preferred means of acquiring information. Eighty percent of TN dairies had 1–4 employees. Most communicated with their employees by casual discussion (81%) or when they observed a problem (64%), whereas only 14% had formal meetings. For independent learning, 59% provided their employees with magazines, 37% would be willing to send their employees for training (with 13% unsure), and 29% would be willing to host on-farm training (with 10% unsure). The results indicate that producers use and prefer non-electronic forms of communication when acquiring new information, thus electronic mediums are not the most effective way to communicate with the majority of Tennessee producers. Communicating new information within a farm may not be efficient as it relies more on casual discussion and troubleshooting rather than structured meetings and/or trainings. This study will aid in better designing and implementing communication strategies with dairy producers, their employees, and affiliated professionals.

204 Key Words: producer, communication Incorporation of palmitic and stearic acids into plasma lipid fractions of lactating dairy cows.

S. Schmidt,* C. L. Preseault, J. E. Rico, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

Transport of fatty acids (FA) in the bloodstream is complex and involves various plasma lipid fractions including phospholipids (PL), cholesterol esters (CE), triglycerides (TG), and NEFA. Effects of dietary FA on plasma lipid fractions have not been well characterized in lactating dairy cows. The mammary gland preferentially utilizes FA from plasma TG and NEFA for milk fat synthesis, thus changes in the profile and concentration of these fractions may impact milk fat synthesis. Effects of dietary palmitic and stearic acids on the concentration and profile of plasma lipid fractions were evaluated in an experiment with a crossover arrangement of treatments. Sixteen Holstein cows (143 ± 50 DIM) were assigned to a treatment sequence; treatments were diets supplemented (2% of diet DM) with palmitic acid (PA; 99% C16:0) or stearic acid (SA; 98% C18:0). Treatment periods were 21 d with plasma samples collected every 15 h between d 17 and d 21 of each period and composited. The statistical model included the random effect of cow and the fixed effects of period, treatment, lipid fraction, and the interaction of treatment and lipid fraction. PA treatment increased MF yield by 6.2% compared with SA treatment ($P < 0.01$). The proportion of total plasma FA in each lipid fraction was not affected by treatment and averaged 50.4, 46.5, 2.3, and 0.83% for PL, CE, TG, and NEFA, respectively (all $P > 0.14$). The PA and SA treatments increased the concentration of C16:0 and C18:0 respectively in TG; for C16:0, values were 29.7 vs. 18.2, and for C18:0 they were 29.5 vs. 36.4 g/100 g FA (PA vs. SA treatment, both $P < 0.0001$). PA treatment also increased C16:0 in NEFA and PL fractions ($P < 0.0001$), but not in CE ($P = 0.24$). Likewise, the SA treatment increased C18:0 in NEFA and PL fractions ($P < 0.01$), but not in CE ($P = 0.9$). The majority of C16:0 and C18:0 were transported in PL with 73.6 vs. 71.4% of total plasma C16:0 (PA vs. SA treatment, $P = 0.08$) and 90.5 vs. 88.3% of total plasma C18:0 (PA vs. SA treatment, $P = 0.006$) within the PL fraction. Results demonstrate that the PA and SA treatments increased the concentration of C16:0 and C18:0, respectively, across plasma TG, PL, and NEFA. Treatment did not however, alter proportions of total FA across lipid fractions. Further work is required to determine if the observed increase in milk fat yield with the PA treatment was due to the increase in C16:0 in TG.

Key Words: plasma lipids, palmitic acid, stearic acid

205 Effect of temperature during drying and mechanical extrusion on soybean meal protein in situ degradability and in vitro digestibility.

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The objective of this study was to investigate the effect of drying and extruding temperature on ruminal degradability and intestinal digestibility of mechanically-extracted soybean meal (M-SBM) crude protein (CP). Whole soybeans were processed at a commercial extrusion facility with the following treatments: drying at 49°C and extruding at 149°C (HD-LE); drying at 49°C and extruding at 160°C (HD-ME); drying at 49°C and extruding at 171°C (HD-HE); drying at 27°C and extruding at 149°C (LDLE); and drying at 27°C and extruding at 160°C (LD-ME). Control was solvent-extracted SBM (S-SBM). Ruminal protein degradability was determined by incubating samples in situ for up to 24 h in the rumen of 3 lactating dairy cows. Following the in situ incubation, a portion of the undegraded meal residues were further processed to estimate intestinal CP digestibility in vitro using incubation in pepsin-hydrochloric acid solution for 48 h. Ruminally degradable (RDP) and undegradable (RUP) protein in samples were estimated based on NRC (2001) and ruminal passage rates calculated from actual intake and body weight of the cows. All M-SBM had higher RUP ($P < 0.001$) content compared with S-SBM (33% RUP), which could be partially explained by the slightly larger geometric mean diameter of the former meals (769 vs. 759 µm, $P = 0.01$). Increasing the extruder temperature

increased ($P < 0.001$) RUP content of the HD (43, 50, and 55%, for HD-LE, HD-ME, and HD-HE, respectively) or LD (43 vs. 49%, LD-LE and LD-ME, respectively) meals. Drying temperature had no effect on M-SBM RUP. Intestinal digestibility of the undegraded in situ CP was similar among treatments ($P = 0.24$), although digestibility of M-SBM was numerically lower than S-SBM CP (65 vs. 71%, respectively). Lys content of in vitro residues was similar among treatments. Meal output was decreased by about 13% by increasing extrusion temperature. In the specific conditions of this study, increasing extruder temperature from 149°C to 171°C (300 to 340°F) increased RUP content of M-SBM by 28% but decreased meal output.

Key Words: soybean meal, processing, ruminal degradability

Animal Behavior and Well-Being: Use of Animal Behavior to Assess Animal Welfare

206 Use of animal behavior to assess animal welfare. E. A. Pajor,* *Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada.*

The science of animal behavior (ethology) has been closely linked to the study of animal welfare. A major advantage of behavior as a welfare indicator is that it can be measured non-invasively. As a starting point, a species' natural behavior is often compared with its behavior in confinement. Although this approach provides some general information about the range and variation in behavior, it does little to indicate anything about animal welfare. A more rewarding approach currently used by many scientists is to try to determine how particular behaviors develop, understand their function and what motivates them to occur. For many animal welfare scientists an animal's subjective stat is an important, if not the most important aspect of animal welfare. Feelings are not directly observable, but have measurable correlates or consequences. They can be assessed either by giving animals some control over their environments and observing the choices and decisions they make, using preference and motivation tests or by looking for signs of deprivation, frustration or distress when the animal is confined in an environment or subjected to a treatment without any means of control. Although preference and motivation tests are techniques under development, if carefully interpreted they can constitute a powerful tool for the assessment of welfare. Another important research area is the study of the causes and prevention of abnormal behaviors such as stereotypies or injurious behaviors. These behaviors have often been interpreted as indicators of poor animal welfare but recent studies suggest that such interpretations are too simplistic. Another promising approach to evaluating animal welfare is through the study of cognition, learning and memory. The focus of scientific inquiry and policy development is shifting to include the study of positive welfare states. Additional research in understanding and quantifying such states is a significant challenge.

Key Words: behavior, welfare, assessment

207 Prevalence of hock, knee and neck injuries, stall dimensions and lying time on Canadian free-stall dairy farms. J. C. Zaffino*[1], C. G. R. Nash[1], T. J. DeVries[2], S. J. LeBlanc[1], D. F. Kelton[1], J. Gibbons[3], E. Vasseur[3,5], A. M. de Passillé[3], J. Rushen[3], K. Orsel[4], H. W. Barkema[4], L. Solano[4], G. B. Bond[4], and D. B. Haley[1], *[1]University of Guelph, Department of Population Medicine, Guelph, ON, Canada, [2]University of Guelph, Department of Animal and Poultry Science, Guelph, ON, Canada, [3]Agriculture and Agri-Food Canada, Agassiz, BC, Canada, [4]University of Calgary, Department of Production Animal Health, Calgary, AB, Canada, [5]Organic Dairy Research Centre, University of Guelph Alfred Campus, Alfred, ON, Canada.*

Hock, knee and neck injuries on dairy cows are important indicators of welfare, management, and inadequate stall design. We investigated the relationship between injuries, lying time and stall dimensions on 90 free-stall dairy farms in Ontario (n = 40) and Alberta (n = 50). We sampled 40 Holstein cows per farm, scoring injury severity on a 4-point (hocks, knees) or 3-point scale (neck). Higher scores indicated greater severity. The same cows were used to calculate farm average lying time by recording their activity over 4, 24-h periods using electronic data loggers. Bed lengths (brisket board to rear curb) and stall widths were recorded on every farm. The association of stall dimensions with herd prevalence of injuries was analyzed in a mixed logistic regression model. The mean herd prevalence (and range) of hock, knee and neck injuries (score > 1) was 33% (0 - 82%), 17% (0 - 81%) and 8% (0 - 65%), respectively. The median farm average lying time was 10.5 h/d (interquartile range: 10.2 - 11.3 h/d). Mean bed length was 178 cm (range: 151 - 226 cm). Mean stall width was 115 cm (range: 104 - 131 cm). Hock injuries were not associated with bed length ($P = 0.82$) or stall width ($P = 0.98$). Knee injuries were less prevalent on farms with wider stalls (odds ratio = 0.3 per 10 cm increase in stall width; $P = 0.002$) and may be attributed to increased lateral lunge space. Neck injuries were more prevalent on farms with longer stalls (odds ratio = 1.4 per 10 cm increase in bed length; $P = 0.04$) and may be related to the placement of the neck rail on these stalls, yet to be analyzed. This is the first study to examine the prevalence of injuries on Canadian free-stall dairy farms. The finding that injuries are common on some farms is concerning, yet the variation between farms demonstrates that a low level of injuries is attainable. Refinement of stall designs may contribute to a reduction of injuries.

Key Words: injury, stall dimensions, animal welfare

208 Gradual cessation of milking reduces milk leakage and anticipatory behavior in dairy cows at dry-off. G. Zobel*[1], D. M. Weary[1], K. Leslie[2], and M. A. G. von Keyserlingk[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [2]Population Medicine, University of Guelph, Guelph, ON, Canada.*

The welfare effects of abrupt cessation of milking at dry-off are not well understood, but the pain-minimizing effects of gradually reducing milk production are frequently discussed in human work. This study aimed to assess the effect of abrupt vs. gradual cessation of milking on dairy cow behavior, milk leakage and somatic cell score (SCS). Eighteen cows (with a mean milk production of 24 ± 5 kg/d) were randomly assigned to either abrupt milk cessation (i.e., dry-off on d0) or gradual milk cessation (i.e., skipped milkings beginning on d0; dry-off on d5) in 3 replicates. Dry cow antibiotic and teat sealant therapy was administered at dry-off. Measurements were taken d-3 to d8. Three periods were identified for behavior data: P0 (baseline; d-3 to d-1), P1 (abrupt cows dry, gradual cows milking; d0 to d4) and P2 (all cows dry; d5 to d8). Lying and feeding behavior did not differ in P1 and P2 so these periods were combined for these measures. Lying time was recorded using data loggers and 5-min video scan samples were used to measure feeding time and anticipatory behavior (i.e., waiting at the pen's exit gate). Milk leakage was monitored every 20 min for 2 h following the times when cows would have been milked before dry-off (0500 and 1500). Leakage was assessed using the periods after full dry-off (P1 for abrupt vs. P2 for gradual). Composite milk samples were taken before dry-off and after calving to determine SCS. Regardless of treatment, dry-off resulted in reduced lying time (877 vs. 799 ± 9 min/d), reduced lying bouts (11.1 vs. 8.6 ± 0.3 bouts/d) and increased feeding time (285 vs. 350 min/d; SE = 8). Compared with P0, abrupt cows showed a greater increase in anticipatory behavior (P1: OR = 6.0; 95% CI: 2.7 – 13.5 and P2: OR = 8.1; 95% CI: 3.1 – 20.8) than gradual cows (P2: OR = 2.7; 95% 1 – 6.9). Frequency of leakage was greater in abrupt vs. gradual cows (89 vs. 22%, Fisher's exact test). SCS increased at calving regardless of treatment (2.6 vs. 4.5 SCS; SED = 0.4) but returned to P0 levels by d6. Gradually reduced milking frequency results in reduced milk leakage and reduced time spent anticipating milking following dry-off.

Key Words: welfare, milking frequency, SCS

209 Physiological and behavioral responses to bovine respiratory disease. R. Toaff-Rosenstein*[1], L. Gershwin[2], A. J. Zanella[3], and C. Tucker[1], *[1]Department of Animal Science, University of California-Davis, Davis, [2]Department of Pathology, Microbiology and Immunology, School of Veterinary Medicine, University of California-Davis, Davis, [3]Chair, Animal Health and Welfare, Scottish Agricultural College, Edinburgh, UK.*

Bovine respiratory disease (BRD) is the most widespread disease in US beef cattle, affecting 14.4% of feedlot animals, yet early detection is relatively poor. An improved understanding of the coordinated sickness response, including behavioral and physiological changes, can help improve disease detection. BRD was predicted to cause fever accompanied by lower feed intake and average daily gain (ADG). It was also expected to decrease grooming and increase lying time, as non-essential behaviors are reduced and those associated with fever maintenance increased with illness. Healthy beef steers (300 kg) were challenged with bovine respiratory syncytial virus on d0 and *Histophilus somni* on d5 (BRD, $n = 10$) or sterile solution (healthy, $n = 10$). Days −2 to 7 from initial viral challenge, unless stated otherwise, and treatment were analyzed using a mixed model. To assess grooming (d −1, 4, 6, 7) a brush was provided 20 min/d and self-licking was recorded simultaneously. Body temperature (d 3 to 7) and lying behavior were measured 24h/d with a data logger. BRD steers had higher body temperature d3 to d6, with the greatest difference on d5 (42.1 ± 0.16 vs. 39.9 ± 0.16°C, $P < 0.001$). Feed intake declined in BRD steers starting d2 and remained significantly lower on all subsequent days (peak difference on d5, 2.4 ± 0.12 vs. 0.3 ± 0.16% body weight, $P < 0.001$). This was accompanied by decreased overall ADG in BRD steers (−2.4 ± 0.36 vs. 1.6 ± 0.36 kg/d, $P < 0.001$). BRD steers spent more time lying down on d3 and 4 (peak difference on d3, 16.1 ± 0.38 vs. 14.1 ± 0.43 h/d, $P < 0.001$). BRD steers explored the brush less overall (8.4 ± 0.17 vs. 15.2 ± 0.17% of observed intervals, $P = 0.029$) and performed less self-licking on d4 (0.3 ± 0.24 vs. 8.9 ± 0.24% of observed intervals, $P < 0.001$) but there was no effect of BRD on brush-grooming ($P = 0.209$), possibly due to insufficient sampling. These results indicate that the BRD sickness response occurs as early as d2 after viral challenge as indicated by decreased feed intake. Behavioral changes can be used detect BRD, but adequate sampling is required for accurate disease recognition. Automated monitoring of behavioral changes may be a promising way forward for improved, early BRD diagnosis.

Key Words: sickness response, bovine respiratory disease

210 Effect of prepartum grouping strategy on agonistic behavior of dairy cows. K. M. Lobeck,* M. I. Endres, P. R. B. Silva, and R. Chebel, *University of Minnesota, St. Paul.*

The objective of this study was to investigate the effect of 2 prepartum grouping strategies on agonistic behavior of dairy cows measured by displacements from the feed bunk. Treatments were 1) All-In All-Out (AIAO) - cows assigned to a pen as a group and no new cows added during a 5-wk close-up period and 2) control (CON) - weekly entrance of new cows to maintain a pen density of 44 cows. The study was conducted in a freestall sand-bedded dairy farm in south-central Minnesota. Eighty-eight AIOA and 138 CON Jersey cows were enrolled in the study over 2 repetitions. Cows were randomly assigned to one of the treatments 5 wk before expected calving date. Cows were balanced for body condition score and those cows with locomotion score >2 were not included in the study. Displacements from the feed bunk were measured during 3 h on the day of move-in (d0) at 13:00 ± 1:00 and following fresh feed delivery (05:00 ± 1:00) on d 1, 2, 3 and 7 of each wk. Displacement rate was calculated as daily displacements divided by the number of cows in the pen to account for stocking density. Data were analyzed by Proc Mixed with day (week) as repeated measures. CON had greater number of displacements than AIAO (22.0 vs. 10.4; SE = 1.0; $P < 0.01$). Displacements during wk 1–5 were 12.7, 13.4, 13.4, 9.5 and 2.7 in AIAO and 32.3, 20.9, 23.1, 14.1 and 19.3 in CON, respectively (SE = 1.7; $P < 0.01$). There was a treatment by week interaction (SE = 2.3; $P < 0.01$). During wk 1, 2, 3 and 5 numbers of displacements were greater in CON than AIAO. Within AIAO, there were fewer displacements during wk 5 than wk 1–4. Within CON, wk 1 had greater displacements than wk 2–5. Displacement rate was greater in CON than AIAO (0.54 vs. 0.31; SE = 0.03; $P < 0.001$). Displacement rates in wk 1–5 were 0.29, 0.36, 0.37, 0.31 and 0.20 in AIAO and 0.78, 0.53, 0.58, 0.34, and 0.49 in CON, respectively (SE = 0.04; $P < 0.01$). There was a treatment by wk interaction (SE = 0.06; $P = 0.01$). During wk 1, 3 and 5, the CON treatment had greater displacement rate than AIAO in corresponding wk. Within AIAO, wk 5 tended to have a lower displacement rate than wk 2 ($P = 0.06$) and wk 3 ($P = 0.05$). In conclusion, AIAO resulted in fewer displacements and reduced displacement rate than CON.

Key Words: dairy behavior, dry cow, displacements

211 Individual differences in calf defense pattern in Red Angus beef cows. C. Flörcke,* T. E. Engle, T. Grandin, and M. J. Deesing, *Colorado State University, Fort Collins.*

Predation on livestock has increased causing difficulties in management of extensive beef systems. This study evaluates different calf defense patterns and maternal protectiveness within the first 24h past parturition. A total of 341 cow-calf pairs (95% Red Angus and 5% Angus x Hereford commercial crossbreds) were approached with an unfamiliar vehicle that performed circling movements, gradually decreased the distance between the vehicle and the cow-calf pair. Approach -, protective-, vocalization - and closest distance were collected with a digital range finder. Yes/No-classifications were made on calf defense patterns: protective behavior toward the calf (99.1% protective), aggressiveness of the cow toward the vehicle (13.2% aggressive), vocalization toward the calf (78% called calf) and flight behavior of cow and calf (no flight, walk and trot). Hair whorl pattern (HW) on the forehead of the animal was used as a measure of individual differences in temperament. HW pattern and age were collected when the animal was in a squeeze chute during routine handling. HW pattern was classified into: high, middle, low, abnormal, multiple HWs and no HW. Data analyses via ANOVA with Post-hoc Fisher's LSD Test showed a trend for the approach distance ($P = 0.057$). Post-hoc tests revealed that cows with a high HW ($P < 0.05$) or multiple HWs ($P < 0.05$) noticed the presence of the car at a further distance. Post-hoc tests for vocalization distance showed that cows with a high HW vocalized earlier (i. e. at a further distance; $P < 0.05$). The age of cows (3–6yrs) influenced protective behavior. Younger cows could be approached closer than older cows (3yrs vs. 5yrs of age: $P < 0.05$). When only high, middle and low HW pattern were analyzed approximately 50% of cows that trotted away performed aggressive movements (Chi^2 = 18.3, $P < 0.001$). Results suggest that individual differences in maternal protectiveness may be associated with HW pattern. The more vigilant a cow is toward her surrounding the more likely she will be able to detect danger for herself and her offspring.

Key Words: calf defense patterns, maternal protective behavior, temperament

212 Physiologic and behavioral responses of horses to shaded or unshaded pens in a hot, sunny environment. K. E. Holcomb*[1], C. L. Stull[1], and C. B. Tucker[2], [1]*University of California at Davis, School of Veterinary Medicine, Population Health & Reproduction, Davis,* [2]*University of California at Davis, Department of Animal Science, Davis.*

Housing recommendations for horses invariably include providing access to shade on hot, sunny days. The documented benefits of shade to livestock are assumed to apply to horses as well. However, this assumption has not been directly addressed and some owners do not believe horses require shade. This study measured physiologic and behavioral responses of individually-housed horses confined to completely shaded (S) or completely unshaded (NSh) dry-lot pens during the summer in Davis, CA. Twelve healthy adult horses in a crossover design experienced both treatments for 5 d each. The mean ambient temperature during observations (1200–1800 h) was 31.2°C in S and 31.9°C in NSh; relative humidity was 37.7% in S, 37.5% in NSh; black globe temperature was 33.4°C in S, 41.2°C in NSh; soil surface temperature was 30.6°C in S, 55.4°C in NSh. Rectal temperature (RT), respiration rate (RR) and skin temperatures (SK) were recorded hourly from 1230 to 1730 daily. RR was measured by observing flank movement. Behavior observations were recorded at 5-min intervals from 1200 to 1800 h daily to evaluate time spent walking, foraging, and standing near or away from water. Behavior and weather parameter data were averaged per hour for analysis. Data were analyzed using the Proc Mixed model in SAS, with horse as a random variable and ambient temperature as covariate, controlling for time of day. Results showed that RT was greater for NSh than for S (mean 37.8°C and 37.6°C respectively, SE 0.05, $P < 0.01$) as was true for RR (25.4 and 20.5 breaths per minute, SE 1.2, $P < 0.01$), and SK (35.7°C and 34.6°C, SE 0.1, $P < 0.01$). Horses in NSh spent more time than S standing near their water source (35.5% of observations versus 18.8%, SE 0.3, $P < 0.01$). There were treatment-by-time effects with larger treatment differences in RT and RR in mid-afternoon. Although RT and RR were within normal reference ranges, horses without access to shade showed significant physiologic and behavioral responses, suggesting the need to mitigate effects of the hot sun. These results can be used in developing and assessing standards of care for horses.

Key Words: horse, shade, welfare

213 Effect of a magnesium rich marine extract on behavior, salivary cortisol levels and skin lesions in growing pigs in response to mixing and an out of feed event. K. K. M. O'Driscoll*[1], D. Lemos Teixeira[3], D. O'Gorman[2], S. Taylor[2], and L. Boyle[3], [1]*Teagasc, Animal and Bioscience Research Department, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath, Ireland,* [2]*Celtic Sea Minerals, Currabinny, Carrigaline, Co. Cork, Ireland,* [3]*Teagasc, Pig Development Unit, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland.*

The aim was to investigate if a magnesium rich marine extract (Acid-Buf) would improve pig welfare in response to mixing and an out-of-feed event. 448 weaned (d 28) piglets were assigned to Control (CL; Mg 0.16%) or Acid-Buf (AB; Mg 0.18%) diets in single sex groups of 14. Seven pigs/pen were mixed with 7 of the same sex and diet from another pen: CL male, AB male, CL female and AB female (n = 4 of each) at d 56. At mixing, aggressive behavior and no. pigs involved per bout was recorded for 3 h from video. Postural behavior was recorded at 10-min intervals. At d 112 feed was removed for 21 h. After re-introduction of the feed pens were observed continuously for 8 × 2-min periods and aggressive behavior was recorded. Skin lesions of 4 focal pigs/pen were scored on the day before, and after, mixing and the out of feed event. Saliva samples were collected on d 56 and d 113 (1 h before and 1, 3 and 8 h after mixing/feed delivery post deprivation) and at 10:00 on d 55, d 57 d 58, d 112 and d 114 by allowing the 4 focal pigs to chew on a cotton bud for 1 min. Cortisol was analyzed by ELISA. Data were analyzed in SAS (Proc Mixed). At mixing, aggressive interactions lasted longer in males than in females (16:55 vs. 34:27 mm:ss, SE 03:38; $P < 0.01$) and more CL than AB pigs were involved/bout (2.13 ± 0.39 vs. 2.08 ± 0.34; $P < 0.05$). There was no effect of diet or sex on skin lesion scores, but AB females had lower cortisol concentrations than CL (1.51 ± 0.12 vs. 1.91 ± 0.13 ng/mL; $P < 0.05$). During the out-of-feed event, neither sex nor diet affected salivary cortisol levels, but males were more aggressive than females (0.182 vs. 0.122 aggressive interactions/pig/min; SE 0.019; $P < 0.05$), and CL pigs had higher skin lesion scores than AB pigs (13.2 ± 1.1 vs. 10.0 ± 1.0; $P < 0.05$). Supplementation with magnesium had some beneficial effects on pig welfare.

Key Words: welfare, magnesium, behavior

214 Neophobic reactions to a new flavored feed are overriden by social learning in pigs. J. Figueroa,* D. Solà-Oriol, J. F. Pérez, and X. Manteca, *Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

Social interactions help animals learn new features of their environment without a trial and error process. This could help to override aversion or neophobia of a particular ingredient or flavor after interacting with a conspecific that has just eaten these components. The aim of this experiment was to evaluate if observer piglets are able to prefer a flavored feed over their common (unflavored) feed by the effect of previous social interactions with models or demonstrators conspecifics. A total of 128 (49d old) weaned pigs, allocated in 16 pens (8 pig/pen), were used in this experiment. Half of animals (8 pens; G1) were exposed to a social learning process and the rest (8 pens; G2) acted as a negative control. In G1, 4 pigs/pen were randomly selected as observers and the rest acted as demonstrators. Demonstrator groups were temporarily moved to an empty pen where a flavored feed (anis (A) or garlic (G); 0.075%) were offered for 30 min. After that, demonstrator piglets were mixed again with the observer animals during 30 min. Flavors were counterbalanced across pens to act as the social flavor. After the interaction time, a double choice test between the flavored feed previously eaten by demonstrators (G1) and a control feed (known unflavored starter diet) was performed with the observer animals (G1) and with 4 animals from each control group. Feed intake was measured after 30 min. Data were analyzed using the GLM procedure of SAS®. Pigs showed higher intakes of the flavored feed in the social learning group (SLG) that in the control group (389 vs. 283g; $P < 0.05$). Higher intakes of socially learned flavored feed compared with the control feed (389 vs. 264g; $P < 0.01$) were observed in the SLG animals (G1). No feed intake differences were observed in the control group between the 2 feeds (283 vs. 325g for flavored and control feed). Social interactions with a conspecific animal that had a recent experience with a flavored feed enhanced the preference for that feed and could even override neophobia to new feed components.

Key Words: neophobia, social-learning, pigs

Animal Health II

215 The effect of yeast cell wall supplementation on the physiological and acute phase responses of crossbred heifers to endotoxin challenge. N. C. Burdick*[1], T. R. Young[2], J. A. Carroll[1], J. R. Corley[3], R. J. Rathmann[2], and B. J. Johnson[2], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]Texas Tech University, Department of Animal and Food Sciences, Lubbock, [3]Lesaffre Feed Additives, Milwaukee, WI.*

This study examined the effect of feeding yeast cell wall (YCW) products on the physiological and acute phase responses (APR) of crossbred newly-received heifers to endotoxin (lipopolysaccharide; LPS) challenge. Heifers (n = 24; 219 ± 2 kg) were obtained from commercial sale barns and transported to the Texas Tech University Beef Center in New Deal, Texas. Heifers were separated into treatment groups receiving a Control Diet (C; n = 8), YCW A (2.5 $g{\cdot}hd^{-1}{\cdot}d^{-1}$; n = 8) or YCW C (2.5 $g{\cdot}hd^{-1}{\cdot}d^{-1}$; n = 8) and were group fed for 52d. On d36 heifers were fitted with vaginal temperature (VT) recording devices and jugular catheters and moved into a barn with individual stalls during which they were individually fed. On d37 heifers were challenged i.v. with LPS (0.5 μg/kg BW) and blood samples were collected every 0.5h from −2 to 8h and again at 24h relative to LPS challenge (0h). Sickness behavior scores (SBS) were assigned following collection of each blood sample. Serum was isolated and stored at −80°C until analyzed for cortisol, interleukin-6 (IL-6), interferon-γ (IFN-γ), and tumor necrosis factor-α (TNF-α). Data were analyzed using the Mixed procedure of SAS specific for repeated measures. There was an increase in VT in all treatments post-LPS ($P < 0.001$), with YCW C (38.90 ± 0.03°C) maintaining lower VT post-LPS than C (39.00 ± 0.3°C) and YCW A heifers (38.99 ± 0.03°C; $P < 0.01$). Post-LPS SBS increased but were not affected by treatment ($P = 0.54$). Cortisol was greatest in C (39.7 ± 1.5 ng/mL) heifers post-LPS than YCW A (31.3 ± 1.7 ng/mL) or YCW C heifers (32.0 ± 1.7 ng/mL; $P < 0.001$). Concentrations of IFN-γ and TNF-α increased post-LPS ($P < 0.001$) but were not affected by treatment ($P = 0.50$ and 0.35, respectively). Serum IL-6 increased post-LPS ($P < 0.001$) and were greater in C (351.5 ± 36.0 pg/mL) than YCW A (85.8 ± 42.9 pg/mL) and YCW C (136.2 ± 36.0 pg/mL; $P < 0.001$) heifers. These data indicate that YCW supplementation can decrease the physiological and APR of newly-received heifers to endotoxin challenge. Therefore, YCW supplementation may be a viable feed supplement for newly received heifers to reduce the negative effects of illness.

Key Words: cattle, immune, yeast

216 OmniGen-AF supplementation modulates the physiological and acute phase responses of Brahman heifers to an endotoxin challenge. N. C. Burdick*[1], J. A. Carroll[1], J. D. Chapman[2], T. H. Welsh Jr.[3], R. C. Vann[4], and R. D. Randel[5], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]Prince Agri Products, Inc, Quincy, IL, [3]Texas AgriLife Research, Texas A&M System, College Station, [4]MAFES, Mississippi State University, Raymond, [5]Texas AgriLife Research, Texas A&M System, Overton.*

This study examined the effect of feeding OmniGen-AF (OG; Prince Agri Products) on the physiological and acute phase responses (APR) of heifers to an endotoxin (lipopolysaccharide; LPS) challenge. Brahman heifers (n = 24; 183 ± 5 kg) from the Texas AgriLife Research Center in Overton, TX were separated into 2 groups at weaning: 1) Control (C; n = 12) and 2) OG (n = 12; fed at 4 g per 45.4 kg BW) and fed for 69d. On d35 heifers were fitted with vaginal temperature (VT) monitoring devices, and were transported from Overton to New Deal, TX on d39. On d40, heifers were fitted with jugular catheters and moved into a barn with individual stalls. On d41 heifers were challenged with LPS (0.25 μg/kg BW i.v.) and blood samples were collected at 0.5h intervals from −2 to 8 h and again at 24h relative to LPS challenge (0h). Additional blood samples were collected every 2h and analyzed for white blood cell (WBC) counts. Sickness behavior scores (SBS) were assigned following collection of each sample. Serum was isolated and analyzed for cortisol, interleukin-6 (IL6), interferon-γ (IFNγ), and tumor necrosis factor-α (TNFα). Heifers were transported back to Overton on d43. Data were analyzed using the Mixed procedure of SAS specific for repeated measures. Post-LPS VT increased ($P < 0.01$) in all heifers, and was lower in OG (38.97 ± 0.01°C) than C heifers (39.03 ± 0.00°C; $P < 0.01$). Post-LPS SBS increased ($P < 0.01$) and were greater in OG (2.34 ± 0.02) than C heifers (2.16 ± 0.02; $P < 0.01$). Cortisol increased post LPS ($P < 0.01$) and were greater in OG (54.8 ± 1.1 ng/mL) than C heifers (48.4 ± 1.1 ng/mL; $P < 0.01$). Pre- and post-LPS WBC and lymphocytes (L) were greater in OG (WBC: 147 ± 4 and 82 ± 2 cells/μL; L: 90 ± 3 and 42 ± 2 cells/μL) than C heifers (WBC: 110 ± 4 and 63 ± 2 cells/μL; L: 68 ± 3 and 35 ± 1 cells/μL; $P < 0.01$). Total WBC, L, and neutrophils decreased 1 h post LPS ($P < 0.01$). Although post-LPS IFNγ, TNFα and IL6 increased ($P < 0.01$), there was no treatment effect ($P > 0.51$). These data suggest that OG-supplemented heifers were primed to produce a quicker APR to LPS challenge (lower VT, greater WBC counts), allowing for the heifers to recover quicker than C heifers.

Key Words: cattle, immune, OmniGen-AF

217 Yeast cell wall supplementation alters the performance and physiological response of beef heifers following an immune challenge. T. R. Young*[1], N. C. Burdick[2], J. A. Carroll[2], M. A. Jennings[1], J. T. Cribbs[1], R. J. Rathmann[1], J. R. Corley[3], and B. J. Johnson[1], *[1]Texas Tech University, Department of Animal and Food Sciences, Lubbock, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Lesaffre Feed Additives, Milwaukee, WI.*

A study was designed to determine the effect of feeding yeast cell wall (YCW) products on the performance and vaginal temperature response of crossbred heifers following a subcutaneous endotoxin (lipopolysaccharide; LPS) challenge. Heifers (n = 83; 225 ± 9.4 kg) were obtained from commercial sale barns and transported to the Texas Tech University Beef Center in New Deal, Texas, sorted by source (n = 2), and arranged in a completely randomized block design (21 pens; 7 pens/treatment; 4 heifers/pen). Heifers were separated into treatment groups receiving a Control Diet (CON; n = 28), YCW A (2.5 $g{\cdot}hd^{-1}{\cdot}d^{-1}$; n = 28), or YCW C (2.5 $g{\cdot}hd^{-1}{\cdot}d^{-1}$; n = 27). On d 56 heifers were fitted with indwelling vaginal temperature (VT) recording devices. Heifers were then challenged subcutaneously with LPS (0.5 μg/kg BW) on d 63. Daily DMI was recorded and individual BW was collected on d 63 and d 77. In Source 1, YCW C exhibited greater ADG ($P < 0.01$) and G:F ($P = 0.01$) compared with CON. There was an increase in VT in all treatments post-LPS ($P < 0.01$), with YCW C (39.14 ± 0.01°C) maintaining greater VT post-LPS than CON (38.89 ± 0.01°C) and YCW A (38.92 ± 0.01°C; $P < 0.05$). In Source 2, no significant differences in performance were observed. There was an increase in VT in all treatments post-LPS ($P < 0.01$), with YCW C (38.91 ± 0.02°C) maintaining greater VT post-LPS than CON (38.83 ± 0.02°C) and YCW A (38.83 ± 0.02°C; $P < 0.05$). Ambient temperature was extremely high during this study (greater than 45°C at certain times), indicating a period of high heat stress. Collectively these data suggest that YCW supplementation can affect the physiological response to a mild endotoxin challenge during high heat stress and thereby alter feedlot performance of newly received beef heifers.

Key Words: cattle, immune, yeast

218 A description of dairy heifer raising operations in the United States.

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The National Animal Health Monitoring System conducted the first national study of dairy heifer raising operations in 2011. Twenty-one states participated in the study. Operations were identified via multiple methods including previous interaction with state or federal animal health officials, Dairy Calf and Heifer Association membership list, and via word of mouth. Operations had to raise at least 20 dairy heifer calves in 2010 for at least one operation other than their own to be eligible for the study. The response rate was 60% with 228 operations completing the questionnaire. Operations were classified as small (20–99 heifers), medium (100–999 heifers), and large (1000 or more heifers). One objective of this study was to describe management practices on these specialized operations. Approximately 85% of operations sourced dairy heifers directly from other dairy operations and the median number of sources was 2. One third of operations (34.2%) reported obtaining primarily preweaned heifers while almost 2-thirds obtained primarily weaned heifers (60.1%) and 5.7% obtained primarily pregnant heifers. The majority of heifers left the heifer-raising operation as pregnant heifers (78.5%) while 21.5% left the operation as weaned heifers. The majority of operations raising preweaned heifers fed only medicated milk replacer (59.2%) while 32.1% fed only milk. Almost 80% of operations housing preweaned heifers reported cleaning and disinfecting or rinsing feeding equipment with water between every feeding. For operations housing weaned and pregnant heifers, more than 70% fed ionophores in the feed. A higher percentage of larger operations used consultants to the operation such as veterinarians, nutritionists, university/extension personnel and state or federal animal health officials. More than twice as many large and medium operations as small operations reported keeping written or computerized records of dairy heifer growth and/or health information (86.6, 73.1 and 32.1% respectively). Heifer raising operation practices are important in understanding the overall impact of this segment of the dairy industry.

Key Words: heifer-raising, milk replacer, record-keeping

219 Biosecurity practices on dairy heifer raising operations in the United States.

J. E. Lombard,* C. A. Kopral, J. M. Rodriguez, B. A. Wagner, and G. W. Hill, *USDA-APHIS-VS-CEAH, National Animal Health Monitoring System, Fort Collins, CO.*

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Key Words: heifer-raising, biosecurity

220 Pre- and postpartum immunomodulatory effects of a dietary supplement on the immune system of dairy heifers.

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The purpose of this study was to evaluate the effect of a dietary supplement (OmniGen-AF) on amplifying heifers' immune response to *Staphylococcus aureus* vaccination. Treated heifers (n = 40) receiving the supplement and unsupplemented controls (n = 43) in 8 age groups were monitored during gestation and into early lactation. For the prepartum parameters measured, there were no differences in body weight, hip height, prevalence of IMI, SCC, or differential mammary secretion leukocyte counts between treated and control heifers. Overall prevalence of IMI was 86% of heifers, with *S. aureus* as the most prevalent pathogen (62.1% of heifers, 25.3% of quarters). Front mammary quarters were 4.5 times more likely ($P \leq 0.001$) to be infected with *S. aureus* than rear quarters. Mean SCC of quarters with *S. aureus* IMI was $3,337 \times 10^3$/mL, while SCC in uninfected quarters averaged $1,846 \times 10^3$/mL. Regardless of infection status, macrophages predominated in mammary secretions followed by neutrophils and lymphocytes. L-selectin mRNA expression of blood leukocytes from group 1 treated heifers was greater ($P \leq 0.04$) than controls, indicating greater leukocyte activity. Additionally, L-selectin mRNA expression in group 2 treated heifers was greater ($P \leq 0.001$) than controls. Interleukin-8 receptor mRNA expression was generally higher in groups 1 and 2 treated heifers but not significantly different from controls. For the postpartum parameters measured, results showed that treated animals exhibited lower SCC than controls (180 vs. 711×10^3/mL) and lower prevalence of mastitis (4% vs. 13%). At 14 d postpartum, treated animals produced a mean of 25.9 kg/d compared with controls producing 21.8 kg/d. Overall, results demonstrated that dietary supplementation with OmniGen-AF improved udder health and milk quality postpartum, resulting in greater milk yield in early lactation.

Key Words: mammary immunity, mastitis, *Staphylococcus aureus*

221 Indoor group housing does not influence performance or measures of innate immune activity of Holstein calves during the neonatal, weaning, and commingling periods. C. J. Cobb,* D. L. Hanson, M. D. Sellers, A. R. Pepper-Yowell, B. S. Obeidat, and M. A. Ballou, *Texas Tech University, Lubbock.*

Objective was to determine if group housing of Holstein calves in indoor pens affects metabolic and innate immunological responses when compared with individually housed calves. Seventy-two calves (2 ± 1 d old) were randomly assigned to 3 treatments: individually housed (G1, n = 29), 2 calves/pen (G2, n = 22), or 3 calves/pen (G3, n = 21). Space allowances per calf were 2.5 m^2. All calves received an identical high plane of milk replacer nutrition. Weaning was initiated during the 7th week by removing the PM feeding and calves were completely weaned when they consumed 800 g dry matter (DM) calf starter after d 53. At d 91, calves were randomly commingled in groups of 5 calves outdoors. Peripheral blood was collected during the neonatal (3, 10, 21 d), weaning (45, 47, 53 d), and commingling periods (91, 94, 99 d) and was analyzed for neutrophil oxidative burst (OB) capacity when cocultured with an *Escherichia coli*, neutrophil L-selectin expression, whole blood secretion of tumor necrosis factor-α (TNF) when cocultured with lipopolysaccharide. Total DM intake was greater ($P < 0.05$) for G2 and G3 during wk 8 and 9 and also at wk 11 for G3 compared with G1. There were no treatment or treatment x time interactions in average daily gain (ADG; $P = 0.589$). Additionally, there were no treatment or treatment x time effects ($P > 0.185$) on any immunological or biochemical variable throughout the entire study. However, during the neonatal period, there were time effects with an increase ($P < 0.05$) in both TNF and neutrophil L-selectin expression with a concomitant decrease ($P < 0.05$) in OB intensity. During weaning, both neutrophil L-selectin expression and OB intensity increased ($P < 0.05$) on d 47 and returned to baseline or below by d 53 ($P > 0.232$). In contrast, commingling decreased ($P < 0.05$) both neutrophil L-selectin expression and OB intensity on d 94. Although group housing increased post-weaning DM intake, it did not influence ADG or any biochemical or immunological measurement throughout neonatal, weaning, or commingling periods.

Key Words: calf, housing, immune

222 Feed intake, rectal temperature and weight gain in *Bos indicus* crossbred steers challenged with bovine viral diarrhea virus. C. A. Runyan*[1], X. Fang[1], E. Downey[1], T. B. Hairgrove[3], J. E. Sawyer[2], J. C. Bailey[1], J. F. Ridpath[4], and A. D. Herring[1], *[1]Texas A&M University, College Station, [2]Texas Agrilife Research, College Station, [3]Texas Agrilife Extension, College Station, [4]USDA-ARS, Ames, IA.*

Yearling, Angus-Nelore half-blood steers (n = 104) born in the spring of 2010 were evaluated for rectal temperature, feed intake and weight gain following vaccination for Bovine Respiratory Disease (BRD) and intranasal challenge with Bovine Viral Diarrhea Virus (BVDV). Steers were tested to be free of BVD persistent infection and stratified by sire across 3 vaccine treatments: killed vaccine (KV; n = 34), modified live vaccine (MLV; n = 35), non-vaccinated group (NON; n = 35). KV steers were administered vaccine at d −49 and d −25. MLV steers received a single vaccine injection at d −25. At d 0, all steers were challenged intranasally with BVDV Type 1b strain CA0401186a. Animals were monitored daily for clinical symptoms of BRD/BVD; weights and rectal temperatures were collected at d 0, 3, 7, 10, 14, 28, and 42. Daily feed intake (DFI) was collected via a 4-pen Growsafe system. A threshold rectal temperature over 40°C was used to classify animals for temperature status during 14 d post-challenge. Mixed model, repeated measures procedures to analyze DFI included models with fixed effects of vaccine treatment (VAC), pen, day, sire, rectal temperature status (RTEMP), and 2-factor interactions. ADG was calculated for the 3–14 d periods following challenge with similar fixed effects plus d-0 weight as a covariate. No steers exhibited visual symptoms that would have led to a morbid classification; however, many had RTEMP over 40°C on evaluation days, including d 0 before challenge and on d 28 and 42; as a result RTEMP alone is likely not an ideal indicator of health status in these data. Also pen and several 2-factor interactions involving pen were important ($P < 0.05$) sources of variation. There was an interaction of RTEMP status and d ($P < 0.01$) where in general, steers exhibiting over 40°C during d 3 to 14 had DFI depressed 0.2 to 0.6 kg/d from d 3 to 10 but appeared to compensate after d 14. A pattern existed in DFI where NON steers consistently ranked lower than KV and MLV steers for d 6–11. No differences in ADG were attributed to VAC or RTEMP status.

Key Words: BVD, feed intake, *Bos indicus* crosses

223 Correlations of temperament with titer and hematological responses of crossbred steers challenged with bovine viral diarrhea virus. X. Fang*[1], E. Downey[1], C. A. Runyan[1], J. E. Sawyer[4], T.B. Hairgrove[2], J. F. Ridpath[3], C. A. Gill[1], W. Mwangi[1], and A. D. Herring[1], *[1]Texas A&M University, College Station, [2]Texas AgriLife Extension, College Station, [3]USDA-ARS, Ames, IA, [4]Texas AgriLife Research, College Station.*

Angus-Nelore F_2 and F_3 yearling steers born in 2009 (n = 78) and 2010 (n = 104) were administered bovine respiratory disease vaccine treatments of killed (2009 n = 28, 2010 n = 32), modified live (MLV) (2009 n = 25, 2010 n = 36) or no (NON) vaccine (2009 n = 25, 2010 n = 36) and stratified by breed composition and sire across vaccine treatment. Temperament scores of steers were evaluated shortly after weaning (8 mo age) on a 1–9 scale by 4 evaluators. After vaccination (25 to 35 d), steers were challenged intranasally with a Type 1b bovine viral diarrhea virus (BVDV). Serum samples for antibody titer of BVDV (Types 1a, 1b and 2) were collected on vaccination days, BVDV challenge day (d 0), and 14, 28, and 42 d after challenge. Whole-blood samples for hematological counts were collected on d 0, 14, 28, and 42. Pearson correlations of temperament score and titer and hematological measures were evaluated. Mean temperament scores were 4.2 in 2009-born steers and 5.9 in 2010-born steers. Several correlations ($P < 0.05$) between temperament score and the titer of BVDV (type 1a, b and 2), lymphocyte (LYM), neutrophil (NEU) and platelet (PLT) counts were found. On d 0 temperament had correlation from −0.20 to −0.24 with BVDV titers. On d 14, these values were reduced (r of −0.15 to −0.20), and became non-significant at d 28 and 42. LYM, NEU and PLT counts at d 0 were not correlated to temperament. Correlation of temperament and LYM at d 14 was similar to correlation of temperament and BVDV titers at d 14. NEU counts were not related to temperament except at d 28 and 42 (r of −0.19 and −0.20, respectively); PLT counts had similar magnitude of relationship with temperament ($P < 0.05$) for d 14, 28 and 42, but were positive (r of 0.17 to 0.20). When mixed model analyses of titer and hematological measures incorporated the regression on weaning temperament score, it became non-significant as the large individual variability overshadowed the temperament influence. The relationships involving animal temperament and immune response warrant further investigation, particularly in *Bos indicus* crosses.

Key Words: BVDV, temperament, immune response

224 *Cis*-9, *trans*-11 conjugated linoleic acid and NF-κB inhibitor pyrrolidine dithiocarbamate decrease prostaglandin production by bovine endometrial cells treated with lipopolysaccharide.

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Uterine bacterial infection or bacterial products suppress pituitary luteinizing hormone (LH) secretion, and are associated with inhibition of folliculogenesis, decreased ovarian steroidogenesis and abnormal luteal phase. To evaluate whether supplemental fatty acids (FA) may attenuate some of the deleterious effects of lipopolysaccharide (LPS) in cattle, we examined the effects of conjugated linoleic acid isomers (100 µM of cis-9, trans-11 and trans-10, cis-12 CLA) on in vitro prostaglandin E2 (PGE2) and F2α (PGF2α) production by bovine endometrial (BEND) cells treated with LPS. The specificity of CLA effects on endometrial PG production was evaluated by using linoleic acid (LA; C18:2) as the control FA. LPS stimulated both PGE2 and PGF2α productions in a dose and time-dependent manner. At 24 h, the concentration of PGE2 in the incubation medium was much higher than that of PGF2α (average ratio of PGE2 / PGF2α = 16.5; $P < 0.01$). The concentration of PGE2 in cell-conditioned media increased ($P < 0.01$) from 2.5 ± 2.0 to 17.4 ± 2.0 ng/mL as the concentration of LPS in the culture medium increased from 0 to 10 µg / mL. Similarly, PGF2α response to LPS increased from 0.2 ± 0.1 to 2.3 ± 0.1 ng / mL as the amount of LPS in the culture medium was raised from 0 to 10 µg / mL. With regard to time effects, the concentration of PGE2 in the culture medium increased ($P < 0.01$) from 0.4 ± 0.2 ng / mL at 3 h to 5.0 ± 0.2 ng / mL at 24 h. Corresponding values for PGF2α were 0.2 ± 0.05 ng / mL at 3 h and 1.0 ± 0.05 ng / mL at 24 h. Addition of FA to the incubation medium decreased ($P < 0.01$) PGE2 response to LPS by 75.6%. The cis-9, trans-11 (c-9, t-11) CLA isomer was more effective (85.1% reduction) than t-10, c-12 CLA (63% reduction) and LA (78% reduction) at decreasing PGE2 concentration. The c-9, t-11 CLA, t-10, c-12 CLA and LA decreased ($P < 0.01$) PGF2α response to LPS by 80%, 40%, and 10%, respectively. Co-incubation with the c-9, t-11 CLA and NF-κB inhibitor pyrrolidine dithiocarbamate decreased PGE2 response to a greater extent than did the CLA or NF-κB inhibitor alone. Results indicate that selective FA and the NF-κB inhibitor are potent inhibitors of LPS effects on endometrial PG secretion. If repeated in vivo, strategic supplementation of CLA may constitute a producer-friendly means of attenuating deleterious effects of the *E. coli* endotoxin in cattle.

Key Words: CLA, prostaglandin, cattle

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225 Peripartum metabolic, immune, and hematological parameters of Jersey cows diagnosed with periparturient diseases.

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Objectives were to evaluate the metabolic, immune, and hematological parameters of Jersey cows diagnosed with postpartum diseases. Blood was sampled weekly from d −21 to 21 (calving = d0) for NEFA concentration (n = 567) and weekly from d −14 to 14 from a subgroup of cows (n = 68) for neutrophil phagocytosis (PHAGO), oxidative burst (OXID), and expression of CD18 and L-selectin, hemogram, and glucose concentration. Cows were examined on d1 for retained fetal membranes (RFM) and on d4, 7, 10, and 14 for metritis (METR) and were observed daily for displacement of abomasum (DA). Data were analyzed by MIXED procedure with disease as the fixed effect (yes vs no) and cow as the random effect. Receiver operator characteristics analyses were used to determine NEFA concentrations that most accurately predicted disease. Interaction of RFM by day and METR by day were ($P < 0.05$) associated with OXID and PHAGO because RFM cows and METR cows had reduced OXID and PHAGO on d0 than normal cows. Interaction of RFM by day tended ($P = 0.08$) to be associated with CD18 expression intensity as RFM cows had higher intensity on d14 than normal cows. Greater percentage of neutrophils from RFM ($P = 0.03$) and METR ($P < 0.01$) cows expressed L-selectin than normal cows. Interaction of RFM by day and METR by day were ($P < 0.04$) associated with leukocyte count because leukocyte count was highest on d0 in normal cows but leukocyte count was highest from d-14 to 0 in RFM and METR cows. Interaction of METR by day tended ($P = 0.08$) to be associated with neutrophil count because only normal cows had increase neutrophil on d0. Interaction of RFM by day was ($P < 0.01$) associated with glucose because on d-7 and 7 RFM cows had greater glucose than normal cows. Interaction METR by day was associated with glucose ($P = 0.02$) and NEFA ($P < 0.01$) concentration because METR cows had greater glucose pre and postpartum and greater NEFA on d −14, 0, and 7 than normal cows. Interaction of DA and day was ($P = 0.03$) associated with NEFA because DA cows had greater NEFA on d −7, 0, 7, and 21 than normal cows. NEFA >0.18 mmol/l on d-7 predicted DA with 66.7% sensitivity and 76.4% specificity and NEFA >0.43 mmol/l on d0 predicted metritis with 46.2% sensitivity and 74.1% specificity. Immune, metabolic, and hematological alterations peripartum were associated with postpartum diseases.

Key Words: prepartum dairy cow, immune parameter, metabolic parameter

Breeding and Genetics: Dairy Cattle Breeding I: Genetic Improvement of Animal Health

226 Genomics of functional traits in dairy cattle. N. Vukasinovic*[1], Y. Li[2], J. D. Nkrumah[1], P. Boddhireddy[1], J. Osterstock[1], F. A. Di Croce[1], M. Kelly[2], M. Hvinden[1], D. J. Weigel[3], and S. K. DeNise[1], *[1]Pfizer Animal Genetics, Kalamazoo, MI, [2]Pfizer Animal Genetics, Brisbane, Australia, [3]Pfizer Animal Health, Kalamazoo, MI.*

Functional traits in dairy cows include fertility, health, longevity, and other traits that affect efficiency of dairy operations by decreasing input rather than increasing output. Genetic improvement of functional traits is challenging because of low heritabilities and difficulties related to phenotype recording. Application of genomics-assisted selection seems to be promising for functional traits. In the scope of this study, genomic predictions for several traits describing various aspects of mastitis, reproduction, and postpartum metabolic disorders were developed using a 50K SNP panel. The reference population included over 4,500 Holstein cows sampled from 9 large commercial herds located in 5 different states in the US. The animals had complete pedigree and extensive phenotype information for the traits of interest. The validation population included about 1,200 Holstein cows from an independent herd. The phenotypes of all animals, along with the pedigree consisting of 14,685 individuals, were used to obtain estimated breeding values (EBVs) for the traits of interest. The EBVs of the reference animals, weighted by their accuracies, were used in the genomic analyses to derive marker effects. The estimated marker effects were then used to obtain direct genomic values (DGVs) for the validation animals. The accuracy of DGVs was assessed by calculating correlations between originally estimated EBVs and DGVs. Preliminary results show that genomic information can be used to predict genetic potential of animals for functional traits.

Key Words: dairy cows, functional traits, genomics

227 Genomic selection for enhanced immune response to improve dairy health. K. Thompson-Crispi*[1], R. Ventura[2,3], F. Schenkel[2], F. Miglior[4,5], and B. Mallard[1], *[1]Department of Pathobiology, Ontario Veterinary College, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]Beef Improvement Opportunities, Guelph, ON, Canada, [4]Guelph Food Research Center, Agriculture and Agri-Food Canada, Guelph, ON, Canada, [5]Canadian Dairy Network, Guelph, ON, 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 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 across Canada and one herd in the US were found to have improved response to commercial vaccination, increased milk and colostrum quality and decreased incidence of diseases including mastitis, metritis, ketosis and retained placenta. The objective of this research was to perform a genome-wide association study to determine genetic profiles associated with antibody-mediated immune responses (AMIR). In collaboration with the Canadian Bovine Mastitis Research Network, 680 Holstein cows from 58 herds across Canada were immunized to measure serum antibody to a putative type 2 test antigen. Cows were classified as High, Average and Low immune responders based on EBV for AMIR. A total of 163 cows (81 High IR and 82 Low IR) were genotyped using the Illumina Bovine SNP50 BeadChip. A generalized quasi-likelihood score method was used to determine SNPs significantly associated with AMIR. Preliminary results show 484 SNPs significantly (comparison-wise $P < 0.001$) associated with AMIR. The majority of the SNPs are on chromosome 23 (98/484) followed by chromosome 9 (32/484), 1 (31/484) and 11 (30/484). Determining potential genes and biological pathways associated with these SNPs is currently underway. Results of this study will help to determine if AMIR could potentially be included in genomic selection indices to decrease the incidence and severity of disease in the dairy industry.

Key Words: dairy cattle, genomic selection, immune response

228 Telomere length assessment of Holstein cows in 10 Pennsylvania dairy herds. D. E. Brown,* C. D. Dechow, W. S. Liu, and K. J. Harvatine, *The Pennsylvania State University, University Park.*

Telomeres are known to shorten in humans with increasing age due to the inability of cells to completely replicate chromosomal DNA. Additionally, stress factors in humans are generally associated with a decrease in telomere length. The objective of this study was to assess telomere length variation in dairy cattle using a quantitative PCR (QPCR) procedure and determine if telomere length varied among herds and with age. DNA samples were obtained from purebred Holstein dairy cows from 10 dairy herds. A monochrome multiplex QPCR method was used to quantify relative telomere length for each cow. Primers were designed to create a 79 base pair telomere product and a 144 base pair standard reference gene product with each amplicon having different melting temperatures. Both primer sets were used in the same QPCR reaction well. This allowed independent measurement of amplification, while decreasing variation due to pipetting error and minimized experimental costs. QPCR results for 201 cows, which were run in triplicate, were analyzed using ASREML. Fixed effects of the model included gene, plate, cow, age, herd, the interaction of gene and plate, the interaction of age and gene, and the interaction of gene and herd. Random effects included the interaction of cow and gene, interaction of cow and plate, and the 3-way interaction of cow, plate, and gene. The effect of herd was significant for telomere length ($P < 0.001$). The effect of cow age was significant ($P < 0.05$), with telomere length decreasing as age increased. Least squares means for herd telomere length were positively correlated with rolling herd average milk production ($P < 0.05$). Herd environment appeared to be associated with a physiological response in the telomere length of dairy cattle. However, higher milk production did not appear to elicit a negative effect on telomere length. Telomere assessment may provide a quantifiable measure for future cattle welfare studies.

Key Words: telomere, telomere length, stress

229 Incidence validation and causal relationship analysis of producer-recorded health event data from on-farm computer systems in the United States. K. L. Parker Gaddis*[1], J. P. Cassady[1], J. B. Cole[2], and C. Maltecca[1], *[1]North Carolina State University, Raleigh, [2]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Substantial progress has been made in the genetic improvement of production traits in dairy cattle. Due to a negative correlation between production and fitness traits, the health and fitness of dairy cattle have declined as yields have increased. Health and fitness traits are generally difficult and/or expensive to measure, but health event data collected from on-farm computer management systems may provide an effective and low-cost source of health event information. The principle objective of this study was to analyze the reliability of health event data recorded with on-farm recording systems throughout the United States. To validate editing methods, incidence rates of on-farm recorded health event data were compared with incidence rates reported in the literature. A second aim of this study was to examine putative causal relationships among common health events using data recorded in on-farm computer systems. Calculated incidence rates ranged from 1.4% for respiratory problems to 8% for clinical mastitis. Most health events reported had incidence rates lower than the average incidence rate found in literature. This may represent under-reporting by dairy farmers who record disease events only when a treatment or other intervention is required. Logistic regression was used to examine putative causal relationships among health events within a lactation for 3 timeframes: 0 to 60 d in milk (DIM), 61 to 90 DIM, and 91 to 150 DIM. Herd, season, parity, breed, and year were included in each model as fixed effects. Health events occurring on average before the health event of interest were included in the model as predictors when significant ($P < 0.05$). Path diagrams developed using odds ratios calculated from logistic regression models for each of 13 common health events allowed putative relationships to be examined. The greatest odds ratios were estimated to be the influence of ketosis on displaced abomasum (15.5) and the influence of retained placenta on metritis (8.37), and were consistent with earlier reports. The results of this analysis provide evidence for the usefulness of on-farm recorded health information.

Key Words: dairy, health, path analysis

230 Genetic relationships of mastitis, cystic ovaries and lameness with milk yield and somatic cell score in first-lactation Canadian Holstein cows.

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The objective of this study was to investigate the genetic relationships of the 3 most frequent dairy cattle diseases (mastitis, cystic ovaries and lameness) with test-day milk yield (MY) and somatic cell score (SCS) in first lactation Canadian Holstein cows using random regression models. Health data recorded by producers were available from the National Dairy Cattle Health System in Canada. Disease traits were defined as binary traits (1 = affected, 0 = unaffected) based on whether or not the cow had at least one disease case recorded within 305 d after calving. Random regressions on second order Legendre polynomials were used to model the daily genetic and permanent environmental variances of test-day MY and SCS, while only the intercept term was fitted for disease traits. Genetic correlations between MY and diseases were unfavorable with estimates ranging from 0.21 to 0.42 between MY and mastitis, from −0.05 to 0.29 between MY and cystic ovaries, and from 0.23 to 0.36 between MY and lameness. In contrast, favorable associations were found between SCS and diseases. Genetic correlations varied from 0.64 to 0.71 between SCS and mastitis, from 0.10 to 0.22 between SCS and cystic ovaries, and from 0.19 to 0.29 between SCS and lameness. Unfavorable associations between MY and diseases imply that production and health traits should be considered simultaneously in genetic selection.

Key Words: genetic correlation, disease, milk yield and somatic cell score

231 Genetic relationships among health related fatty acids in milk of Canadian Holsteins.

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The objective of the present study was to estimate heritabilities of and genetic correlations among fatty acids in milk of Canadian Holsteins. The fatty acids studied were chosen because they are important in human health. One morning milk sample was collected from 3185 dairy cows between February and June 2010 from 52 commercial herds enrolled in Dairy Production Centre of Expertise, Valacta. Individual fatty acid percentages (g/100g of total fatty acids) were determined for each sample by gas chromatography. Edits were applied to the database on registration status of the cow, breed, country, cow and sire and dam identifications, age at calving and stage of lactation. Cows were sampled between 3 to 450 d in milk and were in either parity 1, 2 or 3. Herd-year-season of calving classes were formed considering 2 season effects in a year; that is, March 1 to August 31 and September 1 to February 28/29. Each herd-year-season of calving class was required to have 5 or more observations. Editing reduced the data set to 2573 cows representing 46 herds. Ten fatty acids were studied and included 3 omega-3 fatty acids (C18–3n3ALA, C20:5n3, C22:5n3), 2 conjugated linoleic acids (CLA-9c11t, CLA-10t12c), 2 omega-6 fatty acids (C20:3n6, C20:4n6), C22:0, C23:0 and C24:0. Genetic parameters were estimated using a 10-trait animal model fitted under REML using Wombat software. The model included fixed effects of age at calving and stage of lactation nested within parity; random effects of herd-year-season of calving, animal and residual. The pedigree of animals with data was traced back 5 generations on both the male and female side to account for relationships among animals. The estimates of heritability ranged from 0.01 to 0.21 with standard errors ranging from 0.01 to 0.04. Genetic correlations among fatty acids ranged from 0.74 to −0.72 with standard errors ranging from 0.1 to 0.5. Improvement of the fatty acid proportions in milk through genetic selection is possible as individual fatty acids can respond differently.

Key Words: cow milk fatty acids, health, genetic parameters

232 Crossbreds of Holstein with Jersey and Montbéliarde compared to pure Holsteins for 305-d production and mastitis in a pasture production system.

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Montbéliarde × Holstein crossbred cows (MH, n = 30); Montbéliarde × Jersey × Holstein crossbred cows (MJH, n = 49); Jersey × Montbéliarde × Holstein crossbred cows (JMH, n = 32); Holstein × Montbéliarde × Jersey × Holstein cows (HMJH, n = 47); and Holstein × Jersey × Montbéliarde × Holstein crossbred cows (HJMH, n = 10) were compared with pure Holstein cows (HO; n = 114) for 305-d milk, fat, and protein production; SCS; and mastitis incidence during their first 3 lactations. Cows were housed at the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota, a grazing herd, and calved from March 2006 to June 2011. Best Prediction was used to calculate actual production (milk, fat, protein, and SCS) for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Incidence of clinical mastitis was recorded in a binary manner as treated (1) or not treated (0) during a lactation. Independent variables for statistical analysis were the fixed effects of year-season of calving (6-mo seasons), crossbred group (2-breed, 3-breed, or 4th generation crossbred), breed group nested within crossbred group, parity nested within breed group and crossbred group, and random cow within breed group. Across the first 3 lactations, pure HO cows had significantly ($P < 0.01$) higher milk (7,766 kg) production than JMH (6,790 kg) cows, but were not significantly ($P > 0.05$) different than MH (8,054 kg), MJH (7,562 kg), HMJH (8,041 kg) and HJMH (7,230 kg) cows for milk production. The MH (520 kg), MJH (511 kg), JMH (476 kg), and HJMH (499 kg) cows were not significantly ($P > 0.05$) different from pure HO (499 kg) cows for fat plus protein production during the first 3 lactations; however, the HMJH (526) cows had significantly ($P < 0.05$) greater fat plus protein production than pure HO cows. The crossbred cows were not significantly ($P > 0.05$) different from pure HO cows for SCS during the first 3 lactations. The MH (37.9%), MJH (26.3%), and HJMH (23.7%) cows had significantly ($P < 0.05$) less clinical mastitis than pure HO (56.4%) cows during the first 3 lactations.

Key Words: crossbreeding, mastitis, pasture

233 An update: Responses of production and mastitis to selection for milk yield with a control population in a pasture production system.

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The University of Minnesota initiated a designed study of yield selection in 1964 that included an unselected control group of cows. The study continues at the West Central Research and Outreach Center (WCROC), Morris, Minnesota, and is currently part of the low-input sustainable and organic grazing dairy project. At time of dispersal from the Southern Research and Outreach Center, Waseca, in 2003, rolling herd averages were control line (5,964 kg milk, 221 kg fat, 179 kg protein, 3.3 SCS) and selection line (10,099 kg milk, 384 kg fat, 303 kg protein, 2.0 SCS). The control line of cows has not been evaluated in a pasture-based dairy production system. Therefore, control Holstein cows (n = 118) were compared with contemporary Holstein cows (n = 267) for 305-d milk, fat, and protein production; SCS; and mastitis incidence during their first 5 lactations. Cows were housed at the WCROC, a grazing herd, and calved from January 2003 to May 2011. Best Prediction was used to calculate actual production (milk, fat, protein, and SCS) for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Incidence of clinical mastitis was recorded in a binary manner as treated (1) or not treated (0) during a lactation. Independent variables for statistical analysis were the fixed effects of year-season of calving (6-mo seasons), genetic line, parity nested within genetic line, and random cow within genetic line. Across the 5 lactations, control Holstein cows had significantly ($P < 0.01$) less milk (6,034 versus 8,234 kg), fat (205 versus 271 kg), protein (188 versus 254 kg), and fat plus protein (393 versus 525 kg) production compared with contemporary Holstein cows. The control Holstein cows were not significantly ($P > 0.05$) different from contemporary Holstein cows (3.49 versus 3.42, respectively) for SCS during the first 5 lactations. However, the control line cows (31.9%) had significantly ($P < 0.01$) less clinical mastitis than contemporary Holstein cows (47.1%) during the first 5 lactations.

Key Words: genetic selection, mastitis, pasture

234 Genetic analysis of leukosis incidence in a US Holstein cattle population.

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Bovine leukosis (BL) is a retroviral disease caused by the bovine leukosis virus (BLV) that affects only cattle. It is associated with decreased milk production in addition to death losses. On average, a BLV negative cow has a longer life span, produces 3.5% more milk per lactation, and has 48 fewer days open than does a BLV positive cow. The virus also affects the immune system. Infected cows display a muted response to immunization with J5 bacterin. The aim of this study was to estimate the heritability for BL incidence and the genetic merit of sires for leukosis resistance in the US Holstein population. Continuous and binary data of milk ELISA score for 14,120 cows from 114 dairy herds across 16 US states were considered. Data were obtained from commercial testing records at Antel BioSystems located in Lansing, Michigan. Data used for analysis were limited to animals with a minimum of 3 test results. Out of the 14,120 animals tested, 38% were infected with the disease. Linear and threshold animal models were used to analyze the continuous and binary data, respectively. Variance components and breeding values for animals were estimated using the 2 models and the agreement between the estimated breeding values from each model was assessed. Estimates of heritability obtained with the 2 approaches were very similar and around 7%, indicating that there is a considerable genetic component underlying BL disease incidence. The correlation between the estimated breeding values from the 2 methods was 0.797, and the lists of top 10% bulls selected from each model had a 65.3% overlap. In summary, results indicate that the simple linear model approach using the continuous ELISA scores as response variable is a reasonable approach for the genetic analysis of BL incidence in cattle. In addition, the levels of heritability found indicate that selection could also be used to improve resistance to BL in Holstein populations.

Key Words: bovine leukosis, heritability, threshold model

235 Production traits, somatic cell score, and days open of crossbred cows versus pure Holsteins during their first lactation in Italian commercial dairy herds.

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The objective of this study was to compare Swedish Red (SR) × Holstein (HO) crossbred cows (n = 385), Montbéliarde (MO) × HO crossbred cows (n = 71), and Brown Swiss (BS) × HO crossbred cows (n = 52) with pure HO cows (n = 1,583) for production traits. A total of 563,158 test-day information for milk yield and 15,348 for fat and protein, and somatic cell score were recorded on first parity cows milked in 4 herds of northern Italy. Production traits were analyzed through a mixed linear model that included effects of herd-test-day, days in milk based on the Wilmink function, breed group, days open, and the random effects of cow nested within breed group and residual. Days open were grouped into classes of 60 d each, except for the first, which was a class of non-pregnant cows and the last, which was an open class (>240 d). The Wilmink model was used to investigate differences in the shape of lactation curves of milk yield among breed groups. Parameters were estimated for each cow and then used as response variables in linear models including the effects of breed group, herd, and classes of days open. HO produced more milk than SR × HO and MO × HO crossbreds (+2.86 and +2.34 kg/d, respectively) and protein (+0.04 and +0.03 kg/d, respectively), but lower protein percentage (−0.14 and −0.08%, respectively). SR × HO and MO × HO cows became pregnant about 20 d earlier than HO cows. BS × HO produced less milk (−1.47 kg/d) than pure HO cows, but higher (+0.11%) protein percentage. BS × HO and SR × HO had also significantly lower SCS (−0.42 and −0.37, respectively) than HO cows. According to previous results, the Wilmink function showed that milk production was lower for crossbreds compared with pure HO cows, which highlighted stronger increase toward the peak then SR × HO and MO × HO. Breed groups did not differ for the parameter describing the decreasing part of the lactation curve, which was affected by days open. Results indicate that SR and MO are candidate breeds for crossbreeding with HO to maintain good levels of production and improve fertility of dairy herds.

Key Words: crossbreeding, milk traits, days open

236 Birth weight, gestation length, calving-ease and mortality in Holstein, Jersey, and crossbred cows in a pasture-based dairy herd.

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Holstein (H) and Jersey (J) cows were mated to H or J bulls to form purebreds, reciprocal crosses, and backcrosses in a criss-cross mating system in the herd located at the Center for Environmental Farming Systems in Goldsboro, North Carolina. Data for birth weight (BW = 31.1 ± 5.9 kg), calving ease (CE = 0 for unassisted, n = 1106, and 1 for assisted, n = 74), and mortality (0 for alive, n = 1150, and 1 for abortions recorded after mid-gestation, stillborn, and dead within 48 h, n = 30) of calves (n = 1231) were recorded over 9 calving seasons from 2003 through 2011. Gestation lengths (GL = 276.7 ± 5.9 d) were determined from insemination and subsequent calving dates. Linear mixed models for BW and GL included fixed effects of sex, parity (first vs. later parities), twin status, and genetic groups [purebred Holsteins (HH), purebred Jerseys (JJ), reciprocal F1 crosses (HJ, JH), crosses > 50% Holsteins (HX) and crosses > 50% Jerseys (JX)]. The BW model also included GL as covariate. Logistic regression for CE and mortality included fixed effects of sex, parity, and genetic groups. Genetic groups were replaced by linear regression using percentage H genes as coefficients on above models and included as covariates to determine the type of genetic control. Heifer calves, twins and calves born at first parity had lower BW. Differences in genetic groups were observed for BW ($P < 0.01$). Percentage H genes in the calf (direct genetic effects) and percentage H genes in the dams (maternal genetic effects) increased BW ($P < 0.01$). Shorter GL were observed for twin births and for first parity. Direct genetic effects shortened GL ($P < 0.01$), whereas maternal genetic effects increased GL ($P < 0.01$). First parity cows had more assisted births than older cows ($P < 0.01$). Female calves had lower odds ratio (0.27, CI = 0.11, 0.67) for mortality than male calves. Higher percentages of heterosis in the dams (maternal heterosis) reduced calf mortality ($P = 0.015$).

Key Words: crossbreeding, genetic groups, percentage Holsteins

237 Genetic parameters associated with feedlot bovine respiratory disease complex morbidity and mortality.

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Bovine respiratory disease complex (BRDC) is a broad term associated with host of infectious agents that occur in cattle. Morbidity and mortality caused by BRDC in the feedlot is associated with annual costs estimated in excess of a billion dollars. Indirect effects of BRDC include depressed performance and carcass quality. Therefore, the objective of this study was to quantify the genetic control of feedlot morbidity and mortality associated with BRDC. Crossbred steers from a single source were shipped from western Nebraska to southeast Colorado over a 2 year period (year 1 n = 1,551, year 2 n = 1,319). Steers were processed the day following arrival and placed in feedlot pens where they remained unless identified as sick and in need of health treatment by feedlot staff. If an animal was pulled as sick it was treated according to defined protocols and housed separately with other sick animals until recovered. Processing and treatment protocols were nearly identical across the 2 years of the study. In the event of mortality, field necropsies were conducted and biological samples were taken to ascertain the cause of death. Treatment and mortality rates attributed to BRDC varied greatly of the 2 years of the study, in year one morbidity and mortality rates were 45% and 6% compared with year 2 8% and 2% respectively. A probit threshold link function in ASReml was used to convert binary observations for both morbidity and mortality to the underlying scale. Variance components were estimated through univariate sire models using the 2,870 total observations and 3,255 pedigree relationships. Fixed effects included contemporary group (ranch unit and feedlot pen) and year. Heritability and standard errors for feedlot morbidity or feedlot mortality were, 0.17 (0.06) and 0.08 (0.16) respectively. These results suggest some amount of genetic control in the susceptibility to BRDC and the inability to recover from an infection. The ability to select for animals with greater disease tolerance or immune function could result in increased performance and decreased input requirements in the feedlot.

Key Words: feedlot, morbidity, mortality

238 Performance of a German Holstein cattle population under stressful conditions near Benghazi, Libya.

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The aim of this study was to evaluate productive and reproductive performance of German Holstein Friesian dairy cows and subsequent generations that were born in Libya. Animals were managed by a Dutch company from 1986 to 1990, and Libyan managers were used after 1990. The number of cows that had the first lactation record included in the study was 2094. Data were analyzed using REML to estimate factors affecting milk yield and reproductive traits. The model included month, year of calving, management, generation, origin of sire as fixed effects. In addition, age at first calving and lactation period included for milk yield traits as covariates. Total milk yield was generally high (8409 Liters) and achieved with reproductive efficiency (110 d open) during Dutch management, and at the expense of the reproductive traits (161 d open) during Libyan management. Management, calving year, calving month, age at first calving and lactation period had a significant effect on both milk yield and reproductive traits. In addition, milk yield and days open were affected by the temperature-humidity index (THI). Different trends of milk yield and days open were found during cold and hot seasons. However, Days open were more affected by the increasing in THI than does milk yield. Reasons of culling were mainly due to low fertility (37%), mastitis and udder injuries (15%) and accidental defects (16%). Management plays important role to maintain high productivity with reproductive efficiency under heat stress conditions.

Key Words: milk yield, reproductive traits, THI

Companion Animals Symposium: Companion Animal Reproduction: To breed or not to breed?

239 Canine and feline reproductive biology 101. M. Kutzler,* *Oregon State University, Corvallis.*

This lecture is designed to provide a primer on canine and feline reproduction for scientists unfamiliar with this topic as well as lay people. Domestic bitches are nonseasonally monoestrous. As a result of this unique reproductive physiology, bitches spontaneously ovulate only once or twice per year and ovulation can occur at any time of the year. Queens are induced ovulators, requiring external stimulation (such as natural breeding) to stimulate the ovulation of mature follicles. During the breeding season, queens exhibit estrous behavior every 2–3 wks unless ovulation occurs. However, the occurrence of estrus and ovulation are not repetitive, cyclic or predictable. In bitches, ovulation of primary oocytes occurs 36–50 h after the onset of the surge in luteinizing hormone (LH). Oocyte maturation (extrusion of the first polar body) is complete 2–3 d post-ovulation and sperm can penetrate the zona pellucida before extrusion of the first polar body. Queens ovulate secondary (mature) oocytes capable of fertilization immediately following ovulation. Fertilization (extrusion of the second polar body) occurs in the uterine tube. Embryos are present within the uterine tube 7 d past the onset of the LH surge and late morulas and early blastocysts enter the uterus 10 d past the onset of the LH surge. Prior to implantation, embryos float freely within the uterine lumen, nourished by "uterine milk" (histotroph). Embryo migration between uterine horns does occur and blastocysts space themselves out evenly between horns until 16 d after the onset of the LH surge. Embryonic implantation occurs 22 d after the onset of the LH surge. Implantation sites can be observed ultrasonographically at this time. The bitch and queen have an endotheliochorial, zonary (circumferential), modified deciduate placenta. The continuous availability of ovarian progesterone is required for the initiation and maintenance of pregnancy in both species, such that ovariectomy at any time will result in resorption or abortion. No placental or embryonic luteotrophic secretions that have been demonstrated in the bitch or the queen. However, relaxin is only detectable during pregnancy and is the only specific pregnancy-associated protein in dogs and cats.

Key Words: ovulation, pregnancy, placentation

240 Companion animal reproduction and nutrition 101. D. Greco,* *Nestle Purina Petcare.*

This review covers the use of common nutritional supplements for the bitch and puppies. Basic nutrients such as fat, protein, minerals, vitamins, and essential fatty acid supplementation will be discussed. Newer supplements such as probiotics for stimulation of the immune system of the bitch and puppy and use for the non-pharmaceutical treatment of weaning diarrhea will also be outlined.

241 Companion animal population control: Past, present and future. S. Zawistowski,* *The American Society for the Prevention of Cruelty to Animals, New York, NY.*

The euthanasia of pets in US animal shelters likely peaked at an estimated 20 million per year around 1970. It was then that the first major programs appeared to promote and subsidize sterilization of dogs and cats. The relentless efforts of shelter groups in the past 40 years have helped to reduce the euthanasia figure to about 4 million pets per year. This progress has been the result of broad based public education programs and substantial advances in the methods of surgical sterilization. Maintaining this success, and making further progress will likely require the development of non-surgical contraceptives and sterilants that do not call for the substantial infrastructure investments needed for high volume, high quality spay/neuter programs. Current research on non-surgical approaches employ cutting edge approaches in cell, molecular and neuroendocrine biology.

Key Words: companion animal population, spay/neuter, non-surgical sterilization

242 The role of the domestic cat in endangered species conservation. J. Herrick,* *National Foundation for Fertility Research, Lone Tree, CO.*

Domestic cats are highly prolific breeders, so there has been little demand to study reproduction or develop assisted reproductive technologies (ARTs) in this species. As a result, surprisingly little is known about feline reproduction, despite the widespread popularity of cats as pets. However, most of the other 36 species of cats in the world are threatened with extinction. An improved understanding of feline reproduction would greatly benefit conservation efforts and population management for these endangered species. Since nondomestic cats are poor research subjects due to their limited availability and dangerous nature, the domestic cat has become an important model species for reproductive studies. Research in domestic cats has led to the development of techniques for noninvasive hormone monitoring and electroejaculation that have facilitated studies of estrous cycle dynamics and sperm physiology in nondomestic cats. Similarly, protocols for artificial insemination, in vitro fertilization, and embryo transfer developed in domestic cats have been used successfully in some nondomestic cat species. These ARTs could play a valuable role in conservation programs, but current protocols are inefficient and successful offspring production is sporadic. One of the many areas in need of additional research is the culture environment used for feline embryos following in vitro fertilization. During the first few days after fertilization, the embryo is extremely sensitive to its environment (the fluids of the reproductive tract or synthetic culture media). Even brief exposure to sub-optimal conditions during this time can have dramatic effects on embryonic and fetal viability. By developing a culture medium specific to the needs of the feline embryo, we have been able to greatly improve the success of in vitro fertilization in domestic cats, as well as several species of nondomestic cats. However, embryonic development in vitro is still compromised compared with development in vivo. Specifically, the feline embryo undergoes rapid cell division and appears to have unique nutritional requirements to support this growth that are not being met with current media formulations. Research to develop more appropriate culture media and increase the viability of cultured embryos will continue to rely heavily on the domestic cat, as will all research to improve the efficiency of ARTs. The future existence of endangered cats could very well depend on a better understanding of reproductive physiology in their domestic cousin.

Key Words: feline, assisted reproductive technologies, conservation

243 Population control in wildlife: Lessons learned. J. F. Kirkpatrick,* *Science and Conservation Center, Billings, MT.*

The management of certain wildlife populations by means of fertility control has become widely accepted and is now commonly used in species such as wild horses, urban deer, African elephants, bison, and >85 species of captive exotic animals in zoos, worldwide. The most commonly used contraceptive agent is a porcine zona pellucida vaccine (PZP), which operates entirely outside the cascade of reproductive endocrine events. The characteristics of this vaccine come closer to the ideal for use in wildlife than any other form of contraception and include (1) efficacy of at least 90%, (2) remote delivery, (3) reversibility, (4) safe for use in pregnant animals, (5) minimal effects on behavior, (6) no debilitating side effects, (7) inability to pass through the food chain, and (8) low cost. Despite major scientific strides in achieving these goals and demonstrating success in the field, significant opposition remains. This opposition exists in the form of cultural and social biases, economic concerns, agency inertia and political pandering. Regardless of whether the development of this technology is aimed at wildlife or companion animals, involved scientists must understand that unless they are willing to address the points of opposition, as well as regulatory hurdles, much of their work and the resources expended can come to naught.

Key Words: population control, companion animals, wildlife

244 Obesity is associated with adverse cardiovascular outcomes and insulin resistance in dogs. J. L. Adolphe,* T. I. Silver, M. D. Drew, and L. P. Weber, *University of Saskatchewan, Saskatoon, SK, Canada.*

Obesity and cardiovascular disease are strongly linked in humans, but this association is less clear in dogs. The purpose of this study was to evaluate the effects of obesity on cardiac structure and function as well as insulin resistance in dogs. Cardiovascular variables were measured and oral glucose tolerance tests were performed before and after weight gain in 9 beagles. At baseline, dogs were fed a commercial diet in measured amounts to maintain an ideal body weight. Subsequently, for 12 weeks the dogs were allowed free access to the diet to allow weight gain. Echocardiography was used to analyze left ventricular function. Blood pressure was measured by high-definition oscillometry. Serum glucose and insulin were measured before and at specific time points after an oral glucose challenge to determine glucose tolerance and insulin sensitivity. CT (CT) was used to quantify total and visceral fat accumulation in the dogs in the obese state. Body weight increased from 9.8 ± 0.6 kg at baseline to 12.1 ± 0.7 kg (123 ± 3% of ideal body weight) after ad libitum feeding. Systolic left ventricular free wall thickness, heart rate, area under the glucose response curve and peak glucose significantly increased in the obese state compared with the lean state ($P < 0.05$). Systolic free wall thickness was positively correlated with total fat ($r = 0.7$, $P = 0.02$) and visceral fat ($r = 0.7$, $P = 0.03$). Area under the insulin response curve was associated with visceral fat ($r = 0.8$, $P = 0.03$). Increased systolic free wall thickness, coupled with elevated heart rate, in dogs likely reflects hyperdynamic cardiac function which may have negative long-term cardiovascular consequences. Thus, this study supports the hypothesis that visceral fat is linked to detrimental changes in cardiac function and insulin sensitivity in obesity. These results are particularly remarkable considering that the dogs were obese for only 12 weeks.

Key Words: obesity, dogs, insulin resistance

Dairy Foods Symposium: Maximizing Value of Milk Proteins: Manufacture, applications and market opportunities for milk protein concentrate

245 Market trends and opportunities for milk protein concentrates. V. Lagrange,* *US Dairy Export Council, Arlington, VA.*

The US market for milk protein concentrates (MPC42–70) is estimated at 80–85,000 mt, and is complemented by a milk protein isolate (>85% protein) market estimated at 15–20,000 mt. MPC and MPIs range in protein content from approximately 42% to over 90%. Over 60% of the low-protein MPC (MPC 40–59) are used worldwide in dairy products (other than processed cheese). In Europe, yogurt and dairy desserts are an application where MPC's functional properties–improved viscosity, mouthfeel, emulsification, water binding–a favorable nutritional profile and the marketing appeal of a "clean label" increases their appeal. In the United States use in soups and sauces has increased significantly. Processed cheese dominates applications, although in the United States, volume used in this segment has decreased from 60% in 2007 to less than 40% in 2011. Almost all MPC purchases for use in specialty nutrition (sports, medical and clinical nutrition, geriatric nutrition) are high-protein concentration (80 percent or greater) products. The world market for milk protein isolates is estimated at 40,000 mt. These ingredients are highly valued in lactose free formulations and, increasingly, in medical nutrition product where they offer a milk dairy flavor and a desirable blend of "slow" and "fast" proteins. Clinical trials are underway in several locations to measure their effectiveness in the treatment of sarcopenia, the loss of muscle associated with aging.

Key Words: milk protein, milk protein concentrate, milk protein isolate

246 Impact of processing and storage on milk protein concentrate functionality. J. A. Lucey,* *University of Wisconsin-Madison, Madison.*

Milk protein concentrate (MPC) powder is basically skim milk powder with a reduced lactose (higher protein) content. Ultrafiltration (UF) is used to remove some lactose before drying, and UF processing may be adjusted to give MPCs that span a wide range of protein concentrations, for example, 40–85% protein in dry matter. High protein (>70%) MPCs can be slow to dissolve during rehydration and poor rehydration properties negatively affect the use of MPC in many applications. Another serious concern is that high protein MPCs can also exhibit a decrease in solubility during storage especially at storage temperatures > 20°C. Reports have indicated that some commercial MPC samples were prone to a large decrease in solubility during storage while other samples maintained good solubility. Differences in the mineral composition have been suggested as a possible explanation for variations in solubility behavior. High protein MPC requires extensive diafiltration to reduce the lactose content but this procedure also reduces the concentration of soluble salts. We have explored the impact of washing on protein solubility where washing was done with lactose solutions to remove soluble salts but not change the protein content. At least in our low protein MPC experiments, multiple diafiltration steps did not result in a disruption of the casein micelles or poor solubility during powder storage (although there was a loss of insoluble calcium from micelles). There are commercial MPC products that have been depleted of calcium, which presumably alters the micelle structure and casein-casein interactions that can occur during powder storage. High inlet air temperatures during MPC processing have also been suggested to impair solubility. Possible reasons include greater protein denaturation or enhanced Maillard cross-linking of proteins with lactose. A greater understanding is needed of the processing factors that determine MPC solubility.

Key Words: milk protein concentrate, solubility, functionality

247 Advances in processing and development of new milk protein products. H. Singh,* *Riddet Institute, Massey University, Palmerston North, New Zealand.*

The global demand for milk protein has increased significantly in recent years due to better understanding of its nutritional value, physiological and bioactive properties, and newly developed functional uses. In particular, consumer awareness of the benefits of protein in sports performance, weight management, lean muscle mass retention, satiety and general wellbeing has improved considerably over the last decade. Consequently, the demand for milk protein-enriched food and beverage products has moved into the mainstream as they appear to deliver these benefits more readily than other food proteins. The dairy industry produces a vast range of milk protein products, specifically designed for particular applications. These products include the traditional milk protein products, such as skim milk powder and whey powders, and higher protein products, such as caseins and caseinates, whey protein concentrates and isolates and milk protein concentrates and isolates. Among the higher protein products, milk protein concentrates (MPCs) and whey protein isolates (WPIs) have become very important for the dairy industry, as they provide several processing and functional/nutritional advantages over traditional milk powders. MPCs are now commonly added to milk or cheese formulations to enhance the protein content and to improve texture of yogurts. The use of MPCs in nutritional products is growing. In this application, MPC provides both casein and whey proteins in the same ratio as in milk, but without the high lactose content. However, several functionality problems are associated with high protein MPCs, including cold water solubility. Various patented processes have been developed for manufacturing MPC powders with improved functional characteristics, involving alterations in mineral balances and/or the state of aggregation of whey proteins. Development of high protein foods poses several functionality challenges, such as self-association/aggregation and high viscosity of proteins. New types of protein products and associated processes are being developed to overcome some of these technical challenges.

Key Words: milk protein, processing, functionality

248 Manufacture and application of micellar casein concentrates. D. M. Barbano,* *Cornell University, Department of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY.*

Micellar casein concentrate (MCC) is currently produced by removal of intact casein micelles from skim milk by microfiltration. The casein micelles may be further concentrated by ultrafiltration or evaporation. Liquid MCC may be used directly as a fresh ingredient, concentrated and stored as a long shelf-life refrigerated ingredient, or dried and stored for later use as a powdered ingredient. The MCC are different from caseinates, and acid and rennet caseins because the casein in MCC still retains its micelle structure and bound calcium. Casein in MCC is in the same form as casein in NDM powder and milk protein concentrates (MPC) produced by ultrafiltration. The difference between MCC and

NDM or MPC, is the presence of other dairy solids that will cause differences in functionality among these 3 products. The MCC can be produced in a range of purities. The key compounds being removed by microfiltration in the manufacture of MCC are milk serum proteins, lactose, soluble calcium phosphate, monovalent ions, and nonprotein nitrogen compounds. A technically feasible microfiltration process could continuously discharge a high-purity liquid MCC which has been 95% reduced in serum protein and soluble NPN compound contents at 9% true protein and < 0.2% lactose (both on wet bases). This liquid MCC could be further concentrated or dried. The liquid protein concentrate is bland in flavor, white, and viscous. Highly concentrated liquids have some unique properties. The MCC has excellent heat stability; when used as an ingredient in retorted beverage production, there is minimal browning and cooked flavor formation during sterilization. While MCC could be used as an ingredient in making nonstandardized cheeses in the US, the higher value uses for MCC may be as an ingredient in retorted, shelf-stable, high protein beverages and as an ingredient in low-fat natural cheese manufacture.

Key Words: micellar casein concentrate, microfiltration, serum protein removal

249 Performance of spiral wound microfiltration membranes during production of micellular casein concentrate. L. E. Metzger,* C. Marella, and P. Salunke, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Micellar casein concentrate can be manufactured from skim milk by microfiltration that utilizes membranes with an average pore size of 0.1 - 0.2µm. The microfiltration process concentrates micellar casein by selectively permeating whey proteins, lactose, and soluble minerals. In contrast to other processes for isolating casein (isoelectric precipitation or rennet induced coagulation), microfiltration has the advantage of concentrating micellar casein in its native state. The most common types of membranes used to microfilter milk are ceramic or spiral wound. In general ceramic membranes have an advantage in terms of performance whereas spiral wound membranes have an advantage in terms of cost. The data related to microfiltration of milk using spiral wound membranes has been collected using small scale manufacturing systems and short processing runs. This is an issue for manufacturers that attempt to scale up and commercialize microfiltration since the performance characteristics of spiral would microfiltration membranes are influenced by a variety of operating conditions and the selectivity of the membrane can vary substantially during a production run. In this study the performance of a 4 stage microfiltration system during a 15–20 h production run at 2 serum protein removal levels (40% and 85%) was determined. Relative to small scale systems, the continuous, single pass 4 stage process resulted in improved whey protein removal over the processing run. However, data on flux rates and selective passage of the major whey proteins showed that even though flux rates remained fairly constant, the membrane selectivity varied during the process run. This flux rate and selectivity data can be utilized by manufacturers to design a spiral wound microfiltration process to achieve their desired whey protein removal targets.

Key Words: micellar casein concentrate, spiral wound, microfiltration

Graduate Student Competition: ADSA Production Division Graduate Student Paper Competition, MS Division

250 Neutrophil function in the transition period and reproductive tract health in dairy cows. J. A. M. Wittrock,* T. F. Duffield, D. Bienzle, and S. J. LeBlanc, *University of Guelph, Guelph, ON, Canada.*

The study objective was to evaluate the relationship between neutrophil function during the transition period and reproductive tract disease in dairy cows. Phagocytic and killing ability of polymorphonuclear neutrophilic leukocytes (PMNL) are commonly reduced around calving. Cows (n = 81) were followed for 8 wk through the transition period. At −2, −1, 1, 2, 3, and 5 wk relative to calving, PMNL were isolated from the blood and phagocytosis and oxidative burst function were evaluated by flow cytometry, and serum glucose, NEFA, BHB, haptoglobin, insulin, and IGF-1 were measured. Endometritis and cervicitis were diagnosed at 5 wk postpartum by cytobrush cytology, with a positive diagnosis based on >5% PMNL. There were 27 cows (34%) with endometritis, and 22 (27%) with cervicitis. There was no difference in PMNL phagocytosis between cows with or without endometritis ($P = 0.2$). Cows with endometritis at wk 5 had 21% lower PMNL oxidative burst function at 2 wk after calving than unaffected cows ($P = 0.01$). Oxidative burst function of PMNL in cows with cervicitis was not different from healthy animals ($P = 0.2$). Cows with cervicitis had 28% lower PMNL phagocytosis than healthy cows 2 wk before calving ($P = 0.03$). Compromised phagocytosis and killing ability of PMNL may precede and contribute to cervicitis and endometritis after calving.

Key Words: transition cow, neutrophil, reproductive health

251 Effects of intrauterine infusion with *E. coli* lipopolysaccharide on systemic and local inflammatory and immune response. J. G. N. Moraes*[1], P. R. B. Silva[1], L. G. D. Mendonça[1], J. Silva[1], M. A. Ballou[2], K. N. Galvão[3], and R. C. Chebel[1], [1]*Department of Veterinary Population Medicine, University of Minnesota, St. Paul,* [2]*Department of Animal and Food Sciences, Texas Tech University, Lubbock,* [3]*Department of Large Animal Clinical Sciences, University of Florida, Gainesville.*

Objectives were to evaluate the effects intrauterine infusion with *E. coli* lipopolysaccharide (LPS) on periperal neutrophil function, hematology, intrauterine cell population, and expression of endometrial interleukin-1 (IL-1). Cows (31 ± 3 d postpartum) diagnosed with endometritis by Metricheck were assigned to receive 0 (NC, n = 31), 150 (150LPS, n = 33), or 300 (300LPS, n = 34) μg of *E. coli* LPS. A sub-sample of cows (n = 25/treatment) had blood sampled on the day of infusion (d0) before treatment and at 2 and 6 h after treatment for determination of neutrophil phagocytosis (PHAGO) and oxidative burst (OXID) and expression of CD18 and L-selectin. All cows had blood sampled at 0, 2, 6, 24, 48 h after infusion for hemogram and were examined for endometritis using Metricheck on d 1, 2, 7, and 28 and for sub-clinical endometritis using cytrobush on d 0 (before infusion), 1, 2, and 7. Data was analyzed by ANOVA for repeated measures or by chi-squared using MIXED and FREQ procedures, respectively. Percentage of neutrophils positive for PHAGO was ($P = 0.02$) greater for 300LPS (66.8 ± 1.5%) compared with NC (61.7 ± 1.5%) and 150LPS (61.9 ± 1.5%), but the intensity of PHAGO was not different ($P = 0.36$). Treatment did not affect percentages of neutrophils positive for OXID ($P = 0.49$) and for expression of CD18 ($P = 0.76$) and L-selectin ($P = 0.80$). Intensity of OXID tended ($P = 0.08$) be affected by treatment. Treatment had no effect on hematological parameters. Percentage of cows with endometritis 7 (59%; $P = 0.47$) and 28 (16.7%; $P = 0.92$) d after treatment was not affected by treatment. No differences in percentage of polymorphonuclear cells in uterine cytology were observed on d0 ($P = 0.35$) or thereafter ($P = 0.55$). Percentage of cows with >10% of PMNC in uterine cytology was not different among treatments on d 0 (48.5%;$P = 0.27$) and d 1 (85.3%;$P = 0.27$), but on d 7 150LPS (51.7%) and 300LPS (50%) cows tended ($P = 0.08$) to be less likely to have >10% of PMNC in uterine cytology than NC (75.9%) cows. Intrauterine infusion with 300μg of LPS resulted in slight increase in percentage of neutrophils positive for PHAGO.

Key Words: lipopolysaccharide, uterus

252 Effects of fresh-cow diseases on reproduction in a large commercial dairy herd. R. P. Tollefsrud*[1], R. L. Larson[1], H. M. Scott[1], G. A. Hanzlicek[1], and D. E. Little[2], [1]*Kansas State University, Manhattan,* [2]*DairyNet Incorporated, Brookings, SD.*

The 2007 NAHMS (National Animal Health Monitoring System) survey indicated that early lactation health issues are major factors influencing reproduction and culling on US dairy herds. The objective of this study was to evaluate fresh-cow health during the first 30 d in milk, and its association with days to pregnancy in the concurrent lactation. Data were collected on cattle that calved over a 2-mo period (July and August 2009) on a dairy farm located in the Upper Midwest region of the US Health and production data were collected daily for each cow from the beginning of lactation until the majority of the study population was confirmed pregnant. Both a competing risk analysis and a semi-parametric Cox proportional hazard regression model were completed, and the association between specific health-related events and days to pregnancy was investigated and compared between the models. These analyses showed metritis and dystocia in the first 30 d of lactation were associated with greater days to pregnancy. No difference was noted between parities, except lactation-5 and greater cows were significantly associated with greater days to pregnancy. These 2 analyses showed conflicting significance of association between retained placenta, ketosis, twinning, lameness, and other non-specific illnesses with days to pregnancy. This study found that a competing risk analysis and a semi-parametric regression model were appropriate methods to analyze time sensitive data such as reproductive efficiency. This study supports the evidence that parity, metritis, retained placenta, ketosis, dystocia, twinning, lameness, and other non-specific illnesses can affect reproductive inefficiencies.

Key Words: reproduction, animal health, dairy

253 Using temperature-sensing reticular boluses to aid in the detection of disease in dairy cows. A. E. Adams,* F. J. Olea-Popelka, and I. N. Roman-Muniz, *Colorado State University, Fort Collins.*

The objective of this study was to examine the feasibility of using a temperature-sensing reticular bolus (TSRB) to aid in the early detection of common dairy cow diseases. Approximately 2175 primiparous and multiparous Holstein dairy cows were utilized in this study. Each cow received an orally administered TSRB after parturition. Reticular temperature (RT) measurements were obtained for approximately 350 d, as cows equipped with a TSRB passed the reading panels located at the exit lanes of the milking parlor. Over the 350 d study period, health data were collected for all cows diagnosed by dairy personnel with the following production disorders: mastitis, metritis, lameness, or pneumonia. A retrospective analysis of all health and RT temperature data was conducted. For analysis of RT data, a cow was determined to have a fever if RT exceeded baseline temperature by 0.8°C during the 4 d before diagnosis, determined by a logarithm in the TempTrack software (DVM Systems LLC, Greeley, CO). The health and RT data were combined and analyzed to examine the relationship between fever and disease. A logistical regression model was used to determine the likelihood of a cow with a fever (as defined by TSRB data) being diagnosed with one of the listed diseases by dairy personnel. A total of 218 health events were included in this data set. Odds ratio analysis indicate that a cow presenting a fever is 6.73 times as likely to be diagnosed with mastitis ($P < 0.0001$) and 7.50 times as likely to be diagnosed with pneumonia ($P = 0.0183$), as one that did not present a RT change. No difference in RT was found between cows diagnosed as being lame or with metritis when compared with the "healthy" controls. These data suggest that RT monitoring coupled with routine observation and the prompt assessment of cows has the potential to aid in the early detection of mastitis and pneumonia in dairy cows.

Key Words: reticular temperature, dairy cow, disease

254 Optimization of methods for the detection of *Mycobacterium avium* ssp. *paratuberculosis* in milk and colostrum of naturally infected dairy cows with Johne's disease.

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Mycobacterium avium ssp. *paratuberculosis* (MAP) is the causative agent of Johne′s Disease (JD), a chronic enteritis that occurs in dairy cattle and other ruminants. A 2007 NAHMS Dairy Study demonstrated that over 68% of dairy herds are infected with JD so the risk of exposure within a herd is high. MAP is primarily shed in the feces but it is also shed into the milk and colostrum of infected cows. Because of this, there exists concern about transfer of the organism from dam to calf and the prevalence of MAP in the milk supply. The amount of MAP shed into milk is not well defined because the complexity of the milk matrix and presence of confounding microorganisms makes it difficult to recover MAP via culture methods. The objective of this study is to optimize the decontamination of whole raw milk for the isolation of viable MAP and compare recovery rates in liquid culture mediums. The efficacy of 2 liquid culture mediums, TREK-ESP and BD Bactec 12B were compared for recovery speed and thresholds, incidence of contamination, and reproducibility of results. Milk collected from a non-infected cow was spiked with known concentrations of MAP (10^2 to 10^8 cfu/mL). Two chemical decontaminates were investigated, hexadecylpyridinium chloride (HPC) and N-acetyl-L-cysteine-sodium hydroxide (NALC-NaOH). It was found that NALC-NaOH was the superior chemical for decontamination ($P < 0.01$) and that MAP recovery from milk was highest and contamination was lowest when decontaminated with 1.5% NaOH for a 15-min exposure time. In comparing the 2 liquid culture mediums, Bactec 12B was superior in recovery especially at low spiking levels ($P < 0.01$) with a detection threshold of less than 10^2 cfu/ml and superior in speed of recovery of viable MAP. TREK-ESP culture demonstrated an increased incidence in false positive and false-negative results that were not observed in Bactec 12B medium. Optimized methods will be used to assess the frequency and level of MAP shed into milk during a complete lactation period of naturally infected dams.

Key Words: Johne's disease, milk, cattle

255 Effects of transient silage DM concentration variation on dairy cows.

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Transient changes in silage DM concentration, if unaccounted for, will cause a diet to become unbalanced. We hypothesized that a transient decrease in silage DM% would have a negative effect on DMI and milk yield and composition. Holstein cows (24) at 116 DIM were used in 8 replicated 3 × 3 Latin squares with 21-d periods. The treatments were 1) Control (CON), 2) Unbalanced (UNB), and 3) Balanced (BAL). The CON diet was formulated to have a consistent silage DM% and forage:concentrate (F:C) of 55:45 throughout the period. Forage consisted of 67% alfalfa silage (53%DM) and 33% corn silage (36%DM). The UNB and BAL diets were the same as the CON for most of the period except during 2 3-d bouts when water was added to the silage (simulating a rain event) to cause a 10%-unit decrease in silage DM%. During the bouts, the UNB diet was the same as CON on an as-fed basis, but the F:C changed to 49:51 (DM basis), changing diet DM (67.2 vs 64.0%), NDF (32.0 vs 30.7%), and starch (29.8 vs 31.5%). The BAL treatment corrected for the change in silage DM concentration by an increase in silage inclusion to rebalance the F:C to 55:45. Daily DMI and milk yield were measured and milk composition was measured 3 times during the bouts and 3 times during the normal time. A mixed model including parity, cows within parity, period, bout, and treatment with repeated measures (i.e., bout (wet and dry) within period) was used. Over the 21-d period, treatment did not affect DMI (24.0, 24.1 and 23.8 kg/d for CON, UNB and BAL), milk yield (39.4, 39.9 and 39.6 kg/d), milk fat (3.41, 3.42 and 3.33%), and milk protein (2.78, 2.80 and 2.79%). No differences were observed between wet and dry bouts within each treatment for DMI and milk yield; but for UNB, milk fat (3.48 vs 3.35%) increased and milk protein (2.78% vs 2.82%) decreased during wet bouts. A significant decrease in milk yield between wet bouts occurred within the UNB treatment (40.3 vs 39.4 kg/d). Overall, a large decrease in silage DM% (10%-unit) over short-term bouts (with or without TMR adjustment) had only minor effects on DMI, milk yield and composition. Therefore, with drier silages adjusting for short-term, transient changes in silage DM was not necessary.

Key Words: silage variability, precision feeding, DM change

256 Development of a merit-based genetic selection index for dairy grazing systems.

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Pasture-based dairy producers face different costs, revenues and management challenges from those with conventional production systems. These differences have led many graziers to question whether the US Lifetime Net Merit (NM$) index is appropriate to achieve maximum economic gain when selecting dairy cows and bulls for their breeding programs. A Grazing Merit index (GM$) parallel to the US NM$ index was constructed using costs, revenues, and management characteristics representative of grazing systems. Inputs were obtained from surveys, literature, and farm financial record summaries. Derived weights for GM$ were then multiplied by Predicted Transmitting Abilities of 584 active Artificial Insemination Holstein bulls to compare with NM$. Spearman rank correlation between GM$ and NM$ was 0.93 ($P < 0.0001$). Traits included in GM$ (and their percentage of weight) include: milk volume (24%), fat yield (16%), protein yield (4%), productive life (7%), somatic cell count (−8%), Feet and Leg Composite (4%), Body Size Composite (−3%), Udder Composite (7%), daughter pregnancy rate (18%), calving ability (3%), and dairy form (6%). Weights in NM$ were 0, 19, 16, 22, 10, 4, 6, 7, 11, 5, and 0% for the same traits, respectively. Dairy form was added to GM$ to offset the decrease in strength that arises from selection to reduce stature by selecting against Body Size Composite. Relative importance of milk volume was greater due in part to a difference in the milk prices used and the increased marginal value of milk yield when production is less in grazing systems. There is a large decrease in the emphasis placed on productive life probably because grazing cattle tend to remain in the herd longer; therefore, the marginal value of increasing length of productive life is decreased. This trend is reflected in the relative weight for productive life in GM$ (18%) vs NM$ (22%). It appears that NM$ may provide guidance for pasture-based dairy producers, however a GM$ index based upon appropriate costs and revenues, is more beneficial.

Key Words: grazing, Holstein, selection index

257 Effects of stocking rate, supplement strategy and breed in a pasture-based automatic milking system.

C. Nieman,* S. Utsumi, D. K. Beede, and J. Rowntree, *Michigan State University, East Lansing.*

The influence of 2 grazing and supplementation strategies on the performance of 14 United States Holstein (564 ± 38 kg BW; mean ± SD) and 14 New Zealand Friesian (393 ± 27 kg BW) cows in a pasture-based automatic milking system (AMS) was investigated. The study was a 2 × 2 factorial of the 2 breeds and 2 stocking rate treatments lasting 56 d. The low stocking rate (1.92 cows/ha) treatment was offered pasture plus concentrate (PC), whereas the high stocking rate (2.81 cows/ha) treatment was offered PC plus a partial totally mixed ration (pTMR; 60% forage). Amount of pTMR fed was adjusted weekly and used to supplement deficits in pasture allowances and growth rate. Each stocking rate treatment had voluntary access to a single stall AMS where cows were offered 1 kg of concentrate per 6 kg of milk. Voluntary access to pastures was controlled via automated gates. Fresh pasture allocations were opened daily at 0500 h. Targeted pre- and post-grazing pasture biomass was 2,400 kg/ha and 1,600 ± 200 kg/ha, respectively. Pre- and post- grazing biomass was recorded daily with a rising plate meter. Milk yield (MY), daily milking frequency (MF), Milk fat and Milk protein were analyzed with a repeated measures mixed model for a completely randomized design ($P < 0.05$). There was a week by treatment interaction for MF, likely influenced by weekly MF increases for pTMR. The MY followed a similar week by treatment interaction trend ($P = 0.08$), likely explained by MY increases for pTMR during the final weeks of the study. No treatment by breed or week by breed interaction was detected, but significant differences in milk production and composition were detected between the 2 breeds (Table 1). Results suggest a higher milk productivity for the high stocking rate and pTMR supplemented system and superior milk production for United States Holstein cows.

Table 1. Milk production and composition by breed

Variable	New Zealand Friesian	United States Holstein
Milk yield, kg/d	15.3^{b}	27.9^{a}
Milking frequency,/d	2.2^{b}	2.5^{a}
Milk fat %	4.2^{a}	3.6^{b}
Milk protein %	3.3^{a}	3.1^{b}

^{a,b}Means within a row with different superscripts differ ($P < 0.05$).

Key Words: pasture-based dairy, automatic milking, feeding systems

Physiology and Endocrinology: Estrous Cycle Manipulation–Beef

258 Mean and basal LH concentrations increased in peri-puberal beef heifers during early exposure to androgenized steers. C. Fiol*[1], N. Curbelo[2], G. Larraz[2], L. de Melo Menezes[3], and R. Ungerfeld[2], *[1]Departamento de Bovinos, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay, [2]Departamento de Fisiología, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay, [3]Universidad de Pelotas, Rio Grande del Sur, Brazil.*

The aim of the experiment was to characterize the LH secretion pattern in peri-puberal beef heifers exposed to androgenized steers (AS) during 80 d. Thirty anestrous Hereford heifers (24-mo-old, 257.5 ± 32.5 kg) and 3 AS were used. Since D0, 15 heifers were exposed to AS during 80 d (group EH), remaining 15 heifers isolated from AS or any other male (group IH). Both groups grazed low quality native pastures in 2 paddocks separated by 600 m. From D-10 to D30, daily ovarian ultrasonographic evaluations were done in all the heifers to determine the presence of corpus luteum and the onset of cyclic activity. Thereafter, ovarian ultrasonographic determinations were done every week (D32 to D60) and every 10d (D60 to D80) to determine the presence of corpus luteum. At 10 d intervals (D-10 to 30), 8 heifers per treatment were housed in individual cages and blood samples were collected at 15-min intervals for 6h. Concentrations of LH were determined by RIA, and compared with repeated measures ANOVA; cyclic activity was compared with chi-squared test. Cumulative proportion of cyclic heifers was greater for EH than IH on D60 (33.3 vs 0%, $P = 0.01$), 70 (47 vs 0%, $P < 0.005$) and 80 (53 vs 0%, $P < 0.001$). On D10 of the exposure period, mean and basal concentrations of LH were greater in EH than IH (Table 1). The frequency of LH pulses was greater in D10 compared with D0 and 20, and tended to be greater to D30 (Table 1). In conclusion, exposure to AS stimulated LH secretion pattern during the first days of the exposure period.

Table 1.

	Mean LH, ng/mL		Basal LH, ng/mL		LH pulse frequency, pulses/6h
Day	EH	IH	EH	IH	
−10	1.18 ± 0.09	1.27 ± 0.09	1.05 ± 0.08	1.12 ± 0.08	3.12 ± 0.25
0	1.08 ± 0.09	1.19 ± 0.09	0.96 ± 0.08	1.02 ± 0.08	2.81 ± 0.25^{y}
10	1.68 ± 0.09^{a}	0.88 ± 0.09^{b}	1.53 ± 0.08^{a}	0.75 ± 0.08^{b}	3.68 ± 0.25^{x}
20	1.83 ± 0.09	1.82 ± 0.09	1.66 ± 0.08	1.63 ± 0.08	2.68 ± 0.25^{y}
30	1.45 ± 0.09	1.94 ± 0.09	1.26 ± 0.09	1.77 ± 0.08	2.96 ± 0.26

Different superscripts indicate significant differences between treatments (in the same row; a vs b) and days (in the same column; x vs y). a vs b, x vs y: $P < 0.05$.

Key Words: LH profiles, male effect, puberty

259 Plasma progesterone concentration in beef heifers receiving exogenous glucose, insulin, or bovine somatotropin. B. I. Cappellozza*[1], R. F. Cooke[1], M. M. Reis[2], F. N. T. Cooke[1], D. W. Bohnert[1], and J. L. M. Vasconcelos[2], *[1]Oregon State University - EOARC, Burns, [2]UNESP - FMVZ/DPA, Botucatu, SP, Brazil.*

Three experiments evaluated plasma concentrations of glucose, insulin, IGF-I, and progesterone (P4) in pubertal beef heifers receiving exogenous glucose, insulin, or sometribove zinc. All heifers utilized had no luteal P4 synthesis but received a controlled internal drug releasing device containing 1.38 g of P4 to estimate treatment effects on hepatic P4 degradation. In Exp. 1, 8 nulliparous Angus × Hereford heifers (initial BW = 442 ± 14 kg; initial age = 656 ± 7 d) were randomly assigned to receive, in a crossover design containing 2 periods of 10 h: 1) intravenous (i.v.) insulin infusion (1 µg/kg of BW; INS) or 2) i.v. saline infusion (0.9%; SAL). Treatments were administered via jugular venipuncture in 7 applications (0.15 µg of insulin/kg of BW per application) 45 min apart (from 0 to 270 min). Blood samples were collected immediately before each infusion, as well as at −120, −60, 330, 390, and 450 min relative to the first infusion. Heifers receiving INS had greater ($P < 0.01$) plasma insulin, reduced ($P \leq 0.04$) plasma glucose and IGF-I, but similar ($P = 0.62$) plasma P4 concentrations compared with SAL heifers. In Exp. 2, the same heifers were assigned to receive, in a similar experimental design as Exp. 1: 1) i.v. infusion containing insulin (1 µg/kg of BW) and glucose (0.5 g/kg of BW; INS+G) or 2) SAL. Heifers receiving INS+G had greater ($P \leq 0.02$) plasma insulin, glucose, and P4, but reduced ($P = 0.01$) plasma IGF-I concentrations compared with SAL heifers. In Exp. 3, the same heifers were assigned to receive, in a crossover design containing 2 periods of 14 d: 1) subcutaneous injection containing 250 mg of sometribove zinc (BST), or 2) SAL. Blood samples were collected 3 h apart (from 0900 to 1800 h) on d 6, 8, and 10 relative to treatment administration (d 1). Heifers receiving BST had greater ($P < 0.01$) plasma glucose and IGF-I, and similar ($P \leq 0.67$) plasma insulin and P4 concentrations compared with SAL heifers. Results from this series of experiments suggest that concurrent increases in glucose and insulin are required to reduce hepatic catabolism and increase plasma concentrations of P4 in bovine females.

Key Words: heifer, insulin, progesterone

260 Prediction of estrus in beef cows using ruminal temperature. B. H. Boehmer* and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Core body temperature increases at estrus in beef cows. Monitoring ruminal temperature (RuT), a measure of core body temperature, may be useful for the prediction of estrus. The objective of this experiment was to evaluate the use of RuT in beef cows for the prediction of estrus. Hourly reporting temperature boluses (SmartStock, LLC) were administered to Angus cows (n = 60) with a balling gun. Estrus was synchronized with $PGF_{2\alpha}$ at 66 ± 2 d postpartum. The onset of estrus was determined as a 0.7°C increase in mean RuT of a cow for any 9 h period compared with the mean RuT 12 to 84 h before the 9 h identification period. The onset of estrus was determined by HeatWatch (CowChips, LLC). Ambient temperature (Tamb; www.mesonet.org) and RuT were analyzed using the UNIVARIATE and MIXED procedures (SAS). Mean Tamb for the experimental period was 19.1 ± 0.1°C (range: 16 to 32°C). Maximal daily Tamb (Tmax) was ≥32°C in only one of the 13 d. Mean RuT for all cows was 37.96 ± 0.01°C. The beginning of the 9 h mean increase of 0.7°C in RuT occurred 8.4 ± 6.1 h before the onset of estrus, as determined by HeatWatch. During the 9 h after the onset of estrus (HeatWatch), RuT was greater ($P = 0.001$, 38.54 ± 0.09°C) compared with 16 to 24 h before (37.92 ± 0.09°C) and 24 to 32 h after (37.98 ± 0.09°C) onset of estrus. Ruminal temperature correctly identified estrus in 79% of cows and identified a non estrus cow as estrus in 40% of cows. Diurnal variation in RuT was maximal at 2300 h (38.22 ± 0.03°C) and had a nadir at 1200 (37.70 ± 0.04°C). The magnitude of the increase in

RuT at estrus (9 h period compared with the previous 12 to 84 h) was greater when estrus occurred from 1700 to 0000 h compared with 0100 to 0800 h ($P = 0.009$; 0.98 ± 0.15°C vs. 0.49 ± 0.09°C, respectively). The magnitude of increase in RuT at estrus tended to be greater when estrus occurred from 1700 to 0000 h compared with 0900 to 1600 h ($P = 0.079$). These results indicate that RuT can be used for the prediction of estrus in beef cows. Diurnal variation in RuT should be incorporated in a model that utilizes RuT to predict estrus in beef cows.

Key Words: beef cow, ruminal temperature, estrus

261 Comparison of three CIDR-based fixed-time AI protocols for beef heifers.

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Several effective fixed-time AI (FTAI) protocols have been developed to facilitate AI while eliminating the need for estrus detection. Among these are the 5-d CO-Synch+CIDR (5d), PG 6-d CIDR (PG-CIDR), and 14-d CIDR-PG (CIDR-PG) protocols. While each of these protocols vary in duration and approach to synchronizing estrus and ovulation, each has been reported as an effective method to facilitate FTAI in beef heifers. Therefore, the objective of this study was to compare FTAI pregnancy rates in beef heifers synchronized with these 3 CIDR based protocols. Virgin beef heifers (n = 801) at 4 locations were synchronized with one of 3 protocols: 1) (5d) an injection of GnRH (100 µg; i.m.) and insertion of a CIDR on d −5, PG (25 mg; i.m.) and CIDR removal on d 0 and a second injection of PG (>4 h after CIDR removal) on d 0 and FTAI at 72 h after CIDR removal, 2) (PG-CIDR) PG (25 mg; i.m.) on d −9, GnRH (100 µg; i.m.) and insertion of a CIDR on d −6, PG and CIDR removal on d 0, and FTAI at 66 h after CIDR removal, or 3) (CIDR-PG) a CIDR insert from d 0 to 14 and PG (25 mg; i.m.) on d 30 and FTAI at 66 h after PG. All heifers received an injection of GnRH (100 µg; i.m.) concurrent with FTAI. Timing of treatment initiation was offset to allow all heifers to receive FTAI concomitantly and at random. Pregnancy success was determined between 35 and 40 d after FTAI by transrectal ultrasonography. Blood samples were collected approximately 12 d before the beginning of each protocol and at the initiation of each protocol to determine estrous cycling status (77%). Data were analyzed using the GLIMMIX procedures of SAS. Fixed-time AI pregnancy success did not differ between treatments ($P = 0.13$; 62.5%, 56.9%, and 53.3%, for 5-d, PG-CIDR, and CIDR-PG; respectively) or location ($P = 0.16$; 51.5%, 62.7%, 56.1%, and 58.6% for location 1, 2, 3, and 4; respectively). However, heifers that had reached puberty had greater ($P < 0.01$) pregnancy success compared with heifers that were prepubertal (60.7% and 47.3%; respectively). In summary, all 3 protocols had similar FTAI pregnancy success, and puberty status had the greatest impact on pregnancy success.

Key Words: fixed-time AI, beef heifer, pregnancy

262 Ovarian dynamics and AI pregnancy rates with PGF2α administration 2 d prior to the onset of a 5-d CO-Synch + CIDR program in beef cattle.

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The 5-d CO-Synch + CIDR program was used in heifers and postpartum beef cows across 2 studies to compare ovarian dynamics and AI pregnancy rates when animals received PGF 2 d before onset of the program. In all animals in both studies; blood samples were collected on d −17 and −7 of the expt. to assess reproductive status based on plasma progesterone (P4) concentration, 100 µg GnRH (GnRH-1; Cystorelin) was given at CIDR insertion on d −5, CIDR was removed on d 0 coincident with PGF injection (heifers, 25 mg; cows, 50 mg; Lutalyse). In Expt 1, prepubertal heifers (n = 35) and anestrous cows (n = 50) were randomized by age and body weight, and age and days postpartum (DPP), respectively, to receive or not, 25 mg of PGF on d −7. On d 3, all females received 100 µg GnRH (GnRH-2).Ovarian ultrasonography was conducted on d −7, −5 and −3 to determine ovulatory response to GnRH-1, d 0 to 3 to evaluate ovarian follicular dynamics during synchronization, and on d 3, 5, and 9, concurrent with blood samples to evaluate P4, size of ovulatory follicle (OF) at GnRH-2, and the proportion of females induced to ovulate and develop a functional CL following GnRH-2. In Expt 2, postpartum beef cows (n = 410) in 3 locations were randomized by DPP and age to receive or not the PGF treatment on d – 7. Estrus was detected for 60 h after PGF and AI according to the AM/PM rule. Cows not bred at estrus were timed AI on d 3 following GnRH-2. In Expt 1, ovulation response to GnRH-1, ovarian follicular development during the program, size of the OF and ovulation response to GnRH-2, size of the CL and P4 on d 9 did not differ between treatments within animal class. In Expt 2, synchronized AI pregnancy rate did not differ between cows that did and did not receive PGF on d −7 (47.3% and 50.7%, respectively). Interactions of treatment with reproductive status, estrus detection, location, AI technician and sire for AI pregnancy rate were not detected. In conclusion, PGF administration 2 d before the onset of the 5-d program did not influence ovarian dynamics in anestrous females or synchronized pregnancy rate in postpartum cows.

Key Words: beef cattle, PGF, AI

263 Efficacy of a new, once-used, or twice-used CIDR in a 5-day CO-Synch + CIDR estrous synchronization protocol in suckled beef cows.

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The objective of this experiment was to compare timed-AI (TAI) pregnancy rates (PR) in suckled beef cows treated with either a new, once-used, or twice-used CIDR within the 5-d CO-Synch + CIDR protocol. Angus-cross beef cows (n = 307) from 2 locations were stratified by estrous cycling status as determined by identification of a corpus luteum (CL) via transrectal ultrasonography on d −11 and −1 (d 0 = CIDR insertion, d 8 = TAI), age (2 yr old; n = 68 vs. ≥ 3 yr [mature]; n = 239), and BCS and randomly allotted to 1 of 3 treatments. Cows were enrolled in the 5-d CO-Synch + CIDR protocol that included either: 1) a new CIDR (NEW); 2) a CIDR previously used once in a 5-d estrous synchronization protocol (1X); or 3) a CIDR previously used in 2, 5-d estrous synchronization protocols (2X). Blood samples were collected

at d −11, d −1 and d 15 for analysis of progesterone (P4) to confirm ultrasound findings for cycling status and to assess the proportion of previously anestrous cows that ovulated and developed a functional CL following TAI. Determination of pregnancy was performed by transrectal ultrasonography 31 d after TAI. Categorical and continuous data were analyzed with the GLIMMIX and MIXED procedures of SAS, respectively. The proportion of cows cyclic by d −1 (75.8%) did not differ between treatments. TAI PR did not differ ($P = 0.40$) among NEW (55.7%), 1X (57.8%), and 2X (49.5%) treatments. However, there was a treatment × age interaction ($P < 0.001$). In 2 yr olds, the 2X (78.3%) treatment had greater ($P = 0.003$) TAI PR than the NEW (34.7%) treatment, with 1X treatment being intermediate (59.1%). In mature cows, the NEW (61.7%) and 1X (57.5%) treatments had greater ($P \leq 0.02$) TAI PR than the 2X (41.0%) treatment. In addition, TAI PR was greater ($P = 0.008$) in cyclic (56%) than non-cyclic (50%) cows. On d 15, the proportion of previously anestrous cows that had greater than 1 ng/mL of P4 (94.7%) and mean P4 concentrations (4.37 ± 0.20 ng/mL) did not differ among treatments. In summary, cow age affects the number of times a CIDR can be effectively used in the 5-d CO-Synch + CIDR protocol.

Key Words: beef cow, CIDR, timed AI

264 Fixed-time AI in lactating beef cows after GnRH on day 9 of a 14-d CIDR.

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Most progestin-based estrous synchronization protocols focus on inducing a new follicular wave before progestin removal by administering GnRH at the initiation of the protocol. However, lack of response to GnRH due to stage of the estrous cycle when given and incomplete corpus luteum regression upon progestin removal contribute to failure to conceive to timed-AI (TAI). Our objectives were (1) to determine the effectiveness of an extended controlled internal drug release (CIDR) protocol with 2 induced follicular waves, and (2) determine the efficacy of initiating the 14-d CIDR treatment with GnRH analog (Factrel) or prostaglandin F$_{2\alpha}$ (PG) injections. Lactating beef cows at 4 locations (n = 264, location 1; n = 94, location 2; n = 139, location 3; n = 128, location 4) were randomly assigned to 3 treatments. Cows in the 14-d GnRH group received a CIDR (1.38 g progesterone) and 100 µg GnRH im on d 0, 100 µg GnRH im on d 9, CIDR removal with 50 mg PG im on d 14, and 100 µg GnRH im with TAI 72 ± 3 h after CIDR removal. Cows in the 14-d PG group were assigned the same protocol as 14-d GnRH cows except that 25 mg PG im was given at CIDR insertion instead of GnRH. Cows in the control treatment, 5-d CO-Synch + CIDR (5-d CO-Synch), received a CIDR and 100 µg GnRH im on d 9, CIDR removal and 25 mg PG im on d 14, 25 mg PG im 6 ± 1 h later, and 100 µg GnRH im with TAI 72 ± 3 h after CIDR removal. Body condition scores for the 14-d GnRH, 14-d PG, and 5-d CO-Synch treatments averaged (±SD) 4.8 ± 0.82, 4.9 ± 0.85, and 4.8 ± 0.82, and postpartum intervals at TAI were 75 ± 17.2, 76 ± 17.0, and 78 ± 16.7 d, respectively. Pregnancy status to TAI was determined 40 ± 2 d after TAI by ultrasonography. With no treatment x location interaction ($P > 0.05$), combined pregnancy rates to TAI were higher ($P < 0.05$) in 14-d PG cows (70.4%, 2 = 205) than 14-d GnRH (54.4%, n = 214) and 5-d CO-Synch cows (53.5%, n = 206). There was no increase in pregnancy rate to TAI with inclusion of 2 GnRH injections within a 14-d CIDR, however replacement of GnRH with PG at the initiation of the 14-d PG treatment improved TAI pregnancy rates compared with the 5-d CO-Synch treatment.

Key Words: CIDR, estrous synchronization, PGF$_{2\alpha}$

265 Comparison of long-term CIDR-based protocols to synchronize estrus and ovulation prior to fixed-time artificial insemination in postpartum beef cows.

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This experiment compared 2 long-term CIDR-based protocols to synchronize estrus and ovulation before fixed-time AI (FTAI) in postpartum beef cows. Cows were assigned to treatments by age, body condition score (BCS), and days postpartum (DPP). Cows in treatment one [T1 (n = 92)] received CIDR inserts (1.38 g progesterone) from d 0 to d 14, and PGF$_{2\alpha}$ (PG; 25 mg i.m.) 19 d after CIDR removal on d 33. Cows in treatment 2 [T2 (n = 90)] received CIDR inserts from d 3 to d 17, and PG 16 d after CIDR removal on d 33. Cows in both treatments were inseminated 72 h after PG with GnRH (100 µg i.m.) at FTAI. Blood samples for progesterone were collected at d −10 and d 0 to determine pretreatment estrous cyclicity status, and again at PG. HeatWatch estrus detection transmitters were applied at CIDR removal and replaced at PG to determine onset of estrus following CIDR removal and PG. Dominant follicle diameter was determined via transrectal ultrasonagraphy at PG and FTAI. Pregnancy diagnosis was performed via transrectal ultrasonagraphy 70 d after FTAI and confirmed at 180 d gestation. Age, BCS, DPP, P4 concentrations, and follicle diameters were analyzed by PROC TTEST. Pregnancy rates for FTAI and final pregnancy were analyzed by PROC GLIMMIX. There were no differences between treatments for cow age, BCS, or DPP. Progesterone concentrations at PG were higher ($P = 0.04$) for cows assigned to T2 than T1 (2.4 versus 1.9 ng/mL, respectively). Estrous response after PG and before FTAI was higher ($P = 0.05$) for cows assigned to T1 (45%) compared with T2 (31%). There were no differences between treatments in mean diameter of dominant follicles at PG or FTAI. Despite differences in estrous response between treatments after PG, there was no difference between treatments for FTAI pregnancy rate ($P = 0.23$; T1 52/92 = 57%; T2 42/90 = 47%) or final pregnancy rate ($P = 1.00$; T1 76/91 = 84%; 76/90 = 84%). In summary, both protocols worked effectively to synchronize estrus and ovulation before FTAI in postpartum beef cows, suggesting that a range in interval from CIDR removal to PG may be feasible when using long-term CIDR-based protocols.

Key Words: fixed-time AI, CIDR, beef cow

266 Determination of concentrations of anti-Müllerian hormone at estrus during a synchronized and a natural bovine estrous cycle.

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Concentrations of anti-Müllerian hormone (AMH) have been correlated to antral follicle counts, which are indicators of fertility. The effects of exogenous hormones on AMH have not been evaluated. Therefore, the objective of this experiment was to determine if concentrations of AMH at estrus differ in a synchronized compared with a natural estrous cycle. Nulliparous heifers (11 to 15 mo; n = 68) consisting of Angus (n = 19), Charolais (n = 5), Holstein (n = 34) and Jersey (n = 10) breeds were synchronized using the Select Synch + CIDR protocol (GnRH^{+}CIDR-7 d-CIDR removal+PGF$_{2\alpha}$). Heifers were observed for expression of synchronized estrus every 6 h until 84 h after the injection of PGF$_{2\alpha}$. Ovarian structures were evaluated by transrectal ultrasonography performed on heifers detected in standing estrus or with an activated heatmount detector and secondary signs of estrus. Blood samples were collected at estrus via venipuncture of the coccygeal vein of the tail for analysis of concentrations of AMH during the synchronized and natural estrous cycles. Visual detection of the subsequent estrus, considered natural estrus, occurred every 6 h from d 16 to 24 after synchronized estrus. The number of days between synchronized and natural estrus was 20.05 ± 1.60 (mean ± SD). Concentrations of AMH were determined using the Beckman-Coulter AMH Gen II ELISA kit. The GLM, CORR and REG procedures of SAS were used to analyze data. Concentrations of AMH between natural and synchronized estrus were highly correlated ($r = 0.67$, $P < 0.001$). A 0.100 ng/mL increase in the concentration of AMH in a natural estrous cycle was associated with a 0.077 ng/mL increase in the concentration of AMH in a synchronized estrous cycle ($P < 0.001$). The mean concentration of AMH did not differ ($P > 0.05$) between the natural (0.0543 ± 0.008 ng/mL) or synchronized (0.0428 ± 0.008 ng/mL) estrous cycles. In conclusion, concentrations of AMH were similar between a natural and a synchronized estrous cycle.

Key Words: anti-Müllerian hormone, bovine, estrus synchronization

267 Effect of time of insemination relative to ovulation on pregnancy rate of Nelore cows submitted to TAI protocols. M. Maturana Filho, R. Germano de Rezende, J. R. Naves,* G. A. Fonseca, T. K. Nishimura, V. B. Nunes, and E. H. Madureira, *FMVZ/USP, Pirassununga, SP, Brazil.*

The economic efficiency of cattle is related to the production of calves. The time of insemination relative to ovulation is an important factor in conception rate due to 2 physiological factors, time required for sperm capacitation in the female genital tract and survival of both gametes (spermatozoa and oocyte). The present study aimed to evaluate the influence of time of artificial insemination (AI) on pregnancy rate. The experiment was conducted on the campus of University of São Paulo (USP) Pirassununga, College of Veterinary Medicine and Animal Science (FMVZ). We used 665 Nelore cows submitted to timed artificial insemination protocol. The TAI protocol consisted of d 0 — insertion of an intravaginal progesterone-releasing device on a random stage of estrous cycle, and an injection of 2.0 mg of estradiol benzoate (EB). On d 8, the implants were removed and the cows received an injection of 0.150 mg of PGF2α and 300 IU of equine chorionic gonadotropin (eCG). On d 9, they received an injection of 1.0 mg of EB. AI was performed at 10 d and expected to ovulation time was 1900 h. The cows were randomly divided into 3 experimental groups, according to the time of insemination, being performed using semen of 2 Nelore bulls: Group 1 (G1) inseminated between 1330 and 1450 h, Group 2 (G2) between 1451 and 1610 h and Group 3 (G3) between 1611 and 1730 h. Pregnancy rate was obtained after 30 d using ultrasound Aloka SSD 500, using linear probe. The pregnancy rate obtained in G1, G2 and G3 were 63.8, 75.4 and 54.7% respectively. The semen of 2 bulls used to AI, was distributed in a balanced form among the groups, however, there was no difference in pregnancy among them. The time of AI influenced ($P < 0.05$) fertility, was observed that the best time to perform the AI is between 6 and 4 h before the expected ovulation.

Key Words: Nelore cows, ovulation, protocols

268 Substituting ground redberry juniper leaves and stems for oat hay in lamb feedlot diets: Growth performance, serum urea nitrogen, serum insulin-like growth factor-1, and wool characteristics. T. R. Whitney*[1], C. D. Swening[1], J. P. Muir[2], C. J. Lupton[1], and W. C. Stewart[1], [1]*Texas AgriLife Research, San Angelo,* [2]*Texas AgriLife Research, Stephenville.*

The abundance of redberry juniper throughout southwest rangelands presents rangeland management challenges, yet presents opportunity as an untapped feed resource. Drought and rising feed costs also make ground redberry juniper forage a cost-effective alternative roughage. Rambouillet lambs (n = 45) were used to evaluate effects of substituting redberry juniper for oat hay on feedlot performance, serum urea nitrogen (SUN), IGF-1 concentrations and wool characteristics. In a completely randomized design study with 2 feeding periods (Period 1 = 64% concentrate diet, 35 d; Period 2 = 85% concentrate diet, 61 d), lambs were individually fed ad libitum diets containing 40% dried distillers grains with solubles (DDGS) and ground juniper leaves and stems that replaced 0%, 33%, 66%, or 100% of the ground oat hay. In Period 1, a positive quadratic effect was observed in lamb ADG and DMI as juniper replaced 0% to 100% of oat hay ($P < 0.003$). In Period 2, a linear response occurred in lamb ADG as juniper replaced up to 100% of oat hay ($P = 0.007$), whereas DMI was unaffected ($P > 0.10$) after d 49. Overall, final BW of each period quadratically increased ($P < 0.04$) and there was no effect ($P > 0.32$) of treatment on G:F. During Period 2, a positive quadratic effect on SUN ($P = 0.002$) and a linear effect on fecal N ($P = 0.001$) were observed, due in part, to a combined effect of DMI and dietary urea concentrations. No differences ($P > 0.18$) were observed in serum IGF-1, Ca, P, or fecal P. Wool characteristics were unaffected by treatments with the exception of a negative quadratic effect in grams of wool produced/kg of BW. From these findings we can conclude that redberry juniper stems and leaves can effectively replace oat hay in lamb feedlot diets and is a viable alternative roughage source for lamb diets.

Key Words: lamb, feedlot, juniperus

269 Dietary betaine improves physiological responses in sheep under chronic heat load in a dose dependent manner. K. DiGiacomo,* S. Simpson, B. J. Leury, and F. R. Dunshea, *Melbourne School of Land and Environment, The University of Melbourne, Parkville, Vic, Australia.*

Heat stress (HS) results in decreased production, health issues and economic losses in ruminants. Dietary betaine is an organic osmolyte implicated in maintaining cellular osmotic balance and reducing energy expenditure and may help to maintain thermal tolerance. Thirty-six Merino ewe's (40 kg, n = 6 per group) were housed in climate chambers maintained at either thermoneutral (TN) (n = 18, 21°C) or cyclical HS (n = 18, 18–43°C) conditions for 21 d, and supplemented with either 0, 2 or 4 g betaine/d. Animals had ad libitum access to water and were pair fed such that TN intake matched that of HS animals who were fed ad libitum. Water and feed intake was measured twice daily, and plasma samples were obtained at 1500h 3 times per week. Heart rate (HR), respiration rate (RR), skin temperature (T_S) and rectal temperature (T_R) were measured at 0900, 1300 and 1700 h daily. Betaine supplementation did not alter feed intake ($P = 0.66$). All physiological measures differed with time of day ($P < 0.001$) and average daily T_R was increased by HS (39.4 to 40.1°C, $P < 0.001$) and altered by betaine supplementation (39.7, 39.6 and 39.8°C for 0, 2 and 4 g betaine respectively, $P < 0.001$). Heat increased T_S (38.0 to 39.1°C, $P = 0.002$), while betaine did not affect T_S ($P = 0.48$). Heat increased RR by 47 breaths min^{-1} ($P < 0.001$) and 2 g betaine decreased RR (113, 102 and 116 breaths min^{-1} for 0, 2 and 4 g betaine respectively, $P < 0.001$). Heat increased HR by 8 beats min^{-1} ($P < 0.001$), while 2 g betaine decreased HR (95, 88 and 99 beats min^{-1} for 0, 2 and 4 g betaine respectively, $P < 0.001$). Heat stress did not alter plasma glucose and NEFA concentrations ($P > 0.50$), while betaine supplementation decreased plasma NEFA concentrations (80, 55 and 54mM for 0, 2 and 4 g betaine respectively, $P = 0.05$). These data suggest that dietary betaine supplementation in sheep has dose dependent responses, with the 2 g betaine dose able to decrease heat load in sheep.

Key Words: betaine, heat stress, ruminants

270 Evaluation of body temperature and sweating rate of Senepol and crossbred heifers in the tropics. R. W. Godfrey*[1], A. J. Weis[1], P. E. Hillman[2], K. G. Gebremedhin[2], C. N. Lee[3], and R. J. Collier[4], [1]*University of the Virgin Islands, St Croix, VI,* [2]*Cornell University, Ithaca, NY,* [3]*University of Hawaii, Manoa,* [4]*University of Arizona, Tucson.*

Heat stress is a common problem in livestock production throughout the tropics. Senepol (SEN) cattle are well adapted to the tropical environment but other *Bos taurus* breeds are not as well suited for the climate. The objective of this study was to compare the body temperature and sweating rate of SEN (n = 6) and Charolais × Angus × SEN (XBRED; n = 4) heifers. All heifers were nulliparous and 1.3 y of age. Temperature data loggers, programmed to record vaginal temperature (VT) at 10-min intervals, were inserted into the vagina of each heifer and removed after 72 h. Rectal temperature measured using a digital veterinary thermometer (RT), eye temperature measured using infrared images of the left eye (IREYE), surface temperature over the rump measured using a hand-held infrared thermometer (IRR), respiration rate measured as breaths per minute (bpm) using visual observation (RR) and sweating rate (SWR) measured at a site on the rump of each heifer using a hand-held closed-chamber VapoMeter were collected between 1200 and 1430 h. Heifers were evaluated in the shade on d 1 and d 3 and in the sun on d 2 and d 4. Data were analyzed using GLM procedures of SAS with breed, sun exposure and the interaction in the model. Serial VT measurements were analyzed using time and breed in the model. Mean temperature, relative humidity and THI during the data collection were 28.3°C, 83.7% and 80.6, respectively. There was no difference between SEN and XBRED heifers in IREYE or RR ($P > 0.10$). The SEN heifers had lower ($P < 0.05$) VT and RT than XBRED heifers (38.87 ± 0.11 vs. 39.22 ± 0.13°C and 39.14 ± 0.07 vs. 39.36 ± 0.09°C, respectively). There was no difference ($P > 0.10$) in RT or VT between heifers in the sun or shade within breed. The VT of SEN heifers in the shade was lower ($P < 0.06$) than VT of XBRED heifers in sun or shade (38.75 ± 0.15 vs. 39.22 ± 0.18°C, respectively). The IRR of SEN heifers was lower ($P < 0.008$) than that of XBRED heifers (37.39 ± 0.21 vs. 38.38 ± 0.28°C, respectively) and IRR was higher ($P < 0.0001$) in the sun than in the shade (40.60 ± 0.26 vs. 35.16 ± 0.24°C, respectively). The SWR of SEN heifers was higher ($P < 0.001$) than that of XBRED heifers (23.96 ± 0.71 vs. 19.75 ± 0.93 g/m^2, respectively). The SWR of SEN heifers in the sun was higher ($P < 0.03$) than SWR of SEN heifers in shade or XBRED heifers in sun or shade (27.37 ± 1.08 vs. 20.54 ± 0.93 vs. 20.48 ± 1.32 vs. 19.03 ± 1.32 g/m^2, respectively). The higher SWR of SEN heifers may play a role in their lower RT and VT and their adaptation to the tropical climate.

Key Words: heat stress, sweating rate, Senepol

271 Evaluation of body temperature and sweating rate of Senepol cows in the tropics. R. W. Godfrey*[1], A. J. Weis[1], P. E. Hillman[2], K. G. Gebremedhin[2], C. N. Lee[3], and R. J. Collier[4], *[1]University of the Virgin Islands, St Croix, VI, [2]Cornell University, Ithaca, NY, [3]University of Hawaii, Manoa, [4]University of Arizona, Tucson.*

Senepol cattle are well adapted to the tropical environment and there is interest in determining what physiological traits contribute to their adaptation. The objective of this study was to evaluate the body temperature and sweating rate of Senepol cows in the tropics. Primiparous (n = 3) and multiparous (n = 7) cows were evaluated in July (2.3 to 11.4 y of age). Three cows were pregnant (6 mo of gestation) at the time of data collection. Temperature data loggers, programmed to record vaginal temperature (VT) at 10-min intervals, were inserted into the vagina of each cow and removed after 72 h. Rectal temperature measured using a digital veterinary thermometer (RT), eye temperature measured using infrared images of the left eye (IREYE), surface temperature over the rump measured using a hand-held infrared thermometer (IRR), respiration rate measured as breaths per minute (bpm) using visual observation (RR) and sweating rate (SWR) measured at a site on the rump of each cow using a hand-held closed-chamber VapoMeter were collected. Evaporative heat loss (EVHL) was calculated from measured air properties passing over a sample area of the cows' body by a Bovine Evaporation Meter. Cows were evaluated over 3 d in the shade and in the sun after a 20 min acclimation to each condition on each day. Data were analyzed using GLM procedures of SAS with sun exposure and time of day as the main effects in the model. Serial VT measurements were analyzed using time and pregnancy status in the model. Mean temperature, relative humidity and THI during the data collection were 28.3°C, 83.7% and 80.6, respectively. There was no difference ($P > 0.10$) in SWR or VT between the sun and shade (20.95 ± 2.6 vs. 22.98 ± 2.9 g/m^2 and 38.86 ± 0.22 vs. 38.41 ± 0.23°C, respectively). The IREYE, IRR, RT, RR and EVHL were higher ($P < 0.02$) in the sun than in the shade (38.87 ± 0.14 vs. 38.19 ± 0.19°C, 40.16 ± 0.25 vs. 34.64 ± 0.27°C, 39.15 ± 0.06 vs. 38.93 ± 0.06°C, 72.4 ± 0.9 vs. 68.1 ± 1.0 bpm and 344.8 ± 13.7 vs. 179.5 ± 14.9 $g{\cdot}m^{-2}{\cdot}h^{-1}$, respectively). Pregnant cows had a lower ($P < 0.01$) RT than open cows (38.88 ± 0.07 vs. 39.12 ± 0.05°C, respectively). Pregnant cows had higher ($P < 0.0001$) VT than open cows at all times of the day except during the morning (0600 to 1200 h). These data provide more information on the heat tolerance traits of Senepol cattle.

Key Words: heat stress, sweating rate, Senepol

272 Variation in skin surface temperature in different body parts of pigs in response to varying air temperatures. A. Sapkota* and J. J. McGlone, *Pork Industry Institute, Texas Tech University, Lubbock.*

Surface skin temperature may vary with the environmental temperature in mammals and may be a non-invasive method to evaluate the welfare of pigs. Surface skin temperatures may vary with body regions. The objective of this study was to evaluate how surface skin temperature of pigs varied with changes in external environmental temperature (both warm and cold) and over time. An infrared thermometer was used to record surface skin temperature every minute on body parts: rooting disc, bridge, ear, neck, throat, thorax, loin, abdomen, front leg, hind leg and ham of market size pigs. Data were recorded in the home pen (HOME), hallway (HALL), outside the building (OUT), back again in hallway (HALL2) and in home pen (HOME2) during cold (n = 24) or warm (n = 24) weather. Statistical models included the effects of air temperature and time (per min for 5 min; linear and quadratic effects). During winter, pigs in HOME (avg temp = 17.8 C) showed no time effects. When pigs were moved to the HALL (avg temp = 16.4 C), there was a quadratic effect ($P < 0.05$) for bridge, thorax, loin, abdomen, front leg, hind leg and ham. When pigs were moved to OUT (avg temp = 6.3 C), the disc and bridge regions showed a quadratic change over time ($P < 0.05$). When again moved to HALL2 (avg temp = 9.6 C), the quadratic effect over time ($P < 0.05$) was seen in all body parts except ear and thorax. Finally, when pigs were moved to HOME2 (avg temp = 16.4 C), the quadratic change over time was observed for all body parts except bridge, ear and thorax ($P < 0.05$). During summer, pigs in HOME (avg temp = 31.8 C) showed no time effects. When pigs were moved to HALL (avg temp = 32.4 C), there was quadratic time effect ($P < 0.05$) only for ham. When pigs were moved to OUT (avg temp = 35.6 C) and HALL2 (avg temp = 33.9 C), the quadratic time effect was observed in all body parts except disc ($P < 0.05$). Finally, when pigs were moved to HOME2 (avg temp = 32.3 C), there were no time effects. When body parts were compared, the rooting disc was the coolest body part in summer. However, during the winter, body regions had more uniform surface temperatures. Only some of the pigs' body regions (esp. rooting disc) were responsive to warm air temperature. More data are needed to model surface temperature effects on core body temperature and behavior.

Key Words: surface temperature, pigs, welfare

273 Routine exercise of feedlot cattle: Implications for stress response, productivity, and beef quality. N. Miller,* B. Gerlach, H. Glynn, K. Miller, C. van Bibber, L. Edwards-Calloway, J. Drouillard, and T. Houser, *Kansas State University, Manhattan.*

Feedlot cattle normally are limited in the amount of physical activity in which they regularly participate. The objectives were to determine if cattle become conditioned to handling with routine exercise during the finishing period, and to determine if routine exercise affects behavioral and physiological changes, growth performance, and carcass characteristics. Steers (n = 419) were stratified by weight and randomly assigned within strata to one of 4 treatments: 1) exercised 3 times/wk for the entire finishing period (ALL); 2) exercised 3 times/wk for the first 10 wk (E); 3) exercised 3 times/wk for the last 7 wk (L); and 4) no exercise during the 116-d finishing period (CON). Cattle were exercised by animal handlers for a minimum of 20 min at a trotting pace. Temperament scores (TS) and BW were obtained from all cattle on d 0, 72 and 116. Blood was obtained from 3 cattle randomly selected from each pen (n = 84) on these days and at exsanguination for analysis of serum concentrations of cortisol, insulin, glucose, and lactate, and plasma concentrations of epinephrine, norepinephrine, and β-endorphins. Data were analyzed as a mixed model, with fixed effect of treatment and random effect of pen. Date was included as a fixed effect for analyses of blood constituents and TS. There were no treatment x date interactions for blood constituents ($P > 0.10$) or TS. Exercise influenced pre-harvest insulin ($P < 0.01$; 0.75, 0.47, 0.60 and 0.78 ng/mL for ALL, E, L, and CON, respectively), but had no impact on other pre-harvest or post-harvest blood measurements ($P > 0.10$). TS were similar across treatments ($P > 0.10$), indicating no adaptation due to routine exercise or handling. Treatments did not differ with respect to ADG ($P > 0.8$). DMI were 10.29, 10.44, 10.26, and 10.58 kg/d ($P = 0.10$); G:F were 0.197, 0.197, 0.176, and 0.189 ($P = 0.28$); and HCW ($P = 0.77$) were 390, 391, 393, and 389 kg for ALL, E, L, and CON, respectively. Other carcass characteristics were unaffected by exercise regimen ($P > 0.10$). In summary, routine exercise had little impact on blood parameters, feedlot performance, or carcass traits of finishing steers.

Key Words: exercise, cattle, stress

274 Effects of different implant management options on performance of pre and post weaned calves.

H. B. Jones*[1], J. D. Rivera[1], and R. C. Vann[2], [1]*MAFES South Mississippi Branch Experiment Station, Poplarville,* [2]*MAFES Brown Loam Branch Experiment Station, Raymond, MS.*

Fifty-one head of crossbred (primarily *Bos taurus*) beef steers (BW = 166 kg) were used in year one of a multi-year study to evaluate effects of growth implants on performance, in a randomized complete block. Calves were implanted either at calfhood vaccination (approximately 3.5 mo old) with 100 mg of progesterone and 10 mg estradiol benzoate (CALF); at calfhood and again at weaning with 40 mg of trenbolone acetate and 8 mg of estradiol (WEAN); or not implanted (NONE). Cattle were weighed at weaning, and subsequently on d 28, 45, and 80 post weaning. On d 80, all steers were ultrasounded to measure longissimus area (LMA), intramuscular fat (IMF), and fat thickness. Data were analyzed using PROC GLM of SAS, steer was the experimental unit. At weaning, steers implanted at calfhood, had greater pre-weaning ADG compared with non-implanted steers (1.12 vs 1.0 kg, respectively; $P = 0.04$). At 28 d post weaning, no differences were detected among groups regarding ADG. Additionally, at 45 d post weaning, no differences were noted for BW; however, a difference was noted in ADG from weaning to d 45 between CALF and NONE (0.61 vs. 0.48 kg, respectively; $P < 0.10$). Surprisingly, no difference was detected in ADG between NONE and WEAN (0.48 vs 0.52 kg, respectively). Moreover, a tendency was noted in ADG ($P = 0.14$) between NONE and both implanted groups for the period between weaning and d 80 (0.82, 0.90, and 0.90 kg, respectively). Overall ADG was greater ($P < 0.10$) for cattle that were implanted compared with untreated controls (0.88, 0.98 and 0.92 for NONE, CALF and WEAN, respectively). Ultrasound measurements noted a tendency for increased LMA in CALF group ($P = 0.12$), and a tendency for decreased IMF for the CALF and WEAN compared with controls ($P = 0.12$). Results suggest that use of growth promoting implants may be of benefit to cattle producers; however, longer retention periods post weaning may be needed to realize full benefit of implanting.

Key Words: beef cattle, growth, implants

275 Comparison of chelated versus inorganic trace minerals on rate and efficiency of gain and pregnancy rates in beef heifers.

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Objectives of this experiment were to compare rate and efficiency of gain, and conception rates of yearling heifers supplemented with Cu, Zn and Mn as either metal methionine hydroxy analog chelated trace mineral (CTM; provided as Mintrex) or the same trace minerals in an inorganic SO_4 form. The experimental design utilized 3 ranches, each having 2 replications per treatment with pen as the experimental unit for ADG, DMI and G:F. Individual heifer was the experimental unit for pregnancy rates. Ranch A contained 498 Angus cross heifers, ranch B, 236 Red Angus cross heifers, and ranch C, 1,742 Angus cross heifers. All heifers were fed silage based diets that contained approximately 13.5% CP, 64% TDN (DM basis) and had no significant levels of SO_4, Mo, or Fe in feed or H_2O. Diets contained an average of 24 ppm Cu, 70 ppm Zn and 64 ppm Mn. Supplements were fed for 181 d (Ranch A), 149 d (Ranch B) and 151 d (Ranch C) before breeding. Heifers were weighed once at trial initiation (initial BW 270 kg ± 2.8), end of drylot feeding, at breeding and at pregnancy diagnosis. Ranch A heifers were bred by AI followed by natural service (45 d breeding), Ranch B heifers were bred by natural service (50 d breeding) and Ranch C heifers were bred by AI once. Pregnancy was determined via ultrasound using trained technicians. Ranch effects were significant ($P < 0.001$) for gain, ADG, G:F and overall pregnancy rate, but not for conception in the first 21 d. No ranch x treatment interactions were detected for any measurements ($P \geq 0.47$) and no differences ($P \geq 0.46$) were detected between treatments for total gain, ADG, G:F or the number of heifers that conceived during the first 21 d on Ranches A or B. Conception rate increased ($P = 0.03$) for CTM heifers from ranch C with one AI breeding. Across ranches, conception rates during the first 21 d of breeding did not differ ($P = 0.12$) between treatments but overall pregnancy rate was greater ($P = 0.05$) for heifers supplemented with CTM. Under the conditions of this experiment results suggest that supplementation with CTM contributed to higher pregnancy rates in heifers.

Key Words: chelated minerals, mineral nutrition, fertility

276 Relationships between postweaning residual feed intake in heifers and efficiency, digestibility, and productivity of Bonsmara cows.

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The objective of this study was to examine phenotypic relationships between heifer postweaning residual feed intake (RFI), and performance, efficiency, digestibility and productivity of mid-gestation cows. RFI_h was measured in growing Bonsmara heifers (n = 115) during 2 yr. Dry matter digestibility (DMD) was measured in 38 heifers with divergent RFI. Low RFI_h heifers consumed 20% less feed ($P < 0.05$) compared with those with high RFI_h heifers, but had similar BW, ADG and backfat depth. DMD was not affected by RFI group. Heifers with the lowest (n = 12/yr) and highest (n = 12/yr) RFI_h were retained for breeding and use in the cow feeding trial. Subsequently, the midgestation females (19 s-parity cows, 23 primiparous heifers) were fed chopped hay (ME = 2.11 Mcal/kg DM) in pens equipped with GrowSafe bunks to measure individual intake. BW were measured at 7-d intervals and BCS and ultrasound measurements of rump fat thickness obtained on d 0 and 77 of trial. DMD was measured on 32 of the pregnant females. Mixed model included fixed effect of RFI_h class, age and 2 way interaction. Low RFI_hfemales had lower ($P < 0.01$) DMI (9.00 vs 11.6 ± 0.54 kg/d) compared with females with high RFI_h, but initial BW, ADG, BCS and rump fat thickness were similar. Age at calving was not affected by RFI_h classification. An interaction ($P < 0.05$) between RFI_h classification and female age group was found for calf birth weight. Calves from primiparous heifers with low RFI_h were lighter at birth (27 vs 32 ± 1.2 kg; $P < 0.05$) compared with high-RFI_h females, but RFI classification did not affect BW of calves born to second-parity cows. RFI for pregnant cows (RFI_c) was calculated as the residual from the linear regression of DMI on conceptus-adjusted ADG and mid-test $BW^{0.75}$. RFI_c was highly correlated with DMI (0.79), but not BW, ADG, backfat depth or BCS. Moreover, RFI_c was moderately correlated to RFI_h (0.50). DMD tended ($P < 0.08$) to be greater (58 vs 54 ± 1.6%) for cows classified as having high RFI_h. Heifers classified as having low RFI continued to consume 22% less feed during mid-gestation with similar BW and BCS compared with heifers classified as having high RFI. While some reranking of animals occurred between RFI in heifers and mid-gestation females, differences in intake were still evident. Between-animal variation in digestibility and body composition did not contribute to variance in RFI in this study.

Ruminant Nutrition: Beef

277 Effect of yeast β-glucan and antibiotics on growth and gastrointestinal development in pre-ruminant calves. Y. Zhou, Y. Tu,* Q.-Y. Diao, Q. Yun, X.-H. Gao, and L.-H. Zhao, *Feed Research Institute of Chinese Academy of Agricultural Sciences, Beijing, China.*

This experiment was conducted to investigate the effect of yeast β-glucan and bacitracin zinc on growth performance and gastrointestinal morphological development of pre-ruminant calves. Twenty healthy Holstein male neonatal calves were randomly allotted to 4 treatments with 5 replicates each. The calves were fed diets supplemented with 0 (Treatment A), 75 mg yeast β-glucan/kg (Treatment B and C), 60 mg bacitracin zinc /kg (Treatment D). The experiment lasted for 28 d. Feed intake (FI) was recorded daily, body weight was measured every 2 weeks, and average daily gain (ADG) was calculated every 2 weeks. On d 21, the calves of Treatments A,B and D were challenged orally with *Escherichia coli* (O141:K99), with Treatment C fed normally. The rectal content was collected after challenged and diluted for microorganism counts. On d 28, calves were slaughtered and tissues from saccus cranialis, duodenum, jejunum and ileum were obtained and used in tissue slice. Data were analyzed using the GLM procedure of SAS software. The results showed as following: Comparing with Treatment A, the ADG of calves in Treatment B increased by 26.17% and 24.93% in the 2 phases before the *E. coli* challenged ($P < 0.05$), the ADG of calves in Treatment B and D increased by 30.38% and 30.81% after the *E. coli* challenged ($P < 0.05$). As for the F/G, which in Treatment B and D were significantly lower than that in Treatment A ($P < 0.05$). Compared with Treatment A, the amount of *E. coli* in rectum at 12h and 24h in Treatment B and D were significantly decreased ($P < 0.05$), and the amount of *Lactobacillus* was significantly decreased in the Treatment D ($P < 0.05$). Compared with the control treatment, the rumen papilla height and width of yeast β-glucan were significant higher than the control treatment ($P < 0.05$). The crypt depth of duodenum in treatment C and D were significant lower than the control treatment and the treatment D ($P < 0.05$), the ratio of villous height to crypt depth (V/C) in treatment B, C and D were higher than the control treatment ($P < 0.05$). It could be concluded that yeast β-glucan at the dosage of 75 mg/kg could erase the decrease of growth performance of pre-ruminant calves, improve the gastrointestinal morphological development and protect pre-ruminant calves, which challenged with *E. coli* K99, thus using β-glucan in calves feed may decreased the usage of antibiotics.

Key Words: calves, intestinal microflora, yeast β-glucan

278 Effect incremental levels of exogenous enzyme preparation on extent of ruminal fermentation, nutrient digestibilties and average daily gain in steers. H. Gado*[1], A. Z. M. Salem[2], and B. E. Borhami[3], [1]*Department of Animal Production, Faculty of Agriculture, Ain Shams University, Cairo, Egypt,* [2]*Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma del Estado de México, Toluca Estado de México, México,* [3]*Department of Animal Production, Faculty of Agriculture (El-Shatby), Alexandria University, Alexandria, Egypt.*

The aim of this experiment was to investigate the effect of the gradual increasing levels of an exogenous enzymes preparation (mixture of cellulase, xylanase, α-amylase and proteases enzymes) in the diet on ruminal fermentations activates, nutrients digestibility and animal performance in steers. Forty 8 steers (Baladi × Friesian, 151 ± 0.95 kg BW) were randomly allocated in 3 experimental groups of the following treatments (12 steers for each): 0 (control, ENZ0), 40 (ENZ40) and 60 (ENZ60) g of ENZ/head/d. A complete randomize block design was set up and a repeated measurement in time model used to analyze the data. The ENZ doses were mixed daily with a part of their daily ration. Steers were fed a total mixed ration (TMR) contained: 11% cracked corn, 8.5% agwa (minced date), 26.5% biscuits (bakery waste), 10% sugar cane molasses, 19% sesame cake, 2% soybean meal, 6% beans, 14.2% rihan straw, 1% salt, 1% limestone and, 0.3 mixture of mineral and vitamins. Steers were fed the TMR for 206 d as experimental period. Feed and orts samples were collected twice weekly to calculate dry matter intake and animals were weighted each 2 weeks during the experiment. At the end of experiment, rumen liquor of 3 animals of each treatment (fitted with permanent rumen fistulated) was collected to determine the concentrations of volatile fatty acids (by gas liquid chromatography) and NH3-N. Nutrients digestibility were determined during the last week of the experiment, using chromium, as a marker, in fecal samples by atomic absorption spectrophotometry. Total digestibility of nutrients, was increased ($P < 0.01$) by addition of ENZ (ENZ40 and ENZ60) vs control (DM, 65.1 and 69.8 vs 61.7%; CP, 66.1 and 68.9 vs 60.3%; NDF, 50.8 and 54.7 vs 41.7%; ADF, 40.8 and 43.5 vs 32.2%, respectively). Average daily gain also improved by the addition of the 2 doses of ENZ (1.45 and 1.58 vs 1.25 kg/d, respectively- $P < 0.05$). Ruminal fermentation activities were improved by the addition of the 2 ENZ doses, however, VFA were higher ($P < 0.05$) in ENZ40 and ENZ60 compared with ENZ0 (120 and 128 vs 100 mM/100mL), respectively), and NH3-N were higher ($P < 0.05$) in the same treatments vs control (ENZ0) (65 and 63 vs 54 mg/L, respectively). Supplementing steers with ENZ could enhance animal performance, ruminal activities and nutrient digestibility in fattening steers.

Key Words: beef production, exogenous enzyme, steers

279 Effect of a blend of castor oil and cashew nut shell liquid on performance, eating pattern, rumen health and carcass quality in Holstein bulls fed high-concentrate rations. M. Devant*[1], A. Aris[1], A. Bach[2,1], and J. Torrent[3], [1]*IRTA-Ruminant Production, Animal Nutrition, Management, and Welfare Research Group, Torre Marimon, Caldes de Montbui, Barcelona, Spain,* [2]*ICREA, Barcelona, Spain,* [3]*Oligo Basics USA LLC, Excelsior, MN.*

This study evaluated the effects of a blend of castor oil and cashew nut shell liquid (Essential, Oligo Basics, Brazil) on the performance, eating pattern, rumen health and carcass characteristics of Holstein bulls. A total of 120 bulls (295 ± 2.5 kg of BW and 214 ± 1.1 d of age) were divided into 2 treatments: 1) control and 2) supplemented with Essential (0.5 g/kg of concentrate as fed). Individual concentrate intake and eating pattern were recorded daily with a computerized concentrate feeder, and BW was recorded every 14 d. Rumen fluid was collected through rumenocentesis for pH and VFA analysis at d 114 of study. Animals were slaughtered after 124 d and HCW, rumen wall ulcers, papillae clumpings, parakeratosis and color, as well as liver abscesses were evaluated. Data were analyzed using a mixed-effects model with repeated measures that included initial BW, Essential supplementation, time, and the interactions among these factors, as fixed effects, and animal as a random effect. The statistical model for rumen pH included previous meal size, total daily concentrate intake and time since last meal as covariates. Essential supplementation improved ($P < 0.001$) ADG (1.6 and 1.4 ± 0.07 kg/d, respectively), and decreased ($P < 0.001$) the CV of daily concentrate intake (14.3 and 20.4% ± 0.96, respectively) during the first 2 wk of the trial, but these differences in both parameters were not observed thereafter. Ruminal pH, VFA, HCW and carcass characteristics were unaffected by dietary treatments. Control bulls tended ($P = 0.08$) to have darker rumen walls (3.4% and 0% black, for control and Essential, respectively), more ($P = 0.09$) papillae clumpings (3.5% and 0% clumping, for control and Essential, respectively), and greater ($P = 0.10$) presence of liver abscesses than supplemented bulls (31.1 and 13.3%, for control and Essential, respectively). Essential® improves intake and growth during the first 2 wk of supplementation, but no further effects are observed thereafter. However, Essential tends to improve rumen wall integrity and decrease liver abscesses.

Key Words: beef, eating pattern, functional oil

280 Yeast cell wall supplementation alters the performance of beef heifers during the receiving period. T. R. Young*[1], N. C. Burdick[2], J. A. Carroll[2], M. A. Jennings[1], J. T. Cribbs[1], R. J. Rathmann[1], J. R. Corley[3], and B. J. Johnson[1], *[1]Texas Tech University, Department of Animal and Food Sciences, Lubbock, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Lesaffre Feed Additives, Milwaukee, WI.*

A study was designed to determine the effect of feeding yeast cell wall (YCW) products on feedlot performance of newly-received crossbred heifers. Heifers (n = 140; 225 ± 9.4 kg) were obtained from commercial sale barns and transported to the Texas Tech University Beef Center in New Deal, Texas. Heifers were sorted by source (n = 2) upon arrival and arranged in a completely randomized block design (35 pens; 7 pens/treatment; 4 heifers/pen). Heifers were separated into treatment groups receiving a Control Diet (CON; n = 28), YCW A (2.5 $g \cdot hd^{-1} \cdot d^{-1}$; n = 28), YCW AA (5.0 $g \cdot hd^{-1} \cdot d^{-1}$; n = 28), YCW B (2.5 $g \cdot hd^{-1} \cdot d^{-1}$; n = 28), or YCW C (2.5 $g \cdot hd^{-1} \cdot d^{-1}$; n = 28) and were fed for 56 d. Daily DMI was recorded and individual BW was collected every 14 d. A significant source by treatment interaction was detected, and data were analyzed accordingly. In Source 1, YCW A (278 ± 8.0 kg) and YCW C (285 ± 8.1 kg) showed a greater increase in 28 d BW compared with CON (272 ± 8.0 kg; $P = 0.03$). YCW C exhibited a higher 42 d BW compared with all other treatments ($P = 0.02$). From d 0 to 28, YCW A (1.87 ± 0.09 kg) and YCW C (2.10 ± 0.10 kg) had higher ADG compared with CON (1.65 ± 0.09 kg; $P = 0.03$). YCW C showed improved ADG from d 0 to 42 compared with all other treatments ($P < 0.01$). DMI was improved for YCW AA (7.27 ± 0.20 kg) and YCW C (7.92 ± 0.23 kg) compared with CON (6.75 ± 0.20 kg; $P = 0.04$) for d 0 to 42. YCW C had higher DMI vs. CON from d 14 to 28 and d 28 to 42 ($P = 0.05$ and 0.02, respectively). Cumulative F:G was lower for YCW B compared with all other treatments ($P = 0.03$). In Source 2, a linear effect for YCW A was detected from d 0 to 14 in BW, ADG, and G:F ($P = 0.01$, 0.02, and 0.03, respectively). Collectively these data suggest that YCW supplementation can offer advantages in performance of newly received beef heifers.

Key Words: cattle, performance, yeast

281 Feedlot performance of Nellore young bulls fed biodiesel coproduct. R. L. Oliveira*[1], C. H. da Cruz[1], N. B. de Santana Filho[2], W. G. Cerutti[3], C. A. dos Santos Dias[2], E. I. de Souza Costa[1], O. L. Ribeiro[1], A. G. Leão[1], M. C. A. Santana[1], and A. A. Pinheiro[1], *[1]Universidade Federal da Bahia, Salvador, Brazil, [2]Universidade Federal do Recôncavo Baiano, Cruz Das Almas, Brazil, [3]Universidade Federal de Santa Maria, Santa Maria, Brazil.*

Feedlot performance of Nellore young bulls fed diets with different levels of palm kernel cake (PKC) was evaluated by analysis of average daily weight (ADW), dry matter intake (DMI) and feed conversion ratio (FCR). Thirty-two Nellore breed young bulls (420 ± 2.0 kg) were used in a completely randomized experimental design and allocated into 4 treatments: 0, 7, 14 and 21% PKC inclusion on DM basis. Diets consisted of forage (Tifton-85 hay, as 35% of diet), concentrate (corn and soybean meal and palm kernel cake) and mineral salt. The animals were fed during 92 d and weighted at the beginning of the experiment and every 28 d, after fasting for 16 h. Feeding level was adjusted according to individual intake to remain between 10 and 20% of orts. FCR was obtained using the ratio between DMI and ADW. Data were submitted to regression and variance analysis using a significance level of 5%. The bulls' DMI and ADW average were, respectively, 10.16 and 1.15 kg per day. There were no effects of PKC level ($P > 0.05$) on the animal's ADW (SE = 0.06) and FCR (SE = 0.85) The DMI ($P = 0.037$, SE = 0.32) linearly decreased ($\hat{Y} = 11.235 – 0.1021X$) as PKC was included to the diet. PKC addition to a diet of Nellore young bulls did not compromise feedlot performance on despite of the decreasing on DMI.

Key Words: beef cattle, palm kernel cake, performance

282 Effect of corn oil or corn protein supplementation on performance and rumen fermentation characteristics of feedlot lambs consuming a 90% concentrate diet containing 30% DDGS. C. L. Shelley,* M. Pimienta, J. Caballero, J. Browne-Silva, S. L. Lodge-Ivey, and S. A. Soto-Navarro, *New Mexico State University.*

Feeding values of corn dried distillers grains with solubles (DDGS) are best when included in concentrate diets at 20 to 30% of the diet. When DDGS are included at levels greater than 30%, high EE or CP content may cause a decrease of feeding value. This study evaluated effects of corn oil and corn protein supplementation on feedlot diets containing dry rolled corn (DRC) and DDGS. Twenty-one Suffolk cross wethers (average BW = 41.8 ± 1.95 kg) were randomly assigned to 1 of 4 treatments and were individually fed once daily. Experimental diets were DRC based containing 10% alfalfa (DM basis). Treatments included: 1) DDGS at 30% of the diet (30%), 2) DDGS at 60% of the diet (60%), 3) DDGS at 30% of the diet containing similar EE to the 60% diet supplied by corn oil (OIL), and 4) DDGS at 30% of the diet containing similar CP to the 60% diet with protein supplied by corn gluten meal (PROTEIN). Animals were weighed on d 1 and d 56 of the 56 d experiment. Ruminal fluid samples collected on d 48 via oral lavage 4 h post feeding were analyzed for pH, VFA, ammonia, and bacterial populations. Final BW and DMI were not affected ($P \geq 0.13$) by treatments. Average daily gain and G:F were 69% higher ($P = 0.01$) for 30% than OIL. Ruminal pH tended to be lower for 30% than for 60% or OIL ($P \geq 0.06$). Ammonia concentrations increased 47% when 60% was fed compared with 30% ($P = 0.01$). Total VFA production was not affected ($P > 0.20$) by treatment. Bacterial populations were analyzed using PCR-denaturing gradient gel electrophoresis (DGGE) using the 16S rDNA gene. Bacterial presence or absence was analyzed using Richness index and was not affected ($P = 0.89$) by treatment. Overall, all samples were 60.21% similar in DGGE banding pattern. Animals fed OIL had the least similar DGGE banding pattern (57.73%) when compared with all other treatments. In conclusion, adding enough corn oil to match the EE of 60% DDGS decreased animal performance and resulted in shifts in bacterial populations.

Key Words: sheep, distillers byproducts, rumen bacteria

283 Prospects of raising Sahiwal cow calves for veal production under tropical environment. S. A. Bhatti*[1], K. Nazir[1], M. J. Basra[2], M. S. Khan[3], M. Sarwar[1], and M. A. I. Mughal[2], [1]*Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Punjab, Pakistan,* [2]*Livestock and Dairy Development Department, Punjab, Lahore, Pakistan,* [3]*Department of Animal Breeding and Genetics, University of Agriculture, Faisalabad, Punjab, Pakistan.*

Sahiwal is a tropical dairy cattle breed of Pakistan known for its heat tolerance and tick resistance. Potential of Sahiwal calves for veal production has not been explored. The objective of present study was to evaluate the growth potential of Sahiwal calves for veal production on whole milk or a combination of whole milk and milk replacer in a ratio of 50:50. For this purpose, 48 Sahiwal calves (both male and female) were assigned to 4 dietary treatments having 12 animals/treatment. Calves in the first 2 treatments were fed milk 15 or 20% of their body weight (BW) upto d 84 adjusted on weekly basis. The calves in remaining 2 treatments received the same amount of milk as in the other 2 treatments till d 21; after which 50% of the milk offered was replaced with a blend of chickpea *(Cicer arietinum)* flour and vegetable (corn) oil mixed in water (MR) till d 84.The constituted MR had 3.1, 2.8 and 14.3%, CP, EE and DM, respectively. The growth and intake data were analyzed using repeated measures analysis, with MIXED Procedures of SAS in 2 × 2 factorial arrangements. The 2 factors were feeding level and feeding source. Calves offered whole milk grew faster ($P < 0.05$) and had greater weaning weights ($P < 0.05$) than those offered milk + MR (606.4 ± 18.1 vs 331.3 ± 18.1 g/d and 70.4 ± 1.5 vs 47.8 ± 1.5 kg, respectively). Greatest daily BW gain (656 ± 26 g/day) and weaning weight (74.6 ± 2.1 kg) were observed in calves offered milk 20% of body weight. Numbers of scour days were higher in calves fed milk + MR than those offered milk. Calves offered milk 15% of their body weight had the lowest production cost per kg of daily BW gain (≈US$3.5 ± 0.1). Replacement of 50% milk with a blend of chickpea flour and vegetable oil was neither able to support growth equivalent to whole milk nor was effective for reducing feeding cost during weaning period. Greatest average daily BW gain of Sahiwal calves during 12 weeks period was 650 g/d. However, daily BW gain of calves from 5 to 8 and 9–12 weeks was 717 and 837 g/d, respectively. Sahiwal calves have a promise for being raised for veal production under tropical environments.

Key Words: calf nutrition, Sahiwal calves, veal

Ruminant Nutrition: Dairy Production II

284 Effect of diet composition and incubation time on feed indigestible NDF concentration in dairy cows. S. J. Krizsan* and P. Huhtanen, *Swedish University of Agricultural Sciences, Department of Agricultural Research for Northern Sweden, Umeå, Sweden.*

Indigestible NDF (iNDF) predicts forage OM digestibility accurately and precisely when determined by a 288-h ruminal in situ incubation, and it is an important parameter in mechanistic rumen models. The long incubation time required is a disadvantage. Further, intrinsic cell wall characteristics of feeds should be determined in ideal conditions for fiber digestion. The objective with this study was to determine effects of diet composition and rumen incubation time on iNDF over a wide range of feeds in dairy cows. In this study concentrations of iNDF were evaluated using 18 feeds and 4 cows in a split-split plot design. Ten feeds were concentrates and 8 were classified as forages. Treatments were in a 3 × 3 factorial arrangement, consisting of different diets and incubation times. Diet composition was primarily varied by changing concentrate inclusion between 17 (low), 42 (medium) and 62% (high) of diet DM. Grass silage was used as basal forage to all cows during the incubations. The feeds were incubated for 144, 216 and 288 h. Indigestible NDF was determined from 2 g sample weighed to polyester bags of Saatifil PES (Saatitech S.p.A., Veniano, Como, Italy) with pore size of 12 µm and a pore area equal to 6% of the total surface, providing a sample size to surface ratio of 10 mg/cm^2. Across all feeds concentration of iNDF ranged from 6 to 515 g/kg of DM. Feed iNDF concentration was not affected by cow ($P = 0.14$). The effect of diet composition on feed iNDF concentration was significant ($P < 0.01$). Concentrations of iNDF across feeds were 178, 186 and 197 g/kg of DM when cows were fed the low, medium and high diet, respectively. The effect of incubation time on feed iNDF concentration was significant ($P < 0.01$). Concentrations of iNDF across feeds were 199, 185 and 177 g/kg of DM for 144, 216 and 288 h, respectively. There were also significant ($P < 0.01$) interactions between incubation time and diet, incubation time and feed, and diet and feed. Indigestible NDF should preferentially be determined from 288-h ruminal in situ incubations in cows fed diets with low concentrate inclusion to be representative of the feed fraction that is unavailable to the animal.

Key Words: dairy cow, digestibility, fiber

285 Effect of corn snaplage on lactation performance of Holstein dairy cows. M. S. Akins*[1], M. Digman[2], and R. D. Shaver[1], [1]*Department of Dairy Science, University of Wisconsin-Madison, Madison,* [2]*U.S. Dairy Forage Research Center, Madison, WI.*

The objective of this study was to compare the effects of feeding TMR containing either corn snaplage (SNAP), corn snaplage with dry ground shelled corn (SPDC; 70% SNAP and 30% dry corn on DM basis), or high moisture shelled corn (HMSC) on lactation performance. Corn snaplage (67.6% DM; 61.0% starch DM basis) and HMSC (74.4% DM; 71.2% starch DM basis) were harvested from the same field of corn and stored in separate silo bags. Mean particle size of the SNAP, HMSC, and dry ground corn were 1764, 1335, and 825 microns, respectively. Sixty Holstein cows (30 primiparous and 30 multiparous) at 100 ± 23 DIM were housed in a pen with 30 electronic feeding gates to deliver the TMR teatments and measure DMI. Cows were blocked by parity (primiparous and multiparous), stratified by DIM, and randomly assigned to gates. Gates were randomly assigned to treatments with 10 for each treatment and 5 each for primiparous and multiparous cows. Primiparous or multiparous cows on each treatment could access all 5 gates. A 2-wk covariate adjustment period with all cows fed a 50:50 mix of the SNAP and SPDC treatments was followed by an 8-wk treatment period with cows fed there assigned treatment TMR. The TMR nutrient content (DM basis) for SNAP, SPDC, and HMC were 26.3, 27.5, and 23.9% starch, respectively and 22% NDF from forages for all treatments. Cows fed HMSC had greater ($P < 0.01$) DMI than SNAP and SPDC. Milk yield and fat corrected milk (FCM) yield were similar ($P > 0.10$) across treatments. Milk production efficiency was lower ($P < 0.01$) for cows fed HMSC than SNAP and SPDC, and cows fed SPDC tended ($P = 0.06$) to have greater efficiency than SNAP. Cows fed HMSC also had lower ($P = 0.01$) FCM/DMI than SNAP and SPDC. Milk fat percentage was greater ($P = 0.02$) for cows fed HMSC than SNAP with SPDC intermediate, however milk fat yield was not different ($P = 0.15$) across treatments. Milk protein percentage and yield were similar ($P > 0.10$) across treatments. Milk urea nitrogen was greater ($P < 0.01$) for cows fed SNAP than HMSC, and greater ($P < 0.01$) for HMSC than SPDC. Overall, cows fed SPDC had better lactation performance than SNAP or HMSC.

Key Words: corn snaplage, dairy cow, high moisture corn

286 Dry heat popping of sorghum grain to increase ruminal starch digestion in dairy cattle. A. R. Anstis[1], D. G. Barber[1], E. Raffrenato*[2,3], and D. P. Poppi[2], [1]*Agri-Science Queensland, Department of Employment, Economic Development and Innovation, Lawes, Queensland, Australia,* [2]*School of Agriculture and Food Sciences, The University of Queensland, Gatton, Queensland, Australia,* [3]*Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria, Gauteng, South Africa.*

Sorghum grain is commonly fed to dairy cattle across Australia. However, starch digestibility of sorghum within the rumen is limited by its structure and the protein matrix surrounding the starch granules. Steam-flaking consistently improves digestibility. Dry popping using heat could also increase digestibility through gelatinization of the starch molecule and increased surface area for microbial digestion. The aim was to increase the rate and extent of ruminal starch digestion with dry popping compared with other processing methods. Sorghum grain was sourced from a local feed mill in Queensland, Australia, and the following treatments were imposed: disc-milled (DM), hammer-milled (HM), rolled (R), steam-rolled (SR), popped (P), popped and hammer-milled (PHM), popped and disc-milled (PDM), semi-popped and disc-milled (SPDM). The HM and DM treatments had a particle size of 2 and 1.2 mm, respectively. All other treatments were ground to 4 mm. The grain was fermented in vitro using rumen fluid from 2 fistulated steers that were fed 3 kg of rolled sorghum per day while grazing kikuyu pasture ad libitum. Data used for rate estimations were in vitro starch fermentation residues, fermented for 0, 3, 7, 12, 18, 24, 36 and 48 h. A first-order decay model was run to estimate rates of digestion, assuming no lag or indigestible starch present. Digestion rates were also derived using the 7 h starch digestibilities according to Roe (1994) and pair-compared with the rates estimated using the non-linear model. The non-linear model resulted in R^2 between 0.92 and 0.99 and rates of starch degradation between 0.0451 and 0.1157 h^{-1}. The PDM and PHM sorghums resulted in the highest rates ($P < 0.05$), followed by the SPDM, SR and P treatments. Similar results ($P = 0.65$) were obtained using the 7 h values, except for DM and HM, which were underestimated compared with the non-linear procedure. Across all intermediate time points, the PDM and

PHM sorghum resulted in the highest starch digestibilities. Dry popping of sorghum grain has a greater potential than steam rolling to increase ruminal starch degradability when the grain is disc or hammer-milled after being popped.

Key Words: sorghum, starch digestibility

287 Daily methane emission profile in Holstein heifers fed rice straw. G. D. Cruz*[1], P. H. Hai[2], S. Polyorach[3], N. Anantassok[3], P. Beelen[4], H. D. Rosa[5], and E. Kebreab[1], [1]*University of California, Davis,* [2]*Institute of Agricultural Science for Southern Vietnam, Hochiminh City, Vietnam,* [3]*Khon Kaen University, Khon Kaen, Thailand,* [4]*Federal University of Alagoas, Rio Largo, Brazil,* [5]*Sao Paulo State University, Botucatu, Brazil.*

In South East Asia, rice straw is the principal crop residue fed to livestock; it is estimated that 40% of total rice straw produced goes to animal feed. Rice straw is a high lignin, high silica and low digestibility feedstuff, therefore a method to increase its nutritional quality would benefit animal production. The objectives of the study were to 1) improve the utilization of rice straw by increasing dietary nitrogen or energy availability and consequently reduce methane emissions, 2) analyze the daily profile of methane measured in ventilated hood chambers (VHC) and 3) investigate intake variability of heifers in VHC compared with group pen. Nine Holsteins heifers were fed in a 3 × 3 Latin square design, with 3 dietary treatments and 3 periods. Animals were fed twice daily at 0900 and 1700 h. Treatments were: control (14.3 CP% and 2.35 Mcal ME/kg DM), high energy (14.2 CP% and 2.45 Mcal ME/kg DM) and high protein (16.5 CP% and 2.36 Mcal ME/kg DM). Each period consisted of 14 d of adaptation and 1 d in the VHC. During the adaptation period heifers were kept in a group pen equipped with Calan gate system to measure individual feed intake. Feed offered and refused in the VHC was weighted individually. Dry matter intake (DMI) of the day that animals were in the VHC was used as a covariate to analyze the total methane emitted. Increase in nitrogen or in energy in the diet did not have an effect on daily methane emission ($P \geq 0.35$), with heifers in control, higher energy and high protein treatments emitting a daily average of 396, 393 and 414 g/d, respectively. A 37% decrease in DMI between heifers in VHC and previous day in group pen was observed (6.4 vs. 10.2 kg/d, $P < 0.001$, respectively). Methane emission peaks occurred between 1 to 1.5 h after feeding, the morning peak averaged 20 g/h and the afternoon 24 g/h. Daily lowest values were observed early morning, 1 to 2 h before feeding with average values of 10g/h. Even though heifers were provided with the best management conditions during the VHC day, DMI was drastically reduced, which may have affected methane productions. Caution needs to be taken when making inference in methane production data when using VHC method and when few hours of observation are extrapolated to daily emission.

Key Words: dairy heifers, methane emission, rice straw

288 The effects of a two ration feeding regimen on intake, milk production, and rumen fermentation in dairy cows. L. W. Rottman, Y. Ying, P. A. Bartell, and K. J. Harvatine,* *Penn State University, University Park.*

In the dairy cow there is a circadian pattern of feed intake and milk synthesis, consequently a single total mixed ration fed once a day may not stabilize rumen fermentation and synchronize nutrient absorption and milk synthesis. The object of this study was to determine if feeding multiple TMRs that complement the pattern of feed intake over one day would stabilize ruminal fermentation and increase milk synthesis. Nine ruminally cannulated cows were arranged in a replicated 3 × 3 Latin square design with 23 d periods. Diets were control (33.2% NDF), a low forage diet (L; 29.5% NDF), and a high fiber diet (H; 34.8% NDF). The L and H diets were balanced to provide the same composition as the control diet when combined in a 3:7 ratio of L:H. The control (Con) treatment was fed control diet at 0900 h, the high/low treatment (HL) was fed H at 70% of total daily offering at 0900 h and L at 30% of total daily offering at 2200 h, and the low/high (LH) treatment was fed L at 30% of total daily offering at 0900 h and fed H at 70% of daily offering at 1300 h. All treatments were fed at 110% of daily intake. Data were analyzed with mixed model procedures using repeated measures for time course data. Preplanned contrasts compared Con to HL and HL to LH. DMI and digestible DMI were decreased by 1.9 and 0.8 kg/d by HL compared with Con ($P < 0.01$ and $P < 0.05$). Total tract DM and OM digestibility did not differ between Con and HL. Intake and total tract digestibility did not differ between HL and LH. There was no difference between Con and HL for milk yield and composition, but LH tended to reduce milk fat yield compared with HL ($P = 0.06$). There was no effect of treatment on milk *trans*-10 C18:1, *trans*-11 C18:1, and fatty acids less than 16 carbons. There also was no main effect of treatment on empty body weight gain, plasma insulin, glucose, and NEFA, and rumen VFA concentration. There was a significant effect of time on plasma insulin, glucose, and NEFA and rumen VFA concentration ($P < 0.001$), suggesting a circadian rhythm also regulates these variables. Feeding multiple rations over the day decreased intake without decreasing milk or body weight gain. Feeding multiple rations over the day reduced intake with no impact on milk yield or body weight gain, but had little impact on other production and rumen parameters.

Key Words: circadian, rumen fermentation, TMR

289 Validation of an acidosis model. H. M. Golder*[1,2], W. J. Wales[3], M. J. Auldist[3], A. R. Rabiee[1,2], E. Bramley[4], P. Celi[1], R. King[5], and L. J. Lean[1,2], [1]*University of Sydney, Camden, New South Wales, Australia,* [2]*SBScibus, Camden, New South Wales, Australia,* [3]*Future Farming Systems Research Division, Department of Primary Industries, Ellinbank, Victoria, Australia,* [4]*Murdoch University, School of Veterinary and Biomedical Sciences, Murdoch, Western Australia, Australia,* [5]*Dairy Australia, Southbank, Victoria, Australia.*

Twenty 4 rumen fistulated lactating Holstein cows were fed 8, 10, 12, 14 and 16 kg/hd/d of concentrate with either a control diet or partial mixed ration (PMR). These were used to validate an existing acidosis model based on ruminal pH, volatile fatty acid (VFA), ammonia and lactate measures. Controls were fed rolled wheat grain twice a day at milking, and had access to pasture and silage in the paddock. The PMR diet, containing the same amount of grain and silage as controls, was fed twice daily on a feedpad immediately after milking. The target grazed pasture intake for both groups was 8 kg DM/cow/d. Cows were adapted to the diets for 14 d before rumen sampling. Rumen fluid samples were collected 10 times over a 24 h period and rumen pH was immediately measured. Rumen samples were analyzed for VFA, ammonia and lactate concentrations. Milk and milk composition data were collected. The acidosis model was used to assign one of 3 acidosis categories to each rumen sample: acidotic, suboptimum rumen function or normal. Further, the eigenvector values from discriminant analysis were used to estimate the degree of acidosis for each sample on a 0 to 1 scale, with 1 being highly acidotic and 0 not acidotic. A repeated measures ANOVA was used for the analysis of eigenvector data (Table 1). The degree of acidosis linearly increased with increasing the amount of concentrate, and PMR feeding reduced acidosis. Control cattle fed 14 and 16 kg of concentrate were the most acidotic as indicated by the higher eigenvector values. These results validate the ability of the model to predict ruminal acidosis from rumen fermentation measures. The model may be used as an acidosis diagnostic tool and PMR feeding may reduce risk of acidosis.

Table 1. Least squares means ± SE and P-values for eigenvectors (0-1)

	LSM ± SE	*P*-value
Diet		0.06
Control	0.24 ± 0.022	<0.001
PMR	0.09 ± 0.022	<0.001
Rate (kg/d)		0.02
8	0.02 ± 0.036	0.63
10	0.04 ± 0.036	0.26
12	0.08 ± 0.036	0.02
14	0.19 ± 0.036	<0.001
16	0.50 ± 0.036	<0.001
Time		0.92
Diet*rate		<0.001
Diet*time		<0.001

Key Words: acidosis, partial mixed ration, metabolic model

290 Evaluation of two versions of a mechanistic, metabolic model including bacterial pools, to describe FA flux, pH and milk fat in cattle on various pasture supplementation feeding strategies.

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The objectives were to analyze data from a series of experiments with different proportions of grazed pasture and supplements using 2 versions of a mechanistic, metabolic model and to challenge the ability of the models to describe ruminal VFA flux, pH and resultant production variables, including milk fat production. The model was Molly (UC Davis, Baldwin) and an updated version of the Molly model with new VFA stoichiometry and bacterial pools to describe ruminal processes. Holstein dairy cattle were fed a range (approx. Sixteen to 21 kg DM/d) of grazed pasture plus wheat and silage supplementation (6 to 12 kg DM/d total supplement). Cows averaged 22.2 kg (SD 4.3) of ECM for 283 d Molly) is a mechanistic, dynamic model describing ruminal and body processes at an aggregated pathway level. An updated set of VFA stoichiometry, including lactate and valerate based on pools of amylytic and cellulytic bacteria, and protozoa, which all produced VFA from substrates differently, was integrated into Molly. The observed intake and chemical composition were direct inputs, and VFA production, ruminal pH, milk and milk composition were outputs. Inclusion of the bacterial pools allowed for the estimation of lactate and valerate production. Lactate uptake was highly correlated with lower milk fat (RSQ = −0.96, $P < 0.01$); a finding which although has been known for some time, we have not yet had a model which could predict it. Both versions of the model described VFA production, ruminal pH, milk and milk composition within 1 SD of the observed means; for example, rumen pH in a short-term, within day feeding trial was predicted with a root mean square prediction error of 3.7%, primarily composed of random error and a slight (30% of RMSPE) mean error, slope error was not different from zero and RMSPE was 32% of the SD. The newest version of the Molly model opens a new ability to ask more specific, complex research questions into the efficiency of dairy cattle in various situations.

Key Words: acidosis, metabolic model, milk fat

291 Multi-component versus one-component analysis: A different way of assessing the effect of TMR chemical composition on milk, fat, and protein yield individual lactation curves.

M. Caccamo*[1], R. F. Veerkamp[2], G. Licitra[1,3], R. Petriglieri[1], F. La Terra[1], A. Pozzebon[1], and J. D. Ferguson[4], [1]*1CoRFiLaC, Regione Siciliana, Ragusa, Italy,* [2]*WageningenUR Livestock Research, Animal Breeding and Genomics Centre, Lelystad, the Netherlands,* [3]*Catania University, DISPA, Catania, Italy,* [4]*University of Pennsylvania, PA.*

The objective of this study was to examine the effect of chemical composition of TMRs tested quarterly from March 2006 through December 2008 on milk, fat, and protein yield curves for 27 herds in Ragusa, Sicily. Prior to this study, standard yield curves were generated on data from 241,153 test day records of 9,809 animals from 42 herds in Ragusa province collected from 1995 to 2008. A random regression sire-maternal grandsire model was used to develop variance components for yields. The model included parity, age at calving, year at calving, and stage of pregnancy as fixed effects. Random effects were herd × test date, sire and maternal grandsire additive genetic effect, and permanent environmental effect modeled using 3-order Legendre polynomials. Model fitting was carried out using ASREML. Subsequently, the model with fixed variance components was used to examine the influence of TMR CP, soluble nitrogen (Soluble N), acid detergent lignin (ADL), NDF, acid detergent fiber (ADF), starch, and ash on milk, fat, and protein yield curves. The data set contained 46,531 test-day milk yield records from 3,554 cows in the 27 herds recorded during the study period. Initially, an analysis was performed using one-dietary component (one-component) within each model as fixed effects associated with the test day record closest to month the TMR was sampled within each herd. An interaction was included with the nutrient component and DIM. The effect of the TMR chemical component(s) was modeled using a 9-order Legendre polynomial. Conditional Wald F statistic on fixed effects revealed significant effects ($P < 0.001$) for ADF, NDF, CP, and starch, and their interactions with DIM on milk, fat and protein yield. Based on these results, a multi-component analysis was performed where CP, NDF, and starch were simultaneously included in the model with DIM interactions. Although both analyses revealed diet composition influenced production responses depending on lactation stage, the multi-component analysis showed more pronounced effects of starch and NDF relative to CP for all traits throughout lactation.

Key Words: lactation curve, TMR, test day model

292 Intestinal digestibility of long chain fatty acids in lactating dairy cattle: A meta-analysis.

J. C. Ploetz* and A. L. Lock, *Michigan State University, East Lansing.*

This analysis was performed to examine the intestinal digestibility of individual long chain fatty acids (FA) in lactating dairy cows. Available data were collated from 15 publications containing 61 treatments, which reported total and individual FA duodenal flows and calculations of intestinal digestibility. All studies involved lactating dairy cows and estimates of digestibility were based on measurements either between the duodenum and ileum or between the duodenum and feces. Analysis was performed using Comprehensive Meta Analysis v2 software that calculated the effect size using a random effects model. FA digestibility was calculated for C16:0, C18:0, C18:1 (*cis* and *trans* isomers), C18:2, and C18:3. Initially, intestinal FA digestibility was determined by pooling data regardless of site of collection. Percent digestibility (mean ± SE) were 75.9 ± 1.4, 73.3 ± 1.4, 80.7 ± 1.5, 77.9 ± 1.4, and 76.9 ± 1.6 for C16:0, C18:0, C18:1, C18:2, and C18:3, respectively. Digestibility of C18:0 was lower than for C18:1 ($P < 0.05$). Digestibility estimates for 18-carbon FA were subsequently separated according to site of collection (ileal vs. fecal). Ileal vs. fecal digestibility for C18:0 was 74.3 ± 2.0 vs. 68.7 ± 4.2. Digestibility of C18:1 was 80.1 ± 1.6 vs. 81.8 ± 0.6 for ileal vs. fecal. Comparing results for C18:0 and C18:1 calculated at the ileum indicate that the digestibility of these FA was not different ($P > 0.05$). Site of collection altered digestibility estimates for C18:2

(70.3 ± 2.8 vs. 79.7 ± 1.3; ileal vs. fecal, $P < 0.05$) and C18:3 (66.9 ± 4.5 vs. 79.4 ± 0.6, ileal vs. fecal, $P < 0.05$). In summary, digestibility estimates differed based on collection site (ileal vs. fecal) and degree of unsaturation of FA. These results suggest that unsaturated FA are biohydrogenated in the large intestine which would result in an over-prediction of unsaturated FA digestibility and an under-prediction of saturated FA digestibility when calculated from fecal collection. Since the amount of unsaturated FA reaching the large intestines is small, differences associated with digestibility estimates for unsaturated FA due to site of collection can be large. Relative differences in the digestibility of individual FA are minimal in lactating dairy cattle.

Key Words: fatty acid, digestibility, meta-analysis

293 Effect of replacing dietary soybean meal with canola meal on production of lactating dairy cows. G. A. Broderick*[1], A. P. Faciola[2], L. Nernberg[3], and D. Hickling[3], *[1]U.S. Dairy Forage Research Center, Madison, WI, [2]University of Wisconsin, Madison, [3]Canola Council of Canada, Winnipeg, MB, Canada.*

Previous research suggested that CP from canola meal (CM) was used more efficiently than CP from solvent soybean meal (SBM) by lactating dairy cows. We compared supplementation of either CM or SBM on both low CP (14.9% CP) and high CP (16.8% CP) diets and tested whether feeding rumen-protein Met plus Lys (RPML) was advantageous. Fifty lactating Holstein cows were blocked by DIM and parity into 10 squares in a replicated 5 × 5 Latin square trial. Five squares were fed: 1) low CP with SBM, 2) low CP with CM, 3) low CP with SBM + CM, 4) high CP with SBM, and 5) high CP with CM; the other 5 squares were fed the same diets except with added RPML (20 g/d of Met and 69 g/d of Lys). Diets contained (DM basis): 40% corn silage, 26% alfalfa silage, 13–23% corn grain, 2.4% mineral-vitamin premix and 31–33% NDF. Periods were 3-wk (total 15 wk); data from the last wk were analyzed using the Mixed procedure of SAS. LS-means and contrasts are reported in the table. There were no significant effects of RPML in this trial ($P \geq 0.11$). Increased CP (diets 4 and 5 vs. 1 and 2) increased fat yield and greatly elevated MUN. Relative to SBM, feeding CM increased DMI, and yield of milk and protein, and depressed MUN. At 14.9% CP, there was similar response in DMI and weight gain on CM and SBM + CM vs. SBM. In this trial, replacing SBM with CM resulted in improved production and N-efficiency at both 14.9 and 16.8% CP.

Table 1.

CP, %:	15	15	15	17	17		Contrasts[1]		
Protein:	SBM	CM	SBM +CM	SBM	CM	SE	[CP]	S vs C	S vs CS
Variable									
DMI, kg/d	24.8	25.3	25.3	25.2	25.5	0.4	0.29	0.04	0.04
BW gain, kg/d	0.28	0.54	0.47	0.50	0.41	0.09	0.78	0.33	0.04
Milk, kg/d	39.5	40.2	40.2	39.9	41.1	0.8	0.06	<0.01	0.08
Milk/DMI	1.59	1.59	1.59	1.59	1.62	0.02	0.24	0.15	0.97
Fat, kg/d	1.56	1.59	1.58	1.60	1.65	0.04	0.03	0.10	0.39
Protein, kg/d	1.19	1.21	1.21	1.21	1.24	0.02	0.10	0.04	0.28
SNF, kg/d	3.47	3.51	3.51	3.49	3.57	0.07	0.31	0.11	0.39
MUN, mg/dL	9.9	8.7	9.6	13.2	12.0	0.2	<0.01	<0.01	<0.01

[1][CP] = CP content; C = CM; S = SBM; CS = SBM + CM.

Key Words: canola meal, rumen-protected AA, soybean meal

294 Milk yield and composition of dairy cows fed diets combining pasture and total mixed ration. A. Mendoza[1,2], C. Cajarville[3], E. de la Quintana[1], M. E. Garmendia[1], E. Mutuberría[1], E. de Torres[4], and J. L. Repetto*[1], *[1]Facultad de Veterinaria, Departamento de Bovinos, Montevideo, Uruguay, [2]Instituto Nacional de Investigación Agropecuaria, Programa de Producción de Leche, Colonia, Uruguay, [3]Facultad de Veterinaria, Departamento de Nutrición Animal, Montevideo, Uruguay, [4]Facultad de Veterinaria, Campo Experimental N°2, Libertad, Uruguay.*

To establish the effects of time of access to fresh pasture on milk yield and composition of cows fed a total mixed ration (TMR), 9 Holstein cows (mean BW = 572 kg; SD = 76) fed a TMR were assigned to three 3 × 3 Latin squares, with 20-d periods and sampling on the last 10 d of each period. Treatments evaluated were: 0 (TMR0), 4 (TMR4) or 8 (TMR8) hours of daily access to fresh pasture. Pasture (*Lolium multiflorum*; 22.1% CP, 24.0% ADF) was daily cut and offered ad libitum from 0800 h in individual stalls and TMR (16.8% CP, 16.4% ADF) was offered ad libitum during the remaining time. Cows were milked twice daily. Milk yield was measured during 5 consecutive days and individual milk samples were taken during 4 consecutive milkings of each period and analyzed for milk composition. Data were analyzed with a general linear model. There were no differences between TMR0 and TMR4 for any trait. However, compared with TMR0, an allowance of 8 h per day of access to fresh pasture decreased ($P < 0.05$) milk yield (32.7 vs. 34.4 kg/day; SEM = 1.5), 4% solids-corrected (32.5 vs. 34.8 kg/day; SEM = 1.0), protein (1.06 vs. 1.13 kg/day; SEM = 0.04) and total casein yield (0.80 vs. 0.86 kg/day; SEM = 0.03), and tended to decrease ($P < 0.10$) milk fat (1.29 vs. 1.40 kg/day; SEM = 0.05) and lactose yield (1.62 vs. 1.70 kg/day; SEM = 0.08). Milk fat (4.01%; SEM = 0.22), protein (3.31%; SEM = 0.13), total casein (2.50%; SEM = 0.11), lactose (4.94%; SEM = 0.06) percentage, total casein / protein ratio (0.756; SEM = 0.005) and MUN (19.9 mg/dl; SEM = 0.97) were not affected by treatments. It was concluded that time of access to fresh pasture influenced both milk and solids yield but not composition of TMR-fed dairy cows.

Key Words: milk composition, pasture, total mixed ration

295 Effects of dietary fiber source on lactation performance, nutrient digestion, and rumen microbial protein synthesis in early-lactating dairy cows. W. Zhu,* Y. Fu, B. Wang, Y. M. Wu, and J. X. Liu, *Institute of Dairy Science, MoE Key Laboratory of Molecular Animal Nutrition, College of Animal Sciences, Zhejiang University, Hangzhou, China.*

The objective of this study was to evaluate the effects of fiber source on lactating performance, rumen fermentation, nutrient digestion, and microbial protein synthesis in early-lactating dairy cows. Three multiparous (BW = 608 ± 20.0 kg, parity = 2 to 4) and 12 primiparous (BW = 552 ± 16.0 kg) Chinese Holstein cows at 45 (±6.0) d in milk were used in a multiple 3 × 3 Latin square involving 3 dietary treatments. All diets were isonitrogenous and isocaloric with ratio of forage to concentrate at 45: 55 (DM basis), and contained nearly the same concentrate mixture, but different forage source (%): corn silage 21, corn stover 19, and alfalfa hay 5 (CS); corn silage 19, Chinese wild rye hay 21, and alfalfa hay 5 (CW); and corn silage 19, Chinese wild rye hay 9, and alfalfa hay 17 (AH). Each period lasted for 21 d with the first 14 d for adaptation. Neither dry matter intake nor milk yield was significantly affected by the source of fiber. However, an increased trend occurred in milk yield for diet AH. Percent of milk protein was higher ($P < 0.05$) in cows on diet AH than that on CW (3.00 ± 0.104 vs. 2.91 ± 0.192%), with an intermediate value (2.94 ± 0.200%) for diet CS, but milk fat, milk lactose, and total solid content were not affected across the treatments. Milk efficiency (milk yield / DM intake) was higher for diet AH than for CS (1.55 ± 0.032 vs. 1.42 ± 0.032, $P < 0.05$) with medium value for diet CW (1.49 ± 0.039). Rumen fluid pH was not affected, but ammonia-nitrogen concentration was higher ($P < 0.05$) for diet CS than for CW or AH. Volatile fatty acid concentrations were higher ($P < 0.05$) in cows consuming diet AH than those on CS (113 vs. 103 mmol/L), with no difference between diets CW and AH or CS. Apparent total tract digestibility of DM was higher ($P < 0.05$) for diet AH than for CS or CW (70.2 vs. 63.7 or 64.5%), while the digestibility of NDF (61.8 vs. 57.2 or 56.9%) and ADF (58.8 vs. 53.2 or 52.5) was higher ($P < 0.05$) for diet CS than for CW or AH. Excretion of purine derivatives (374 vs. 323 or 338 mmol/d) was higher for diet AH than for CS or CW but with no difference between diets CS and CW, and microbial N flow to the duodenum (215 vs. 186 or 195 g/d) was higher in cows on diet AH than in those on CS with no difference between diets CW and AH or CS. These results indicated that corn stover could replace Chinese wild rye grass in the diets for lactating cows, and that high proportion of alfalfa hay in the diet is beneficial for milk protein production.

Key Words: dietary fiber source, microbial protein, lactation performance

WSASAS Symposium-Beef: Beef Production in Arid Environments

296 Significant research accomplishments applicable to arid environments. J. Paterson,* *Montana State University-Bozeman, Bozeman*

The improvement in the production and sustainability of beef cattle in the US has been remarkable over the past 50 yrs. Research has been responsible for producing beef cattle which require 10% less feed energy, 30% less land, 14% less water and produce 18% less greenhouse gases. Beef produced per cow has more than doubled during the past 50 yr (91 vs. 227 kg/cow/yr) and yet we have the lowest cow inventory since 1952. Thirty years ago it required approximately 600 d to grow calves from birth to slaughter; today its 480 d. Research has shown the benefits of crossbreeding, and its effects on weaning weights (25% improvement), genetic correlations, survivability, stayability, performance testing, accurate selection decisions based on EPDs and evaluation of sires based on residual feed intake (RFI). Selection of animals for low RFI can result in 10% lower feed intakes and a 25% reduction in methane production; clearly desirable under drought conditions. Using DNA from a Line 1 Hereford was the basis of a bacterial artificial chromosome library and the bovine genome sequence. Sixty years ago, ranchers did not have ready access to frozen semen, estrus synchronization, prostaglandins, ultrasound, freezing of embryos or vaccines for reproductive diseases. One of the most widely adapted management strategies has been the use of body condition scoring and its relationship with return to estrus, conception rates, and feeding strategies. Research have shown the consequences of protein restriction of the cow on the depression in the productivity of her calves (fetal programming). To improve nutrient utilization, routine usage of ionophores ($250 million dollar savings in feed), implants, grain byproducts and non-protein nitrogen usage have been widely adopted. Sixty years ago, one of the major accomplishments was the benefits of supplementation with P and protein to increase forage intake, growth and reproductive efficiency. Laboratories that routinely provide nutrient analyses are based on forage and grain chemistry research and confirmatory trials conducted during the 1970s and 1980s. Consumer concerns over animal care has resulted in implementation of beef quality assurance programs. Beef cattle production in the western US will depend on the utilization of high forage diets for the cowherd. Challenges for the future will include high input costs, consumer perception about beef safety, animal welfare, carbon footprint and end product quality. Research will be judged as to whether the outcomes are sustainable in terms of economic, social and environmental acceptance.

Key Words: beef research, arid environment

297 Cows that fit arid environments. B. H. Dunn,* *South Dakota State University, Brookings.*

For any cow, the challenge to be both biologically and economically efficient in the production system they are in is the basic measure of fitness. The ability of a cow to annually reproduce within its given feed environment over a relatively long period is the most important factor in the determination of fitness. For cows in production systems located in arid environments, this basic production phenomenon becomes even more critical, as the feed environment, when compared with that found in more temperate environments, is not only regularly restricted by drought, but subject to greater levels of change, and the importation of supplements expensive. Climate change could also be altering the boundaries associated with historic climatic regions, and exasperate the average, as well as the range, associated with annual precipitation within regions. It follows then, that a functional understanding of how a cow partitions feed energy first to maintenance, second to growth, then to lactation, and lastly to reproduction, is critical in determining cows that fit arid environments versus those that do not. Also, it is important to understand the limitation of using genetic selection as a tool for improving fitness to arid environments because of the low level of hereditability for reproductive traits when compared with other economically important traits. As breed differences for economically important traits continue to moderate, using mating systems to breed cattle that have the genetic potential to thrive in arid environments becomes more challenging. In the future, masking problems associated with raising cattle in arid environments that do not fit, by supplementing them with imported feed resources could be increasingly problematic, as transportation costs, as well as opportunity costs for alternative uses, price supplements beyond economic reason.

Key Words: beef cattle, cow size, cow efficiency

298 Supplementation strategies in arid environments. D. W. Bohnert,* *Eastern Oregon Agricultural Research Center, Oregon State University, Burns.*

The principle goal of most supplementation programs designed for beef cattle is to improve performance by providing the limiting nutrient(s) for the specific production scenario; however, in arid environments most supplementation strategies routinely have this and one other equally important goal: modifying grazing behavior. When this is taken into consideration, along with extensive pastures, variable topography, limited water availability, herd sizes, and inconsistent forage production common to the arid regions of the western US, developing effective supplementation strategies can be a challenge. Also, many of the arid regions grazed by beef cattle in the western US contain sensitive resource areas, such as riparian zones, critical wildlife habitat, and recently burned areas, which should be considered when developing a supplementation program. This is further complicated with the management challenges often faced by producers that utilize public lands in their grazing programs. Areas of research that I will discuss include grouping animals into contemporary groups, infrequent supplementation, variation in supplement intake due to form of supplement, and supplement placement as a tool to modify grazing behavior. This presentation will provide information that can be used in developing supplementation strategies that decrease the costs associated with supplementation while meeting acceptable levels of production. In addition, concepts that can be used to develop supplementation strategies that attract cattle away from critical areas and lure them into underutilized areas while maintaining or improving performance, thereby meeting production and conservation goals, will be provided.

Key Words: behavior, cattle, supplementation

299 Restocking the cow herd. D. Peel,* *Oklahoma State University, Stillwater.*

The US beef cow herd has decreased 14 of the last 16 years. On January 1, 2012, the beef cow inventory was 29.88 million head, the lowest beef cow inventory since 1962. The drought in 2011 pushed cow inventories lower despite growing market incentives for herd expansion. At the same time, high concentrate feed prices are affecting forage values with implications for all sectors of the cattle industry. Record high feeder prices increases profit potential for cow-calf production but rising and volatile input prices makes cost of production uncertain. Rebuilding the cow herd will be a slow and difficult process due to the critically low numbers and the record high prices for breeding animals. This symposium presentation will cover factors that have contributed to the continued decline in cow inventories; the implications of the current herd size; and the challenges of rebuilding the herd in coming years.

Key Words: beef cow inventory, herd expansion

300 A systems approach to ranching in arid environments. C. P. Mathis,* K. C. McCuistion, and R. D. Rhoades, *King Ranch Institute for Ranch Management, Texas A&M University-Kingsville, Kingsville.*

Ranches are complex systems driven by internal and external forces. All ranches are different, but are still affected by the laws of systems. The laws of "unintended consequences," "worse before better," and "compensating feedback" are all real in ranching or any other business organization. It may not be obvious, but success in ranching is affected by how well managers understand the reality of these laws as they make decisions affecting complex ranching systems. In arid environments where variable precipitation and low forage production associated with drought is generally the greatest risk to a sustainable ranching operation, often the most important decision a manager makes is the selection of enterprises in which the ranch engages. The thoughtful mix of cow-calf, stocker, and other livestock enterprise, especially when complemented with wildlife enterprises, helps create income diversification and the flexibility in stocking rate needed to cope with drought or capitalize on excess forage availability. The external forces of nature and commodity prices cannot be controlled; however, adaptability and diversification can help mitigate those risks. In arid environments in North America, cow-calf enterprises are generally the core of the ranching operation. Management decisions relating to the cow-calf enterprise should also incorporate consideration of the effect of those decisions on the ranch as a whole. According to standardized performance analysis (SPA) data from the Southwestern US, labor, depreciation, and purchased feed comprise the majority of costs to a cow-calf enterprise. These categories are also generally the top 3 expenses to arid land ranching operations as a whole. Further, SPA data reveals that ranches in the top net income quartile not only raise the highest value calves at weaning, but they also have the lowest cost of production compared with the less profitable quartiles. Understanding individual drivers of profitability is important; however, managers are encouraged to look past simply optimizing the pieces of the ranch operations. To develop a highly successful and sustainable ranching business, the relationship among the enterprises on the ranch must be maximized.

Key Words: systems, ranching, drought

Tuesday, July 17, 2012

POSTER PRESENTATIONS
Animal Behavior and Well-Being: Physiology Emphasis

T1 Stress affects plasma serotonin, but not tryptophan, in Holstein steer calves. A. L. Adams,* T. H. Friend, G. A. Holub, L. R. Berghman, P. K. Riggs, S. M. Garey, C. L. Terrill, and M. J. Carter, *Texas A&M University, College Station.*

Cortisol is a well-known indicator of stress, but little is known about the effects of stress on serotonin and tryptophan in livestock. Previous studies in humans have shown that the brain uses serotonin, derived from tryptophan in the bloodstream, to cope with stress. As serotonin production in the brain increases, plasma tryptophan concentrations are expected to decrease. Furthermore, previous studies in humans have also shown that 90% of serotonin is located in the intestines and released into the bloodstream as an individual experiences stress. The objective of this study was to determine how stress affected plasma serotonin and tryptophan concentrations in calves during handling and transport. Thirty-six 4-mo-old Holstein steer calves were housed in groups of 6 with each group randomly assigned to either transport or control treatments. Transported calves were hauled for 6 h in their groups in a 7.3 m × 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 (pre), and after 2, 4, and 6 h of transport. Plasma samples with the highest cortisol concentrations from each treatment (transport: n = 11, control: n = 8) and sampling period (pre: n = 6, 2 h: n = 3, 4 h: n = 6, 6 h: n = 4) were analyzed for concentrations of serotonin and tryptophan. Pearson correlation coefficients were used to determine associations and mixed model ANOVA determined treatment and sampling period effects on serotonin and tryptophan. Serotonin was not correlated with cortisol ($P = 0.54$) or tryptophan ($P = 0.45$), but tryptophan and cortisol were correlated (r = - 0.52, $P = 0.02$). Treatment did not affect serotonin ($P = 0.79$) or tryptophan ($P = 0.15$). Serotonin was highest (148 ± 16 ng/mL) after 4 h and lowest (46 ± 21 ng/mL) after 6 h ($P = 0.0004$), but tryptophan was not affected by sampling period ($P = 0.64$). These results suggest that stress (handling and/or transport) may cause an intestinal response that releases additional serotonin into the bloodstream.

Key Words: serotonin, stress, tryptophan

T2 Development of a novel method for measuring stress in beef cattle. D. Moya*[1], K. S. Schwartzkopf-Genswein[1], and D. Veira[2], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*Agriculture and Agri-Food Canada, Agassiz, BC, Canada.*

A study was conducted to a) determine if bovine hair contains cortisol at measurable levels, and b) identify the effect of hair location and collection method on hair cortisol levels. Hair samples (0.5 g) from the head, neck, shoulder, hip, and switch were collected from 12 Angus crossed bulls (313.1 ± 14.7 kg BW) using 2 sampling methods: plucking, to ensure collection of the hair follicles; and clipping, using an electric razor to ensure collection of the hair as close as possible to the skin. After a wash with isopropanol, hair samples were ground with a ball mill for 5 min at 22 rps, sonicated with methanol for 30 min, and incubated on a shaker for 18 h, at 50°C and 100 rpm. The supernatant was pipetted off and evaporated in a block heater, at 45°C under a stream of nitrogen. Samples were reconstituted with phosphate buffered saline before quantification of cortisol with a competitive immunoassay. Data were analyzed with a factorial design, considering hair location and collection method as main factors, using the mixed procedure of SAS. Differences were declared at $P < 0.05$. The described method was successful in detecting cortisol in 87.8% of the hair samples, with concentrations ranging from 0.07 to 6.62 pg/mg. A value of zero was used for samples in which no cortisol was detected. The intra-assay coefficient of variation (CV) ranged from 5.91 to 9.96%, while the inter-assay CV ranged from 5.04 to 10.48%. Hair from the switch had the greatest cortisol concentration (3.32 ± 0.20 pg/mg) compared with all other sampling locations, while hair from the head and the neck (2.14 and 1.86 ± 0.20 pg/mg, respectively) had greater cortisol concentrations than from the shoulder and hip (0.83 and 0.62 ± 0.20 pg/mg, respectively). Cortisol was greater in hair samples collected by clipping than by plucking. Results indicate that hair can be used to measure cortisol levels in beef cattle. Future studies will assess hair cortisol concentration as a biomarker of stress and animal welfare under chronic stress conditions, as well as its relationship with other physiological and behavioral measures of animal welfare.

Key Words: hair cortisol, biomarker, welfare

T3 Body temperature and panting in feedlot cattle. J. B. Gaughan*[1] and T. L. Mader[2], [1]*The University of Queensland, Gatton, Qld, Australia,* [2]*University of Nebraska, Concord.*

Assessment of thermal status during periods of high heat load is essential for the maintenance of cattle wellbeing. Respiration rate (RR) and body temperature (BT) are routinely used as indicators of thermal status. However, they are difficult to obtain under commercial conditions. The panting score (PS) system was designed as a visual assessment of the thermal status of cattle. The PS system uses a 7 point score (0, 1, 2, 2.5, 3, 3.5 and 4) where PS0 indicates no elevation in RR (no thermal stress) and a PS4 indicates severe thermal stress (open mouth, tongue fully extended, head drooped, rapid labored breathing). A PS2 (closed mouth, drooling, elevated RR) indicates that the animal is under moderate heat load. A PS3 (open mouth, tongue extended, drooling, further elevation of RR) is an indicator of high heat load. In this study BT and PS data were obtained from 48 Angus steers over 120 d. Steers were implanted with a BT transmitter on d −31, and BT data were obtained at 30 min intervals. The cattle were housed in 2.43 m × 7.4 m pens (8 steers/pen: 3 transmitter steers/pen), and were fed a finisher diet (NEg = 1.44 Mcal/kg). The PS of the steers was obtained daily (±15 min) at 0600 h (AM), 1200 h (MD) and 1600 h (PM). At the same times, climate variables were obtained from an on-site weather station. Observations were made from outside the pens so as not to influence cattle responses. The 2 closest BT values to the time when PS was obtained were retrospectively downloaded from a logger and averaged. A total of 15,361 observations were used and 2nd order polynomial response curves generated: (AM) $y = 39.28 – 0.295x + 0.125x^2$ ($R^2 = 0.99$); (MD) $y = 38.27 + 0.853x – 0.0554x^2$ ($R^2 = 0.99$); (PM) $y = 38.68 + 0.869x – 0.071x^2$ ($R^2 = 0.99$), where y = BT (°C) and x = PS. These data suggest that PS is a good indicator of BT. The BT at MD corresponded to slightly lower PS compared with PM, e.g., for PS1; BT at MD = 39.6°C and

40.1°C at PM. However during AM, BT was lower at PS1, 2 and 2.5 (highest AM value) compared with MD and PM, e.g., for PS2.5; BT at AM = 40.2°C, MD = 40.8°C and PM = 41.1°C. The AM response curve suggests an attempt to increase heat dissipation during the cooler AM period relative to MD and PM.

Key Words: panting, body temperature, heat stress

T4 Use of artificial shade during grazing and its effects on body weight at the end of gestation in red deer (*Cervus elaphus*).

N. G. Mejía, A. Sánchez, A. Paez, and L. Alvarez,* *Facultad de Medicina Veterinaria y Zootecnia, UNAM, México DF, México.*

In grazing animals, solar radiation and high temperatures can seriously compromise the performance and welfare if they lack the necessary protection. The aim of this study was to determine whether the resource shade affects the body weight and behavior of female red deer during the last 2.5 mo of pregnancy. Two groups (n = 23 each) of pregnant does were grazed in different pens of similar botanical composition and size. In the shaded group, a mesh shade (>80% protection, 60m2) was placed. A behavioral scan sampling (10 min) was used to determine the location of animals and their behavior inside the paddock. Ambient and black globe temperature were also measured. All females were weighed at the beginning of the experiment and immediately before delivery. Data was arcsin transformed to be analyzed using a repeated measures ANOVA, correlation and linear regression. Percentage of animals using the shade during daytime was highly correlated with ambient [$R^2 = 0.7$, $P < 0.05$, $y = (2.45x) + (-6.91)$] and black globe temperature [$R^2 = 0.9$, $P < 0.05$, $y = (2.40x) + (-49.24)$]. There were no differences in the percentage of animals grazing during the day ($P > 0.05$). More animals were seen drinking water, and more thermoregulatory behaviors (to get muddy, to introduce forelegs in troughs) were recorded in the unshaded animals (11.1 ± 1 versus 6.3 ± 1 and 10 ± 1.4 versus 3.3 ± 1.4 respectively, $P < 0.05$). The average daily gain of weight was higher in the shaded group (215 ± 24.1 versus 127.1 ± 23.6, g ± SE, $P < 0.05$). It is concluded that artificial shade during the last 2.5 mo of gestation reduces the thermoregulatory behaviors and improves the average daily gain of weight. PAPIIT IN205810, UNAM.

Key Words: animal welfare, body weight, solar radiation

T5 Evaluation of on-farm methods assessing locomotor disorders of individual or group housed sows.

S. Conte*[1], J. Grégoire[1], R. Bergeron[2], S. D'Allaire[3], M.-C. Meunier-Salaün[4], and N. Devillers[1], [1]*Agriculture and Agri-Food Canada, Dairy and Swine R & D Centre, Sherbrooke QC, Canada,* [2]*University of Guelph, Alfred Campus, Alfred, ON, Canada,* [3]*Faculty of Veterinary Medicine, University of Montreal, St-Hyacinthe, QC, Canada,* [4]*Institut National de la Recherche Agronomique, UMR1348 Pegase, Saint-Gilles, France.*

The aim was to evaluate methods for on-farm assessment of locomotor disorders in gestating sows, and the influence of housing system on the prevalence of locomotor disorders. Of the 311 sows studied across 10 farms, 120 sows were housed in groups of 4–8 sows per pen and 191 sows were housed in individual stalls. Data recorded were: 3-point gait score, walking speed (≤0.8, ≤1.25, >1.25 m/s), stride length (<83, <100, ≥100 cm), number of steps during 30s at feeding (<3, <6, ≥6), latency to lie down after feeding (≤30, ≤60, >60 min), ability to stand up after being stimulated ("stand-up test": moving freely, hesitancy, refusal), number of feet with uneven toe size and bursitis (0, 1, >1), and presence of cracks (>1 cm) on the side wall. The percentage of sows in each category was calculated. Cochran-Mantel-Haenszel and Chi-squared tests were used to determine the association between variables and housing systems. Following gait scoring, 49% of sows were sound (score 0), 35.5% walked stiffly (score 1) and 15.5% were visibly lame (score 2). There were no differences between housing systems in the percentage of sows within each gait score ($P > 0.05$). The percentage of sows having feet with uneven toe size, bursitis or cracks on the side wall was higher in stalls than in pens ($P < 0.05$). No associations were found between the 3-point gait score and the number of steps during 30s, the stand-up test score or the latency to lie down after feeding ($P > 0.05$). The percentage of sows having reduced walking speed and stride length was higher for sows scored 2 than for sows scored 0, in stalls only ($P < 0.05$). Results indicated no differences in the prevalence of locomotor disorders between housing systems based on the gait score, but highlighted more foot problems in stalls than in pens. New quantitative indicators such as stride length and walking speed seem to be good indicators of locomotor disorders for sows housed in stalls but not in pens. This suggests that methods used to detect lameness are not always applicable from one housing system to another. Other factors associated with the housing system such as the possibility to exercise may interfere with the assessment.

Key Words: gestating sow, locomotor disorders, housing system

T6 Effectiveness of a non-penetrating captive bolt for the euthanasia of nursing and weaned piglets from 3 to 9 kg.

T. M. Casey-Trott*[1], S. G. Nykamp[1], P. V. Turner[1], S. T. Millman[2], and T. M. Widowski[1], [1]*University of Guelph, Guelph, Ontario, Canada,* [2]*Iowa State University, Ames.*

A non-penetrating captive bolt (NPCB) has been shown to be highly effective for euthanasia in neonatal piglets. The objective of this study was to determine the effectiveness of the NPCB for euthanasia of nursing and weaned piglets from 3 to 9kg (5–49 d of age). The NPCB was used by 15 stock people from 6 farms to euthanize 150 compromised piglets (3 kg: 55 piglets, 5 kg: 45 piglets, 7 kg: 25 piglets, 9 kg: 25 piglets). The NPCB was placed on the frontal bone and fired twice in rapid succession. Piglets were monitored for signs of sensibility using brainstem and spinal reflexes. Duration of neuromuscular leg spasms and time to cardiac arrest were also recorded. CT scans and macroscopic scoring were completed post mortem to quantify the degree of skull fracture and brain hemorrhage. Data were analyzed in SAS 9.2 using proc mixed with an age, weight interaction. The NPCB caused immediate and sustained insensibility until death in 98.6% of piglets. Leg spasms ceased in <5 min in 97.3% of the piglets and cardiac arrest was achieved by 98% in <10 min. Stock person variation was significant for duration of leg spasms ($P = 0.0443$), but not time to cardiac arrest ($P = 0.2022$). There were no significant differences among weight groups for either the duration of leg spasms ($P = 0.7338$) or time to cardiac arrest ($P = 0.6585$). However, age significantly affected the duration of leg spasms ($P = 0.0417$) with younger piglets (≤21 d) having a shorter duration than older piglets (≥22 d). Average fracture displacement was 8.3 mm (±1.0SE). Two piglets from the 9kg category had fractures present but no displacement. Moderate to severe subdural-dorsal (SDD) hemorrhage was reported in at least 85% of piglets in each weight category. Moderate to severe subdural-ventral (SDV) hemorrhage was reported in at least 60% of piglets from weight categories 3, 5, and 7kg; whereas the SDV hemorrhage for the 9kg category was predominantly minimal to mild (56%). The NPCB was highly effective for the euthanasia of piglets up to 9kg (49 d) based on immediate insensibility until death. However, age affects should be further studied to ensure the technique remains effective if it is used on piglets beyond this range.

Key Words: euthanasia, piglet, captive bolt

T7 Trailer compartment and trip duration affect stress of pigs transported under Canadian conditions. Y. M. Seddon*[1], J. Brown[1], T. Crowe[2], R. Bergeron[3], T. Widowski[3], L. Faucitano[4], and H. Gonyou[1,2], [1]*Prairie Swine Centre, Saskatoon, SK, Canada,* [2]*University of Saskatchewan, Saskatoon, SK, Canada,* [3]*University of Guelph, Guelph, ON, Canada,* [4]*Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada.*

Long transport times and trailer designs in use in western Canada have raised concerns regarding the welfare of pigs transported to market. Objectives of this study were to assess the effects of the internal trailer compartments (C) and trip duration on measures of stress in pigs transported in western Canada. Over 4 weeks in winter (W) and 4 weeks in summer (S), pigs from one farm (121 ± 0.35 kg) were monitored during transport to market. Each week, market pigs were weighed, identified and loaded onto 3 pot-belly trailers at a density of 0.38 m^2/pig. Trailers were loaded at 6-h (h) intervals to complete journey times of 6, 12 and 18 h, arriving at the abattoir at the same time. The study focused on pigs located in 4 C, namely C1 and C4 (front and rear of the upper deck), C5 (front of the middle deck) and C10 (rear of the bottom deck). At the abattoir, pigs were rested for 1.5 h before slaughter. Blood was collected from 4 pigs per C at exsanguination (total n = 384), and analyzed for packed cell volume (PCV), creatine phosphokinase (CPK), cortisol and lactate. Statistical analysis using the PROC mixed procedure in SAS determined the effects of season, week, travel duration and C on the stress measures. CPK levels were affected by trip duration (6 h: 4172, 12 h: 6552, 18 h: 9697 ± 1659 IU/L; $P < 0.05$) and C (C1: 3834, C4: 8676, C5: 5754, C10: 8968 ± 1455 IU/L; $P < 0.0001$). Despite longer trip durations, CPK levels did not alter in C1, but rose in C4, C5, and C10 (12 h), with C4 and C10 showing the highest levels following 18 h transport ($P < 0.05$). Cortisol was higher ($P < 0.05$) in S than W. C and season affected lactate, with lactate levels being significantly higher ($P < 0.05$) in pigs transported in C1 and C4 than in the other C in W. Data suggest longer trip durations caused increased stress, and seasons present challenging conditions, yet the compartment location can either mitigate or aggravate the stress response. Therefore, determining conditions within the C, such as temperature and humidity extremes, vibrations and G-forces would help to understand these negative effects and assist in the development of targeted improvements to trailer design.

Key Words: transport, stress, pig

T8 Effect of commercial transport by road on prevalence of bruises and meat pH of beef cattle in Brazil. M. H. Romero*[1], M. J. R. Paranhos da Costa[2], L. F. Uribe[1], J. Braga[2], and A. Riobueno[2], [1]*Universidad de Caldas, Manizales, Caldas, Colombia,* [2]*La Universidad Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

Cattle are exposed to various handling and transport conditions during marketing and previous to slaughter. Brazil is the principal meat producer in South America. Commercial crossbreds of Zebu cattle (n = 1841) were evaluated to determine prevalence and risk factors for carcasses with bruises in a slaughterhouse that had modern facilities and had implemented animal welfare practices and driver training. Measurement of pH was performed in the *Longissimus thoracis* muscle at the level of the 5th and 6th rib, approximately 24 h after slaughter in refrigerated carcasses. A logistic regression analysis was done. Bruise prevalence was 59%. A total of 2041 bruises were found (mean 1.1 bruises/carcass). Bruises in subcutaneous tissue (939, 76%) were more frequent than bruises in muscle tissue (24%). The mean time transport was 4.51 ± 1.21 h, and distance ranged between 65 Km and 334 Km. The fat cover was associated with the presence of bruises. Thin animals bruised more easily than fat animals due to a lack of fat cover ($P \leq 0.01$). Average incidences of meat pH greater than 5.8 and 6.0 were 24.6% and 0.3% respectively. Time of transport and distance were related with high pH ($P \leq 0.01$). Prevalence of bruises was not significantly associated ($P \geq 0.01$) with increased carcass pH values, transport time and type of truck. The results suggest that transport time and distance can affect meat quality.

Key Words: bruises, slaughter, well-being

T9 The effect of water sprinkling on behavior and core body temperature of market hogs transported during summer. J. Fox*[1], T. Widowski[1], S. Torrey[2], E. Nannoni[4], R. Bergeron[5], HW Gonyou[6], JA Brown[6], T. Crowe[7], and L. Faucitano[3], [1]*University of Guelph, Guelph, ON, Canada,* [2]*Agriculture and Agri-Food Canada, Guelph, ON, Canada,* [3]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada,* [4]*University of Bologna, Bologna, Italy,* [5]*University of Guelph, Alfred, ON, Canada,* [6]*Prairie Swine Centre, Saskatoon, SK, Canada,* [7]*University of Saskatchewan, Saskatoon, SK, Canada.*

Hogs are often transported to slaughter under conditions exceeding their thermo-neutral zones, which can lead to reduced welfare and increased in-transit loss. Water sprinkling during lairage decreases micro-climate and hog body temperatures and improves welfare, but there is no clear evidence of these effects during transport. The aim of this study was to observe if sprinkling hogs in stationary trailers before and after transport decreased signs of heat stress. In each of 12 weeks from May to September 2011, 2 pot-belly trailers with 208 hogs per trailer were transported 2h to slaughter. One was outfitted with a custom made sprinkler system that ran for 5min (~125 L) immediately before departure from the farm and immediately before unloading at the plant. In each trailer, 4 test compartments (1 on the top deck, 2 on the middle deck, and 1 on the bottom deck) were outfitted with cameras, and the core body temperature (CBT) of 4 randomly chosen hogs (n = 384) in each were recorded using orally administered iButtons. Trailer and deck loading order were randomized. Behaviors during transport, unloading and during lairage were recorded from video or live observations. Data were analyzed through ANOVA with ambient temperature external to the truck (AmbT) as a co-variant. AmbT averaged 19.5°C ± 3.8°C (range: 14–26°C). At AmbT > 23°C, there was no effect of sprinkling on behavior on-truck (standing, sitting or lying), but at AmbT < 23°C, more hogs stood on sprinkled trucks ($P < 0.05$). Sprinkling did not affect slips or falls during unloading. In lairage, latency to lie was shorter when AmbT exceeded 23°C ($P < 0.05$) and sprinkled hogs spent more time lying and less time sitting ($P < 0.05$) and had fewer drinking bouts than controls ($P < 0.0001$) regardless of AmbT. CBT increased between loading and departure and decreased while in transit for all hogs ($P < 0.0001$) and sprinkling further reduced CBT at arrival at AmbT > 23°C ($P < 0.05$). Therefore, sprinkling hogs when ambient temperature exceeds 23°C can help to alleviate transport-related heat stress without detrimental effects on unloading.

Key Words: pigs, transport, heat stress

T10 Characteristics of bruises in carcasses of commercial zebu cattle in Colombia. M. H. Romero,* L. F Uribe, J. A. Sánchez, and H. Mesa, *Universidad de Caldas, Manizales, Caldas, Colombia.*

Bruises detected on carcasses at the abattoir, may provide information about the traumatic situations the animal endure during the pre-slaughter period. The objective of this study was to describe the gross characteristics of bruises in commercial zebu cattle of different methods of selling and management. The number of bruises and their distribution on the carcass, as well as their severity, shape and size were assessed

post mortem in a slaughterhouse in Colombia. A descriptive statistical analysis was done. A total of 1195 bruises were found on 453 (38.3%) of the carcasses evaluated (n = 1177). Females (n = 453) had 649 bruises (mean 3.2 bruises/carcass) whereas males (n = 250) had 530 bruises (mean 2.1 bruises/carcass). Cattle transported from livestock market had 3 times more bruises than cattle transported directly from the farm (35% and 59%, respectively). The pin (*tuber isquiadicum*), the hip (*tuber coxae*) and the loin were the more frequently observed bruises (32.9, 25 and 21.3%, respectively). Bruises with muscle tissue affected (grade 2) were more prevalent (80%); however, the bruises were small (≥2 and ≤ 8 cm). Circular shaped bruises were most frequent (71%, n = 850), followed by irregular, linear, speckled and tramline shaped bruises (21, 3.6, 3.4 and 1.0%, respectively). speckled shaped bruises were located predominantly in the loin, and can be caused by electric prod or pointed sticks. The model of logistic regression showed that sex and time of transport were associated with the presence of bruising ($P \leq 0.01$). Lairage time was not considered a risk factor for the presence and severity of bruises ($P \geq 0.1$). The presence of bruises located more frequently in the pin and the hip suggest that bruises are inflicted by rude handling and inadequate design of the trucks and facilities. Cattle transport infrastructure must be improved in the area being studied, as must driver training; animal welfare practice must be promoted in all links of the meat chain and research developed in this particular area.

Key Words: bruises, cattle, welfare

Animal Health II

T11 Intravaginal administration of lactic acid bacteria modulated selected plasma metabolites in transition dairy cows. Q. Deng, J. F. Odhiambo, T. Lam, S. M. Dunn, and B. N. Ametaj,* *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

Transition dairy cows experience dietary changes, negative energy balance, and suppressed immunity after parturition, which enhances their susceptibility to uterine infections. The objective of this study was to evaluate blood metabolite responses of periparturient cows administered intravaginally a mixture of lactic acid bacteria (LAB) around calving. One hundred fifty-two pregnant Holstein cows were randomly (based on parity and BCS) assigned to 3 groups 2 wk before the expected day of parturition. Cows received intravaginal LAB or carrier (sterile skim milk) once a wk at −2, −1 and +1 wk relative to calving as following: treatment 1 (TRT1) - 2 consecutive LAB and 1 carrier dose; treatment 2 (TRT2) - 3 consecutive LAB doses; control (CTR) - 3 consecutive carrier doses. Probiotics were a mixture of 3 LAB including *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138, and FUA3140, which were infused at 10^8-10^9 cfu per dose. Blood samples were collected from the tail vein once per wk, before treatment, from −2 to +8 wk. A subset of serum samples from 32 cows were used to evaluate concentrations of glucose, cholesterol, nonesterified fatty acid (NEFA), β-hydroxy butyric acid (BHBA), and lactate. Results showed that concentrations of glucose were 60.8 ± 1.1, 65.2 ± 1.1, and 59.3 ± 0.9 mg/dL ($P < 0.01$) in TRT1, TRT2, and CTR, respectively. Serum cholesterol was 121.5 ± 2.3, 113.8 ± 2.1, and 106.2 ± 1.9 mg/dL ($P < 0.001$) in TRT1, TRT2, and CTR, respectively. Furthermore, concentrations of BHBA in the serum were at 738 ± 39, 555 ± 37, and 623 ± 33 µmol/L ($P < 0.01$) in TRT1, TRT2, and CTR, respectively. Treatments had no effect on serum concentrations of NEFA and lactate ($P > 0.05$). Serum glucose, cholesterol, NEFA, BHBA, and lactate were greater ($P < 0.05$) and glucose was lower ($P < 0.001$) in multiparous cows than those in primiparous cows. The concentrations of all metabolites measured changed in relation to wk ($P < 0.05$). In conclusion, data indicated that administration of LAB in the vaginal tract of periparturient dairy cows affected serum concentrations of selected metabolites related to carbohydrate and lipid metabolism and showed differences between multiparous and primiparous cows.

Key Words: dairy cow, lactic acid bacteria, serum metabolites

T12 Indoor versus outdoor housing during the neonatal, weaning, and commingling periods influences innate immune responses in single-housed Holstein calves. M. D. Sellers,* C. J. Cobb, D. L. Hanson, A. R. Pepper-Yowell, and B. S. Obeidat, *Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

Objective was to determine if housing environment (indoor vs. outdoor) influences metabolic and innate immune responses during the neonatal, weaning, and commingling periods in single-housed Holstein calves. Forty-three Holstein calves (2 ± 1 d old) were housed either in indoor pens (n = 21) or outdoor hutches (n = 22). Weaning started during the wk 7 by removing the PM milk feeding and calves were fully weaned after d 53 when daily starter consumption was 800 g dry matter. Calves were randomly commingled in outdoor group hutches (n = 5/pen) on d 91. Peripheral blood samples were collected during the neonatal (3, 10, 21 d), weaning (45, 47, 53 d), and commingling periods (91, 94, 99 d) and analyzed for neutrophil oxidative burst (OB) capacity when cocultured with an *Escherichia coli*, neutrophil L-selectin expression, whole blood secretion of tumor necrosis factor-α (TNF) when cocultured with lipopolysaccharide, as well as plasma concentrations of haptoglobin, glucose, and urea nitrogen. The study concluded on d 99. Data within each period were analyzed by ANOVA with repeated measures. Within the neonatal period, Indoor calves had more neutrophils producing an OB on d 10 and 21 ($P < 0.05$), as well as a more intense OB response on d 3, 10, and 21 ($P < 0.05$). In addition, Indoor calf neutrophils expressed higher L-selectin on d 21 ($P < 0.05$) and had greater TNF secretion on d 10 ($P < 0.05$). During weaning, Indoor calves had greater OB capacity on d 45, 47 and 53 ($P < 0.05$), and lower haptoglobin concentration on d 47 ($P < 0.05$). Urea nitrogen and glucose decreased ($P < 0.05$) over time across both treatments during the weaning period. During commingling, Indoor calves had a lower ($P < 0.05$) percentage of neutrophils positive for OB on d 94 relative to d 91 when compared with Outdoor calves. Indoor housed calves had heightened innate immune responses during both the neonatal and weaning periods compared with Outdoor calves. In contrast, when calves were commingled, Indoor calves had decreased innate immune responses, which could be due to Indoor calves being moved outside during commingling.

Key Words: calf, housing, immune

T13 Prevalence of nematodes eggs of the genera *Cooperia*, *Ostertagia*, and *Haemonchus*, before and after treatment of dairy heifers with commercial anthelmintics in commercial dairy farms in Puerto Rico. L. López-Soberal,* A. Ruíz-Lugo, Á. González-Sanabria, M. Pagán, and G. Ortiz-Colón, *University of Puerto Rico, Mayagüez Campus.*

A total of 316 dairy heifers, between 3 and 12 mo of age, were evaluated in 18 commercial dairy farms in Puerto Rico to determine the prevalence of gastrointestinal nematodes eggs before and after anthelmintic treatment. Three grams (3g) of feces were collected directly from the rectum of each heifer in 2 different visits (d0) and (d7). After feces collection on d 7, treatments: Ivomec (ivermectin) (n = 111), Dectomax (doramectin) (n = 98), and Valbazen (benzimidazole) (n = 107) were randomly administered to heifers according to manufacturers' instructions. Fourteen (14) days after treatment, 3 g of feces was collected again and the number of parasite eggs per gram of feces was counted using the Modified McMaster Technique. A total of 1,230 eggs were counted before treatment. Nematode genera were identified by a combination of microscopic egg visual evaluation (20×), and egg measurements. Before treatments, the prevalence of nematode eggs were *Cooperia* (19%), *Ostertagia* (62%), *Haemonchus* (13%); *Strongyloides* (5%) and *Trichuris* (1%). Overall, 489 parasite eggs were counted after the administration of anthelmintics. After treatments, the prevalence of nematode eggs were *Cooperia* (6%), *Ostertagia* (76%), *Haemonchus* (14%), *Strongyloides* (2%) and *Trichuris* (2%). The number of *Cooperia* eggs before treatments was 109.2 ± 21 eggs/gram feces (EGF), and it was reduced in all treatments to 20.8 ± 28 EGF ($P < 0.03$). *Ostertagia* averaged 166 ± 23 EGF before treatments, and the EGF was reduced by Dectomax and Valbazen treatment to 87 ± 19.3 and 32.4 ± 18.2 EGF respectively ($P < 0.03$). Conversely, Ivomec treatment did not affect the number of *Ostertagia* eggs ($P = 0.63$). *Haemonchus* averaged 76.5 ± 27.7 EGF before treatments, and the egg count was reduced by Dectomax and Valbazen treatment to 30.7 ± 8.7 and 32.4 ± 11.7 EGF respectively ($P < 0.001$). Ivomec treatment did not affect the number of *Haemonchus* eggs ($P = 0.63$). These data suggest that *Ostertagia* and *Haemonchus* populations have developed resistance to ivermectin in Puerto Rico.

Key Words: ivermectin, doramectin, benzimidazole

T14 Eicosapentaenoic acid and NF-κB inhibitor pyrrolidine dithiocarbamate attenuate prostaglandin production by bovine endometrial cells treated with lipopolysaccharide.

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The recognition that n-3 polyunsaturated fatty acids (n-3 PUFA) possess anti-inflammatory properties has prompted a series of studies investigating their efficacy in animal and human models of inflammatory disease. Although their action in antagonizing arachidonic acid metabolism is a key anti-inflammatory effect of n-3 PUFAs, these FA have several other anti-inflammatory effects which might occur downstream of altered eicosanoid production or might be independent of this activity. The objective of this study was to examine the effects of α linolenic (ALA, C18:3; 100 μM), eicosapentaenoic (EPA, C20:5n-3; 100 μM) and docosahexaenoic (DHA, C22:6n-3; 100 μM) acids on prostaglandin E2 (PGE2) and F2α (PGF2α) production by bovine endometrial (BEND) cells treated with lipopolysaccharide (LPS, 10 μg / mL). Concentrations of PGE2 and PGF2α in the culture medium increased ($P < 0.01$) in a dose and time-dependent manner following treatment with LPS. Addition of omega-3 PUFAs to the incubation medium decreased ($P < 0.01$) PGE2 response to LPS by 70.2%. Alpha linolenic acid and EPA were equipotent in reducing PGE2 response to LPS (89% reduction). A smaller but statistically significant reduction of PGE2 production was detected ($P < 0.01$) when BEND cells were co-treated with LPS and DHA. ALA and EPA decreased ($P < 0.01$) PGF2α response to LPS by 63 and 79%, respectively. In contrast, DHA increased ($P < 0.01$) PGF2α response to LPS by 42%. Addition of an NF-κB inhibitor (50 μM pyrrolidine dithiocarbamate) to the culture medium decreased ($P < 0.01$) PGE2 response to LPS to a greater extent than did EPA. Results indicate that omega-3 FA and the NF-κB inhibitor attenuate LPS effects on endometrial PG secretion and that these molecules may act trough distinct signaling pathways. Additional studies are needed to fully characterize the mechanism by which omega-3 FA modulate pro-inflammatory eicosanoid biosynthesis in the bovine endometrium

Key Words: eicosapentaenoic acid, prostaglandin, cattle

T15 Plane of milk replacer nutrition influences the acute phase response of weaned Jersey calves to an oral *Salmonella typhimurium* challenge.

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Objective was to determine if previous plane of milk replacer nutrition influences the acute phase response to an oral *Salmonella typhimurium* (ATCC14028) challenge in weaned Jersey calves. Twenty Jersey bull calves (77 ± 1 d old) that were previously fed either a Low Plane (LP; 409 g/d of a 20/20 milk replacer) or a High Plane (HP; 610 and 735 g/d of a 28/25 milk replacer for wk 1 and wks 2–6, respectively) of milk replacer were enrolled in the study. All calves were offered ad libitum access to calf starter after the 1st wk of life. Calves began weaning by removing the PM feeding during wk 7 and were completely weaned when they consumed 600 g of calf starter / d after the 7th wk. Calves were orally challenged with 1.5×10^7 colony forming units of *Salmonella typhimurium*. Indwelling rectal temperature probes collected a measurement every 5 min. from −16 h to the conclusion of the study at 236 h post-challenge. Peripheral blood samples were collected daily at 0800 throughout the study and analyzed for oxidative burst capacity when cocultured with an *Escherichia coli*, whole blood secretion of tumor necrosis factor-α when cocultured with lipopolysaccharide, as well as plasma concentrations of haptoglobin, glucose, and urea nitrogen. The percentage of neutrophils producing an oxidative burst was greater ($P < 0.05$) among HP calves from d 1— 5 after the challenge. Similarly, the intensity of the oxidative burst tended to be greater ($P < 0.10$) among HP calves on d 2 and 3 after the challenge. In addition, the secretion of tumor necrosis factor-α tended ($P < 0.10$) to be greater on d 1 and was greater ($P < 0.05$) on d 5 and 6 after the challenge among HP calves. Median ranks of haptoglobin concentrations were lower ($P < 0.05$) among HP calves throughout the study; however, there was no difference in rectal temperature ($P = 0.99$) between LP and HP calves. Data was analyzed using ANOVA with repeated measures. These data support that calves fed a HP of milk replacer nutrition have a more aggressive innate immune response to an oral *Salmonella typhimurium* challenge, which may improve resistance to disease.

Key Words: calf, immune, nutrition

T16 Intravaginal probiotics expedited uterine involution in postpartum dairy cows.

Q. Deng, J. F. Odhiambo, T. Lam, S. M. Dunn, and B. N. Ametaj,* *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

Uterine involution and resumption of ovarian cyclicity are good indicators of uterine status and reproductive performance of postpartum dairy cows. The objective of this study was to investigate the effect of intravaginal probiotics on uterine involution and resumption of ovarian cyclicity in postpartum dairy cows. 154 pregnant Holstein cows were randomly assigned (based on parity and BCS) to 3 groups 2 wk before the expected day of calving. Cows received intravaginally a mixture of lactic acid bacteria (LAB) or carrier (skim milk) once a wk at −2, −1 and +1 wk relative to calving as following: treatment 1 (TRT1) - 2 consecutive LAB and 1 carrier dose; treatment 2(TRT2) - 3 consecutive LAB doses; and control (CTR) - 3 consecutive carrier doses. LAB used in this study were a mixture of 3 bacteria: *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138, and FUA3140 and infused at a dose of 10^8-10^9 cfu per dose. Uterine involution was evaluated by rectal ultrasonography using a Sonosite ultrasound fitted with a 7.5MHz probe once a wk at +2, +3, +5, +7 wk to obtain images of the cervix, uterine body and horns, follicles, and corpus luteum. Data were analyzed with the mixed procedure of SAS including treatment, parity, and wk. Results showed differences among treatments in terms of the cross-sectional areas of gravid horn and uterine body. TRT1 had smaller cross-sectional areas of the gravid horn than TRT2 (3.98 ± 0.13 vs. 4.48 ± 0.14 cm^2; $P < 0.01$) and CTR (3.98 ± 0.13 vs. 4.23 ± 0.12 cm^2; $P > 0.05$). The cross-sectional areas of uterine body were smaller in TRT1 compared with TRT2 (5.41 ± 0.16 vs. 5.90 ± 0.17 cm^2; $P < 0.05$) and CTR (5.41 ± 0.16 vs. 5.95 ± 0.15 cm^2; $P < 0.01$). Multiparous cows had larger gravid horn cross-sectional areas than primiparous cows (4.57 vs. 3.90 cm^2; $P < 0.001$). Parity also affected cervix and uterine body cross-section areas ($P < 0.05$). Week had an effect on the cross-sectional areas of gravid horn, cervix, and uterine body ($P < 0.001$). Based on the presence of corpus luteum, data showed that the number of cows that had resumed their cyclic activity by wk +7 were 57%, 67%, and 55% ($P = 0.08$) in TRT1, TRT2, and CTR, respectively. Overall, intravaginal LAB treatment expedited involution of the uterine gravid horn and body, and had a tendency to hasten the resumption of ovarian cyclicity in postparturient dairy cows.

Key Words: dairy cows, lactic acid bacteria, uterine involution

T17 Plane of nutrition during the pre- and post-weaned periods influences the innate immune activity of Holstein calves. B. S. Obeidat[1], C. J. Cobb[1], M. D. Sellers[1], A. R. Pepper-Yowell[1], D. L. Hanson[1], T. J. Earleywine[2], and M. A. Ballou*[1], [1]*Department of Animal and Food Sciences, Texas Tech University, Lubbock,* [2]*Land O'Lakes, Animal Milk Products Co., Shoreview, MN.*

Objective was to determine the influence of plane of nutrition during the pre- and post-weaned periods on the performance and innate immune activity of Holstein calves. Thirty 9 (2 ± 1 d old) calves were randomly assigned to 2 treatments. Treatments were a low (LPN; n = 18) and high plane of nutrition (HPN; n = 21). Calves in LPN treatment were fed 409 g/d dry matter (DM) of a 20% CP/20% fat milk replacer; whereas calves in HPN treatment were fed 756 and 910 g/d DM of a 28% CP/20% fat during the 1st wk and wk 2–6, respectively. Weaning was initiated during the 7th wk by removing the PM feeding and calves were completely weaned when they were consuming 800 g DM of calf starter after d 53. Calves were fed their respective calf starter until the end of the study at 91 d. Peripheral blood samples were collected on d 3, 10, 21, 45, 47, 53, and 91 for ex vivo immunological and biochemical analyses. Data were analyzed by ANOVA with repeated measures. Metabolizable energy intake, crude protein intake, and average daily gain were greater ($P < 0.001$) for HPN calves compared with LPN calves. No difference between treatments was observed for secretion of tumor necrosis factor-α when whole blood was cocultured with lipopolysaccharide. On d 3 and 21 neutrophil L-selectin expression was greater ($P < 0.05$) in LPN than HPN. The percentage of neutrophils producing an oxidative burst when cocultured with *Escherichia coli* tended ($P = 0.06$) to be greater and was greater ($P < 0.05$) in LPN than HPN on d 10 and 21, respectively. In addition, neutrophils from LPN had greater ($P < 0.01$) oxidative burst intensity throughout the study. On d 3, 10, 21, and 45 plasma glucose concentrations were greater ($P < 0.02$) in calves fed the HPN. The innate immune responses of calves fed a LPN were more active during the pre-weaning period than calves fed a HPN; however, this response was not observed during the immediate post-weaned period. The exact mechanism underlying the more active innate immune responses of the LPN during the pre-weaned period is not known, but could be due to either increased immunogenic stimulation or decreased stress.

Key Words: calf, immune, plane of nutrition

T18 Pathophysiological response to an oral *Salmonella typhimurium* challenge is influenced by the inoculum dose in newborn colostrum-fed Jersey calves. A. R. Pepper-Yowell,* D. L. Hanson, M. D. Sellers, C. J. Cobb, B. S. Obeidat, and M. A. Ballou, *Texas Tech University, Lubbock.*

Objective was to determine how the pathophysiology of newborn Jersey calves changed over time at increasing doses of an oral *Salmonella typhimurium* (ATCC14028) challenge. Twenty Jersey bull calves (4 ± 1 d old) were orally inoculated with one of 5 doses (n = 4) of *Salmonella typhimurium*: saline, 1×10^4, 1×10^6, 1×10^8, or 1×10^{10} colony forming units. Peripheral blood samples were collected daily from −2 to 11 d and on d 14 relative to the challenge and analyzed for glucose, urea nitrogen, and haptoglobin. Indwelling rectal temperature probes collected hourly measurements throughout the study. Both 10^8 and 10^{10} were 100% lethal doses (LD_{100}) occurring between 2 and 8 d post challenge; whereas 10^6 was an LD_{50} occurring between 10 and 11 d post challenge. None of the 10^4 calves showed any visual signs of disease during the observation period. All values are expressed as differences from the mean of the saline at each time point. Time to reach nadir glucose values for 10^8 and 10^{10} was faster than 10^4 and 10^6 ($P < 0.01$; 3.5, 1.0, 9.0 and 7.8 ± 1.04 d). Average nadir glucose value for 10^8 was lower than 10^4 ($P < 0.05$; −44.9 and −28.6 ± 4.91 mg/dL). Time to peak urea nitrogen was faster for 10^{10} than 10^4, 10^6 and 10^8 ($P < 0.01$; 1.0, 6.0, 6.0, and 3.8 ± 0.94 d). Peak urea nitrogen was lower for 10^4 and 10^{10} than 10^6 and 10^8 ($P < 0.05$; 8.2, 5.8, 14.9 and 15.6 ± 2.12 mg/dL). Time to peak haptoglobin was faster for 10^8 and 10^{10} than 10^4 and 10^6 ($P < 0.01$; 1.8, 1.0, 4.0 and 4.0 ± 0.63 d). Time to peak rectal temperature was faster for 10^8 and 10^{10} than 10^4 and 10^6 ($P < 0.01$; 1.5, 1.0, 3.5 and 3.3 ± 0.33 d). There was no treatment effect on peak haptoglobin values and peak rectal temperature ($P = 0.22$ and $P = 0.13$). However, when the animals were classified by survivability the calves that died had higher average haptoglobin than calves that survived ($P < 0.01$; 3.5 and 1.8 ± 0.38 OD). Increasing the dose of *Salmonella typhimurium* in newborn Jersey calves shortened the timeframe that calves reached a peak immune reaction, and increased the magnitude of the reaction for metabolic parameters.

Key Words: bacteria challenge, calf, health

T19 Effect of dietary supplementation with *Curcuma longa* (turmeric) during *Eimeria maxima* and *Eimeria tenella* infection of chickens. D. K. Kim*[1], H. S. Lillehoj[1], S. H. Lee[1], S. I. Jang[1], M. S. Park[1], and D. Bravo[2], [1]*Animal Parasitic Diseases Laboratory, Animal and Natural Resources Institute, United States Department of Agriculture, Beltsville, MD,* [2]*Pancosma SA, Geneva, Switzerland.*

The effects of orally administered *Curcuma longa* (turmeric) on the classic criteria of coccidiosis in chicken was evaluated during experimental *Eimeria maxima* (EM) or *Eimeria tenella* (ET) infection and the modification of genome-wide profile was analyzed in uninfected condition. Broiler chickens continuously fed from hatch with *Curcuma Longa* supplemented diet and orally challenged with live EM or ET had increased body weight gain, greater antibody responses to microneme protein 2 from ET (EtMIC2) compared with chickens fed a non-supplemented diet. However, the chickens fed turmeric-supplemented diet shed significantly decreased fecal oocyst excretion only in ET infected chickens, not in EM infection group. Differences between groups were considered statistically significant at $P < 0.05$ by one-way ANOVA. Differential gene expression by microarray hybridization using a cutoff of >2.0-fold changes identified 601 transcripts whose levels were significantly altered in intestinal lymphocytes of turmeric-fed birds without *Eimeria* infection compared with non-supplemented controls (287 upregulated, 314 downregulated). Biological pathway analysis identified the most significant function belonging to the categories of "Disease and Disorder" as "Nutritional Diseases." The levels of local cytokine transcripts of IL-1β, IL-6, IL-15, and IFN-γ were consistently greater in the turmeric-fed no-infection group compared with the controls fed only the standard diet. These results suggest the immunologic and genomic changes that occur in chickens following dietary supplementation of turmeric that are relevant to protective immunity during avian coccidiosis.

Key Words: *Curcuma longa*, turmeric, coccidiosis

T20 Detection of neutralizing antibody titration against rabies virus in dogs. A. E. Gazi*[1] and S. Ak[2], [1]*Tarim Ilce Mudurlugu, Bozyazi, Turkey,* [2]*Istanbul University, Veteriner Fak. Microbiology, Istanbul, Turkey.*

The aim of this study was to determine the titers of neutralizing antibodies against rabies virus in 5 hundred vaccinated owned and stray dogs within the Istanbul province. The levels of the neutralizing antibody titration in the blood serum were evaluated by ELISA method. Sixty-five

(13%) of the dogs examined had adequate level (0.5 IU/ml and over) of antibody titration. In addition, the effects on the formation of the neutralizing antibody levels following the vaccination of some factors, such as being owned or stray, the number of repetition of vaccination, the age, living area, sex, interval between the last vaccination and sampling, have been evaluated. The statistical comparisons of the ages, number of repetition of vaccination, interval between the last vaccination and the sampling dates of the groups were analyzed by using one way ANOVA. *t*-test procedure was used to evaluate rest of the data. As a result of the statistical evaluations, it has been determined that interval between the last vaccination and sampling had an important effect on formation of the neutralizing antibody titration ($P < 0.001$). Moreover, the effect of the age of the dogs was also significant for the neutralizing antibody levels ($P < 0.05$). In contrast, being owned or stray, sex, living area and the number of repetition of the vaccination had no effects on the neutralizing antibody levels.

Key Words: rabies, vaccines, immunogenicity of rabies vaccine

T21 Dairy health records use and management by producers in Washington and Idaho.

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Nationally, more than 90% of large dairy herds use computerized records, making it possible to use epidemiologic techniques to evaluate management of the herd. However, accuracy and consistency of these data are often lacking. Dairy management software prescribes the way reproduction records are entered but health data entry is user-defined and highly variable within and between farms. Therefore, the ability to meaningfully summarize and evaluate health data are limited. The purpose of this study was to evaluate the use and perceived value of health data on dairies. Mail and online survey that focused on perception of health data utility and how health data were recorded was pre-tested and then provided to 951 dairy producers in Washington and Idaho. Comparisons of proportion of respondents to a question were made using a chi-squared test for homogeneity of proportions. A total of 242 (25.4%) surveys were returned. About 65% of producers used commercial dairy management software and just over half recorded some health events in the computer. Of the 116 that used commercial software and recorded some health events, 85% indicated that their disease and treatment records were most useful for making culling decisions for individual cows but were less confident about the ability of their computerized health records to track drug withdrawal times, monitor disease in the herd or evaluate the effectiveness of management practices for groups of cows. Of all the respondents, 45.6% (108) agreed that better guidelines on how to record disease and treatment records are needed while 16.5% (39) disagreed. Few respondents agreed that disease and treatment data are recorded the same way on most dairies (11.4%). A minority of respondents (16.5%) were dissatisfied with the quality of their records. A higher percentage of dissatisfied respondents agreed that better guidelines for recording health data were needed versus the need for better guidelines on reproduction data (90 vs 51%; $P < 0.001$). Most producers saw value to their health data but primarily for making individual cow decisions. Improvements in health data quality allowing epidemiological evaluation to inform herd-level decision making will require on-farm health data entry industry standards as currently exist for milk production and reproduction records. Such standards would be best implemented by a change from user-defined to prescribed data entry in dairy management software.

Key Words: dairy, health, records

T22 Effect of method of detection and uterine dimensions in the diagnosis of endometritis in lactating dairy cows.

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Objectives of this study were to 1) identify the agreement among different methods to detect endometritis and, 2) determine interactions among uterine measurements, parity, BCS and endometritis diagnosis. Three-hundred and forty-seven diagnoses were performed in lactating Holstein cows from the UBC Dairy Centre. Cows were diagnosed at 30 and 44 ± 3 d in milk by gloved hand (GH) and Metricheck (MC) exams based on vaginal discharge that were scored on a 1–5 scale (>3 considered positive), and ultrasonography (US) of the uterus (presence of ecogenic fluid in lumen) as the gold standard. Blood samples and BCS (Low <2.75 > Moderate) were collected on the same dates of uterine exams. Major US measures of the uterus were diameter of the endometrium in both horns (Small <18mm > Large), asymmetry between horns (Moderate <3mm > High), and diameter of the inner layer of cervix (Small <18mm > Large). Data was analyzed by logistic regression using SAS (significant if $P < 0.05$). Results show that endometritis was diagnosed in 10.6% of the time, whereas MC and GH were diagnosed in 15.7% and 13.4% of the time. Considering US as the reference method, agreement with MC and GH was 35.3% and 32.3%, respectively. A large uterine horn (22.8% vs. 12.8%), high asymmetry of uterine horns (16.3% vs. 6.2%) and a large cervix (15.5% vs. 5.8%) measured by US were more likely to be diagnosed with endometritis. When diagnosis was done with MC or GH, the high asymmetry between uterine horns proved significant (20.3% vs. 9.8%) to predict endometritis, but only in the GH a large cervix was more likely to predict endometritis (18.9% vs. 8.2%). Primiparous cows were also more likely to be diagnosed with endometritis based on vaginal discharge (20.2% vs. 12.6%) compared with multiparous cows. BCS had no influence in the diagnosis of endometritis. In conclusion, methods that used solely vaginal discharge to detect clinical cases of endometritis overestimated the number of endometritis cases and were inaccurate compared with US diagnosis. Methods using vaginal discharge are likely diagnosing vaginitis or cervicitis more accurately than endometritis.

Key Words: dairy cows, endometritis, ultrasound

T23 Effects of phytoncide supplementation on growth performance, nutrient digestibility, blood profiles, diarrhea score, and fecal microbial shedding in weaning pigs.

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A total of 140 weaning pigs [(Landrace × Yorkshire) × Duroc, BW = 6.47 ± 0.86 kg] were used in a 5-week growth trial to determine the effects of phytoncide supplementation on growth performance, apparent total tract digestibility (ATTD), blood profiles, diarrhea score, and fecal microbial shedding. Pigs were randomly assigned into 1 of 5 treatments. Dietary treatments were: NC, basal diet (without antibiotics); PC, NC + 0.05% tylosin; EO, NC + 0.1% essential oil; PP, NC + 0.2% PP (phytoncide with 2% citric acid), and PA, NC + 0.2% PA (phytoncide). Each treatment had 7 replicate pens with 4 pigs per pen. All pigs were housed in pens with a self-feeder and a nipple drinker, and allowed ad libitum access to feed and water throughout the experiment. Statistical analyses were conducted in accordance with mean separations performed by the Duncan multiple range test using the GLM procedure of the SAS statistical software package (1996). During 0–2 weeks, the gain to feed (G/f) ratio in EO and PP treatments were increased ($P < 0.05$) compared with PA treatments. During 2–5 weeks, PA treatment had the highest ($P < 0.05$) G/f among treatments. Pigs fed the PC and PP diets had higher ($P < 0.05$) ATTD of gross energy than those fed the NC and EO diets at 2 week. The ATTD of dry matter (DM) was improved ($P < 0.05$) in PC, PP and PA treatments compared with NC treatment at 5 week. The PP treatment increased ($P < 0.05$) the concentration of immunoglobulin G (IgG) in blood compared with NC, PC and EO treatments at 2 week. These pigs fed PP diet showed greater ($P < 0.05$) amounts of fecal *Lactobacillus* compared with NC treatment. However, no difference ($P > 0.05$) was observed in diarrhea score among treatments. In conclusion, dietary supplementation with 0.2% PP may improve nutrient digestibility, increase blood IgG concentration, and the amounts of fecal *Lactobacillus* in weaning pigs, which indicated that phytoncide with 2% citric acid could be used as an alternative for antibiotics in weaning pigs.

Key Words: blood profiles, phytoncide, weaning pigs

T24 Influence of tannins extract supplementation on feedlot performance of receiving bull-calves naturally infested with gastro intestinal parasites. R. Barajas*[1], B. J. Cervantes[2], M. A. Espino[1,3], A. Camacho[1], I. Enriquez[1], C. Barraza[1], L. R. Flores[1], J. J. Lomeli[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*, [3]*Pronutrient Developers, León, Guanajuato, México.*

Sixty-five bull-calves 171 ± SE 2.77 kg were used to determine the influence of tannins extract supplementation on feedlot performance of receiving bull-calves naturally-infested with gastro intestinal parasites. Bull-calves were individually weighed, ear-tagged, and grouped in 4 blocks using initial weight criteria for reduction of social interaction, and allotted in 16 ground floor pens (6 × 12 m). Bull-calves were weighed d 1 and 28 when feces and blood samples were taken from each bull-calve to exploring the presence of gastro-intestinal parasites, blood parasites, and plasma urea nitrogen (PUN) determination. Inside each block, pens were randomly assigned to receive 1 of 2 treatments: 1) Feeding with a 70% concentrate ground sorghum-DDG-canola meal based diet (CTRL; n = 32); or 2) Diet similar to CTRL, added with 0.3% (dry matter basis) of tannins extract (TE; n = 33). Tannins extract was supplied as TMP-Protein Enhancer (Técnica Mineral Pecuaria; Mexico), a premix that contains 56% of a condensed (Quebracho tree) and soluble (Chesnutt) tannins-blend. Number of infested animals was compared using Chi-squared test. Number of parasites-eggs by gram of feces data (NEGF) was transformed to square-root before analyses. NEGF, PUN, final weight and Average daily gain were analyzed by ANOVA. No blood-parasites were found. Eggs of found parasites corresponded to: < i (85%), *Eimeria* sp. (72%), *Cooperia* sp. (71%), *Trichostrongylus* sp. (52%), and *Esophagostomus* sp. (32%). In d 1 and 28 the amount of infested-calves and the NEGF were similar ($P > 0.50$) between treatments. TE supplementation decreased ($P = 0.03$) 15.5% PUN concentration (14.06 vs. 11.88 mg/dL). Final weight was similar between treatments ($P = 0.51$). Average daily gain tended to be higher ($P = 0.07$) in bull-calves fed-TE (1.370 vs. 1.191 kg/day for TE and CTRL, respectively. It is concluded that tannins extract supplementation in dose near to 0.3% of dietary DM, did not produce changes on GI parasites population of receiving bull-calves.

Key Words: feedlot-calves, parasites, tannins

T25 Effects of different levels of fermented oat on growth performance, diarrhea score, fecal microbial shedding, and fecal noxious gas emission in weaning pigs. J. P. Wang,* J. P. Lee, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to investigate the effects of different levels of fermented oat on growth performance, diarrhea score, fecal microbial shedding, and fecal noxious gas emission in weaning pigs. A total of 125 weaning piglets [(Landrace × Yorkshire) × Duroc, BW = 7.31 ± 0.24 kg] weaned at 21 d of age were assigned to 5 treatments in randomized complete block designs based on the initial BW and sex. This experiment included 2 phases. In phase 1 (0–21 d), there were 5 treatments: T1, basal diet + 15% nature oat; T2, basal diet + 3.7% fermented oat + 11.3% nature oat; T3, basal diet + 7.5% fermented oat + 7.5% nature oat; T4, basal diet + 11.3% fermented oat + 3.7% nature oat, and T5, basal diet + 15% fermented oat. In phase 2 (21–35 d), it also included 5 diets, an half of dose in phase 1 were supplemented in phase 2. Pigs were allowed ad libitum access to feed and water and their BW and FI were measured by each phase for entire experiment. During the phase 1, the use of 7.5%, 11.3%, 15% fermented oat to replace nature oat improved ($P < 0.05$) ADG and G/f compared with T1 and T2 treatments. Use of fermented oat up to 7.5% replacing nature oat showed the highest ($P < 0.05$) ADG and G/f among dietary treatments. During the phase 2, pigs fed the 3.5%, 5.3%, and 7% fermented oat substituted diets showed higher ($P < 0.05$) ADG compared with those fed the basal diet. Overall, ADG and ADFI were higher ($P < 0.05$) in T3, T4 and T5 treatments compared with T1 and T2 treatments. Different levels of fermented oat had no effect ($P < 0.05$) on diarrhea score, nutrient digestibility, fecal microbial shedding, and fecal noxious gas emission. Collectively, we could conclude that supplementation with 50% fermented oat to replace nature oat is an appropriate dose to achieve a better growth performance in weaning pigs.

Key Words: fermented oat, growth performance, weaning pigs

T26 GPR109A mediates calcium mobilization induced by BHBA in isolated bovine monocytes. L. K. Mamedova*[1], E. C. Titgemeyer[1], G. M. Pighetti[2], J. Y. Lu[1], D. H. Hua[1], and B. J. Bradford[1], [1]*Kansas State University, Manhattan*, [2]*University of Tennessee, Knoxville.*

Ketosis is a common in early lactation dairy cows, and ketosis greatly elevates the risk of subsequent infections. In vitro administration of β-hydroxybutyric acid (BHBA) has inhibitory effects on the function of bovine neutrophils, monocytes, and lymphocytes. However, mechanisms linking BHBA to altered immune function remain unknown. Our objective was to evaluate the potential role of the BHBA receptor GPR109A in leukocytes. Blood was collected from 3 healthy Holstein cows in mid-lactation and peripheral blood mononuclear cells (monocytes) and polymorphonuclear neutrophils were isolated. Protein and RNA were extracted, mRNA abundance of GPR109A was determined by quantitative RT-PCR, and protein abundance was determined by Western blot. Results demonstrated strong expression of GPR109A at the mRNA (mean Ct = 22.7 ± 0.6) and protein levels in both cell types. Next, isolated monocytes and neutrophils were exposed to BHBA (1 mM) or niacin (10 μM), a potent agonist of GPR109A. Immediately after exposure to treatments, cytosolic calcium concentrations were monitored by fluorescence assay. Both BHBA and niacin elevated cytosolic calcium in both monocytes and neutrophils (all $P < 0.01$). Finally, RNA interference was used to knock down the protein before exposure to agonists. Isolated monocytes were transfected with siRNA (scrambled or GPR109A) and incubated for 24 h. Cells were then treated with 1 mM BHBA and calcium mobilization was assessed, or cells were harvested to determine knockdown efficiency. Although incubation time was short due to the limited viability of isolated monocytes, densitometry analysis of Western blot revealed that GPR109A protein was significantly knocked down by the siRNA treatment (36 ± 10% decrease, $P < 0.05$). As in the initial study, BHBA caused a significant increase in cytosolic calcium, and GPR109A siRNA decreased this response by 63 ± 3% ($P < 0.001$). Collectively, these results suggest that GPR109A at least partially mediates calcium mobilization responses to BHBA in bovine leukocytes. Further research is required to determine whether such mechanisms underlie the effects of BHBA on immune function.

Key Words: G protein coupled receptor, ketone, immunity

T27 Effects of bacteriophage as an alternative for antibiotics on egg performance, egg quality, fecal microbial shedding, and fecal moisture content in laying hens.

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A total of two hundred forty 40-wk-old ISA-brown laying hens were used in a 6-week feeding trial to evaluate the effects of bacteriophage as an alternative for antibiotics on egg performance, egg quality, fecal microbial shedding, and fecal moisture content. Hens were allotted to 1 of 4 dietary treatments with 10 replications (6 adjacent cages per replication and 1 hen per cage) in a completely randomized design. Dietary treatments included: 1) CON, basal diet; 2) BPS1, CON + 0.020% bacteriophage; 3) BPS2, CON + 0.035% bacteriophage, and 4) BPS3, CON + 0.050% bacteriophage. Bacteriophage used in our study contains *Salmonella gallinarum*, *S. typhimurium*, *S. enteritidis*, *S. pullorum*, *Staphylococcus aureus*. The counts of bacteriophage are 10^8 pfu/gram. All diets were formulated to meet or exceed the NRC (1994) requirements for laying hens. Hens were provided with basal diet for a 7 d adjustment period before the beginning of the experiment. All hens were allowed ad libitum access to water and feed through nipple drinkers and feeders, respectively. The hens were housed in a windowless and environmentally controlled room that was maintained at 21°C, and had a daily lighting schedule of 16 h light and 8 h dark. During 0–6 weeks, no difference ($P > 0.05$) was observed in egg production and egg weight among dietary treatments. At 4 and 5 weeks, birds in BPS2 group had higher ($P < 0.05$) Haugh unit (HU) than those in CON group. HU in birds fed the BPS1 and BPS3 diets was greater ($P < 0.05$) than those fed the CON diet at 5 and 6 weeks. However, egg weight, egg shell color, yolk height, yolk color unit, egg shell strength, egg shell thickness, egg gravity, fecal microbial shedding, and fecal moisture content were not influenced ($P > 0.05$) by dietary treatments during the entire experimental period. In conclusion, bacteriophage supplementation in our study had beneficial effects on HU, which related to a higher egg albumen contents, thus led to fresher eggs in laying hens.

Key Words: bacteriophage, egg quality, laying hens

T28 Effects of bacteriophage as an alternative for antibiotics on growth performance, nutrient digestibility, blood profiles, fecal microbial shedding, diarrhea score, and fecal moisture content in growing pigs.

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A total of 96 growing pigs [(Landrace × Yorkshire) × Duroc, BW = 28.85 ± 1.63 kg] were used in a 6-week feeding trial to investigate the effects of bacteriophage as an alternative for antibiotics on growth performance, apparent total tract digestibility (ATTD), blood profiles, fecal microbial shedding, diarrhea score, and fecal moisture content. Pigs were randomly allotted to 4 treatments with 6 replicate pens (4 pigs per pen) per treatment according to their initial BW. Dietary treatments were: 1) NC, negative control diet (without antibiotics); 2) PC, NC + 22ppm tylosin; 3) BP1, NC + 0.025% bacteriophage and 4) BP2, NC + 0.05% bacteriophage. Bacteriophage used in our study contains *E. coli* K88, *E. coli* K99, *Salmonella typhimurium*, *S. enteritidis*, *S. cholerasuis*, *Clostridium perfringens* type A & C, *Staphylococcus aureus*. The counts of bacteriophage are 10^8 pfu/gram. No difference ($P > 0.05$) was observed in growth performance and blood profiles among treatments throughout the experimental period. The ATTD of DM was higher ($P < 0.05$) in PC, BP1, and BP2 treatments than that in NC treatment. The ATTD of N was improved ($P < 0.05$) in bacteriophage treatments than that in NC treatment. The ATTD of energy was higher ($P < 0.05$) in PC treatment than that in NC treatment. Fecal *Lactobacillus* counts were increased ($P < 0.05$) in BP2 treatment compared with NC and PC treatments, whereas fecal *Escherichia coli* population was reduced ($P < 0.05$) in PC and BP2 treatments compared with NC treatment. No significant difference ($P > 0.05$) was noted in diarrhea score and fecal moisture content among treatments. In conclusion, supplementation with 0.05% bacteriophage in growing pig diet improved nutrient digestibility, benefited the fecal *Lactobacillus* population, and inhibited the growth of *Escherichia coli*, indicating bacteriophage can be used as an alternative for antibiotics in growing pigs.

Key Words: bacteriophage, nutrient digestibility, growing pig

T29 Effects of bacteriophage as an alternative for antibiotics on growth performance, nutrient digestibility, relative organ weight, blood profiles, and fecal microbial shedding in broilers.

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A total of 720 1-d-old ROSS 308 broilers (BW = 44.2 ± 0.2 g) were used in a 32-d trial to investigate the effects of bacteriophage as an alternative for antibiotics on growth performance, apparent total tract nutrient digestibility, relative organ weight, blood profiles, and fecal microbial shedding. Broilers were randomly assigned to 1 of 4 treatments (12 replicate pens per treatment with 15 broilers per pen). Dietary treatments were: 1) NC, basal diet (without antibiotics); 2) PC, NC + 0.05% tylosin; 3) BP1, NC + 0.025% bacteriophage; 4) BP2, NC + 0.05% bacteriophage. Bacteriophage contains *Salmonella gallinarum*, *S. typhimurium*, *S. enteritidis*, *Clostridium perfringens* type A & C, and *Staphylococcus aureus*. The counts of bacteriophage are 10^8 pfu/gram. This trial was separated into starter phase (d 0–14) and finisher phase (d 15–32). Broilers were allowed *ad libitum* access to feed and water. The feed conversion ratio (FCR) decreased ($P < 0.05$) in BP2 treatment compared with NC treatment. No difference ($P > 0.05$) was found in BWG, FI and FCR among treatments during neither period nor overall period. The apparent total tract nutrient digestibility was unaffected ($P > 0.05$) by dietary treatments. The relative liver weight was higher ($P < 0.05$) in BP1 treatment than NC treatment. The meat quality and other relative organ weights were not affected ($P > 0.05$) by dietary treatments. There was no difference ($P > 0.05$) in blood profiles among treatments. The fecal *Lactobacillus* counts were increased ($P < 0.05$) in BP2 treatment compared with NC treatment. The fecal *E. coli* population was reduced ($P < 0.05$) in PC, BP1 and BP2 treatments compared with NC treatment. Collectively, the dietary bacteriophage supplementation at the level of 0.05% could benefit intestinal beneficial bacteria, and inhibit the growth of pernicious bacteria, thus maintained the intestinal health of broilers.

Key Words: bacteriophage, broilers, microbial shedding

T30 Changes in bacterial communities in bovine milk when comparing low and high somatic cell count quarters using culture independent analysis. S. M. Buttram*[1], K. M. Hunt[1], L. K. Fox[2], and M. A. McGuire[1], [1]*Department of Animal and Veterinary Science, University of Idaho, Moscow,* [2]*Department of Animal Science, Washington State University, Pullman.*

Many believe that bovine milk is sterile unless infectious mastitis is occurring. However recent reports indicate the presence of microbial communities in milk of healthy mammary glands, but little is known about these communities when there is an increase in somatic cell count (SCC). The objective of this study was to characterize the microbial communities in bovine milk, to determine if sampling type affected bacterial diversity, and to compare how communities changed with an increase in SCC. Milk was collected once from 6 Holstein cows that had at least one high SCC (≥400,000 cells/ml) quarter and one low SCC quarter using 4 sampling techniques: fore strip, needle aspirate of foremilk, residual strip, and needle aspirate of residual milk. To characterize the microbial communities, culture independent pyrosequencing of the 16S ribosomal RNA gene was used to determine percentage relative abundance. Results (mean ± SEM) demonstrated that the most abundant bacterial genera in low SCC milk included: *Clostridium* (29.6 ± 4%), *Sporacetigenium* (11.6 ± 1.7%), *Pelomonas* (10.9 ± 2.4%), *Turicibacter* (5.8 ± 1.0%), and *Staphylococcus* (5.1 ± 1.7%). The most abundant genera in high SCC milk included: *Staphylococcus* (63 ± 7.3%), *Peptoniphilus* (7.9 ± 3.7%), *Enterococcus* (6.1 ± 4.2%), *Arcanobacterium* (4.5 ± 2.1%), and *Sporacetigenium* (2.8 ± 1.0). Milk collected from high SCC quarters displayed increased *Staphylococcus* and reduced bacterial diversity (number of genera above 5% relative abundance). This occurred across all sample types. These results suggest that bovine milk is not sterile and contains diverse microbial communities when SCC is low. When an increase in SCC occurs, these bacterial communities are altered as bacterial diversity is diminished.

Key Words: microbial communities, somatic cell count, bovine milk

T31 Group housed Holstein bull calves have suppressed innate immune function compared to individually housed calves during weaning. L. E. Hulbert*[1], M. S. Calvo[1], M. A. Ballou[2], K. C. Klasing[1], and F. M. Mitloehner[1], [1]*Department of Animal Science, University of California-Davis, Davis,* [2]*Animal and Food Sciences, Texas Tech University, Lubbock.*

Objectives were to (1) determine if housing calves in groups of 3 (Group; n = 9 pens) or individually (Indv; n = 18) influences the innate immune responses of Holstein calves during weaning and (2) determine whether the response of grouped calves is influenced by their ADG ranking within a pen (Low = 0.80 ± 0.116; Mid = 1.27 ± 0.116; or High = 1.68 ± 0.116 kg/d). Calves were fed 227 g of milk replacer (MR) twice-daily until weaning and offered ad libitum calf-starter throughout the experiment. Weaning was initiated at age 53 d by removal of pm MR and was completed at age 64 d by removal of am MR. Peripheral whole blood (WB) samples were collected before the am MR at age 53, 57, 64, 67 and 71 d. In all calves, plasma cortisol and urea nitrogen (UN) increased at 67 d from pre-weaning concentrations ($P \leq 0.05$). Indv-housed calves had greater haptoglobin at 67 d ($P \leq 0.05$). Overall, neutrophil oxidative burst (OB) and phagocytosis (PG) to heat-killed *E. coli* was lower in Group calves compared with Indv-calves ($P \leq 0.05$). In addition, Group-calves had lower ($P \leq 0.05$). Tumor Necrosis Factor (TNF)-α concentrations from WB stimulated with endotoxin than Indv-calves at pre-weaning ($P \leq 0.05$). Indv-calves also had greater WB killing (WBK) of *E. coli* than Group-calves at 64 d of age ($P \leq 0.05$). Within Group, Low-ranked calves had the least glucose ($P \leq 0.05$), greatest UN ($P \leq 0.05$), and least OB and PG ($P \leq 0.05$) than other Group-calves. Mid-ranked calves had increased TNF-α responses at 67 and 71 d ($P \leq 0.05$). In addition, secretion Interferon-γ by WB stimulated with phytohemagglutinin was greater among Mid-ranked calves at 57 and 64 d ($P \leq 0.05$). Lastly, High-ranked calves had greater WBK at 57 and 64 d than other Group-calves ($P \leq 0.05$). Weaning may have a more negative effect on innate immune function for group-housed calves than individually housed calves, especially the lowest performing calves.

Key Words: bovine, commingle, immunity

T32 Effects of dietary herb supplementation on growth performance, and appearance of diarrhea in weaning-growing pigs. J. P. Wang,* X. Y. Guo, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choongnam, South Korea.*

A total of 200 weaning pigs [(Landrace × Yorkshire) × Duroc, BW = 7.00 ± 0.86 kg] were used in a 10-week feeding experiment to determine the effects of dietary supplementation of herb extract on growth performance, and appearance of diarrhea in weaning-growing pigs. Pigs were randomly allocated into 1 of 5 treatments with 2 replicate pens per treatment and 20 pigs per pen. Dietary treatments were: 1) CON, basal diet; 2) A, CON + 0.1% anti-diarrhea herb seed; 3) B, CON + 0.05% (*Lonicera japonica* + *Japanese atractylodes*); 4) C, CON + 0.1% (*Scutellaria baicalensis* + *Houttuynia cordata*); 5) D, CON + 0.1% anti-diarrhea herb extract. All pigs were housed in pens with a self-feeder and a nipple drinker to allow *ad libitum* access to feed and water throughout the experimental period. The experiment included weaning phase (0–5 weeks) and growing phase (5–10 weeks). In each phase, body weight and feed consumption were recorded to calculate ADG, ADFI, and G/f. Diarrhea pig number was recorded daily from d 0 to 6 in each phase. During 0–5 weeks, ADG and G/f were higher ($P < 0.05$) in B, C and D treatments than those in CON and A treatments. ADFI was increased ($P < 0.05$) in D treatment compared with CON and A treatments. During 5–10 week, pigs fed the B, C and D diets had a greater ($P < 0.05$) ADG and ADFI than those pigs fed the CON and A diets. Overall, pigs fed the B, C and D diets had a higher ($P < 0.05$) ADG than those fed the CON and A diets. From d 2 to 6 in weaning phase and d 1 to 6 in growing phase, the number of diarrhea pigs was decreased ($P < 0.05$) by the application of herbs. In conclusion, dietary supplementation of 0.05% (*Lonicera japonica* + *Japanese atractylodes*), 0.1% (*Scutellaria baicalensis* + *Houttuynia cordata*), and 0.1% anti-diarrhea herb extract could improve the growth performance, and decrease the diarrhea rate in weaning-growing pigs.

Key Words: growth performance, herb, weaning-growing pigs

T33 Efficacy of a yeast cell wall-derived mycotoxin adsorbent on excretion of aflatoxin B_2 in rats. B. Walters,* T. Smith, and M. Crump, *University of Guelph, Guelph, Ontario, Canada.*

Mycotoxins are natural contaminants of livestock feeds and impair production efficiency. One method to reduce exposure of animals to mycotoxins is by using specialized feed additives known as mycotoxin adsorbents (MA). These use nonspecific binding to sequester mycotoxins preventing them from being absorbed into the bloodstream. Current research has shown that MA can reduce symptoms of mycotoxicoses but quantitative evidence of reduced exposure has yet to be demonstrated. The current study sought to quantify the adsorptive capabilities of a yeast cell wall-derived MA (GMA). In the first experiment, male Sprague-Dawley rats were randomly placed in groups of 10 and were fed either a control diet or a diet containing 1, 3 or 5% w/w GMA (Integral, Alltech Inc., Nicholasville, KY). Rats were fed this diet for 7 d and then exposed by oral gavage to a tracer dose of ^{3}H-8,9-aflatoxin B_2. Feces and urine were collected 24 h after dosing. The rats were sacrificed by CO_2. The dose collected in each sample was compared between groups using SAS and no significant difference was observed between any GMA group and the control. Due to the kinetics of the digestive pathway, it was thought that total excretion after a set time did not provide as much information as excretion over time. In the second experiment, rats were grouped as before using only the 5% GMA and control diets. Feces and urine were collected for 6, 12, 18, 24, 48 and 72 h after dosing. The amount of excreted dose was higher among the GMA-treated rats compared with the control during the first 18 h after the initial dosing. After 18 h, excretion of dose in both groups was lower. Using ANOVA with a factorial design indicated a significant interaction between diet and time ($P < 0.05$). The natural logarithm of the excreted dose was used for linear regression analysis and showed that the excretion rate in the GMA-treated rats ($r^2 = 0.88$) was faster than the control ($r^2 = 0.80$). Based on this model, it was concluded that GMA reduces transit time of aflatoxin and reduces exposure in rats.

Key Words: aflatoxin, adsorbent, glucomannan

T34 Biotransformation approaches to alleviate the toxic effects induced by Fusarium toxins in swine. B. Grenier*[1,3], A. P. Loureiro-Bracarense[2], J. Lucioli[2], A. M. Cossalter[1], W. D. Moll[3], G. Schatzmayr[3], and I. P. Oswald[1], *[1]Institut National de la Recherche Agronomique-ToxAlim, Immuno-Mycotoxicology, Toulouse, France, [2]Universidade Estadual de Londrina, Lab Patologia Animal, Londrina, Brazil, [3]Biomin Research Center, Tulln, Austria.*

Mycotoxins are secondary metabolites of fungi that can cause serious health problems in animals, and may result in severe economic losses. Therefore, development of control strategies is necessary. Based on enzymatic reactions, we evaluated the efficiency of detoxifying agents into the gastrointestinal tract of piglets fed a co-contaminated diet with low doses of deoxynivalenol (DON) and fumonisins (FUMO). Four diets were formulated and given to piglets for 5 weeks; a control diet with or without the detoxifying agents (DA), and a co-contaminated diet with both Fusarium toxins (3 mg DON/kg, 6 mg FUMO/kg of feed) with or without DA. At d 4 and 16, the animals were subcutaneously immunized with ovalbumin (OVA) to assess the specific immune response. A decreased proportion of blood neutrophils was observed in the animals fed DON+FUMO diet ($P = 0.04$), and by contrast animals fed this diet with DA were not affected. Microscopical lesions (mild to moderate) were recorded in liver and lungs of piglets exposed to mycotoxins. Addition of the DA did not significantly reduce the hepatic lesion score, but significantly counteracted the effects on the proliferation index of hepatocytes ($P < 0.01$). Similarly, in lung, occurrence and extent of lesions were strongly reduced after inclusion of DA in the co-contaminated diet ($P = 0.01$). Assessment of the specific immune response at d 35 showed a restoration of immune parameters in presence of DA in contaminated feed. Indeed, the ability of lymphocytes to proliferate upon OVA stimulation was significantly enhanced in the DON+FUMO+DA diet (by 2.2 fold, $P = 0.05$). The concentration of IgG anti-OVA was partially increased in plasma of animals fed the co-contaminated with DA (+33%, $P = 0.28$). In spleen, the profile of cytokines expression (IL-1β, IL-6, IL-8 and IL-12p40) in the group containing both toxins with DA was similar in comparison to both control groups, whereas the association of the mycotoxins significantly depressed the mRNA levels ($P < 0.05$). In conclusion, the adverse effects induced by the ingestion of both DON and FUMO in piglets were partially to totally counteract in presence of DA in this diet.

Key Words: Fusarium toxins, biotransformation, immune response

T35 Impact of cow genetics regarding the osteopontin gene for the immune response to MAP infection. C. Thibault[1], P.-L. Dudemaine[2,1], and N. Bissonnette*[1,2], *[1]Agricultre and Agri-Food Canada, Dairy and Swine Research and Development Center, Sherbrooke, Quebec, Canada, [2]Université de Sherbrooke, Sherbrooke, Quebec, Canada.*

Bovine paratuberculosis is a pandemic infection that affects much of the world′s ruminant population. The causative pathogen is *Mycobacterium avium* ssp. *paratuberculosis* (MAP). The goal of this study was to measure the effect of cow genetics regarding the osteopontin (OPN) gene for the immune response to MAP infection. The importance of gaining insight into the unique interactions between host macrophages and mycobacteria is explained. MAP evades host immune responses and is able to persist and multiply in macrophages which generate granuloma formation. Granulomas are characterized by a mononuclear cell infiltration of macrophages and lymphocytes, by the formation of giant cells and epithelioid cells, and by fibrosis, sometimes with calcification. Previous investigations observed that OPN, an early T-cell activating factor, is more abundant in granulomas. In addition, studies confirmed the increased susceptibility of OPN-null mice to intracellular mycobacteria. MAP is believed to grow and survive in macrophages. Thus, the role of OPN in the mycobacteria–macrophage relationship is of considerable interest. In a previous study, our team found that OPN was correlated with bovine mastitis susceptibility and that expression of the OPN gene was correlated with the genotypes (i.e., gene haplotypes). We have undertaken a study of gene expression changes after ex vivo MAP infection using macrophage from different bovine genotypes (SPP1 haplotypes). Four reference genes were also measured; UXT and PPIA were selected by BestKeeper. The qRT-PCR results were analyzed according to the relative quantification method ($2^{-\Delta\Delta Ct}$). Results show that MAP induces a marked increase in cytokines, including interleukin (IL)-1β, −6, −8, −10, and −23 and TNF-α (but not IL-12, SPP1, NOD-2, and SLC11A1 also known as NRAMP1). SPP1 genotype has an effect on IL-6 at 6 h, −8, −10, and −23 gene expression at 24 h ($P < 0.05$) with a tendency for IL-1β at 24 h ($P = 0.09$). The strategy of identifying host genes altered by infection whose expression is linked to animal genetics can provide valuable information for targeting improved disease resistance in genetic selection.

Key Words: bovine paratuberculosis, osteopontin, macrophage

T36 Polymorphisms in the osteopontin gene are associated with *Mycobacterium avium* ssp. *paratuberculosis* infection status.

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The Canadian dairy industry is aware of the importance of considering resistance to bovine paratuberculosis as a target trait for improvement. The objective of the study was to detect and assess whether DNA polymorphisms in the bovine candidate gene, osteopontin (OPN), are associated with susceptibility to paratuberculosis in dairy cattle. Johne′s disease (JD) is a debilitating and chronic enteritis in ruminants caused by an intracellular pathogen called *Mycobacterium avium* ssp. *paratuberculosis* (MAP). JD and bovine paratuberculosis causes significant economic losses to the Canadian dairy industry. Because of the limited sensitivity, diagnosis of paratuberculosis is difficult because animals remain asymptomatic for years. Variability in the susceptibility of cattle to MAP infection is evident. To detect genetic variations (single nucleotide polymorphisms (SNP), the 10-kilobase DNA fragment carrying the encoding OPN gene has been sequenced using 108 Holstein cows from the same group of age. The MAP status of the cows was determined using serum or milk ELISA combined to fecal culture assays. Fifty-seven cows were positive to both tests and considered infected. Fifty-one cows tested negative over a 6-mo period (2 consecutive tests) and were declared negative). Logistic regression was used to determine the association of SNPs and reconstructed haplotypes with MAP infection status. A total of 9 informative SNPs were identified. The SNPs *SPP1c. 1301G>A* and *SPP1c. 1251C>T* (numbering according to GenBank no. AY878328) genotypes were confirmed and found tightly linked ($P = 0.0007$, Chi-Square) with MAP infection status. In our previous study, these SNPs were associated with the mammary health status of lactating cows. As OPN is now recognized as an important proinflammatory cytokine with pleiotropic beneficial functions, including intracellular pathogen clearance, the presence of genetic variations and their association with infection status confirms the importance of this candidate gene in JD disease. It may be possible to use OPN gene in selective breeding strategies to enhance health status including resistance to MAP infection.

Key Words: bovine paratuberculosis, osteopontin, susceptibility/resistance

T37 Phytonutrients affect the integrity of the mucus layer and susceptibility to enteric pathogens.

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Plant extracts, also known as phytonutrients, are gaining interest for their use as health promoting feed additives in animal production. Their mechanism of action, however, is still unknown. We hypothesize that phytonutrients may function by acting on the large intestine to alter the microbial ecosystem, strengthen mucosal defenses, and stimulate innate immunity. Mucus secretion and thickness is thought to play a major role in both health and disease by providing a protective yet permeable barrier between intestinal contents and host tissue. The mucus layer in the large intestine consists of 2 stratified layers, mainly composed of the secreted mucin, Muc2. The inner layer is of dense composition and devoid of commensal bacteria, while the outer layer is built as a loose matrix housing commensal bacteria. Six phytonutrients: anethol, capsicum oleoresin, carvacrol, cinnamaldehyde, eugenol, and garlicon40, with known antimicrobial and anti-inflammatory properties were evaluated in C57Bl/6 mice for their effect on the mucus layer, microbial composition, and colitis induced by the natural mouse pathogen, *Citrobacter rodentium* (*C. rodentium*). Each phytonutrient was given to mice through their drinking water for 7 d. Of the 6 phytonutrients tested, eugenol-fed mice were found to have increased Muc2 expression ($P = 0.06$) and a significantly thicker inner mucus layer ($^*P = 0.02$) in the large intestine compared with untreated mice. Eugenol-fed mice were less susceptible to *C. rodentium*-induced goblet cell depletion in the large intestine ($^{***}P = 0.0004$) and showed a decrease in systemic pro-inflammatory cytokines, TNF-α ($^*P = 0.02$), IFN-gamma and MCP-1, 6 d post infection. These results suggest that eugenol acts to strengthen the mucosal barrier by increasing the thickness of the inner mucus layer, which protects against invading pathogens and intestinal inflammation.

Key Words: phytonutrient, mucus, pathogen

Breeding and Genetics: Applications and Methods in Animal Breeding

T38 Effect of diet and sex on growth of cattle evaluated with non-linear mixed effects models. A. Dufek*[1,2] and E. Vacatko[1,2], [1]*Research Institute for Cattle Breeding, Ltd., Rapotin, Czech Republic,* [2]*Agriresearch Rapotin Ltd., Vikyrovice, Czech Republic.*

Accurate statistical model is a reliable basis for testing hypothesis especially in cases of non-linear relationship between variables. The aim of this study was to analyze mass growth pattern in beef cattle in the *R* software. We used the Gompertz and logistic function to describe the mass vs. age relationship and to test differences in growth patterns among groups of 2x2 experimental design (heifers, bulls vs. intensive fattening system: IF = maize silage in feedlot, extensive fattening system: EF = grazing, finishing on brewer's grains). Repeated measures growth data (8 measures per animal, n = 76) were evaluated in the package *nlme* (3.1–92) in the *R* (2.9.1). The Gompertz [y = A*exp(-exp(-K*(x-Ti))] and logistic [y = A/(1+exp(-K*(x-Ti)))] functions were parameterized in the *R* where A = a response (body mass [kg]) that approaches a horizontal asymptote as $x \to \infty$, exp = exponential function, K = a rate constant, x = age, Ti = the inflection point representing age with the highest growth rate. The values of the parameters for the basic models including all animals were A = 613, K = 0.004, Ti = 240 for Gompertz and A = 565, K = 0.006, Ti = 299 for logistic function. Based on the lower residual sum of square, the logistic function was selected to build the mixed model with one random effect: animal, 2 fixed effects: sex, fattening system and one covariate: the day of birth of an animal in a suckler herd representing the effect of season. Significance of the effects was determined using likelihood ratio test. The effects of sex, diet and interaction on the A and Ti were significant on the level $P < 0.001$; the A-values were 897, 470, 703, 372 and the Ti were 348, 278, 345, 205 for IF bulls, EF bulls, IF heifers, EF heifers, respectively. The date of birth had no effect on the A ($P = 0.67$) or Ti ($P = 0.12$). Analysis of residual variability showed differences between groups of sex ($P < 0.001$) and diet ($P < 0.001$): the standard error for the heifers was 49% of that for the bulls and for the IF group was 68% of that for the EF group. The results revealed that fattening system and sex affected both growing pattern and its variability. The *nlme* in the *R* is very effective tool for non-linear analyses.

Key Words: growth, nonlinear, mixed

T39 The effect of the ancestor on inbreeding depression in milk yield during the first lactation. J. Bezdicek*[1], L. Stadnik[2], F. Louda[3], and O. Latal[1], [1]*Agrovyzkum Rapotin Ltd., Vikyrovice, Czech Republic,* [2]*Czech University of Life Sciences Prague, Prague, Czech Republic,* [3]*Research Institute for Cattle Breeding, Ltd., Vikyrovice, Czech Republic.*

The objective of this study was to examine the effect of ancestor on inbreeding depression in milk yield (in kg) in Holstein cows. In total we evaluated differences in 9 ancestors. The database included Holstein cows (215,000) calved in the Czech Republic in the years 1995–2006. For proper comparison, each inbred cow was assigned an outbred equal. Inbred cows were matched with their outbred equals on characteristics such as identical sire, first calving on the same farm, in the same year and period (±2 mo) and dam reaching the same breeding value of milk production (±5%). In each group of ancestors, the goal to create pairs of inbred and outbred cows equivalent in terms of origin (the same sire, dam with similar breeding value) and which would also produce in the same environment. The PROC GLM of SAS® with fixed effects (F_X, ancestor, age at first calving, year of birth, milk production, breeding values of the sire and dam) was applied to all data. For evaluation of F_X level we used the software B-calc. The level of inbreeding was between F_X = 3.125–6.25%. Differences in the inbreeding depression of the 9 ancestors with the following number of inbred daughters (144; 107; 24; 48; 40; 25; 21; 20; 20) were evaluated. The total group of inbred cows (n = 449 cows) showed a significant decrease in milk production (−269 kg; $P < 0.001$) compared with their outbred equals (n = 449). A decrease in milk production was also found after dividing the studied group according to the 9 ancestors. The decrease was in the range −151 to −466 kg. These differences were significant within groups 1 and 9 ($P < 0.05$) and non significant within other groups. An effect of ancestor and breeding value of dam and sire as well was found to be highly significant ($P < 0.001$). Coefficients of determination varied within different groups of ancestors rating from 0.1552 to 0.5601 (total group 0.3514). The correlation coefficient (negative) between milk production and calculated coefficient F_X was significant (r = −0.09; $P < 0.01$). This study showed an inbreeding level F_X = 3.125–6.25% depression effect on milk production. There was also a significant effect of ancestor found.

Key Words: ancestor, inbreeding, milk production

T40 Association between milk production and Holstein fraction of upgraded dairy cattle in the Thai tropics. S. Koonawootrittriron[1], P. Yodklaew[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

Upgrading local dairy cattle to Holstein (H) has been used as a strategy to increase milk production in many tropical countries. The expectation is that milk production will increase alongside increments in H fraction of upgraded animals. However, lack of adaptation of high percent H cattle to tropical conditions may prevent them from achieving their expected production potential. The aim of this study was to evaluate the association between milk production and H fraction of high percent upgraded cattle in Central Thailand using 305-d milk production (MY) of 3,222 first lactation cows from 304 farms. Data were gathered between 1990 and 2011. Eight high H fraction groups were defined: BG1 ($H < 0.625$), BG2 ($0.625 \le H < 0.6875$), BG3 ($0.6875 \le H < 0.75$), BG4 ($0.75 \le H < 0.8125$), BG5 ($0.8125 \le H < 0.875$), BG6 ($0.875 \le H < 0.9375$), BG7 ($0.9375 \le H < 1$) and BG8 (H). The model included herd-year-season subclass, calving age (month) and breed group as fixed effects, and residual as a random effect. Least squares means (LSM) of MY were estimated for each breed group and then used to fit a second degree polynomial function to explain the change in MY for every 0.0625 H fraction in cows 62.5% H and above. The average milk production of all cows in this study was 4,145 kg (SD = 1,115 kg). Milk production differed across herd-year-seasons, calving ages, and breed group subclasses ($P < 0.01$). Cows with H fraction from 0.8125 to less than 0.875 had the highest MY of all breed groups. The LSM of MY tended to increase as H fraction increased from BG1 (4,075 ± 109 kg) to BG5 (4,285 ± 47 kg) and then it decreased toward BG8 (4,120 ± 76 kg). This association between MY and H fraction can be explained with a second degree polynomial equation: MY = 2,055 + 5,082(H fraction) - 2,957(H fraction)^2 ($R^2 = 0.61$). The quadratic association between MY and H fraction found in Central Thailand stressed the limitations of upgrading adapted local dairy cattle to H as a means of increasing milk production under tropical conditions.

Key Words: milk production, tropics, upgrading

T41 Genetic analysis of longevity traits in a Holstein cattle population near Benghazi, Libya.

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The aim of this study was to estimate the longevity of 2196 German Holstein Frisian cows under Libyan conditions. Three different longevity measurements were used to estimate the effect of inbreeding and management on the survival of those cows. True herd life (THL), which is the period in days from birth of an animal until culling, productive life (PL), which is the period in days from birth an animal until culling and number of lactations were used as measurements of longevity. Cows were distributed in 6 generations in the period from 1989 to 2004. In 1996, Libyan dairy cattle producers faced some difficulties in importing semen from foreign countries so they started using local sires. The analysis was performed using linear animal model. Origin of sire, generation, age at first calving, level of milk production, year and month of calving were considered as fixed effects. Additive animal effect was the only random effect in the model and days open was included as a covariate. All factors included in the model showed a highly significant effect ($P < 0.001$) on THL, PL, number of lactations and 305-d milk yield with the exception of true herd life, which was independent of age at first calving and month of calving. Daughters of local sires compared with daughters of North American and European sires, had a shorter THL and PL ($P < 0.01$). They also had less number of lactations and lower 305-d milk yield at the same significant level. Heritability estimates of longevity traits and 305-d milk yield were low because the effect of inbreeding in the last 3 generations. Effect of inbreeding was also clear on longevity traits. Very high genetic and phenotypic correlations were found between longevity traits. Genetically, 305-d milk yield was moderately correlated with longevity traits.

Key Words: longevity, heritability, genetic correlations

T42 Ranking of Brown Swiss cattle based on genetic evaluation and grades in judgment at the show ring.

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The objective was to determine the association between ranking of animals based on grades of conformation in judgment of cattle (JUD) at the show ring and their predicted transmitted abilities (PTA), for registered Brown Swiss cattle in Mexico. Ranking values obtained in JUD were transformed using the rankit transformation, assigning the highest rankit to the first place. Correlation analyses were performed between JUD and PTA. Records of JUD were used for the total of 735 animals; by sex (454 males and 194 females), in 6 years of livestock national show ring competitions (2003, 2004, 2005, 2006, 2009 and 2010) and 3 categories (adult, youth and calf). PTA values came from the most recent national genetic evaluation (2009) for milk yield adjusted to 210 d. Additionally, averages of the PTA and percentage of animals with positive PTA from those used in JUD were estimated. Using the complete data set, correlation between JUD and PTA was different from zero (0.17, $P < 0.05$). This result suggests a low association between both ways to evaluate animals. The correlation between JUD and PTA of adult animals was higher than using those of young animals and calves, which indicates a better association for adults. Correlations by sex and category varied throughout the years; this could indicate differences in the ability to judge animals by evaluators. Averages of the animals′ PTA were positive and the percentages of animals with positive PTA fluctuated between 67 and 86%, indicating just a tendency of Brown Swiss breeders to use animals genetically superior in the JUD.

Key Words: breeding value, judgment of cattle, Brown Swiss

T43 Genetic evaluation of mobility for Brown Swiss dairy cattle.

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Genetic parameters were estimated for mobility score and 16 current linear type traits for Brown Swiss dairy cattle. Mobility is defined as a composite trait measuring the cow's ability to move as well as the structure of her feet, pasterns, and legs. Scores from 50 to 99 were assigned by appraisers for the Brown Swiss Cattle Breeders Association beginning in June 2007. Only scores made before 69 mo of age were used. After edits, 32,710 records were available for 19,472 cows in 819 herds. The model included fixed effects for the interaction of herd and appraisal date (2109 groups); appraisal age within parity (46 groups); lactation stage within parity (21 groups), as well as random effects for animal, permanent environment and residual error. A multitrait analysis was run using canonical transformation, multiple diagonalization, and a decelerated expectation-maximization REML algorithm. Resulting heritability was 0.21 for mobility, and ranged from 0.06 to 0.37 for the other 16 type traits. The traits with the highest genetic correlation with mobility were final score (0.78), rear legs rear view (0.74), rear udder width (0.52) and foot angle (0.51). Predicted transmitting ability (PTA) for mobility was calculated using the current Brown Swiss multitrait type evaluation system, but using only appraisals where all traits were scored. For 1868 bulls evaluated, PTA mobility ranged from 1.6 to −1.8, standard deviation 0.5, and was most highly correlated with the PTA for final score (0.88), rear legs rear view (0.77), rear udder height (0.70) and rear udder width (0.69), similar to the trait correlations as was expected. When matched with official evaluations from August 2011, PTA mobility had moderately high correlations with PTA of milk, fat, protein, and productive life (0.31 to 0.41). The mobility trait may increase accuracy and timeliness of predictions of productive life by increasing the accuracy of the foot and leg composite.

Key Words: mobility, type trait, genetic evaluation

T405 Covariance functions, genetic parameters and breeding values for longitudinal ultrasound measures of ribeye area in a Colombian multibreed cattle population.

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The objective of this research was to obtain restricted maximum likelihood estimates of covariance functions and predictions of breeding values for longitudinal records of ribeye area measured by ultrasound in a Colombian multibreed cattle population. The data set contained 708 records from 340 calves progeny of 37 sires from 9 breeds (Gray Brahman, Red Brahman, Guzerat, Blanco Orejinegro, Romosinuano, Braunvieh, Normand, Limousine and Simmental) mated to Gray Brahman Cows. The model was a random regression model that used Legendre polynomials (LP) of order 1 to 3. Fixed effects were age of animal, dam parity, contemporary group (herd-year-season-sex), breed additive genetic and heterosis, whereas direct and maternal additive genetic and maternal permanent environment were random effects.

Residual variances were modeled as constant or changing across the growth trajectory. Models were compared with the corrected Akaike's information criterion and the Schwarz's Bayesian information criterion. The best model had first order LP and constant residual variance. This model was used to obtain genetic parameters and breeding values. Direct additive genetic variance decreased until 156 d of age and increased afterward. Maternal additive genetic and maternal permanent environment variances increased with age. Direct heritability estimates for REA at 4 mo, weaning, 12 and 15 mo (taken as target ages) were 0.004, 0.01, 0.03 and 0.06, respectively. Maternal heritabilities for the same ages were 0.32, 0.35, 0.37 and 0.38. Direct additive correlations ranged from −0.7 to 1. Maternal additive genetic and permanent environmental correlations were close to unity across the entire range of ages. According to these results selection for maternal ability appeared to be feasible in this multibreed population and maternal effects showed an important influence on REA pre and postweaning. Validation of these results with larger multigenerational multibreed populations is required.

Key Words: carcass composition, covariance functions, crossbred cattle

T44 Considerations in using residual feed intake to define feed efficiency in dairy cattle.

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With the advent of genomic selection, the dairy industry will soon be able to focus more directly on selection for feed efficiency. Thus, it is important that geneticists and nutritionists agree on how best to define and measure feed efficiency. The objective of this study is to quantify relationships among factors that affect feed efficiency in dairy cattle. Residual feed intake (RFI) is a measure of actual versus predicted intake for an individual. Predicted intake can be determined from nutritional models, or it can be determined statistically as the deviation from average intake of cohorts, after adjustment for differences in production, body weight (BW), and/or BW changes. A cow with negative RFI is more efficient than her cohorts because she has lower maintenance requirements, digests feed more efficiently, or uses digested feed more efficiently for maintenance, gain, or milk. Decisions about whether and how to adjust for differences in BW or BW change are critical to selection strategies focused on improving feed efficiency. Inappropriate adjustment for BW and body energy change may cause inadvertent bias toward cows that are larger, lose body condition to support milk output, or gain body condition when fed a high energy diet. Moreover, adjustment for BW change requires accurate measures of BW that are not unduly influenced by gut fill. Daily feed intake and milk production, and weekly body weight and milk composition data were recorded on 500 cows for 8 wk starting at approximately 70 DIM. RFI was calculated as the deviation from average intake of cohorts, after appropriate adjustments. Metabolic BW was a significant contributor to variation in intake. However, it accounted for only 10% of the variation whereas milk energy output accounted for 60%. BW change accounted for even less variation in intake, but its consideration likely is essential to ensure improvement in feed efficiency does not occur at the expense of health and fertility. Careful consideration of all factors affecting feed efficiency, including RFI, maintenance requirements, and production, will be necessary to achieve continued improvement of feed efficiency.

Key Words: genomic selection, feed efficiency, residual feed intake

T45 Contribution of heredity, nutrition and management to milk yield improvement in Shanghai from 1998 to 2010.

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Milk yield of Chinese Holstein cow is influenced by a variety of factors, including management, genetic effect, nutritional status, disease and environment. The purpose of this work was to establish the contribution of heredity, nutrition and management to milk yield improvement in Shanghai area. Milk yield changes were analyzed with total 68,138 milk yield records of 17,034 cows in 10 dairy farms from Shanghai Dairy Herd Improvement Project (from 1998 to 2010). The nutritional statuses of the 10 dairy farms were evaluated through 120 TMR diet samples assays. The management statuses were quantified through Brightdairy Thousand Points Evaluation. The hereditary effects were analyzed with breeding value of sires and maternal grandsires of the 17,034 cows. Hereditary effect, nutritional status and management status were defined as independent variables, and milk yield change as dependent variable. The results indicated that average 305-d milk yield increased from 7,418 kg in 1998 to 8,356 kg in 2010. Hereditary effect, nutritional status and management status were the significant factors ($P < 0.05$) affecting milk yield improvement. The results of path analysis revealed that management status (cumulative effect was 0.3324) had the highest positive relationship with milk yield improvement followed by hereditary effect (0.2816) and nutritional status (0.2086).

Key Words: heredity, nutrition, management

T46 Multiple trait analysis for milk yield and milking time of Holstein Cows.

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Test-day milk yields and milking time of 2,175 first lactation Holstein cows of one herd of southeast region of Brazil, calving from 1997 to 2005 were analyzed by standard multiple trait model (MT), principal components (PC) and by random regression models (RRM). Cows were milked 3 times a day, by electronic machines, totalizing 18,666 records. The reduced rank analysis adjusted the first 2, 3, or 4 genetic principal components. RRM fitted Legendre polynomials (LP) for random additive genetic and permanent environmental trends, respectively with 4 and 5 coefficients. For all models, fixed effects included contemporary groups (year-month of test), linear and quadratic effects of age of cow at calving, and management group. For RRM only, the average trend of milk yield and milking time were fitted by a third order LP and residual variances by step functions considering 4 heterogeneous classes. Comparing MT and PC models, a PC with 2 genetic principal components (PC2), with 220 parameters, was enough to fit the data. Heritability estimates for milk yields ranged from 0.10 to 0.32 and from 0.07 to 0.29 for milking time, considering PC2. For RRM the estimates ranged from 0.17 to 0.35 for milk and from 0.23 to 0.33 for milking time. Both models estimated higher heritability at the end of lactation. The RRM was less parameterized (105 parameters) and produced higher heritability estimates than PC2, but unexpected negative genetic correlation between some milk yields were estimated by RRM, differently from those estimated by PC2 model. Genetic correlation for PC2 were all positive and higher estimates were found among closer test-days, ranging from 0.38 to 0.99 for milk yields and from 0.33 to 0.99 for milking time. The genetic correlations of milk yields and milking time at the same test-days were negative

between records of the first half of lactation (−0.38 to 0.99) and positive on the second half (0.06 to 0.61), but the association was stronger for the first 5 mo. The negative genetic correlation at the first half of lactation is in desirable direction, suggesting that greater production is associated with smaller milking time or higher milk flow. This could be related to a scaling factor because the milk yield is higher during early lactation

Key Words: dairy cattle, functional traits, longitudinal data

T47 Milk fat:protein ratio in lactating dairy cows: Effects on conception at first postpartum AI. A. H. Souza*[1], L. F. Ferraretto[1], P. D. Carvalho[1], A. R. Dresch[1], L. M. Vieira[1,2], R. A. Cerri[3], M. C. Wiltbank[1], and R. D. Shaver[1], *[1]University of Wisconsin-Madison, Madison, [2]University of Sao Paulo-VRA, SP 05508, Brazil, [3]University of British Columbia, BC, Canada.*

Objectives of this retrospective study were to use information of milk composition from the first 5 DHIA milk test results to predict conception at 1st postpartum AI (CRAI1) in lactating Holstein cows. Specific interest was to study if milk fat:protein ratio (FPR) was associated with CRAI1. Edits in the data set were: Holstein herds only, herd size ≥ 100 lactating cows only, herds with CRAI1 between 20 to 60% only, DIM at 1st AI between 30 to 200d, only confirmed pregnancy outcomes included, lactation number 1 to 6 only, 305ME ≥ 20.000, %protein between 2.0 to 4.5, and %fat between 1 to 8. After edits, data from 207.506 1st postpartum breedings performed in 648 herds in Midwest-USA from July/2009 to July/2010 were included in the analysis. A scoring system based on FPR in a scale from 0 to 5 was as follows: FPRS0, cows with zero milk tests with FPR within 1 to 1.4 included; FPRS1, cows with only 1 out of first 5 milk tests with FPR within 1 to 1.4 included; FPRS2, cows with 2 out of 5 milk tests with FPR within 1 to 1.4; so forth. The procedure Glimmix of SAS using cow within herd and herd as random effects was used. The software Weka was used to find thresholds of milk composition and CRAI1. At first test, only about 50% of the cows had their FPR within 1 to 1.4, but this percentage increased to ~70% at 2nd through 5th tests. Most cows not 1–1.4 FPR were above (~45% of the cows at 1st test), and only minority (~5% at 1st test) below these thresholds. At 5th test % of cows above 1.4 FPR decreased to only ~10%; but, % of cows below 1.0 FPR increased to ~18%. This pattern did not ($P > 0.10$) seem to change throughout different seasons. In addition, FPRS5 cows presented significantly ($P < 0.01$) greater CRAI1, followed by FPRS4, and cows with FPRS0 to 3 did not differ in terms of conception at 1st AI (FPRS5 = 38.8%a, FPRS4 = 36.8%b; FPRS3 = 35.2%c; FPRS2 = 34.4%c, FPRS1 = 34.7c; FPRS0 = 34.2%c). Interestingly, an interaction between FPRS and season was found in which cows with FPRS5 had essentially same CRAI1 across all seasons; however, FPRS ≤ 3 had considerably lower CRAI1 in warmer months compared with cooler months of the year. In conclusion, cows presenting 4 or more out of the first 5 postpartum milk tests within FPR range of 1 to 1.4 seem to have improved fertility after 1st postpartum AI. Possible underlying reasons for this lower fertility in cows deviating from 1 to 1.4 FPR at beginning of lactation need to be further investigated through manipulative studies. Supported by AgSource Cooperative Services, USDA Grant 2010–85122–20612.

Key Words: milk composition, fertility, dairy cow

T48 Prediction of milk and fat production and estimation of breeding values in Holstein dairy cows using neuro-fuzzy and artificial neural networks. S. Shahinfar*[1], H. Mehrabani-Yeganeh[1], C. Lucas[2], A. Kalhor[2], A. Kazemian[2], and K. A. Weigel[3], *[1]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [2]Center of Excellence: Control and Intelligent Processing, Faculty of Electrical and Computer Engineering, Tehran, Iran, [3]Department of Dairy Science, University of Wisconsin-Madison, Madison.*

New computational techniques enable for rapid data analysis and fast decision making on dairy farms. The goals of such techniques are to detect short-term management changes and adjust the breeding strategies in real time. The objective of this study was to investigate the potential of 2 types of intelligent learning methods, artificial neural networks (ANN) and neuro-fuzzy systems (NFS), for computing the estimating breeding values (EBV) and production potential of Iranian dairy cattle. The back propagation algorithm was used to build ANN that could predict breeding values from the performance data of selection candidates. Subsequently, fuzzy logic was incorporated into the ANN to form a NFS that was also used to predict the breeding values and performance records. Explanatory variables included age at first calving, days in milk, ambient temperature, ambient humidity, length of the photoperiod, raw and adjusted (ME) milk and fat production and average production of contemporaries, and milk and fat EBV of parents. Correlations of 0.7 and 0.8 were achieved between predicted and actual values for milk and fat production, respectively. Correlations between EBV for milk yield and predictions from the ANN and NFS learning method were 0.917 and 0.926, respectively, whereas for fat yield correlation were 0.926 and 0.932, respectively. Finally, correlations between multi-trait predictions of BLUP EBV for milk and fat yield and corresponding predictions from a multi-trait implementation of ANN were 0.925 and 0.930, respectively; correlations with predictions from a multi-trait implementation of NFS were 0.935 and 0.949, respectively for milk and fat yield.

Key Words: artificial neural networks, neuro-fuzzy systems, machine learning

T49 New software for sparse matrix factorization and inversion using the supernodal techniques. Y. Masuda* and M. Suzuki, *Obihiro University of A & VM, Obihiro, Japan.*

We developed a set of subroutines for various sparse matrix operations including symbolic and numerical factorization, solution, and sparse inversion by using some modern sparse algorithms. Some programs for ordering or symbolic operations were imported from public domain packages. Ordering routines (AMD, QAMD, and AMF) were extracted from the MUMPS package. Symbolic factorization was performed by SMBFCT from the public domain version of SPARSPAK with some modifications. Supernodal left-looking approach for factorization and inverse-multifrontal method for sparse inversion were implemented. They relied on Basic Linear Algebra Subprograms (BLAS). When a highly optimized BLAS library was used, supernodal algorithms for factorization and inversion were 5 and 10 times faster than traditional approaches for a coefficient matrix of order 1 million or more from an animal model with random regressions. The time-efficiency was more improved as increasing the order. For solution of mixed model equations, estimation of genetic parameters by restricted maximum likelihood, and calculation of reliabilities, computing time would be greatly reduced. All programs were written in standard Fortran 95 and packaged into several modules. The source codes are available by requests to the first author for the academic and noncommercial purposes.

Key Words: computation, algorithms, mixed model equations

T50 Genotype × climate interaction in the genetic evaluation for growing traits in Braunvieh cattle.

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The presence of genotype × environment interaction causes changes in ranking of breeding values (BV) of sires from one environment to another, which affects genetic progress. The objective was to determine the magnitude of genotype × climate interaction (G×C) for growth traits in the genetic evaluation of Braunvieh cattle. Traits studied were weaning weight (WW) and yearling weight (YW). Records provided by the Asociación Mexicana de Criadores de Ganado Suizo de Registro, were grouped based on the meteorological variables recorded nearest to the herd by the National Weather System. The CLUSTER procedure in SAS was used to classify herds into 3 climates: dry tropic (DT), wet tropic (WT) and temperate (TE). Records of WW were 5348, 4501 and 2515 in DT, WT and TE, respectively, with 25173 animals in the pedigree. For YW, there were 3811, 2652 and 1528 records in DT, WT and TE, respectively, with 18072 animals in the pedigree. An animal model with ASReml software was used to estimate genetic parameters and to predict BVs. Bivariate analyses were carried out for pairwise combinations of climates for each growth trait. The criteria to evaluate G×C were: 1) genetic correlations (r_g) in bivariate analyses, and 2) frequencies of coincidence (FC) in the ranking of top 25 sires. Estimates of r_g between DT and WT, DT and TE, and WT and TE were −0.36, 0.84 and 0.72 for WW, and 0.23, 0.99 and 0.23 for YW, respectively. The FC between DT and WT, DT and TE, and WT and TE were 0.16, 0.92 and 0.76 for WW, and 0.60, 1.00 and 0.64 for YW, respectively. The size of r_g and FC imply the presence of G×C when compared WT with DT or TE, suggesting that genetic evaluations should be carried out separately for animals performing under wet tropical conditions.

Key Words: genotype by environment, weaning weight, Braunvieh cattle

T51 Relationships among visual scores with feedlot performance and feed efficiency in *Bos indicus* cattle.

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Visual evaluation of live beef cattle have been largely used to identify more adequate animals for meat production and, in Brazil, even as selection criteria in breeding programs. However, the relationship of these evaluations with feed efficiency traits in feedlot are unknown. The objective of this work was to evaluate phenotypic correlations of visual scores of conformation (C), precocity (P) and muscularity (M) with feedlot performance. Forty 3 bulls and 43 steers of Nellore were visually evaluated by an experienced technician twice. In the first evaluation (VS16), cattle (16-mo old, 313 ± 25 kg BW) was grazing in *Brachiaria* spp. pastures. At 22-mo of age, they were fed ad libitum for 84 d for individual dry matter intake (DMI) and average daily gain (ADG) records. A second evaluation of visual scores (VS22) were carried out on d 21 of the 84-d period. The body weight (BW) was measured each 28 d to calculate average daily gain (ADG) and gain to feed ratio (G:F). The visual were assigned to each animal in a within-gender comparison and the relationship among traits was evaluated by Pearson correlation. Visual scores showed moderate to high correlations with BW in both evaluations. The correlations between BW and C were 0.75 and 0.35 in VS16 and VS22, whereas with P the correlations coefficients were 0.46 and 0.29, respectively. For muscularity, the correlation with BW was 0.5 in both evaluations. Conformation score was positively correlated with DMI and ADG in both VS16 (0.47 and 0.27) and VS22 (0.33 and 0.13) and negatively with G:F in both evaluations (−0.15 and −0.19). Correlation of P with DMI was low and positive (0.25) in VS16 and nonsignificant ($P > 0.05$) with the rest of traits in both evaluations. Visual evaluation of M had nonsignificant correlations with all efficiency traits in both evaluations, except with DMI in VS22 (0.25; $P < 0.05$).The visual score of conformation may be an indication that animals with larger frame sizes, can ingest more food than the others. Visual assessments for precocity and musculature appeared as features of low accuracy to select efficient cattle.

Key Words: conformation, precocity, muscularity

T52 Genetic parameters for carcass traits and weaning weight of composite beef cattle in Brazil.

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Heritability and genetic correlations for weaning weight (WW; n = 328,326) and real-time ultrasound measurements of ribeye area (REA), subcutaneous fat thickness (BF) and rump fat (RF) from 863 calves were estimated using data from the Montana Tropical composite beef cattle population in Brazil. Images of carcass traits were obtained for ultrasound scanning (Aloka, SSD 500, with linear transducer of 3.5 megahertz and 172 mm long and acoustic guide attached) and analyzed using LINCE software. Calves were weaned at 6 m (205 d). of age, and ultrasounds were collected at 21 m (639 d) of age. Single-trait and multi-trait analyses with direct additive effects only were considered. The maternal additive effects was considered only for WW. Models included contemporary group (herd of birth-herd of weaning-herd of measurement-year of birth-season of birth-sex of animal) as a fixed effect, and age of dam, individual and maternal heterozygosity, and age at measurement as covariates for single trait analyses. Two-trait analyses excluded the covariate for age of dam. Random effects were animal and residual. The A^{-1} matrix contained 536,120 animals. Variance and covariance components were estimated using REML methodology and ASREML software. Heritabilities (h^2) and standard error (in parenthesis) for WW, BF and RF were 0.31(0.0104), 0.13(0.1320), 0.10(0.1278) respectively. The h^2 for REA was close to zero. Maternal (h^2) was 0.1940(0.0066) for WW. The genetic correlation between WW and BF was near zero (0.038), low and negative between WW and RF (−0.26), and positive between WW and REA (0.20) with standard errors of 0.23, 0.27 and 0.24. The low heritability estimates for ultrasound traits indicated that selection for these traits at this age would be rather ineffective. Selection for WW may reduce RF. In the 2-trait analysis, the h^2 were 0.36 (0.0047) and 0.14 (0.1322) for WW and BF, 0.36 (0.0047) and 0.12 (0.1322) for WW and RF and 0.36 (0.0047) and 0.01 (0.0829) for WW and REA. These results should be considered with caution because of the small number of observations for ultrasound carcass traits.

Key Words: beef cattle, tropical composite, ultrasound traits

T53 Influence of maternal genetic effect on the estimation of genetic parameters in post-weaning traits. G. A. Oliveira Júnior*[1], F. M. Rezende[1], J. B. S. Ferraz[1], J. P. Eler[1], and G. B. Mourão[2], [1]*Faculdade de Zootecnia e Engenharia de Alimentos - Universidade de São Paulo, Pirassununga, São Paulo, Brazil,* [2]*Escola Superior de Agricultura Luiz de Queiroz - Universidade de São Paulo, Piracicaba, São Paulo, Brazil.*

The maternal genetic effect may interfere with the performance of the animal's post-weaning traits in beef cattle. The aim of this study was to estimate the importance of maternal effects on genetic analyses of post-weaning traits in Nellore cattle. The database used for estimation of (co)variance components contained information from 115,922 animals corresponding to 176,679 animals in the pedigree, with 80,581 different dams. The traits analyzed were scrotal circumference (SC), visual score of muscling (MUSC) and post weaning weight gain (PWGAIN), measured around 18 mo of age. (Co)variance components and direct breeding value estimates were predicted using restricted maximum likelihood and univariate animal model analyses as implemented in the MTDFREML software. Two models were evaluated for each trait: one including only the direct animal effect, and the other including a maternal effect. Contemporary group, the age of animals at the measurement and the age of dam at delivery (AOD), considered as a covariate with quadratic effects, were considered as fixed effects. The AOD was not used for MUSC. The management group at weaning was fitted as a random effect for all analyzed traits. Basic edits involved the exclusion of all information out of the interval between −3.5 and 3.5 standard deviations for each trait, data from contemporary groups including fewer than 20 animals, and data from progeny of sires or dams with only one offspring in the data set. Likelihood ratio tests and Pearson and Spearman correlations were used to compare models. The likelihood ratio test showed that the inclusion of the maternal genetic effect was statistically significant ($P < 0.01$) in the prediction of (co) variance components for all post weaning traits analyzed. However, the rank of the animals did not change, indicating that there is no gain from including genetic maternal effects in the model. The results of the estimates of direct additive heritabilities with no maternal effect were 0.23, 0.21, and 0.55 for PWGAIN, MUSC and SC respectively. When we added the maternal additive effect in the analyses, these results didn't vary significantly (PWGAIN = 0.22, MUSC = 0.23), except for SC, with 0.44 for heritability. The maternal additive heritabilities were lower than the direct additive heritabilities for all traits considered, that was expected. The estimates for maternal additive heritabilities were 0.05 for PWGAIN, 0.01 for MUSC and 0.10 for SC. The prediction of maternal additive genetic merit can be an indicator of maternal effect, mainly on the post weaning weight gain and scrotal circumference traits. However, due to the low value of maternal heritability of these traits, the value of accuracy of these predictions might be low as well and they must be used carefully.

Key Words: *Bos indicus* cattle, genetic parameters, variance components

T54 Selection for resistance to *Haemonchus contortus* in Santa Ines hair sheep: Comparisons of methods of animal evaluation at countryside and in the laboratory. P. S. Oliveira,* J. B. S. Ferraz, J. P. Eler, L. S. Oliveira, C. T. Moncau, M. D. Poleti, B. Silva, F. M. Rezende, G. A. Oliveira Júnior, J. Daniel, and E. C. Mattos, *Faculdade de Zootecnia e Engenharia de Alimentos - Universidade de São Paulo, Pirassununga, São Paulo, Brazil.*

The use of new tools to assist selection resistant or susceptible animals to gastrointestinal parasites, associated with the fecal egg counts (FEC), have been developed and applied to Santa Ines hair sheep to distinguish between resistant and susceptible individuals, without the need for laboratory tests. Distinguishment is needed to identify animals to be used in a DNA marker association study that is being developed. Thus, this study aimed to evaluate possible correlations between traits evaluated at countryside in the animals (Conjunctival Mucous Color (FAMACHA) and body score (BS) and in the laboratory (the Fecal Egg Counts (FEC), Hemoglobin (HGB) and Packed Cell volume (PCV)) in 503 sheep from Santa Ines, from 4 herds located in 3 different states of Brazil. For the laboratory analysis were collected individual samples of blood for the determination of HGB and PCV, and feces for FEC. FAMACHA test consisted in the visual evaluation of the color the ocular mucosa (scale from 1 to 5), where the higher value meant more anemic animals. The assessment of BS was performed by palpation in the lumbar region, where 0 meant cachectic animals and 5 meant obese animals. Subsequently, simple correlation coefficients between all variables were obtained by SAS PROC CORR. The correlations of greater magnitude ($P < 0.0001$) were found for FAMACHA with HGB and PCV ($r = -0.63$ and -0.64 respectively) and BS with HGB and PCV ($r = 0.68$ and 0.65 respectively). Lower magnitude correlations were found for FEC with FAMACHA, BS, HGB and PCV ($r = 0.21$, 0.25, -0.30 and -0.29 respectively) and between BS and FAMACHA ($r = -0.44$). Analyzing the study it can be concluded that the association of the method FAMACHA with BS can be considered an efficient method to diagnosis of anemia in Santa Ines sheep at countryside. Furthermore, increase in FEC also reduces levels HGB and PCV, however, this can't be considered as the only cause of anemia in sheep.

Key Words: FAMACHA, body score, packed cell volume

T55 Test-day model for milk yield of dairy buffaloes in Colombia. N. Hurtado Lugo*[1,2], G. M. F. de Camargo[1], R. Aspilcuelta[1], S. Gutiérrez[2], E. Taccari[1], F. M. M. Gil[1], L. G. Albuquerque[1], M. Cerón[2], and H. Tonhati[1], [1]*State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil,* [2]*University of Antioquia, Medellín, Ant, Colombia.*

The test-day model is the preferred method for genetic evaluations in dairy cattle. The aim of this study was to estimate the genetic parameters for the milk yield at the Test-Day (TD) in dairy buffalo in Colombia. Test-day records were collected from 7 dairy herds, members of the Colombian Buffalo Breeders Association (ACB). The TDs were separated in 9 classes of 30 d each, for total of 9 test-day controls (TD, 1 to 9). For this study, 28372 TDs records of 1220 lactations from 1997 to 2009 were used. Single and multiple trait analyses were used and variance components were estimated by Restricted Maximum Likelihood. The (co)variance components were estimated with the MTDFREML software. The model used in the TDs analysis included the additive genetic, permanent environment and residual as random effects; and the contemporary group (herd, year, and season of calving) as fixed effect. The buffalo age at calving was considered as covariate (linear and quadratic). The calving seasons were January–April, May–July, August–October, and November–December. The TDs varied from 4.84 to 3.2 kg/day. The heritability estimations for TD varied from 0.07 ± 0.087 to 0.16 ± 0.11 for single-trait analyses and from 0.31 ± 0.098 to 0.45 ± 0.198 for the multiple-trait analyses. The genetic correlations for single and tetra-trait TD models were high, bigger and varied from 0.36 to 0.96 and from 0.41 to 0.99, respectively. Correlations among TD increased as time between observations decreased for single- and multiple-trait models. In conclusion, the results of this study suggest that selection of buffaloes in Colombia should use breeding values obtained in a multi-trait test-day model, because of their high heritability.

Key Words: buffalo, genetic correlation, yield

T56 Random regression models for test-day milk production for first lactation in Colombian buffaloes.

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The Random regression models for genetic evaluation in dairy cattle consider individual lactation curves using ordinary polynomials of linear functions. Alternative models to understand the genetic variability for milk yield along the lactation curve are required for genetic evaluations of the buffalo population in Colombia. The knowledge of the lactation curve may be of interest for production and management requirements of this specie. This study has the aim to estimate the genetic parameters using RRM for the milk yield at the Test-Day in Colombian buffalo dairy. A total of 9432 milk yield records were analyzed, corresponding to 1,746 first lactations of crossbred buffalo cows. The fixed effects were: contemporary group that was composed by farm, month and station of parity and milking days and age of the cow at calving (linear effect) as fixed effects and the random effects were the direct genetic and the permanent environment. The variance components were estimated using the statistical package WOMBAT. The residual variances were heterogeneous, modeled by a step function (LRT), containing 4 classes of variances. Results from different models of analyses were compared by the Restricted Maximum Likelihood (REML) form of the Akaike information criterion (AIC), the Schwarz Bayesian information criterion (BIC) and by inspecting the variance component and genetic parameter estimates. The most appropriate model was the one using a Legendre's polynomial function of 4rd order for the genetic effect and 5th order for the permanent environmental effect (4,5,4). The phenotypic mean for test-day was 3,6 ± 1,42 kg. The heritabilities for all models test ranged from 0.38 to 0.01. For the best model (4,5,4) the heritabilities ranged from 0.38 to 0.12. The highest values were observed between the 2 and 5 test day. For genetic and phenotypic correlation estimates ranged from 0.39 to 0.96 and from 0.42 to 0.91, respectively. Genetic correlations were higher than phenotypic ones. The results of this study indicate the necessity to consider the heterogeneity of residual variances to model changes in the variations for days in milk.

Key Words: animal model, Legendre polynomial, heritability

T57 Genetic parameters for growth curves in free range chickens.

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Nonlinear models have been used to describe growth in different species. These models feature parameters of biological meaning, and they have proven quite effective, especially in research related to animal breeding programs. The estimation of genetic parameters for growth curves fitted by nonlinear models provides the identification of animals that were more suitable for certain purposes of selection, for example, the optimum age of slaughter. Growth models usually have 2 parameters with biological meaning. The asymptotic weight (A) estimates the adult weight, whereas mature rate (k) is an indicator of the rate at which the animal approaches the adult body weight. The objective of this study was to estimate the genetic variance for the parameters A and k of the growth curves in free-range chickens by univariate and bivariate models. For this experiment we used an experimental lineage called 7P. Data from 11 weights of 934 chickens, being 470 males and 464 females, collected from birth to 84 d of age, totaling 5183 observations. The growth curve was estimated by nonlinear logistic model by OLS. The (co) variances were estimated using the methodology REML by ASREML® software. The coefficients of heritability (h^2) for A were 0.1816(0.0618) and 0.1888(0.630) and for k were 0.1571(0.0569) and 0.1567(0.0568), for the univariate and bivariate, respectively, with little difference between the values obtained for the models. The correlation between A and k, found for the bivariate model was −0.77, indicating that animals that grow faster have lower adult weight.

Key Words: variance components, heritability, performance

T58 Comparative analyses of proximate and chemical characteristics of eggs from six indigenous bird species.

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Birds are raised mainly for their meat, eggs or feathers. Egg is a common food and the cheapest per unit source of animal protein and serves as a good source of vitamins and minerals. However, despite its nutritional value some health issues may arise as a result of its consumption. This study was aimed at assessing the inter specie differences in the physical characteristic, proximate composition and chemical constituents of eggs from 6 species (Chicken, Duck, Guinea Fowl, Pigeon, Quail and Turkey) of extensively managed indigenous birds. A total of 240 eggs comprising 40 eggs from each of the 6 species were sampled. The eggs were cleaned, labeled and measured with digital weighing scale and vernier calipers for its physical characteristics (egg weight, length, width, vertical, and horizontal circumferences). Proximate composition (moisture content, dry matter, total ash, crude protein, crude fat and carbohydrate) of the eggs along with mineral analyses (calcium, magnesium, manganese, iron, zinc and cobalt) were conducted using standard laboratory procedures for proximate and mineral assay procedures. All statistical analyses (descriptive and model fitting) were conducted using the JMP software. The one way ANOVA procedure for each of the response variable investigated was fitted by the model $Y_{ij} = \mu + a_i + e_{ij}$, while species was the sole predictor variable. Further comparison of the means was done after a significant ANOVA using the Tukey's post-hoc method. Specie was a significant ($P < 0.001$) source of variation in all the 5 physical characteristics accounting for over 90% of the variation, while its effect was significant ($P < 0.001$) and moderate to high on proximate composition with the exception of crude fat ($P > 0.05$). In the same vein species was a significant ($P < 0.001$) source of variation on mineral content except ($P > 0.05$) for magnesium and zinc. The nutritive value of Quail eggs are quite promising considering its proximate and mineral content mix which makes it a safer and healthier dietary source of nutrients and minerals when compared with Pigeon eggs.

Table 1. Means of proximate composition and mineral content of eggs

Species	N	DM (%)	Crude ash (%)	CP (%)	Carbohydrate (%)	Ca (%)	Fe (ppm)	Co (ppm)	Mn (%)
Chicken	40	26.59^{b}	5.50^{ab}	6.51^{c}	33.12^{c}	0.050^{b}	25.71^{b}	0.375^{b}	21.67^{b}
Duck	40	34.40^{a}	4.00^{bc}	8.14^{b}	42.35^{abc}	0.049^{b}	30.00^{ab}	0.350^{b}	27.50^{b}
Guinea Fowl	40	29.93^{ab}	6.00^{a}	6.15^{c}	34.78^{bc}	0.053^{b}	22.50^{b}	0.400^{b}	18.75^{b}
Pigeon	40	20.25^{c}	3.14^{c}	13.01^{a}	46.50^{a}	0.053^{b}	41.43^{a}	0.543^{a}	68.57^{a}
Quail	40	30.00^{ab}	3.25^{c}	8.72^{b}	48.35^{a}	0.120^{a}	20.00^{b}	0.400^{b}	24.00^{b}
Turkey	40	33.87^{a}	3.88^{c}	7.04^{c}	45.40^{ab}	0.048^{b}	30.00^{ab}	0.400^{b}	23.75^{b}

Key Words: species, proximate composition, mineral content

T59 Statistical classification of six indigenous bird species based on external and internal qualities of their eggs. O. T. F. Abanikannda,* A. O. Leigh, and O. I. Adekanbi, *Lagos State University, Ojo - Lagos, Nigeria.*

Classification is a method of categorizing organism into different groups based on their biological similarities and differences, and it is a systematic grouping of organisms into categories on the basis of evolutionary or structural relationships between them. Conventionally, such classifications could be traditional, phenetic or cladistic but the objective of this study is to employ statistical techniques to discriminate among the different species based on the external and internal measurements of the birds' eggs. A total of 210 eggs comprising 35 each from 6 free ranging indigenous species (chicken, duck, guinea fowl, pigeon, quail and turkey) were sampled. Five external characteristics (egg weight, egg length, egg width, vertical and horizontal circumference), 3 internal qualities (yolk, albumen and shell weights) were measured and 6 indices (shape index, egg surface area, egg volume, surface area to volume ratio, yolk to albumen ratio and egg density) were computed. All weights were measured with a digital scale sensitive up to 0.00g and linear measures were with digital vernier caliper (0.00mm) and flex tape for the circumferences. The distribution and fit model procedures of JMP statistical software were used to analyze the data and further mean separation after a significant effect was done using the Tukey's method. The model for each of the 14 variables studied is given by $Y_{ij} = \mu + \alpha_i + e_{ij}$. Complete method of hierarchical clustering of JMP was used for classification of the species. Specie was a highly significant ($P < 0.001$) and the largest source of variation in all the parameters studied, accounting mostly for over 95 percent of variation observed except in shape index (31%) and yolk to albumen ratio (36%). Three primary clusters of 2 species each were formed comprising chicken and guinea fowl, duck and turkey, and pigeon and quail, respectively, with the duck and turkey cluster been intermediate in distance between the other 2 clusters. The dendrogram from this clustering is similar to the classification from traditional methods which are used in taxonomy to classify the birds. The result revealed that statistical classification is a reliable and veritable method for specie identification and constellation.

Table 1. Hierarchical clustering history of the 6 species of birds1

Number of Clusters	Distance	Leader	Joiner
5	2.081991550	Pigeon	Quail
4	2.765695694	Duck	Turkey
3	3.539278540	Chicken	Guinea Fowl
2	5.216181164	Chicken	Duck
1	9.632125371	Chicken	Pigeon

[1]Complete method of hierarchical clustering.

Key Words: species, cladistic, cluster analysis

Dairy Foods: Cheese and Dairy Products

T60 Prediction of process cheese functionality using dielectric spectroscopy. J. K. Amamcharla* and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Process cheese (PC) is manufactured by blending and heating of natural cheese, emulsifying agents, sodium chloride, acidifying agents, water and other optional ingredients. The selection ingredients used in PC formulations play a crucial role in the functionality of the finished product. There is a need to develop a rapid method to predict the functional properties of PC. The objective of the study was to predict the functional properties of PC using dielectric spectroscopy. Dielectric properties of the PC were collected over the frequency range 0.2–3.2 GHz at a constant temperature (25°C). Dielectric spectra were collected using an open-ended high temperature dielectric probe (Agilent Technologies, Englewood, CO) connected to a vector network analyzer (Agilent Technologies). Dielectric spectra were collected in triplicate at 4 different locations in each sample. Twenty-four PCs were manufactured using a 3 × 2 × 2 factorial design using Intact casein content (ICC; levels: 14, 15.5, and 17%), cooking temperature (CT; 170 and 190°F), and cooking mixer speed (CMS; 100 and 350rpm) as independent variables. Partial least square regression (PLSR) and neural network (NN) models were developed using the dielectric spectra of PCs to predict the hardness (gf), melting point (°C) and modified Schreiber melt diameter (mm) of PC. Penetrometer, dynamic stress rheometry (DSR), and modified Schreiber melt (MSM) test were used as the reference methods, respectively. The PLSR and NN models were validated using the full cross-validation method. Root mean square error of crossvalidation (RMSECV) for PLS was found to be 2.5°C, 1.96mm, and 15.2gf for DSR melt point, MSM diameter, and hardness of PC, respectively. Similarly, RMSECV for NN was found to be 2.7°C, 2.1 mm, and 22gf for DSR melt point, MSM diameter, and hardness of PC, respectively. Practical utility of the calibration models were evaluated using the ratio of prediction error to deviation (RPD). The RPD was found to be > 2 for the 3 functional properties, indicting a good practical utility of the models.

Key Words: dielectric spectroscopy, process cheese, functional properties

T61 The impact of cation substitution on the flavor of reduced sodium full fat Cheddar cheese. E. Kang*[1], M. Kim[1], D. J. McMahon[2], and M. A. Drake[1], [1]*North Carolina State University, Raleigh,* [2]*Utah State University, Logan.*

Sodium reduction is a key issue in the dairy industry as salt plays a crucial role in flavor and ripening of Cheddar cheese. Previous research showed that more than 30% sodium reduction negatively affected flavor development and consumer acceptance. Substitution of potassium chloride and small amounts of magnesium and calcium chlorides may maintain salty taste while minimizing sodium in cheese. The objective of this study was to evaluate the effect of partial salt substitution on flavor and flavor chemistry of full fat Cheddar cheese. Seven full fat Cheddar cheeses with the molar salt contents equivalent to 1.7% (wt/wt) sodium chloride (NaCl) but different ratios of sodium, potassium, calcium and magnesium cations were manufactured. Cheeses made using only NaCl at 1.7% (wt/wt) (C) served as positive controls while cheeses made using 0.7% (wt/wt) NaCl (LC) served as negative controls (LC). The experiment was replicated 3 times. Cheeses were ripened at 6°C and sampled for sensory, organic acids, and volatile compound analyses through 9 mo of aging. Trained sensory panelists documented flavor attributes. Organic acids and volatile compounds were extracted and separated by high performance liquid chromatography or by solids phase microextraction with gas chromatography mass spectrometry, respectively. Consumer acceptance tests were performed after 6 mo. Salty taste intensity was consistent among cheeses except for the LC cheese, but other aromatic and basic taste differences were documented and these differences (bitter taste, sulfur and brothy flavors) increased with increased sodium cation substitution (>25%) or decreased salt (LC). Citric and lactic acids were higher in LC compared with other cheeses. Volatile compound differences were noted when more than 25% sodium was replaced. No differences in consumer liking were observed with up to 50% replacement of potassium with sodium ($P > 0.05$), and consumers on sodium restricted diets scored low sodium cheeses higher than those on unrestricted diets ($P < 0.05$). These results demonstrate that flavor and taste differences due to different cation salts will not affect consumer liking up to 50% sodium replacement.

Key Words: sodium, cheese, salt replacement

T62 A novel approach to produce low fat Cheddar cheese. I. Amelia*[1], D. M. Barbano[1], and M. A. Drake[2], [1]*Cornell University, Ithaca, NY,* [2]*North Carolina State University, Raleigh.*

Our objective was to develop a new process to make low fat Cheddar cheese (LFCC) and compare its composition and properties to commercial full fat Cheddar cheese (FFCC) and commercial 50% and 75% reduced fat Cheddar cheese (RFCC). A RFCC (53% reduction) was produced using a fat removal process (Nelson and Barbano, JDS 2004) and then combined with dry micellar casein concentrate (MCC), water, and salt to achieve 6% fat, 28% protein, 1.2% salt in LFCC. The 6% fat target (83% fat reduction) was used to comply with the FDA low fat labeling regulation. The pH of the LFCC formulation was adjusted to 5.3 with lactic acid. Rennet was added, followed by pressing and packaging in 40 min total time. The cheese texture was conceptualized as a filled-gel model of protein matrix and filler (100% minus %protein). The filler volumes for FFCC, 50% RFCC, 75% RFCC, and LFCC were 75.8, 70.6, 67.4, and 70.3%, respectively, while the moistures were 35.7, 49.2, 52.5, and 58.1%, respectively. The RFCC had the hardest texture. The texture of the LFCC was more similar to the FFCC than either of the RFCC, even though the filler volume of the LFCC was similar to the 50% RFCC. The soft texture of our LFCC was because the original matrix structure of the starting FFCC was broken by blending. A new matrix structure was formed by the interaction of added rennet with the MCC resulting in a softer texture that was more similar to FFCC. Descriptive flavor scores were used to construct a PCA biplot to visualize flavor profile differences among cheeses. Both RFCC and LFCC were missing typical aged full-fat Cheddar flavor characters (nutty, brothy, catty, milkfat). The 50% RFCC and 75% RFCC were characterized by strong whey and cooked flavors while LFCC had bitter and grape-tortilla flavor which was thought to originate from the dry MCC. The sulfur flavor in LFCC was closer to FFCC, than both RFCC. The LFCC flavor produced by this method could be manipulated by adding flavoring ingredients (e.g., enzyme modified cheese) that could boost typical flavors of FFCC. Progress was made in development of a new LFCC making process that achieves a texture similar to FFCC, but the LFCC still needed improvement in Cheddar flavor characteristics.

Key Words: cheese, low fat, micellar casein

T63 Effect of grazing on Caciocavallo cheese quality produced in Alta Irpinia. G. Esposito*[1,3], A. Di Francia[1], F. Napolitano[2], M. L. Varricchio[1], A. Braghieri[2], and F. Masucci[1], [1]*Dipartimento di Scienze del Suolo, della Pianta, dell'Ambiente e delle Produzioni Animali,Universitá degli Studi di Napoli Federico II, Portici (Napoli), Italy,* [2]*Dipartimento di Scienze delle Produzioni animali, Universitá degli Studi della Basilicata, Potenza, Italy,* [3]*Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa.*

Dairy system in Alta Irpinia (Campania, southern Italy) is characterized by semi-extensive farms where cow feeding is based on grazing pasture in spring, and on hays and concentrates in winter. Milk is used to make a typical cheese named Caciocavallo. The aim of the study was to evaluate the effect of grazing on fatty acid (FA) profile, sensory properties and consumer liking of Caciocavallo made in Alta Irpinia. The study was conducted in 3 farms (A, B, C) and in 2 periods: spring (10 wk) and winter (10 wk). Pasture, feedstuff samples, milk and corresponding Caciocavallo cheeses were collected every 2 wk. Data on milk and cheese composition, cheese sensory properties and consumer acceptability were analyzed by GLM procedure, with season effect, farm and their interaction. To assess the FA transfer from milk to cheese, data of both FA profiles were compared by one-way ANOVA. Spring milk had higher contents of C18:0 (SEM 0.65; $P = 0.011$), C18:1t11 (SEM 0.03; $P < 0.001$), C18:3 (SEM 0.059; $P < 0.001$), CLA c9-t11 (SEM 0.087; $P < 0.001$). The cheese FA profile reflected the one of raw milk with few differences due to the aging process. Higher contents of C18:0 (SEM 1.17; $P = 0.01$), C18:3n-3 (SEM 0.01; $P = 0.007$), and CLAc9-t11 (SEM 0.21; $P = 0.004$) were observed in spring compared with winter cheeses. Sensory profile of spring cheese markedly differed across the 3 farms and the 2 periods. In particular, sensory profile of spring cheese produced from milk of cows fed natural pasture (farm A) differed from cheeses of cows fed sown pasture (farms B and C). A higher color intensity (yellowness) was observed in spring products (SEM 1.95; $P < 0.001$) due to the transfer of pigments (e.g., β-carotene) from fresh plants to the cheeses. Consumers expressed no preference for cheeses produced in different farms or seasons. This may be a consequence of the high temperatures (70–80°C) reached during the cheese making process possibly flattening the differences perceivable by untrained consumers. Overall, it is concluded that our work allowed the characterization and differentiation of Caciocavallo cheese produced in Alta Irpinia by different cattle feeding system.

Key Words: CLA, pasture, sensory properties and cheese quality

T64 Sensory and instrumental measure of temporal volatile release from cheese. S. White,* R. E. Miracle, E. A. Foegeding, and M. A. Drake, *North Carolina State University, Raleigh.*

Understanding what consumers experience during consumption of a food product is of great concern to manufacturers. This not only includes overall flavor and texture profiles, but the temporal duration and intensity of these attributes. Volatile compound and rheological tools have been extensively and successfully related to sensory perception. However, matching temporal changes by sensory and instrumental analyses remains a challenge. The objective of this study was to develop and validate an apparatus to measure dynamic volatile compound release from cheese and to verify this instrument with sensory analysis. Two provolone cheeses, made from the same lot of milk, were selected for their differences in free fatty acid flavor intensity. The free fatty acid profiles of the cheeses were analyzed by descriptive sensory analysis, solid phase microextraction gas chromatography (SPME-GCMS) and sensory time intensity. Additionally, a Seward Stomacher 80 Biomaster lab system was modified to measure dynamic volatile release from these samples. The temporal volatile release (TVR) apparatus was designed to allow N_2 gas flow in the stomacher over the sample and through an outlet equipped for SPME fiber exposure. Volatiles were extracted after 10, 20 and 30 s of compression then quantified by GCMS. All experiments were conducted in triplicate. Statistical differences were analyzed using one-way ANOVA. Both sensory time intensity (TI) of free fatty acid flavor and the TVR showed differences ($P < 0.05$) between the cheeses not observed with traditional SPME-GCMS or by descriptive sensory analysis. The TVR volatile measurements were correlated with the sensory TI results ($r^2 = 0.88$, $P < 0.05$); and the TVR apparatus was able to measure differences in the relative volatile compound intensity of free fatty acids as well as the temporal release of these compounds. When used in conjunction with established sensory and flavor chemistry tools, this instrument can help food scientists understand what volatiles contribute to temporal perception of flavor.

Key Words: cheese flavor, time intensity, flavor release

T65 Light backscatter–Shedding new light on milk coagulation. R. Miller, A. Villarroel, B. Krahn, and L. Goddik,* *Oregon State University, Corvallis.*

The objective of this project was to evaluate the application of light backscatter technology to analyze the influences of somatic cell level, breed, parity, age of milk, and lactation stage on milk coagulation rate. Milk collected from individual cows (n = 31) was centrifuged to equalize fat composition and was tested during chymosin-induced coagulation. Coagulation rate was determined using diffuse reflectance to monitor changes in protein aggregation. Only breed and days in milk were significant with respect to milk coagulation rate. A student *t*-test was performed to evaluate differences in mean coagulation time between Holstein and Jersey milk. Coagulation of Jersey milk was significantly faster than Holstein milk. There was no evidence to suggest that somatic cell level affected coagulation rate. Initial pH of the milk was a significant indicator of SCC level, but was not a significant predictor of milk coagulation rate after the pH was equalized for all of the milks tested, suggesting that discrepancies in pH and not SCC level are what affect milk coagulation rate. The influence of milk age was also considered, using individual cow milk samples (n = 6) held for zero to 5 d. Coagulation rate did not vary significantly over the 5 d period. Overall, the results of this study indicate that only breed and days in milk significantly affect milk coagulation rate as measured by diffuse reflectance. The study also demonstrated that diffuse reflectance can be utilized to monitor milk coagulation rate.

Key Words: coagulation, SCC, quality

T66 Selection criteria for lactic cultures in reduced fat Cheddar cheese. A. C. Biswas,* A. N. Hassan, and L. E. Metzger, *Dairy Science Department, South Dakota State University, Brookings.*

The objective of this research was to screen several commercially available ropy strains of lactic acid bacteria for suitability in making reduced fat cheese with improved textural characteristics. Exopolysaccharide (EPS)-producing lactic cultures have been used to improve texture and meltability of reduced fat Cheddar and process cheeses. In our previous studies, among numerous cultures tested, the most successful strain in making reduced fat cheese was a highly ropy *Lactococcus lactis* ssp. *cremoris* (JFR) isolated from commercial buttermilk. Several single and mixed cultures of *Streptococcus thermophilus*, *Lactococcus lactis*, and *Lactobacillus delbrueckii* ssp. *bulgaricus* were obtained from commercial sources and tested in this study. Cultures were screened for ropiness, and 5 highly ropy strains were selected. Selected strains were then evaluated against 2 control cultures: JFR and an EPS-negative culture. Rehydrated skim milk (11% w/w) steamed (95°C) for 15min. was inoculated with the test culture and fermented at the appropriate temperature (37°C for thermophiles and 32°C for mesophiles) to a pH value of 4.6. After overnight cooling at 4°C, fermented milk was tested for shear and heat stability, viscosity, water-holding capacity (WHC), and flow and viscoelastic properties. Milk fermented with JFR had the highest WHC, yield stress, consistency coefficient, ropiness, viscoelastic moduli, and shear stability. Water holding capacity determines moisture retention in cheese. The increase in viscoelastic moduli in the presence of EPS would indicate EPS-protein interactions which lead to stronger bodied, less pasty cheese, and lower whey viscosity (due to retention of EPS within the protein matrix). High heat and shear stability of EPS are important attributes in process cheese making. No direct relationship was found between ropiness and any of the tested traits. In conclusion, ropy cultures producing high water holding capacity, shear stability, consistency coefficient, yield stress, and viscoelastic moduli in fermented milk would produce reduced fat cheese with improved textural and melting properties.

Key Words: starter cultures, reduced fat cheese, exopolysaccharides

T67 Influence of salt levels, rate of salting and potassium chloride on whey syneresis from Cheddar cheese curd.

Y. Lu* and D. J. McMahon, *Western Dairy Center, Utah State University, Logan.*

There is interest in lowering the sodium content of cheese by either reducing the amount of added salt or by replacing some of the sodium with potassium. Such changes have the potential to affect whey expulsion from cheese curd and subsequent mechanical handling of the curd after salting. Our objective was to determine effects on cheese curd syneresis of salting time intervals, salting levels, and 33% KCl molar substitution of NaCl. Four sets of unsalted fresh Cheddar curds were obtained and salted with different methods, with 3 replicates of each set on separate days.. Set A was salted with 3.0% (wt/wt) NaCl over 3 applications either 5 or 10 min apart. Set B was salted with 3.0, 2.5, and 2.0% NaCl over 3 applications 5 min apart. Set C was salted with 2.0% NaCl using 1, 2, or 3 applications. Set D received salt consisting of a 2:1 molar ratio of NaCl and KCl over 3 applications 5 min apart. Whey was collected every 5 or 10 min until 30 or 40 min after the start of salting. Salted curds were pressed for 3 h. In general, whey expulsion started after the second salt addition, and with rapidly after the third application. Using 10-min salting intervals delayed whey syneresis but after pressing there was no significant influence on final cheese composition. Lowering salting levels significantly reduced the amount of whey expelled before pressing from a mean of 25 g/kg with 3.0% salt to 13 and 4 g/kg with 2.5 and 2.0% salting, respectively. This resulted in corresponding cheeses with higher moisture (35.6, 35.9, 37.0%) and slightly lower pH (5.3, 5.3, 5.2), respectively. In Set C cheese, adding 2.0% salt over one, 2, or 3 applications did not significantly affect cheese composition, with mean whey expulsion being ≤7 g/kg. Partial substitution with KCl did not affect amount of whey expelled or cheese moisture composition, although there was a slightly faster whey expulsion when using the NaCl/KCl mixture.

Key Words: cheese, salting, sodium

T68 Effect of different gums supplementation on textural properties of goat milk yogurts.

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Texture plays a significant role in sensory quality and consumer acceptability of fermented dairy foods. Casein gels are responsible for various rheological and textural properties of dairy products, such as yogurt and cheese. A study was conducted to evaluate the differences in textural properties of caprine milk yogurts fortified with 7 different kinds of gums during 4 weeks refrigerated storage. The experimental caprine yogurts were manufactured using goat milk produced at the Georgia Small Ruminant Research and Extension Center, Fort Valley State University, Fort Valley, with 0.2% addition of 7 different gums to pasteurized milk (w/v), which were: (1) xanthum, (2) modified food starch with agar pectin, (3) carrageenan, (4) locust bean, (5) carrageenan, maltodextrin, and dextrose, (6) guar, (7) modified food starch with gums 3, 4 and 5, and the yogurts were stored for 0, 2, and 4 wk at 4°C. Textural characteristics of all yogurts were determined using a texture analyzer (model TA.XT2i, Texture Technology Corp., Scarsdale, NY). Viscosity of the yogurts was measured by firmness (g force) and consistency, and adhesiveness or stickiness was measured by cohesiveness (g force) and index of viscosity. Firmness of control and 1 to 7 different gum added yogurts for the 0 and 4 wk storage were: 19.1, 23.0; 41.8, 63.7; 20.6, 22.2; 19.7, 20.9; 50.2, 64.7; 18.9, 19.7; 20.0, 20.8; 19.3, 21.1, respectively, indicating firmness of xanthum and locust bean fortified yogurts had significantly higher than control and the other gum treated groups. Locust bean showed the highest textural integrity among all tested gums. Viscosity, cohesiveness, and adhesiveness of #1 and #4 gums added yogurts were also significantly higher than the other yogurts. It was concluded that locust bean and xanthum were choice of gums for the best textural quality of caprine milk yogurt.

Key Words: goat milk yogurt, gums, texture

T69 The role of different sweeteners on WPI flavor contributions in acidic protein beverages.

S. White* and M. A. Drake, *North Carolina State University, Raleigh.*

The modern consumer demands that food products have high nutritional value without sacrificing flavor. Among these products are high protein beverages that may contain low calorie sweeteners. Previous research has documented that processing steps in protein beverage manufacture may increase off flavors in the finished product. This objective of this study was to determine if different sweeteners affected WPI flavor contributions in WPI beverages after acidification and pasteurization. Duplicate lots of WPI were rehydrated to 10% solids (w/v) and sweetened with fructose, sucralose, or stevia followed by acidification to pH 3.2 and heat treatment at 85C for 30 s. The experimental controls included unsweetened WPI, as well as deionized water sweetened with fructose, sucralose and stevia; all processed in the same manner. All treatments were evaluated by descriptive sensory analysis, solid phase microextraction gas chromatography mass spectrometry and gas chromatography-olfactometry. The experiment was repeated in triplicate and statistical differences were analyzed using one-way ANOVA and principal component analysis. WPI with different sweeteners were distinct in sensory and volatile profiles ($P < 0.05$). After acidification and heating, model beverages made with sucralose and stevia had higher soapy flavors than those sweetened with fructose; beverages with sucralose were also metallic. WPI model beverages with fructose had higher cabbage flavor, and higher dimethyl trisulfide concentrations after processing. However, other sensory differences were not confirmed by volatile analysis suggesting additional cognitive effects on sensory perception. A comparison of sweetened water and sweetened WPI indicated that processing effects (heat and acidification) on the sweetener alone did not impart unique flavors. Sweeteners influenced sweet taste quality and temporality and enhanced soapy or cabbage flavors contributed by WPI. These results demonstrate that sweetener type influences sensory properties (aromatics and basic tastes) of whey protein beverages.

Key Words: WPI, protein beverages, sweeteners

T70 Concentrations of IGF-1 and IGFBP-3 in several Korean commercial dairy products by immunoradiometric assay. S. H. Kang,* D. W. Kim, K. H. Kim, K. S. Kim, and S. C. Baick, *Seoul Dairy Cooperative R&D Center, Shingil-dong, Ansan-si, Kyunggi-do, Republic of Korea.*

Insulin-like growth factor-1(IGF-1) is a mitogenic polypeptide with a molecular structure similar to that of insulin which stimulates growth, differentiation and metabolism in a variety of cell types by acting through IGF-1 receptors. Milk-derived growth factors may also mediate the growth of tissues not directly associated with the GI tract and may have greater implications for overall growth and development of the neonate. The objectives of this study were to determine the change of insulin-like growth factor-1(IGF-1) and of insulin-like growth factor binding protein-3(IGFBP-3) content in commercial dairy products marketed in Korea. IGF-1 content was determined by immunoradiometric assay (IRMA). All the experiments were triplicated and the data were analyzed by the SAS system using a procedure of ANOVA. There were no significant differences in IGF-1 content by different pasteurization methods between HTST and UHT heat treatment. The mean IGF-1 content of commercial market milk, plain yogurt, skim milk powder, infant formula and sweet cheese whey powder was 2.3 ± 0.6, 8.7 ± 0.8, 4.8 ± 0.1, 4.1 ± 0.4 and 7.8 ± 0.2 ng/mL, respectively. However, the concentrations of IGFBP-3 in all the dairy products could not be measured by using commercially available human IGFBP-3 IRMA kits (<1.0 ng/mL), because the kits were generated against human IGFBP-3 epitopes and failed to recognize bovine milk IGFBP-3. The IGF-1 content in unprocessed milk has been reported in the range of 1.27 - 8.10 ng/mL. It was concluded that the concentration of IGF-1 in the examined milk products was not altered by homogenization, conventional heat treatment or spray drying.

Key Words: IGF-1, IGFBP-3, immunoradiometric assay

T71 The fatty acid composition of butter and cultured butter with lactobacillus acidophilus added to starter. O. Tsisaryk*[1], L. Musij[1], and O. Golubets[2], [1]*Lviv National University of Veterinary Medicine and Biotechnologies, Lviv, Ukraine,* [2]*Ukrainian State Research and Production Centre for Standardization, Metrology, Certification and Consumer Rights Production, Kiev, Ukraine.*

Our purpose was to create butter which would combine functional properties probiotics and increase the content of CLA. Some fermented dairy products contain higher levels of CLA than non-fermented, and the yield of CLA was dependent on the species of lactic acid bacteria inoculated. Some studies have shown that among lactic cultures inoculation of L. acidophilus into milk was most effective in promotion c-9,t-11-CLA formation. The objective of the study was to determine the fatty acid composition of sweet butter and cultured butter when a L. acidophilus was added to the starter. Control butter was churned from sweet cream (SB) and cultured butter (CB) from fermented cream. The cream was fermented by the starter Flora Danica Chr. Hansen (*Lac. lactis*, *Lac. cremoris*, *Leu. cremoris*, *Lac. diacetylactis*) at 20°C (CB1); Flora Danica and *L. acidophilus* La-5 (1:1) at 20°C (CB2); and Flora Danica and *L. acidophilus* La-5 (1:1) at 30°C – a more comfortable temperature for *L. acidophilus* (CB3). The experiment was replicated 3 times. Butter samples were stored at –20°C until the fatty acid analysis by GLC. The FAME were separated on a column (100 m × 0.25 mm × 0.2 µm [HP-88] 88%-cyanopropyl aryl-polysilixane, Agilent Technologies) in a chromatograph (Hewlett Packard 6890). All samples of butter contained similar concentrations of total trans-isomers, transvaccenic acid (4.0%) and c-9,t-11-CLA (1.9%). The content of butyric acid increased from 4.0 in SB to 4.3–4.4% in CB ($P < 0.05$). The sum of branched-chain fatty acids decreased from 2.6 in SB to 1.8% in CB; the percentage anteiso-C14:0 was 0.8% in SB, but it was not detected in CB. The content of C14:1 was 1.74% in cultured samples, but only 0.9% in SB. The sum of unpaired fatty acids was the same in all samples. The percentage of the sum of medium-chain saturated fatty acids (C12-C16) decreased from 40.8 in SB, CB1, and CB2 to 40.5% in CB3 ($P < 0.05$). It was concluded that there were not significant differences in fatty acid composition between the samples of cultured butter, but there were some differences between sweet and cultured butter in content of short- and branched-chain fatty acids.

Key Words: butter, cultured butter, fatty acids

T72 Effect of sodium reduction on the survival of *Listeria monocytogenes* and *Bacillus anthracis* in Cheddar cheese. E. Hystead,* F. Diez-Gonzalez, and T. C. Schoenfuss, *University of Minnesota, St. Paul.*

Reduction in sodium intake is a public health priority. Cheddar cheese is a targeted food for sodium reduction efforts because of its relatively high salt content. One of the roles of salt in cheese is the inhibition of spoilage and pathogenic microorganisms. Additionally, a bioterrorism attack on the milk supply with an agent that survives pasteurization, such as *Bacillus anthracis*, could be used against cheese. The objective of this study was to determine the ability of *Listeria monocytogenes* and *Bacillus anthracis* to survive in Cheddar cheese at reduced and low sodium levels. Stirred curd Cheddar cheese was manufactured separately with 2 different starter cultures, and 5 salting treatments: full sodium, 25%, and 55% reduced sodium with and without potassium chloride (KCl) addition. Shredded cheese from each treatment was inoculated with 5 strains of *L. monocytogenes* or 2 strains of *B. anthracis*, and stored at 4° and 12°C. Enumeration of pathogens, and aerobic count, and lactic acid bacteria was performed at regular intervals over 30 to 60 d. Water activity, pH and moisture were also monitored. *L. monocytogenes* count declined by 4 log cfu/g in all treatments after 60 d at 4°C. Results from subsequent experiments with higher inocula and higher pH, showed no more than 1 log cfu/g decrease in counts in all treatments. Furthermore, the 55% reduced sodium treatment had no reduction at all. The populations of *L. monocytogenes* (at 12°C), *B. anthracis*, aerobic count, and lactic acid bacteria survived consistently at 5, 6, 5.5, and 8.5 log cfu/g respectively, at any temperature or salting treatment. Survival of *L. monocytogenes*, and *B. anthracis* appeared to be due to an increase in pH of stored Cheddar cheese from averages of 4.7 to 5.4 over 6 mo. These results indicate that pathogens were able to survive in Cheddar cheese, regardless of sodium reduction level, but this survival was dependent on pH. In the event of an accidental or intentional contamination, reduction of sodium may increase the risk of pathogen survival if the pH of Cheddar cheese is not sufficiently low.

Key Words: Cheddar cheese, sodium reduction, food safety

T73 Effects of acidification of milk by glucono-δ-lactone (GDL) on the solubility of milk protein concentrate powder. H. Eshpari*[1,2], M. Corredig[1], and P. Tong[2], [1]*University of Guelph, Guelph, Ontario, Canada,* [2]*California Polytechnic State University, San Luis Obispo.*

A limiting factor in using milk protein concentrates (MPC) as a high quality protein source for different food applications is their poor reconstitution properties. It is known that in native casein micelles, there is an optimal balance of hydrophobic and electrostatic interactions; however, acid-induced changes of casein micelles have disruptive effects on the attractive and repulsive forces in casein micelle structure. Depending on the extent of disruption, different structures of acid modified micelles are obtained, that may result in different solubility and functional properties of casein micelles. The main objective of this study was to investigate the effects of acidification of milk by glucono-δ-lactone (GDL) before ultrafiltration on the reconstitutability of MPC powders. Milk protein concentrate 80 powders were manufactured in duplicate by ultrafiltration, diafiltration, and spray-dying using milk (~pH 6.6) and GDL-treated milk (pH 6.0). Powder samples were tested in duplicate for reconstitutability, particle size and microstructure. It was observed that acidification of milk to pH 6 significantly increased ($P < 0.001$) the mean solubility of milk protein concentrate from 79.81 to 90%. Particle size analysis and scanning electron microscopy (SEM) observations showed no significant difference in the mean particle size distribution and microstructure of the powder due to the effect of milk acidification. Mineral content and casein micelle structure of the powders need to be investigated to better understand the beneficial effect of milk acidification on solubility. Overall, this study demonstrates the importance of milk acidification and pH in determining the solubility of milk protein concentrate.

Key Words: acidification, milk protein concentrate, solubility

T74 Influence of ethanol on some characteristics of stirred yogurt. B. Mena*[1,2] and K. Aryana[2,1], [1]*Louisiana State University,* [2]*Louisiana State University Agricultural Center.*

Alcohol is used in manufacture of some products such as egg nog. The objective was to study the effect of ethanol on the growth of yogurt culture bacteria and the physico-chemical characteristics of stirred yogurt. The treatments were 0% (control), 2.5%, 5% and 7.5% v/v of ethanol. The ethanol was incorporated by stirring it into one day old plain yogurt. Product characteristics were studied weekly for 4 weeks of refrigerated (4°C) storage. Data were analyzed using Proc Mixed model of Statistical Analysis System. The ethanol*storage time interaction effect was significant for *Lactobacillus bulgaricus* counts. The storage time effect was significant for *Streptococcus thermophilus*, *Lactobacillus bulgaricus*, pH and titratable acidity (TA). Ethanol incorporation in yogurt did not influence the counts of *Streptococcus thermophilus*, *Lactobacillus bulgaricus* nor the viscosity of the yogurts. Ethanol incorporation in yogurt significantly influenced pH and TA of the yogurts. The pH of the control yogurts were significantly lower than yogurt with 7.5% ethanol, while there were no differences between the control and yogurts with 2.5 and 5% ethanol. Control yogurts had significantly the highest TA followed by yogurts with 2.5% ethanol while yogurts with 5 and 7.5% ethanol had significantly the lowest TA values not different form each other. Yogurts with ethanol can successfully be manufactured without adversely influencing counts of its culture bacteria over product shelf life.

Key Words: yogurt, ethanol, culture

Extension Education

T75 Water use efficiency on small-scale irrigated dairy farms in the Mexicali Valley, México. L. Avendaño-Reyes*[1], F. D. Alavarez-Valenzuela[1], U. Macías-Cruz[1], A. López-López[1], P. H. Robinson[2], and A. Correa[1], *[1]Universidad Autónoma de Baja California, Valle de Mexicali, Baja California, México, [2]University of California, Davis.*

The Mexicali Valley is contiguous to the Imperial Valley in the US state of California and has over 200,000 ha of irrigated land. Under a 1944 water treaty with the United States, Mexicali is guaranteed an annual quantity of 1,850,234,000 m^3 of water to be deliver from the Colorado River. Agriculture depends primarily on this annual quota of irrigation water. The dairy sector is predominantly small-scale and generates income to sustain most agricultural households. However, a proposed concrete lining in the United States on the All-American Channel would cut off billions of leaked gallons of water, which is used to irrigate several crops and livestock use in Mexicali Valley. The aim of this study was to use a survey method to investigate key factors that influence water use efficiency (WUE) in small-holders of the Mexicali Valley, Baja California, México. Descriptive statistics and regression analysis were performed. In the last 5 years there has a been a reduction in the number of dairy small holders because due to economic issues in the Mexicali Valley. Most of the small holder dairy producers are mature to old males (~55 years old), with a low level of education and with about 25 years dairying experience. The general management of the cows is supervised by professionals in less than 50% of the small dairy producers, but almost all participate in the government Brucella surveys. However, largely due to lack of milk management equipment, hygiene of milk is poor and this may lead to disease in the rural population that consumes their milk. Irrigation systems for grazing lands are deficient and a large amount of irrigation water is wasted or poorly managed. Water use efficiency is not associated with milk production or herd size, but it increased with an increase in total irrigated land area. Small dairy producers in the Mexicali Valley require more external support if they are to survive in the current and likely future economic climate, and to avoid other social problems such as migration to the USA to seek out ways to improve their families lifestyle.

Key Words: milk production, irrigation water, grazing dairy cattle

T76 Complexity graphics for complex issues in animal science. M. Boggess,* *USDA-ARS, Beltsville, MD.*

Modern scientific challenges to food animal production are increasingly complex making them difficult to visualize for academics as well as industry stakeholders. Scientists are evolving research models to tackle these complex challenges through larger comprehensive collaborations that feature interdisciplinary approaches to project management and scientific experimentation. Public funding agencies are following suit, requiring larger collaborative programs that feature funding line items for research, education and extension. Administering these programs requires superior leadership, communication and project management. Better tools are also needed to accomplish these goals. “Complexity graphics” are proposed as an innovative tool to visually convey the primary and secondary factors affecting a particular trait, concept or production challenge. Examples include animal production sustainability; sow lifetime productivity; maternal reproduction, bovine viral diarrhea and pork quality, although virtually any complex trait or concept could be illustrated. Sophistication ranges from s simple graphic to serial animation with multiple points of emphasis. These tools have proven to be beneficial with varied animal science and industry audiences to convey and illustrate the factors and relationships influencing complex traits. These tools have also proven beneficial to scientific teams attempting to visualize an interdisciplinary approach to a specific research project in the animal sciences.

Key Words: education, extension, collaboration

T77 Factors limiting productive efficiency in small dairies of central Mexico (Aguascalientes State). R. R. Lozano-Dominguez,* C. F. Arechiga, R. M. Rincon, and L. M. Escareno-Sanchez, *Universidad Autonoma de Zacatecas, Zacatecas, Mexico.*

Objective of present study was to identify the main factors compromising productive efficiency in small and familiar dairy productive systems typical of central Mexico at Aguascalientes state. Data from small dairies (n = 183) was collected including social, agricultural and animal productivity aspects. Such information was analyzed by ANOVA in which main independent variables were location and land property type. Thus, 64% of small familiar dairies are considered as “ejido” properties (communal-type property; $P < 0.01$). Labor is mainly a family responsibility (89.1%). Ejidal-type properties has a reduced number of hectares) compared with private properties (8.1 ± 1.9 vs. 15.9 ± 2.6 ha; $P < 0.01$). Forage corn is the main crop either at irrigated soils (4.0 ± 1.0 ha) as well as a seasonal crop during the rainy season at non-irrigated soils (6.3 ± 1.1 ha) in both property types (i.e., communal or ejido type vs. private property type; $P > 0.05$). Alfalfa is the second most important crop (2.4 ha); However, 79.2% of small-familiar dairies did not produced their own forage crops. Average number of dairy cows on milking line was 15.8 ± 1.4 with an average daily milk yield of 16.2 ± 1.04 kg. Showing differences within location and type of land property ($P < 0.05$). Culling (12.3%) and abortions (8.8%) rates were similar within locations ($P > 0.05$). Milk selling price was of 3.9 ± 0.46 Mexican pesos (MP); generating a daily income for milk sales of $951.50 MP per production unit (around US$75). Therefore, a negative profitability was obtained (-$0.28 cents) per liter of milk sold. Despite the fact, of being small dairy production units with reduced milk yields, when we consider a weekly labor payment for the dairy producer, profitability incomes become negatives. Nevertheless, in most cases such income represents the main and single income for the small and familiar-type diaries of central Mexico.

Key Words: small dairies, milk yield, Mexico

T78 Evaluation of on-farm forage dry matter determined by near infrared spectroscopy. M. S. Akins*[1], M. Dobberstein[2], and R. D. Shaver[1], *[1]Department of Dairy Science, University of Wisconsin-Madison, [2]Dinamica Generale US, DeKalb, IL.*

The objective of this study was to evaluate the use of near infrared spectroscopy (NIRS; Dinamica Generale, Mantova, Italy) for on-farm measurement of forage dry matter (DM) content. The NIRS also measured protein, NDF, ADF, starch, ash and fat, but only DM content was evaluated. To calibrate the NIRS to forages at the University of Wisconsin-Madison Emmons Blaine Dairy Center (Arlington, WI), 10 samples of corn silage (CS) and alfalfa silage (AS) were analyzed using the NIRS to obtain a spectral analysis, then sent to a commercial laboratory (Dairyland Laboratories, Inc., Arcadia, WI) for DM analysis using a 2 step method (microwave drying to 90–95% DM, then use

NIRS to measure total DM content). Spectral and DM analysis data were used to update calibration equations for each forage. Samples of CS and AS were obtained twice weekly on Monday and Thursday for 11 wk. A total of 94 CS samples from 6 silo bags and 2 bunker silos, and 20 AS samples from one bunker silo were analyzed for DM content on-farm using the NIRS. Samples (60–100 g) were put in the scanning tray, compressed, and scanned by moving the tray in the scanning chamber for 10 s. The sample was removed from the tray and the entire sample was dried in an oven at 60°C for 48 h to measure DM content. Bias was calculated for each sample as the difference between oven and NIRS DM. The DM contents using the oven and NIRS were 38.1 ± 4.2% and 37.2 ± 3.9% for CS, and 43.4 ± 3.8% and 41.8 ± 4.4% for AS, respectively. The minimum and maximum DM contents of CS were 27.3% and 47.1% DM using the oven, and 26.5% and 46.7% using the NIRS, respectively. The minimum and maximum DM contents of AS were 31.6% and 47.7% using the oven, and 27.7% and 45.8% using the NIRS, respectively. For CS, the regression equation developed was NIRS DM% = (0.867 × Oven DM%) + 4.23; $R^2 = 0.85$, and the AS regression equation was NIRS DM% = (1.1395 × Oven DM%) − 7.7; $R^2 = 0.95$. The NIRS accurately (bias = 0.8% units) but less precisely (standard deviation of bias = 1.6% units) measured DM content of CS, and consistently measured lower DM content of AS (bias = 1.6 ± 1.1% units). Overall, the on-farm NIRS measured DM content comparable to the oven method.

Key Words: forage dry matter, NIRS

T79 Compliance of small and medium-sized farms in adopting recommendations for improved farm productivity and nutrient utilization.

L. D. Baker,* R. J. Munson, Z. Dou, D. T. Galligan, J. D. Ferguson, C. F. Ramberg, D. W. Remsburg, and Z. Wu, *University of Pennsylvania, Kennett Square.*

Ten dairy farms with less than 200 cows were identified from the Chesapeake Bay watershed in Pennsylvania to participate in an integrated nutrient management program in collaboration with herd veterinarians, nutritionists, agronomists and farm economists to improve farm profitability and to reduce nutrient and phosphorus excretion. Farms were visited quarterly for 2 years by project members to evaluate nutrition and management practices. DHIA records were analyzed monthly to monitor milk production and components, milk urea nitrogen, reproductive performance, and culling practices. Four farms substantially improved their financial situation during the study by making changes in their feeding program when they changed nutritionists, some of them longstanding relationships. Nutrient efficiency was improved on these farms as well. Recommendations by project leaders and collaborators for improvement of feeding and farm management practices were not adopted by all farms. On several farms (6 of 10) small amounts of forages with varying quality were produced and frequent forage changes prevented farms from having a balanced ration for extended periods of time. Conflicts in recommendations between project members and field nutritionists confused producers and resulted in less compliance toward project goals. For example, high quality forage was fed on one farm, but the nutritionist was reluctant to reduce the amount of supplemental grains, therefore increasing feed expense and nutrient excretion for this farm. On another farm the nutritionist was resistant to removing phosphorus from the top dress, resulting in high fecal phosphorus. Agronomists had positive effect on most of the farms, instituting cover crops and manure and soil testing for appropriate application rates and fertilization. There were 2 farms that did not comply with agronomic or project member recommendations, basing their actions on emotions rather than on sound decision making to improve profits. In general veterinarians supported systematic breeding programs recommended by project members with many farms having a positive improvement in pregnancy rate. Partially supported by National Fish and Wildlife Foundation.

Key Words: small farms, dairy farm management, nutrient management

T80 A collaborative bovine artificial insemination course for students attending a Caribbean veterinary school.

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Artificial insemination (AI) is a critical career skill for food animal veterinarians. Consequently, Ross University School of Veterinary Medicine Student Chapter of the American Association of Bovine Practitioners (SCAABP), Select Sires, and University of Idaho Extension have partnered to offer an intensive 2-d course to provide AI training to students attending the Caribbean veterinary school. The program consisted of 7 h of classroom teaching followed by 10 h of live animal experience. Topics included reproductive anatomy and physiology, semen handling, estrous detection, AI technique, estrous and ovulation synchronization protocols, sexed semen, and a virtual AI stud tour. A registration fee of $EC350.00 ($US130.00) included the cost of handouts, and breakfast and lunch on each day. The AI course was held twice in 2010 and 3 times in 2011. A 25-question test was given to participants (n = 83) at the beginning and conclusion of each AI course. The overall mean test score for the pre-test was 77.7%, while the mean for the post-test was 96.2%. The mean difference was 18.5%. Eighty-one students (81/83; 98%) received a certificate of completion by demonstrating sufficient skill at semen handling and AI technique. The course has developed into a high-demand educational program in which priority is given to SCAABP members based on 1) points earned through participation in other chapter events, 2) semester of enrollment at Ross University, and 3) participation in at least 1 chapter-sponsored bovine palpation trip to a local ranch. This collaborative effort ensures students attending the geographically remote veterinary school receive the educational opportunity to increase their knowledge and develop the skill of performing AI in cattle.

Key Words: artificial insemination, cattle, veterinary school

T81 Repro money: A farmer-directed team-based extension program to improve reproductive performance in Wisconsin dairy herds.

M. C. Cordoba,* P. M. Fricke, P. L. Ruegg, R. D. Shaver, K. A. Weigel, and V. E. Cabrera, *University of Wisconsin-Madison.*

Poor reproduction in dairy cattle is a multifactorial problem that includes aspects of physiology, genetics, management, health, and nutrition. Thus, improving reproductive performance requires an integrated approach among farm personnel and consultants that deal with reproduction. Our objective is to improve the reproductive efficiency and profitability of the dairy enterprise through implementation of farmer-directed team-based program called Repro Money. Each farm that enrolls in the Repro Money program agrees to conduct 4 meetings during a 6 to 8 mo period. Before the first meeting, the farm owner selects team members (e.g., veterinarian, nutritionist, AI technician, county extension agent, herd manager) and designates a team leader. At the first meeting, the team leader uses a data gathering and survey tool to analyze and identify farm-specific critical control points for successful reproductive management including: pregnancy rate, insemination risk, conception risk, detection of estrus, male and female fertility, transition cow management, synchronization protocols, and nutrition and heifer management. Based on results from this tool, the team sets goals, develops an action plan, assigns responsibilities, and determines appropriate evaluation strategies for individual team members. Meetings 2 and 3 are structured to ensure that team goals identified at the first meeting are on track. During the fourth and final meeting, the team reassesses the reproductive performance of the dairy using the same tool as the first meeting thereby documenting change. We are now in the process of enrolling farms into the Repro Money program. One of the early adopters of Repro Money increased their 21-d pregnancy rate from 18 to 24% resulting in an estimated $39,000 per year profit increase after implementing management changes identified during the program. With this farmer-directed team-based approach, dairy farmers can best utilize their personnel and advisers in a coordinated way to improve reproductive performance. Supported by AFRI Competitive Grant no. 2010–85122–20612

Key Words: reproduction, dairy cattle, team-based

T82 Calf-ETERIA: Using calf health and productivity as a template for extension and translation of research information for agriculture. V. Bielmann*[1], K. Leslie[1], T. Wright[2], and T. DeVries[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, Ontario, Canada.*

There is increasing evidence from research that calf and heifer management is extremely important for long-term health, production and survival of dairy cattle. In addition, several key risk factors affecting these effects, and management programs for improvement of the situation, have been identified and refined. General adoption of these programs could be improved, and if so, would yield significant financial savings for the dairy industry. Nevertheless, leading producers, extension educators, dairy researchers and veterinarians have been largely unsuccessful in making noteworthy improvements on an industry-wide basis. The Calf-ETERIA Knowledge Translation and Transfer (KTT) project is an extension effort aimed at addressing this dilemma. A key objective of this project was to survey Ontario dairy producers on their calf and heifer management practices. The benefits of benchmarking these practices include using these levels to assess progress over the duration of the project in terms of animal well-being and financial benefit. In total, 3,145 surveys were mailed to Ontario dairy producers who were clients of the CanWest Dairy Herd Improvement program. Once the completed surveys were returned, data was entered into an Access database. The response rate for the survey was 30% (963/3,145). Survey results indicate that navel dipping is no longer routine practice on dairy farms, with only 38% of respondents implementing this practice. Thirty percent of producers indicated that colostrum quality is assessed on farm. However, of this 30%, 91% said the method of assessing quality was by visual inspection (color, consistency or volume), not by using a tool such as a colostrometer. The time of weaning on Ontario dairy farms is primarily decided by the age of the calf, with the majority of calves being weaned at 8 or 11 weeks of age (36% and 31%, respectively). The age at which fresh water is first offered to calves varied with 23% of producers offering water within 5 d of birth, 29% offering water 5–10 d after birth, 30% waited until the calves were older than 10 d of age, and the remaining 17% of producers do not offer water until after weaning. When asked what the cost of raising a heifer was, 58% of producers answered $1500-$2000, while 32% answered $1000-$1500. The remaining 10% answered $1000 (5%), $2500-$3000 (4%) and greater than $3000 (1%). This survey is the most comprehensive data set for calf and heifer management in Ontario since the 1980s and will be the first to evaluate the effect of different KTT approaches intended to positively affect change on dairy farms in Ontario. It is clear from the survey results that there are some areas of calf raising in which management practices vary widely across farms and can be improved upon.

Key Words: calf, heifer, management practices

T83 Comparison of out-of-season estrus synchronization protocols in meat goats. N. C. Whitley[1], K. Moulton*[1], R. A. Franco[1], A. E. Cooper[1], and T. J. Conrad-Acuna[2], *[1]Cooperative Extension Program, North Carolina A&T State University, Greensboro, [2]North Carolina State University Cooperative Extension, Richmond County, Rockingham.*

The objective was to demonstrate different methods for estrus synchronization for out of season breeding in meat goats on a producer-owned farm. The farm owner noted repeated failure of previous spring breeding attempts without hormone use. For this study, 33 mature Boer does were used in April 2011, with 10 receiving CIDR vaginal inserts (CIDR), 10 receiving CIDR inserts along with 400 IU PMSG and 200 IU hCG (5 mL PG600 sc; CP treatment group) and 13 receiving no treatment (CON; buck effect only). Does averaged 3.2 ± 0.2 years of age and were assigned to treatments such that 3 to 5 does from each treatment were represented in each of 3 single-sire mating groups. All males were kept away from sight and smell of the females for at least 3 weeks before the study. The CIDRs were inserted on d 0 and removed on d 13 for 20 does with 10 does receiving PG600 at CIDR removal. Mature Boer bucks were placed with does on d 13 and removed on d 27. On d 66, blood samples were collected via jugular vein puncture to determine pregnancy status (bioPRYN; BioTracking, LLC). Pregnancy and kidding rates were not influenced by treatment or mating group based on Fisher Exact Test analysis. Number of kids born was analyzed using Proc GLM of SAS. Pregnancy rates for CON, CIDR, and CP respectively were 69%, 90%, and 50% and kidding rates for CON, CIDR, and CP were 67, 89, and 40%, respectively. Kidding rates were 60% for 2 mating groups and 73% for the other. Number of kids born per doe kidding was not influenced by treatment, averaging 1.9 ± 0.3, 2.1 ± 0.3 and 2.5 ± 0.4 for CON, CIDR and CP, respectively. Number of kids born per doe exposed tended ($P < 0.10$) to be influenced by treatment, averaging 1.3 ± 0.3, 1.9 ± 0.4 and 1.0 ± 0.4 for CON, CIDR and CP, respectively. For this farm with small sample sizes, the use of the buck effect alone was just as effective as hormonal treatments for inducing out-of-season breeding in meat goat does, though CIDR alone tended to result in more kids born per doe exposed. More research is needed; however, based on these results, the farm owner intends to use CIDRs for out of season breeding this spring.

Key Words: CIDR, estrus synchronization, goat

T84 Using soil moisture monitoring to improve irrigation in dairy pastures. T. W. Downing,* *Oregon State University, Corvallis.*

Irrigating pastures on the Oregon coast has not been emphasized in the past because of the high seasonal rainfall and low return for the investment. As feed costs have risen, more emphasis has been placed on increasing the productivity of coastal pastures and this has stimulated a new interest in improving irrigation. Monitoring soil moisture tension or soil moisture content can help identify problems in irrigation water management that affect pasture yield or water use. Problems include excessive intervals between irrigations, inadequate wetting, too-frequent irrigations and differences in soil moisture type extraction patterns. This project was designed to monitor irrigation effectiveness of 2 types of irrigation systems on 4 dairies over 2 growing seasons. Watermark soil moisture probes were installed in 2 pastures on each dairy and soil moisture tension was recorded every 2 h at 15, 30, 45 and 60 cm deep for 2 years. Irrigation was done with either a traveling big gun irrigator or pod irrigation system. Year 1 dairy operators were asked to irrigate as they normally would and performance was recorded. In year 2 we demonstrated how to use the soil moisture monitoring system for management and reviewed the first years performance. Irrigation dates and volumes were also recorded in year 2. Irrigations done with big gun irrigators applied 4 irrigations averaging 66.25 ± 13.25mm and irrigations made with pod irrigation systems averaged 6 irrigations averaging 40.75 ± 14.87mm. Soil moisture tension measured in ranged from 0 to 97 centibars for the big gun irrigators and soil moisture from pod irrigators ranged from 10 to 62 centibars throughout the second year. Soil moisture monitoring has shown it was extremely beneficial in making decisions in dairy pastures and irrigating effectively was challenging for big gun equipment. Dairies irrigating with pods were over irrigating initially and reduced irrigations by 15% when they used soil moisture data.

Key Words: soil moisture monitoring, irrigating pastures

Food Safety: Food Safety Advances

T85 Occurrence of several antibiotic residues in raw milk in ten provinces of China. R. W. Han[1,2], J. Q. Wang*[1], N. Zheng[1], X. M. Xu[1], Y. P. Zhen[1], X. Y. Qu[1], P. Sun[1], and Z. N. Yu[3], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [2]*College of Food Science and Engineering, Qingdao Agricultural University, Qingdao, Shandong, China,* [3]*Haidu College, Qingdao Agricultural University, Laiyang, Shandong, China.*

The objective of this study was to investigate the occurrence of antibiotic residues in raw milk in China. A total of 199 raw milk samples from 10 provinces of China were examined for β-lactams, tetracyclines, sulfonamides and quinolones. SNAP Beta-Lactam Test kit (Idexx) was used for qualitative detection of β-lactam antibiotics, and sample was positive with the ratio 1.06 or higher. The limits of detection (LOD) of R-Biopharm test kits (Ridascreen) which used for quantitative detection of tetracyclines, sulfonamides and quinolones were 1.5μg/kg, 5.0μg/kg, and 0.25μg/kg, respectively, which were far below the maximum residue limits (MRL, regulated by EU, CAC, and China).Only one positive sample from Beijing for β-lactams was found with a ratio of 1.39. No sample was positive for tetracyclines, while 47.23% samples for quinolones and 20.1% samples for sulfonamides were positive. Sulfonamides and quinolones were positive in all provinces. Shanghai (detection rate 5%) was lowest for quinolones and Hebei (detection rate 80%) was highest. Beijing (detection rate 10%) was lowest for sulfonamides and Shanghai (detection rate 80%) was highest. The maximums detected for sulfonamides and quinolones were 16.28μg/kg (Guangdong) and 23.25μg/kg (Tianjin), respectively. All samples for tetracyclines, sulfonamides and quinolones were under their MRL. In general, the residue levels of the 4 major antibiotics in raw milk in China are safe for people. But stringent measures still needed to control antibiotic residues in raw milk because of the high detection rate of some antibiotics.

Key Words: antibiotic residues, raw milk, China

T86 Occurrence of aflatoxin M1 in raw milk and UHT milk in China. N. Zheng, J. Q. Wang,* R. W. Han, X. M. Xu, Y. P. Zhen, X. Y. Qu, and P. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Aflatoxin M1 (AFM1) can cause teratogenic and mutagenic effects, and has been classified as a secondary group of carcinogenic compounds by the International Agency for Research on Cancer of World Health Organization. AFM1 is the only mycotoxin that has a legal limit in milk worldwide. The limits of 50 ng/L by the European Union and 500 ng/L by the USA have been adopted by many countries and international organization. The objective of the present study was to investigate the occurrence of AFM1 in raw milk and UHT milk in China. 360 raw milk samples and 153 UHT milk samples were collected from primary milk producing regions in China, including Beijing, Hebei, Shanxi, Shanghai, Guangdong provinces. The AFM1 was examined using a competitive enzyme immunoassay kit (R1111, R-Biopharm AG, Darmstadt, Germany), with the limits of detection of 5 ng/L. The data was statistically analyzed using the SPSS version 11.5 (SPSS, Inc., Chicago, IL). 78.1% of raw milk samples and 54.9% of UHT milk samples contained AFM1. It showing that the occurrence of AFM1 in raw milk were higher than that in UHT milk. The concentration of AFM1 in positive raw milk samples and UHT milk samples were in the range of 5 to 123 ng/L and 6 to 160 ng/L, respectively. However, the content of AFM1 between positive raw milk samples and positive UHT milk samples had no significent ($P > 0.05$) difference. AFM1 contents in all positive samples were far below the China and the US legal limit of 500 ng/L, but 10% of the raw milk samples and 20.3% of the UHT milk samples exceeded the EU legal limit of 50 ng/L. Therefore, the potential for contamination of AFM1 in milk in China should be considered, and effective measures should be applied to decrease the contaminant of milk with AFM1.

Key Words: aflatoxin M1, milk, China

T87 Purple prairie clover condensed tannins inhibit *Escherichia coli* through disruption of outer and inner membranes. X. L. Liu*[1,2], L. Jin[1], Z. Xu[1], Y. Q. Hao[2], T. A. McAllister[1], and Y. Wang[1], [1]*AAFC, Lethbridge, AB, Canada,* [2]*Inner Mongolia Agricultural University, China.*

It has been suggested that feeding condensed tannin (CT)-containing forage could be a strategy to mitigate pathogens such as *Escherichia coli* O157:H7 in ruminants. Although antimicrobial activity of CT against G^+ bacteria is well documented, few of them possess activity against G^- bacteria, including *E. coli*. Our previous research revealed that CT isolated from purple prairie clover (PPC; *Dalea purpurea* Vent.) possesses a broad-spectrum of anti- *E. coli* and *E. coli* O157:H7 activity, which was bacterostatic up to the concentration of 400 μg/mL, through an unknown mechanism. The objective of this study was to evaluate the effect of PPC CT on cell aggregation, cell membrane permeability and integrity. *E. coli* (ATCC25922) was aerobically cultured in M9 media containing 0 or a sub-lethal concentration (MIC = 12 μg/mL) of 10 μg/mL of CT at 37°C for 10 h. The bacteria were separated from the media and re-suspended in phosphate buffer (adjusted to $OD_{420} = 1.0$). Inner membrane (IM) permeabilization was determined by measuring cytoplasmic β-galactosidase activity and outer membrane (OM) disruption by fluorescence measurement of the uptake of 1-N-phenylnaphthylamine (NPN) by the cell membrane. Cell aggregation was assessed using fluorescence spectrophotometry and fluorescence microscopy and cell wall integrity was examined by transmission electron microscopy (TEM). All determinations except for TEM were done 3 times over 2-wk period with 4 replicates for each time. *E. coli* cultured with 10 μg/ml CT had higher ($P < 0.01$) extracellular β-galactosidase activity than those cultured without CT, indicating an increase in the IM permeability by CT. The NPN uptake by OM was increased ($P < 0.001$) by culturing *E. coli* with 10 μg/ml of CT. Fluorescence microscopy showed that *E. coli* cells aggregated immediately after CT was added to the cell suspension and this was accompanied by a reduction ($P < 0.01$) in fluorescence. Examination by TEM revealed that the OM structure was also disrupted. These observations suggest that PPC CT inhibit *E. coli* growth through disruption of cell membrane structure and function. Whether inhibition of *E. coli* O157:H7 by PPC CT involves the similar mechanism needs to be further studied.

Key Words: condensed tannin, *E. coli*, cell membrane permeability

T88 Antimicrobial resistance of *Salmonella enterica* isolated from bulk tank milk and milk filters in the United States. J. S. Van Kessel*[1], J. Sonnier[1], S. Zhao[2], and J. S. Karns[1], [1]*Environmental Microbial and Food Safety Laboratory, USDA-ARS, Beltsville, MD,* [2]*Center for Veterinary Medicine, US FDA, Laurel, MD.*

Non-typhoid *Salmonella* is frequently associated with dairy cattle and their environment. Despite well-developed milking hygiene protocols, fecal contamination of the bulk milk can still occur; *Salmonella* has often been isolated from bulk milk. The prevalence of *Salmonella* in US bulk tank milk was determined as part of the NAHMS Dairy Surveys in 2002 and 2007. In-line milk filters were also tested in the 2007 survey. The objective of this study was to determine the level of antimicrobial susceptibilities in *Salmonella* isolated from bulk milk and milk filters in the NAHMS surveys. Susceptibilities to 15 antibiotics were determined for 176 *Salmonella* isolates, representing 26 serotypes, using a Sensititer automated antimicrobial susceptibility system. Resistant isolates were screened by PCR for the presence of the bla_{CMY} gene and class I integrons, and further characterized by pulsed-field gel electrophoresis (PFGE). Thirty isolates (17.0%) including 6 serotypes [Newport (14/14), Dublin (7/7), Typhimurium (3/5), Kentucky (4/22), Anatum (1/13), and Infantis (1/2)] exhibited resistance to at least one antimicrobial agent. Twenty isolates (11.4%) including all 14 *Salmonella* Newport, 2 *Salmonella* Dublin, 2 *Salmonella* Typhimurium and 1 *Salmonella* Infantis displayed the typical MDR-AmpC phenotype, which showed resistance to ampicillin, chloramphenicol, streptomycin, sulfonamide, tetracycline (ACSSuT), plus resistance to amoxicillin/clavulanic acid, cefoxitin, ceftiofur and ceftriaxone. All MDR-AmpC isolates carried the bla_{CMY} gene and 5 resistant isolates contained class I integrons (2.8%). Two-enzyme (*Xba*I and *Bln*I) PFGE discerned clades within serotypes, although it did not discriminate isolates based on year, antibiotic resistance profile, or geographic location. Testing raw milk and milk filters may be a useful means of surveying dairy farms for the presence of antimicrobial resistant *Salmonella*. These data suggest that there is a low but notable presence of antimicrobial resistance in salmonellae from raw milk.

Key Words: antimicrobial resistance, raw milk, *Salmonella*

T89 The effects of tetracycline analogue on prevalence of resistance genes encoded by *Escherichia coli* isolated from feedlot cattle. X. Jin[1,2], T. A. McAllister[1], Q. Li[2], and T. W. Alexander*[1], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China.*

The effects of administering feedlot cattle subtherapeutic levels of chlortetracycline (CT) or CT and therapeutic levels of oxytetracycline (CT-OX) on resistance genotype in *Escherichia coli* were investigated. Fecal samples were collected from cattle that had been housed in commercial feedlots for greater than 60 d and had a documented history of antimicrobial use. Isolates were tested for susceptibility to tetracycline, chlortetracycline, and oxytetracycline using disk diffusion or broth microdilution. Detection of *tet*(A), *tet*(B), and *tet*(C) genes encoded by tetracycline-resistant isolates (n = 176) was performed by multiplex PCR. All isolates encoded at least one or a combination of 2 resistance genes. Prevalence of *tet*(A) was similar between groups of *E. coli*, however prevalence of *tet*(B) was lower (18% versus 34%; $P < 0.05$) and *tet*(C) was greater (46% versus 28%; $P < 0.05$) in CT isolates. The nature of the *tet* determinants was further assessed in a group of intermediately tetracycline-resistant isolates (n = 52). The *tet*(C) gene was present in 92% of these isolates. Minimum inhibitory concentrations showed that susceptibility was dependent on tetracycline analog and the type of resistance determinant. Copies of *tet*(C) transcripts, analyzed by real-time PCR, indicated that upregulation did not occur in tetracycline-resistant isolates when compared with intermediately-resistant isolates. However, sequence analysis of the *tet*(C) gene revealed a T→G substitution at position 1063 in intermediately-resistant isolates that may have affected phenotype. These data provide insight into the relationship between the type of tetracycline analog administered to cattle and the prevalence of resistance genes in *E. coli*.

Key Words: *Escherichia coli*, antimicrobial resistance, tetracyclines

T90 Cranberry juice and cranberry fiber are accepted by newly weaned pigs. S. D. Eicher*[1], B. T. Richert[2], and M. H. Rostagno[1], [1]*USDA-ARS, West Lafayette, IN,* [2]*Purdue University, West Lafayette, IN.*

Cranberry products offer a novel mechanism to control the ability of pathogens to colonize their host. However, it is not known how well pigs will consume juice or feed with cranberry fiber incorporated. The objective of this experiment was to determine if cranberry liquid or fiber products were palatable to newly weaned pigs. Pigs were weaned onto a pelleted diet for 3 d before starting this experiment. In a randomized complete block design, 60 4 recently weaned pigs (22 d of age) were blocked by weight into 8 pens with 4 pens/preference test (pen = experimental unit). Pigs were assigned to treatments to test for preferences of cranberry juice (0, 1, or 10% of 7.5 Brix) or a control dry feed versus dry feed supplemented with 4% cranberry fiber (both cranberry products were from Marshall Ingredients, NY). Control dry feed was provided to pigs on the liquid preference test, and water was provided for those on the dry feed preference test. Liquid choices were added as needed and weighed back every 3-d period. Dry feeds were also added as needed and weighed back every 3 d. Occurrences of eating or drinking of the test liquids and feeds were taken for 2 h from 0900 to 1100 and 1400 to 1600 for the first 3-d period by 1-min duration scan samples every 10 min. Cranberry juice (10%) was consumed more readily than water or than the 1% cranberry juice ($P = 0.01$) during the last 2 periods. Behavior tended to support the consumption of 10% cranberry juice, particularly in the morning observations, but overall was not different among liquid treatments ($P = 0.15$). Although the cranberry supplemented dry feed was eaten more on the first observation period, the treatments were preferred similarly over the remainder of the observations; and overall, the dry feeds were consumed relatively equally, 163 vs. 135 g/d for control and cranberry feeds respectively ($P > 0.10$). Results of this study support the use of cranberry products as a liquid (10%) or as fiber (4%) added to dry feed. Consequently, cranberry products will be used in follow-up research to determine its efficiency as microbial and immune modulators in young pigs.

Key Words: nursery pigs, cranberry

T91 Evaluation of hygienic and sanitary quality of jerked beef commercialized in Salvador city, Bahia, Brazil. L. Pereira, M. Silva, W. Costa, and R. Matoso,* *UFBA, Salvador, Bahia, Brazil.*

The objective of this study was to assess the sanitary quality of jerked beef sold in the city of Salvador, Bahia. We collected 30 samples of dried beef in retail markets located in different neighborhoods of the city. These samples were collected in the form of presentation available to consumers, observing their physical integrity. Each sample was subjected to processing and then plated in liquid and specific solid media to investigate aerobic mesophilic heterotrophic bacteria, coagulase-positive *Staphylococcus*, yeasts and molds. The plates for detection of aerobic heterotrophic bacterial mesophilic and *Staphylococcus* coagulase-positive were incubated at 35°C for 48 h while the plates for the detection of yeasts and molds were incubated at 28°C for 5 d. Afterward colonies were read and counted, in addition to the complementary tests (smear stained by Gram's method, the catalase and coagulase test). It was observed that 100% of samples had counts of aerobic mesophilic microorganisms ranging from 1.2×10^6 to 9.3×10^6 cfu/g, higher than acceptable levels for other meat products contained in Resolution RDC No. 12 of Ministry of Health. Although the counts of molds and yeasts were lower, ranging from 2×10^2 to 8.3×10 cfu/g. When correlating the results with those previously described in literature, it is possible to verify that the samples were in low hygiene conditions. Finally, the presence of *Staphylococcus* coagulase positive in 100% of the samples indicates that there was poor handling of the food product. It is extremely necessary to establish more rigorous standards for the microbiological quality of jerked beef to determine the quality of these products intended for human consumption. These standards should guarantee foods with good hygiene conditions what would increase product lifetime, avoid economic losses and prevent risks to public health.

Key Words: meat products, public health, microbiological quality

Forage and Pastures II

T92 Productive response of finishing young bulls to tannins supplementation. M. Velázquez-Martínez[1], O. Hernández-Mendo[1], S. Pérez-Elizalde[1], E. López-Pérez[2], and G. Aranda-Osorio*[2], *[1]Colegio de Postgraduados, Montecillos, Texcoco, México, [2]Universidad Autónoma Chapingo, Chapingo, Texcoco, México.*

The aim of this study was to evaluate the productive performance of finishing bullocks when adding tannins into their diet. Twenty-seven crossbred (*B. taurus* × *B. indicus*) bullocks, with initial liveweight of 412.3 ± 22.19 kg, were used. They were allocated into 3 groups of 9 animals each, and then distributed, at random, to one of following treatments: T1) control (experimental diet), T2) control + 2,500 IU of vitamin E/animal/day, and T3) control + 4% (kg of DM) of condensed tannins. Quebracho extract (*Schinopsis balansae*, Indunor S.A.C.F.I.F.), was used as source of tannins. Dry matter intake (DMI), average daily gain (ADG), feed conversion (FC), feed efficiency (FE) and hot carcass yield (HCY), were evaluated. Animals were slaughtered at 518.65 ± 33.51 kg of liveweight on average. The variables were analyzed in a completely randomized design with Proc GLM of SAS/STAT. There were no differences ($P \geq 0.05$) among treatments, with averages for DMI, ADG, FC, FE, and HCY, of 10.85 kg, 1.98 kg, 5.60 kg, 183.6 g/kg DM and 57.74%, respectively, which agrees with those results reported by other authors. This study provides evidence that 4% of condensed tannins from Quebracho tree in diets for finishing bullocks did not affect animal performance. However, future studies should take into consideration its effect on ruminal variables, anti-gastrointestinal parasites, and antioxidant effect on meat quality, before its use under commercial conditions.

Key Words: beef cattle, tannins, performance

T93 Pelibuey sheep productive response to different sources of tannins from forage trees. M. Velázquez-Martínez[1], O. Hernández-Mendo[1], S. Pérez-Elizalde[1], E. López-Pérez[2], and G. Aranda-Osorio*[2], *[1]Colegio de Postgraduados, Montecillos, Texcoco, México, [2]Universidad Autónoma Chapingo, Chapingo, Texcoco, México.*

The objective of this study was to evaluate the effect of supplementing tannins from different forage tree species on growth performance and carcass yield of Pelibuey sheep. Thirty-six Pelibuey male sheep were used, with initial liveweight of 23.74 ± 4.57 kg and 5–6 mo of age, on average. The animals were distributed homogeneously into 4 groups of 3 each, with 3 replicates per group, and then randomly assigned to each of the following treatments: T1) control (experimental diet), T2) *Gliricidia sepium* (GS) diet, T3) *Guazuma ulmifolia* (GU) diet, and T4) Quebracho extract (*Schinopsis balansae*, Indunor S.A.C.F.I.F.) diet (QE). All diets were formulated to fulfill the animal requirements (15.4% CP, 33.8% NDF, 2.8 Mcal of ME, 0.92 Ca and 0.32 P, on average). The variables evaluated were dry matter intake (DMI), average daily gain (ADG), feed conversion (FC), feed efficiency (FE), hot carcass yield (HCY) and cold carcass yield (CCY). Animals were slaughtered with an average liveweight of 40.23 ± 4.24 kg. The data were analyzed by using the Proc Mixed from SAS/STAT, and a means comparison with *t*-test (PDIFF). The T3GU had the lowest ($P \leq 0.05$) DMI (1.18 kg) compared with the other treatments, which averaged 1.27 kg. The ADG was not different ($P \geq 0.05$) among treatments (268 g on average). The FC was higher ($P \leq 0.05$) for T2GS (5.22 kg) compared with the other treatments, which averaged 4.60 kg. The T2GS had the lowest ($P \leq 0.05$) FE (195 g/kg) compared with the other treatments, which averaged 220.6 g/kg. The HCY and CCY was higher ($P \leq 0.05$) for T3GU with 52.61 and 50.86% respectively. The results suggest that the use of fodder tree is an alternative for feeding Pelibuey sheep because they do not alter finishing performance and, at the same time, their use may decrease feeding costs. It is important to explore their effects on meat quality.

Key Words: sheep, tannins, performance

T94 Effects of tannin deactivation by alkaline chemicals on in vitro dry matter and organic matter digestibility in sainfoin (*Onobrychis vicifolia*). 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 ruminant animals is inherently variable and depends on many factors including antinutritional factors. 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 nutrient availability from sainfoin. Second cut forage was shade dried and chopped (3 –5 cm length). Forage samples (1 kg, in 3 replicates) were exposed to $KMnO_4$ (0.03 M) and NaOH (0.05 M) solutions and water with forage to reagent ratio of 1:4 (wt/vol). The pH of solutions were determined (12.28 and 12.04 for NaOH and $KMnO_4$, respectively). All of the treatments were carried out in triplicate, in 25°C temperature, for 20 min, with hand shaking. Treated forages were then exposed to 40°C temperature in a forced air oven, for 48 h. All forage samples were ground to pass 0.5 mm screen size (ball mill) for determination of CT concentration using Butanol-HCl reagent. Also grinding with 1 mm laboratory mill was done for in vitro digestibility trial. The in vitro digestion technique used was that of Tilley and Terry (1963) as modified by Wilkins (1966) in triplicates. Rumen liquor was withdrawn from 2 rumen-fistulated Holstein cows fed a balanced diet, exceeded maintenance requirements (CNCPS) in 2 equal meals. Rumen fluids were mixed and then squeezed through 4 layers of cheesecloth. Completely randomized design, GLM PROC of SAS and Duncan's test were used for data analysis ($P \leq 0.05$). Untreated forage have CT concentration of 21.3+0.4 g/kg dry matter, but both the chemicals and water reduced CT levels more than 90 percent. In contrast, treatments were failed to significantly affecting dry matter and organic matter digestibility. It seems that in vitro digestibility (Tilley and Terry) overestimates OM digestibility of untreated tanniferous forages. This effect was explained by rapid passing of phenols through filter paper that entered the digestible fraction. In vitro gas production technique may be a suitable substitute.

Table 1. Effect of treatments on CT content and in vitro digestibility of DM and OM (means ± SD, g/100 g)

Treatment	CT	DMD	OMD
Control	$2.13^a \pm 0.041$	75.6 ± 0.83	68.9 ± 1.24
NaOH	$0.13^c \pm 0.001$	75.7 ± 2.43	69.8 ± 1.53
$KMnO_4$	$0.16^b \pm 0.011$	75.2 ± 2.06	69.9 ± 2.02
Water	$0.17^b \pm 0.012$	76.7 ± 1.98	69.8 ± 2.74

[a–c]Means within each column with different superscript letters are statistically different ($P \leq 0.05$).

Key Words: sainfoin, tannin, digestibility

T95 Different rumen environments can cause different degradation profile of dry matter from tanniferous forages.

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Conventional in situ degradability methods have some problems in the case of tanniferous feeds because of small sample weight in nylon bags and dilution of antinutrients in rumen fluid. Thus we use another method to assess tannin effects on DM degradability in sainfoin. Second-cut sainfoin was dried and chopped (3–5cm length). Polyethylene glycol (PEG) solution in distilled water [6000 MW, 5% (wt/vol), volume to forage weight ratio of 1:1] and distilled water (volume to forage weight ratio of 4:1) were used to treat forage samples. Treatments were carried out at an ambient temperature for 20 min with hand shaking for water and overnight for PEG. Extractable condensed tannin content was determined using butanol-HCl reagent. An in situ experiment was done in 3 × 3 change-over design. Three ruminally fistulated Holstein cows (multiparous, 680 ± 20kg of BW) were used with 10 d for adaptation and 7 d for nylon bag incubation, each period. Forages were fed as sole diet (equals at 0800 and 1600) along with mineral/vitamins to meet 110% of the animal's maintenance requirements. CT content of untrated forage was 21.3, which water and PEG decreased it to 1.7 and 0.3 g/kg DM, respectively. Untreated Forage samples were ground to pass 2 mm screen (Wiley mill) and sieved to remove particles <50 µm. Five gram of samples weighed into nylon bags (10 × 20cm, 50 µm pore size) with sample size:surface area of 12.5 mg/cm^2. Duplicates were incubated for 4, 8, 12, 24, 48, 72 and 96h in ventral rumen. Degradation profiles were calculated by the nonlinear model of Ørskov and McDonald (1979). The effective degradability (ED) was calculated using NEWAY package. PROC MIXED of SAS 9.1 (2002) was used to statistical analysis at 0.05 probability level. Degradation rate increased from 0.0626^{b} (control) to 0.0751^{b} and 0.0961^{a} h^{-1} and lag time decreased from 2.4^{a} h (control) to 1.33^{b} and 0.8 ^{b} h for water and PEG, respectively (^{a} and ^{b} indicate statistical differences between treatments). PEG significantly increased ED from 52.43 to 55.9 and from 47.93 to 51.60 in outflow rates of 0.05 and 0.08 respectively (relative to control). We concluded that PEG and water treatments diminished phenolic compound effects on rumen environment and can increase nutrient availability in situ due to increased microbial activity and nutrient availability.

Key Words: sainfoin, degradability, tannin

T96 Comparisons of metabolizable energy estimates for sainfoin (*Onobrychis viciifolia*) from different in vitro and in vivo methods.

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Sainfoin (*Onobrychis viciifolia* is a non-bloating member of the Fabaceae family. Limitations in nutrient availability data, limited the inclusion of sainfoin in balanced rations. The aim of the present study was to determine and compare the ME content of sainfoin with different methods. Forages were taken from farms (6 farms, 4 samples from each) in Isfahan, Iran. Shade dried, baled and representative samples were obtained and cut into 30–50mm lengths. Chemical analysis were done according to AOAC standard methods. Condensed tannin content was determined by butanol-HCl reagent (21.3 g/kg DM). Hay samples were milled through 2 and 1mm sieves for gas production and Tilley and Terry, respectively. Forages were incubated with rumen fluid in glass syringes following the procedures of Menke et al. Twenty-four hour gas value (34.9 ± 1·03 mL) was used for ME determination using equation 1, ME = 2.2 + 0.1357 GP$_{24}$ + 0.0057 CP (g/kg DM) + 0.0002859 EE^2(g/kg DM) ; equation 2, ME = 2.2 + 0.136 GP$_{24}$ + 0.057 CP (g/100 g DM) + 0.0029 CP^2 (g/100 g DM) and indirectly by equations 3, OMD = 14.88 + 0.8893 GP$_{24}$ + 0.448 CP (g/100 g DM) + 0.0651ash (g/100 g DM) and 4,ME = 0.0157 × DOMD. The in vitro digestion technique used was that of Tilley and Terry (1963) as modified by Wilkins (1966) in triplicates. Three ruminally fistulated Holstein cows (multiparous, 680 ± 20 kg) were used in in vivo trial with 10 d for adaptation and 7 d for sample collection. Forages were used as the sole diet along with mineral/vitamins to achieve 10% more than maintenance energy requirements (NRC, 2001). Total fecal collection, acid insoluble ash (AIA) and chromium oxide were used for determination of OM digestibility. A comparison of means were undertaken using GLM procedure of SAS using a CRD design ($P \leq 0.05$). Organic matter digestibility was 59.23, 59.36, 60.41 and 68.90 for total fecal, Cr2O3, AIA and Tilley and Terry, respectively. The content of digestible organic matter (DOM) was 643.7 g/kg DM, and estimated ME, from Tilley and Terry trial was 10.11 MJ/kg DM. Gas production gave mean estimates of 7.19 MJ/kg DM and the mean of in vivo measurements was 8.75 MJ/kg DM (table1). The OM digestibility in Tilley and Terry method was higher than values determined by in vivo and gas production profiles. Higher OM digestibilities determined by a filtration-based method such as Tilley and Terry for high tanniferous materials, was explained by rapid passing of phenols through filter paper that entered the digestible fraction. Low sample size especially in tanniferous plants can affect gas production results. It seems that in vivo methods are the best for ME estimation in the case of forages with antinutrients.

Table 1. Organic matter digestibility and metabolizable energy estimates of sainfoin with different in vitro and in vivo methods

	Gas production			Tilley and Terry	Total fecal collection	Chromium oxide	AIA	SEM	Error df
	(Eq. 1)	(Eq. 2)	(Eq. 3 & 4)						
ME (MJ/kg DM)	7.87^{c}	8.04^{c}	7.59^{c}	10.11^{a}	8.69^{b}	8.71^{b}	8.86^{b}	0.222	12

$^{a–c}$Means with different superscript letters are statistically different ($P < 0.05$).

Key Words: sainfoin, metabolizable energy, gas test

T97 Deactivation of tannins by chemical materials affect ruminal degradability kinetics and metabolizable protein profiles of sainfoin (*Onobrychis vicifolia*).

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Sainfoin (*Onobrychis viciifolia* Scop.) is tanniferous legume forage. There are few reports about effects of tannin destructive or binding matter on metabolizable protein profile of sainfoin. Second cut forage was shade dried and chopped (3 –5 cm length), and then exposed to solutions of KMnO$_4$ (0.03 M, pH 12.04), NaOH (0.05 M, pH 12.28) and water with forage to reagent volume ratio of 1:4 (wt/vol). All of above treatments were carried out in triplicates, in 25°C temperature, for 20 min, with hand shaking. Treated forages were then exposed to 40°C temperature in a forced air oven, for 48 h. All forage samples were ground to pass 0.5 mm screen size (ball mill) for determinations of condensed (CT) concentrations using Butanol-HCl reagent. Also grinding with 2 mm laboratory mill was done for in situ trial. Crude protein degradability was determined using 3 ruminally fistulated Holstein cows. Samples (5 g) were weighed into nylon bags and duplicates were incubated for

4,8,12,24,48,72 and 96 in the ventral rumen. Effective degradability (ED) was calculated with NEWAY package. Degradation parameters then used to calculate QDP, SDP, RDP, ERDP, DUP, UDP and MP according to formula were presented by AFRC. GLM PROC of SAS and Duncan's Test were used for statistical analysis ($P \leq 0.05$). Control forage had CT concentration of 21.3+0.4 g/kg DM. Sodium hydroxide, KMnO4 and water decreased it by 93.79, 92.41, and 92.06%, respectively. Treatments increased degradability of sainfoin in all of the rumen incubation times (data not shown). Rapid degradable fraction increased with all of treatments. Slowly degradable fraction was not affected by treatments, but rate of degradation of this fraction significantly increased by water and NaOH. Also, treatments significantly improved effective degradability in different rumen outflow rates. All of the treatments improved protein metabolizability of sainfoin. Also, DUP (Digestible undegradable protein) /UDP (undegradable protein) ratio improved by water and $KMnO_4$. Despite that NaOH significantly reduced condensed tannins and improved degradability profiles, cannot increase metabolizable protein. This can be attributed to post ruminal behavior of NaOH treated proteins that reduced digestibility of undegraded protein content. Water as farm available material with no environmental hazard, greatly improved protein metabolism characteristics of sainfoin.

Table 1. Effects of tannin deactivation on MP fractions of sainfoin (g/100 g CP)

	QDP	SDP	RDP	ERDP	UDP	DUP	MP	DUP/ UDP (%)
Control	17.06^{d}	21.15^{b}	38.21^{c}	34.80^{c}	61.79^{a}	27.78^{b}	49.97^{b}	44.96^{b}
NaoH	40.04^{a}	25.26^{a}	65.30^{a}	56.97^{a}	34.70^{c}	12.39^{d}	48.90^{b}	35.77^{c}
Water	39.53^{b}	26.53^{a}	66.39^{a}	58.16^{a}	33.61^{c}	21.42^{c}	58.49^{a}	63.04^{a}
$KMnO_4$	31.78^{c}	16.72^{c}	48.49^{b}	42.14^{b}	51.51^{b}	32.66^{a}	59.51^{a}	63.33^{a}
SEM		1.44	1.49	1.43	1.46	1.29	0.38	1.29

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

Key Words: metabolizable protein, condensed tannin, sainfoin

T98 Correlations between condensed tannins and CNCPS protein fractions of sainfoin. 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.*

Cornell Net Carbohydrate and Protein System (CNCPS) is a growing feed evaluation and ration balancing system in the world but there are few reports about sainfoin. In this study we examine the effects of chemical tannin deactivation methods on CNCPS protein fractions of sainfoin. Also, correlations between condensed tannin (CT) content, acid detergent insoluble nitrogen, neutral detergent insoluble nitrogen, crude protein content, etc. were calculated. Samples of forage were chopped 3–5 cm length, and then treated with solutions of $KMnO_4$ (0.03 M), NaOH (0.05 M), sodium bicarbonate (0.1 M), wood ash (180 g/L) and water with forage to reagent volume ratio of 1:4 (wt/vol). Five percent solution of PEG (6000 MW) was sprayed to forage with 1:1 ratio. Treatment with urea (20 g/100 mL/1 kg of DM) was done using adhesive rubber to create anaerobic conditions for 1 week. All forage samples were ground to pass 0.5 mm screen size. Determinations of CT content of treated and control forages were done using butanol-HCl reagent. The CNCPS protein fractions of sainfoin, determined according to standardized procedure where the A fraction (non-protein N) was determined using TCA solution. Results are presented as percentage of CP. Data was analyzed by SAS using GLM procedure for a completely randomized design ($P \leq 0.05$). In untreated forage a large portion of crude protein was in the C fraction, which is unavailable for animal. This can be due to condensed tannin- protein complexes. Treatments were improved nutritional availability of protein by decreasing the C and increasing the A and B3 fractions. Reduction of antinutritional factors greatly changed protein fractions of sainfoin. For exampleb treatment with water was resulted in 34.2, 1.3, 37.2, 17.1 and 10.2 percentage for A, B_1, B_2, B_3 and C sections, respectively. These values for untreated and PEG treated forage were 16.8, 9.7, 28.6, 13.9, 30.9 and 16.6, 6.7, 52.4, 13.6, 10.6, respectively (other data not shown). Protein content of C fraction had highly positive correlation with CT, ADIN, and NDIN. Conversely, A fraction had negative correlation with this fractions. Correlation coefficients in Table 1 showed that we can attribute increasing in A fraction and reduction of C fraction in treated forages to reduction of CT.

Table 1. Correlation coefficients between CNCPS protein fractions and antinutritional factors in sainfoin

	A	B1	B2	B3	C
CT	−0.261^{NS}	0.262 ^{NS}	−0.367 ^{NS}	−0.153 ^{NS}	0.785***
CP	0.252 ^{NS}	0.359 ^{NS}	0.145 ^{NS}	- 0.309^{NS}	0.059^{NS}
NDF	0.417*	−0.072^{NS}	−0.093 ^{NS}	0.477*	0.064^{NS}
ADF	0.254^{NS}	0.152^{NS}	0.093 ^{NS}	0.225^{NS}	0.368^{NS}
NDIN	−0.361^{NS}	0.535**	−0.359^{NS}	0.310*	0.855***
ADIN	−0.503**	0.778***	−0.227^{NS}	−0.269^{NS}	0.952***

NS = nonsignificant; *$P \leq 0.05$; **$P \leq 0.01$; ***$P \leq 0.001$.

Key Words: CNCPS, sainfoin, antinutrients

T99 Local equations to predict relative feed value for alfalfa in northern Mexico. C. Arzola*[1], F. Carrera[1], R. Copado[1], J. Salinas[2], C. Rodriguez[1], O. Ruiz[1], H. Gaytan[1], and A. Corral[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Chihuahua, Mexico, [2]Universidad Autonoma de Tamaulipas, Cd. Victoria, Tamaulipas, Mexico.*

Knowing the chemical makeup of alfalfa in the field allows dairy producers to pick up the best time to harvest and determine the price of the crop. The use of wet chemistry is time-consuming, so alternative methods such as the predictive equations of alfalfa quality (PEAQ) have been used. Using samples of alfalfa of 15 farms located in the region of Delicias, Chihuahua, Mexico, planted with either one of 2 varieties of alfalfa (excellent or multileaf excellent), local equations (LE) were developed, on the assumption that such equations should reflect more accurately the relationship of ADF and NDF composition to stem length and phenologic stage than equations from PEAQ. Sampling was conducted during one year of alfalfa production on 113 locations, starting at the end of February and ending in late October. Those equations were calculated for each variety and for the whole group (Table 1). Relative feed values (RFV) were calculated with ADF and NDF values obtained with laboratory analyses (LV), LE equations (both varieties and whole group) and PEAQ equations. No additional advantage in terms of accuracy ($P < 0.05$) was obtained when comparing values from equations for separate varieties or the whole group. Calculated values for both ADF and NDF using those obtained with LE were more accurate than those of PEAQ as compared with the laboratory values (LV), but RFV was better estimated with PEAQ than with LE (203, 196 and 198 for LV, LE and PEAQ respectively). Such contradictory response is due to the fact that LE equations rendered lower values for ADF than LV values (21.92 vs 22.03) whereas PEAQ rendered higher values than ¨true¨ values (LV) (24.58 vs 22.03). A general conclusion is that the use of LE does not have advantage over PEAQ

Table 1. Local predictive equations of alfalfa quality

	Whole Group	R^2
ADF	Y =7.095+(0.23*SL)+(0.843*PS)	0.4783
NDF	Y = 11.887+(.276*SL)+(3.290 *PS)	0.5369
	Excellent Variety	
ADF	Y = 7.84+(O.217*SL)+(0.851*PS)	0.4597
NDF	Y = 12.908+(0.268*SL)+(3.081*PS)	0.4947
	Multileaf Excellent Variety	
ADF	Y = 2.162+(0.315*SL)+(0.264*PS)	0.6226
NDF	Y = 5.653+(0.353*SL)+(3.841*PS)	0.8235

SL = stem length in cm; PS = phenologic stage.

Key Words: alfalfa, local equations, RFV

T100 A simplified procedure for measuring NDF within in situ Dacron bags for corn plant components ground to 6 mm. L. J. Nuzback, W. M. Rutherford, and F. N. Owens,* *Pioneer Hi-Bred International, a DuPont Company, Johnston, IA.*

Direct assays of NDF within in situ bags could simplify measurement of in situ NDF disappearance by avoiding re-grinding, compositing, and repackaging of in situ residues for NDF analysis. We compared estimates of NDF using samples ground to 6 mm in 50 micron bags (ONDF) with measured aNDF (samples ground at 1 mm in F-57 bags) using 2 sample sets — 288 samples (whole corn plants plus plant parts) and 90 whole plant corn samples (11 hybrids harvested between 22 and 50% DM). For ONDF analysis, 4 replicate 0.5 g samples of each feedstuff ground to 6 mm in 50 micron Dacron bags (5 by 5 cm) were extracted using automated aNDF procedures (Ankom Technology, Macedon, NY). Residue weights were compared with aNDF values from a lab certified by the NFTA. For the first sample set, ONDF closely matched aNDF ($\text{ONDF} = 1.089 \pm 0.19 \times \text{aNDF} - 5.77 \pm 1.17$; $R^2 = 0.92$; root MSE 4.0) but deviations from regression ($P < 0.05$) were detected in 2 cases. For corn cobs, ONDF exceeded aNDF by 4.4%, presumably reflecting wash loss of finely ground particles. For whole plant samples, ONDF exceeded aNDF by 3.6 and 4.2% in the 2 sample sets. This difference was negatively ($P < 0.001$) related to hemicellulose content of samples and may reflect either particle loss from finely ground samples or incomplete NDF extraction from coarsely ground samples. Though the absolute values differed slightly, correlations between ONDF and aNDF values were sufficiently high ($R^2 > 0.91$) to reliably rank samples and detect differences in NDF content of samples. Direct comparison of 48 h ruminal disappearance with 4 corn silage samples (54 to 68% in situ NDF disappearance) revealed similar means (56.7% in situ ONDF versus 56.4 in situ aNDF) and a high correlation ($R^2 = 0.87$). Through avoiding the needs for sample transfer, compiling multiple residues, and grinding, this modified procedure can simplify measurement of in situ NDF disappearance.

Key Words: NDF, in situ, digestibility

T101 Digestibility and fecal output prediction using acid-detergent lignin, alkaline-peroxide lignin, and acid-detergent insoluble ash in cattle offered bermudagrass hays of varying quality. J. Kanani*[1], D. Philipp[1], K. P. Coffey[1], E. B. Kegley[1], C. P. West[1], S. Gadberry[2], J. Jennings[2], A. Young[1], and R. Rhein[1], *[1]University of Arkansas, Division of Agriculture, Fayetteville, [2]University of Arkansas, Division of Agriculture, Little Rock.*

The potential of acid-detergent insoluble ash (ADIA), alkaline-peroxide lignin (APL), and ADL to predict DM digestibility (DMD) and fecal output (FO) by cattle offered bermudagrass [*Cynodon dactylon* (L.) Pers.] hay of different qualities was evaluated. Eight ruminally cannulated cows (594 ± 100.3 kg) were allocated randomly to 4 bermudagrass hay diets categorized by their low (L), medium low (ML), medium high (MH), or high (H) CP concentrations (7.9, 11.0, 13.0, and 16.4% DM, respectively). Diets were offered in 3 periods to provide 2 replicates per diet per period ($n = 24$). Cows were individually offered hay at a total of 2% of BW in equal feedings at 0800 and 1700 for a 10-d adaptation followed by a 5-d total fecal collection (TC) each period. Hay, orts, and feces were analyzed for ADL, APL, and ADIA concentrations. Actual DMI, DMD, and FO were determined based on hay offered, orts, and feces excreted. Recovery of APL, ADL, and ADIA were expressed as the ratio of the quantity of marker excreted per unit of marker consumed on percentage basis. Data for in vivo DMI, DMD, and FO were analyzed as a replicated 4 × 4 Latin square with one period missing using PROC GLM of SAS, with effects of cow, diet, and period in the model. Data for ADL, APL, and ADIA recovery and marker-based estimates of DMD and FO were analyzed using PROC GLM of SAS, where diet, marker, and the diet by marker interaction were included in the model. Diet affected actual DMI ($P = 0.02$), but not FO ($P = 0.16$), or apparent DMD ($P = 0.23$). Average ADL recovery differed from 100% ($P < 0.05$), and that of APL tended to differ ($P = 0.08$) from 100%, but ADIA recovery was not different from 100% ($P = 0.41$). Estimates of DMD and FO derived using APL and ADIA were not different ($P \geq 0.32$) from TC while those using ADL differed ($P < 0.05$) from that of TC. Therefore, ADIA and APL are potential internal markers to predict DMD and FO of bermudagrass of various qualities fed to cattle.

Key Words: acid-detergent insoluble ash, alkaline-peroxide lignin, bermudagrass digestibility

T102 Diurnal variation in fecal concentrations of indigestible-acid detergent fiber, acid-detergent insoluble ash, and alkaline-peroxide lignin from cattle offered bermudagrass hays of varying quality. J. Kanani*[1], D. Philipp[1], K. P. Coffey[1], E. B. Kegley[1], C. P. West[1], S. Gadberry[2], J. Jennings[2], A. Young[1], and R. Rhein[1], *[1]University of Arkansas, Division of Agriculture, Fayetteville, [2]University of Arkansas, Division of Agriculture, Little Rock.*

The effect of time of fecal sampling on the accuracy of indigestible acid-detergent fiber (IADF), acid-detergent insoluble ash (ADIA), and alkaline-peroxide lignin (APL) for the prediction of fecal output (FO) in cattle fed bermudagrass was evaluated. Eight ruminally cannulated cows (594 ± 100.3 kg) were allocated randomly to 4 bermudagrass hay diets having a wide range of nutritional value (CP content of 7.9 to 16.4% DM) providing 2 replicates per diet for 3 periods ($n = 24$). Cows were individually fed their respective hay at a total of 2% of BW in equal feedings at 0800 and 1700 for a 10-d adaptation period followed by a 5-d total fecal collection (TC) period in 2.7 × 4.3-m pens fitted with rubber mats. Fecal grab samples were taken each day of the fecal collection period at 0600, 1200, 1800, and 2400 either directly from the rectum or from fresh feces, and were composited by cow and time. Duplicate samples of each hay, ort, and fecal sample were incubated for 144 h in the rumen of 2 cows for each period ($n = 6$ cows), followed by a sequential analysis of NDF and ADF to obtain IADF. Additionally, forage, ort, and fecal samples were analyzed for concentrations of APL and ADIA. Time of sampling affected the concentration of IADF ($P < 0.01$) while ADIA and APL concentrations in fecal grab samples were not different ($P \geq 0.24$) across sampling times or from that in total feces. Estimates of DMD by a representative sample from TC and that from all grab sampling times and their different combinations were not different ($P \geq 0.46$) from actual DMD regardless of which internal marker was used. Also, FO estimated by in vivo, samples from TC, or samples from different sampling times, and all different combinations of sampling time were not different ($P \geq 0.22$) across internal markers. Therefore, there is little variation in concentrations of ADIA and APL in daily fecal excretion and a minimum of 2 fecal grab samplings daily can be used in the prediction of DMD and FO.

Key Words: bermudagrass digestibility, fecal sampling time, internal markers

T103 Evaluating particle size of dry and wet forages using the Ro-Tap separator and Penn State Particle Size Separator method. A. D. Kmicikewycz,* D. D. Maulfair, and A. J. Heinrichs, *Pennsylvania State University, University Park.*

Adequate particle length of forages is an important part of a total ration feeding program and is necessary for proper rumen function. There has been considerable effort exerted to developing laboratory and field-based particle sizing techniques that accurately determine particle size (PS) distribution. The objective of this experiment was to compare 3 different methods used by various laboratories to analyze PS distributions of samples of corn silage (CS) and haylage (H). Method 1 involved utilizing the Ro-Tap separator (W. S. Tyler, Mentor, OH) in determining dry CS and H PS. Method 2 utilized the Penn State Particle Size Separator (PSPS; NASCO, Inc. Fort Atkinson, WI) in determining the PS of wet samples of CS and H. Lastly, method 3 utilized the PSPS in determining the PS of dry samples of CS and H. Three replicates were evaluated for each sample, and the log of the mean cumulative percentage for each sieve was analyzed using GLM procedure in SAS. The 3 methods produced different PS distributions for both CS and H ($P < 0.01$), evidenced by differences in the slope of the distributions. The percentage of particles ≥1.18 mm was determined to be 89.8%, 98%, and 92% for CS and 81.4%, 96.9%, and 89.9% for H for method 1, 2, and 3 respectively. Each system of particle sizing of forages yields a different distribution, and results from different methods are not interchangeable.

Key Words: particle size, forage, analysis

T104 In vitro evaluation of *Miscanthus sacchariflorus* var. as a roughage source for ruminants. S. J. Oh,* J. H. Yang, A. R. Lee, C. H. Ryu, J. H. Lim, S. B. Cho, and N. J. Choi, *Department of Animal Science, Chonbuk National University, Jeonju, Korea.*

This study was conducted to evaluate newly developed germtype *Miscanthus sacchariflorus* var. as a roughage for ruminants. *Miscanthus* has been regarded as an environment friend and carbon neutral plant because it does not require nitrogen fertilizer during its growth. *Miscanthus* has been extensively researched in various industry areas such as paper, energy, building materials, and geotextiles, but there are few studies concerning *Miscanthus* as feed for ruminants. In this study, *Miscanthus* from 2 stages of growth (mid and late) was evaluated using in vitro rumen fermentation and rice straw was used as a reference roughage. So, 3 different roughage sources were used to examine their effect on rumen fermentation. All of experiment was conducted in triplicates with same rumen fluid and in vitro fermentative condition, and the results were analyzed using general linear model with SPSS program In vitro rumen fermentation was prepared with rumen fluid from a Korean native steer equipped with cannula. Total gas production, volatile fatty acid production, pH and ammonia nitrogen concentration were investigated during fermentation until 72 h. In acetic acid production, *Miscanthus* in mid growth stages (MM) showed similar patterns with that of rice straw (RS) but *Miscanthus* in late growth stage (ML) was significantly lower than RS ($P < 0.05$). The propionic acid production in RS was significantly higher than *Miscanthus* regardless of growth stages ($P < 0.05$). In butyric acid production, iso-butyrate production in MM was significantly higher than RS, particularly in 72 h of fermentation ($P < 0.05$). Valeric acid production patterns showed similar with butyric acid production across treatments. In pH profiles, MM showed significantly higher than RS ($P < 0.05$). No difference was found in ammonia nitrogen production between MM and RS but that of ML was significantly lower than MM and RS ($P < 0.05$). Total gas production from MM and RS showed same each other but total gas in ML was significantly low ($P < 0.05$). As a result, *Miscanthus* in mid growth stage could be replaced with RS as roughage for ruminants.

Key Words: *Miscanthus sacchariflorus*, roughage, ruminant

T105 Relationship between dynamic degradation and 48-hour degradation of alfalfa hay in Holstein heifers. Y. Tian*[1], Z. Cao[1], S. Li[1], and S. Yan[2], [1]*State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China,* [2]*College of Animal Science, Inner Mongolia Agricultural University, Huhhot, China.*

The objective of this study was to determine the relationship between dynamic degradation and 48 h degradation of alfalfa hay in Holstein heifers. Four Chinese Holstein heifers of average weight 600 ± 30 kg fitted with ruminal cannula were selected. Alfalfa hay samples (n = 9) were incubated in the rumen for 4, 8, 16, 24, 36, 48 and 72h by in situ nylon bag technique. The diet was formulated at a 4:6 (DM basis) concentrate to forage ratio according to 1.3 × maintenance nutrients level. Data were analyzed by ANOVA and Regression analysis procedures (SAS 9.0). The results showed that the Crude protein (CP) degradation rate after 16 h tended to be stable ($P = 0.08$), and degradation rate of DM ($P = 0.08$), NDF (Neutral Detergent Fiber, NDF) ($P = 0.06$) and ADF (Acid Detergent Fiber, NDF) ($P = 0.09$) after 24 h tended to be stable. There was significant correlation between nutrient effective degradation rate and the degradation rate at 48 h in Holstein heifers ($P < 0.001$) (Table 1). In summary, the degradation rate at 48 h for alfalfa hay can be used to predict effective degradation rate.

Table 1. Regression analysis between effective degradation and degradation at 48 h of alfalfa[1]

Index	Regression Equation	R^2	*P*-value
DM	y = 0.804x+1.990	0.978	<0.001
CP	y = 0.898x-4.645	0.995	<0.001
NDF	y = 0.767x-1.964	0.927	<0.001
ADF	y = 1.050x-12.346	0.929	<0.001

[1]Where y = representative effective degradation rate, x = 48-h degradation rate, $P < 0.05$ showed significant difference.

Key Words: alfalfa hay, degradation

T106 In vitro organic matter and nitrogen disappearance of Kenyan browse using rumen from goats ingesting grass versus browse. A. McEwin*[1], C. Wambui[3], J. P. Muir[2], J. Githiori[4], and B. D. Lambert[1,2], [1]*Tarleton State University, Stephenville, TX,* [2]*Texas Agrilife Research, Stephenville,* [3]*Edgerton University, Kenya,* [4]*International Livestock Research Institute, Kenya.*

In vitro organic matter disappearances (IVOMD) of browse species are often thought to be artificially low because of the presence of secondary plant compounds such as condensed tannins (CT). This project investigated how the diet of the wether donating the rumen fluid affected (IVOMD) and in vitro nitrogen disappearance (IVND) results of 11 Kenyan browse species with CT concentrations ranging from 0.2 to 11.9%. The trial consisted of comparing IVOMD and IVND using rumen liquor donated from ruminally cannulated goats that were either fed a Bermudagrass hay diet (no CT) or were allowed to graze freely on natural Texas browse (high CT levels). For 7 of the species, leaf IVOMD was greater ($P < 0.05$) for samples incubated in rumen liquor of goats fed hay but there were no differences ($P > 0.05$) for 2 species without CT or 3 species with CT. Nitrogen in vitro disappearance (as a proportion of the original N) was greater ($P < 0.05$) for 3 species when hay was fed the donor animal, greater 4 species when browse was used, and made no difference ($P > 0.05$) in 4 species, including those without CT. No consistent pattern was discernible between CT concentration and proportion of N disappearing in vitro. These results suggest that when looking IVMD and IVND in browse species that contain secondary compounds, which may interfere with rumen microorganisms, the diet of the rumen fluid donors sometimes but not always make a difference. Further research in needed into determining what factors in the CT or additional factors beyond CT produce differences in IVOMD and IVND.

Key Words: condensed tannins, organic matter disappearances, ruminant

T107 Chemical composition and in vitro gas production of mulberry (*Morus alba* sp.) leaves during regrowth. R. A. Gomes[1], M. H. M. R. Fernandes*[1], I. A. M. A. Teixeira[1], K. T. Resende[1], R. A. Reis[1], F. S. B. Rey[2], and D. C. Soares[1], [1]*UNESP/Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil,* [2]*Faculdade de Medicina Veterinaria e Zootecnia/USP, Pirassununga, Sao Paulo, Brazil.*

Mulberry (*Morus* spp.) is the traditional feed for the silk worm, but its leaves have been widely used as feed for herbivorous animals in several countries, from the temperate areas through the tropics. An experiment was carried out to evaluate in vitro ruminal degradation and to chemically characterize fractions of mulberry leaves harvested at 30, 60, 90, and 120 d of regrowth. Four CHO fractions (A = nonstarch nonfiber CHO, B1 = nonfiber CHO minus sugar; B2 = available fiber and C = indigestible fiber) and 4 CP fractions (A = nonprotein N, B1+B2 = true rapidly and intermediate degraded protein, B3 = slowly degraded protein and C = unavailable protein) were evaluated according to their fermentation characteristics. Incubations were conducted in gas-tight bottles, and the gases accumulated were measured by a pressure transducer. Gas production was recorded from 2 to 124 h, every 2 h. Data were fitted to a modified dual pool logistic equation with a single pool using NLIN procedure of SAS. Polynomial contrasts were used to determine days of regrowth effects. Mulberry leaves had high crude protein (201 ± 5g/kg DM) and high potential of gas production (255 ± 20mL/g DM). Leaves B2(108 to 146 g/kg DM) and C (90 to 108 g/kg DM) carbohydrate fractions increased linearly ($P < 0.05$), and CP (224 to 191 g/kg DM) and degradation rate of non-structural carbohydrates (17 to 8%) decreased linearly ($P < 0.05$) as days of regrowth increased from 30 to 120 d. There was no effect of days of regrowth on leaves CHO fractions A (148 ± 10 g/kg DM) and B1 (280 ± 15 g/kg DM), and protein fractions B1+B2 (49 ± 4 g/kg DM), B3 (48 ± 3 g/kg DM) and C (22 ± 2 g/kg DM), in vitro organic matter digestibility (65 ± 3%) and total gas production ($P > 0.05$). A high proportion of protein fractions A and B1+B2 (up to 62%) relative to the total CP was observed. We concluded that mulberry is a good quality forager, and could be recommended as a protein supplement in ruminant diets based on poor quality forages.

Key Words: carbohydrate, in vitro gas production, protein

T108 Methane-generating potential of *Lotus subbiflorus* 'El Rincón' (LR) and *Lotus uliginosus var. Maku* (LM) harvested in spring. M. de J. Marichal*[1], R. Crespi[1], G. Arias[1], S. Furtado[1], M. H. Guerra[1], and L. Piaggio[2], [1]*Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay,* [2]*Secretariado Uruguayo de la Lana, Montevideo, Uruguay.*

The objective of this study was to evaluate the methane generating potential of forage of *Lotus subbiflorus* 'El Rincón' (LR) and *Lotus uliginosus var. Maku* (LM). Three replicate plots (2 × 2 m) of each Lotus were seeded in August at the Experimental Research Center of the Secretariado Uruguayo de la Lana (S 33° 52·, W 55° 34·). In October, forages were first harvested (plant heights 20 ± 5cm) at ground level using a manual scissor, dried at 60°C (48 h), ground (2 mm screen) and analyzed for NDF, ADF and H_2SO_4 soluble lignin (Lig$_{sa}$). An in vitro gas production procedure was followed using rumen contents of 2 fistulated whethers fed alfalfa hay (17 and 45% CP and NDF, respectively). Rumen contents were collected 2 h after morning feed (alfalfa hay, 1.6 kg DM w^{1}d^1, twice daily), in preheated (39°C) bottles, pooled and blended (less than 1 min) and strained using 4 layers of gauze all maintained at 39°C under CO_2. Samples (500 mg, milled 2 mm) were weighed into 125 mL serum bottles, mixed with ruminal fluid (10mL), and buffer solution (40 mL) and reducing solution (2 mL) of Goering and Van Soest, at 39°C under CO_2. Three batches of 24 of bottles (in each batch 3 bottles by experimental forage and replicate, 3 with alfalfa as standard, and 3 blanks) were incubated (water bath, 39{oC, continuous stirring) for 24 h. Gas was collected at 8 h, and from 8 to 24 hs of incubation in separated bottles and methane in accumulated gas was measured by gas chromatography. Methane production at 8, 8 to 24 and overall 24 h and fiber fractions were analyzed in a complete randomized design (PROC GLM, SAS; Tukey test). Fiber fractions were similar ($P > 0.20$) for both species (47.8 and 44.4; 36.3 and 31.2, and 20.1 and 17.1% NDF, ADF and Lig$_{sa}$, respectively). In gas accumulated up to 8 h, methane production from LR was greater ($P = 0.01$) than for LM (9.2 and 7.6 mg CH4 g OM^1, respectively); however, no differences $P > 0.30$) were registered neither in gas accumulated from 8 to 24 h (10.8 and 10.9 mg CH4 g OM^1, respectively) nor in overall 24h (20.1 and 18.5 mg CH4 g OM^1, respectively) methane production. Both species seemed to be similar in their support of ruminal methane production.

Key Words: methane, *Lotus subbiflorus*, *Lotus uliginosus*

T109 Factors affecting in vitro undigested NDF as estimates of indigestible NDF. D. R. Mertens*[1], D. Taysom[2], and B. Steinlicht[2], [1]*Mertens Innovation & Research LLC, Belleville, WI,* [2]*Dairyland Laboratories Inc., Arcadia, WI.*

Objectives were to evaluate the effects of run (1 vs 2), time (120 vs 262h), single vs double inoculations, blank-correction (bc), ash-correction (om) and substrates on in vitro undigested NDF (uNDF) as estimates of indigestible NDF. Two sources of wheat straw (WS), corn silage (CS), alfalfa haylage (AH), grass hay (GH) and distiller's grains (DG) were fermented in flasks using the method of Goering and Van Soest (1970) with the modification that a composite inoculum containing strained ruminal fluid and blended ruminal solids from 3 steers was used. Donors were fed a TMR (12% CP, 43% aNDF and 18% starch - DM basis). The 262h fermentation was inoculated at 0h (262S), or 0 and 120h (262D), and the 120h fermentation was inoculated at 0h (120S). Two replicates (0.5g) were fermented in each of 2 in vitro runs that were 39d apart. Residues were extracted in neutral detergent with amylase and sulfite and were collected in crucibles with Whatman GF/C filters. Results were analyzed using mixed models with replicate-within-run as a random effect. Blanks were typically greater than zero, and differed by run, time and inoculation ($P < 0.01$). As a fraction of DM, uNDFbc at 262S varied from 0.034 for DG to 0.362 for WS. Blank corrections were large compared with the small uNDF residues of DG yielding erratic results. Results for WS, CS, AH and GH were pooled to evaluate factors affecting uNDF. All uNDF at 120h were larger than those measured at 262S or 262D ($P < 0.0002$). Both uNDF and uNDFom were larger for 262D compared with 262S ($P < 0.0001$). When blank-corrected, uNDFbc ($P = 0.34$) and uNDFombc ($P = 0.27$) were not different between 262D and 262S. Runs differed for all measures of uNDF ($P < 0.04$), while replicates within run did not ($P < 0.63$). Extending fermentation from 120 to 262h reduced uNDF by 5 to 15%; however double inoculation provided minimal reduction. The SEs of LSMeans were lower for 120S and for ash-corrected uNDF. We concluded that blank-correction was critical for the measurement of uNDF and that at least 3 blanks are needed per run. For robust results, uNDF should be replicated across rather than within runs.

Key Words: indigestible NDF, fiber, forage evaluation

T110 Intensive milk production on marandugrass pasture during the rainy season.

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The efficient exploitation of the potential forage production of tropical grasses can bring a great benefit to the producer. Besides the increase in production per area, it is possible to increase the area required to produce forage for the dry season. The objective of this study was to assess milk production, per cow and per hectare, in pasture of *Brachiaria brizantha* 'Marandu' managed under rotational stocking with a fixed rest period of 30 d or variable according to the light interception (LI) of 95% by the canopy. In both treatments, the grazing period was 3 d with 4 Holstein × Zebu cows per paddock. The average size of paddocks was 850 m^2. Assessments were made in summer-autumn period of 2010–2011, considering 5 grazing cycles. The experimental design was randomized blocks with 2 repetitions of the area. To evaluate the milk production each cow was considered as a repeat. Data were analyzed as repeated measures (grazing cycles) using the Mixed Procedure of SAS. Means were estimated using the "LSMEANS" command and comparisons made with Student *t*-test with a 10% significance level. The average milk production per cow did not differ between treatments with values of 15.3 and 14.6 L/day, respectively, for fixed and variable (LI) management. The average daily production decreased in response to grazing periods, from 15.8 to 13.8 respectively for the first and fifth cycle. The average rest period observed was 25.2 and 30 d for the treatment based on light interception and fixed interval, respectively. Consequently, the estimate of the stocking rate shows values of 5.1 and 4.1 cow/ha, representing an increase of 24% in favor of the management based on LI. Thus, the daily milk production per hectare has increased from 63.4 to 73.6 L in response to management that is based on pasture growth and not on pre-defined intervals. These results could be even better considering that in this year there was a long period without rain (38 d). Evaluations of the first year of study (2009–2010) showed an average rest period of 21 d for the management based on canopy light interception. Just as the production per cow, daily production per hectare decreased from 72.3 to 63.0 L in response to the grazing cycles. This reduction is due, in part, to the advancement of the growing season and reduced pasture growth factors. Support: FAPEMIG and CNPq.

Key Words: grazing cycles, light interception, rest period

T111 Nutrient digestibility of annual winter forages using different indigestible markers and fecal collection schedules in growing beef heifers.

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Twelve Angus and Angus-crossbred heifers (364 ± 52 kg of BW) were used to determine the effects of indigestible markers and fecal sample collection schedules on apparent total tract digestibility of nutrients in 3 annual winter forages. The study was conducted at the University of Florida Feed Efficiency Facility (FEF). Winter forages consisted of ryegrass, a blend of ryegrass and Trical 342 triticale, and a blend of oat and ryegrass planted in 0.7-Ha paddocks. On d 0 heifers were randomly assigned to their forage treatments and allowed to graze for 28 d. On d 29 heifers were moved to the FEF (2 heifers/pen) and from d 29 to 44 were offered daily fresh cuts of the same forages. Individual intake was monitored in the FEF using a GrowSafe system (GrowSafe Systems Ltd., Alberta, Canada). From d 29 to 44, heifers received 10 g/d of Cr_2O_3 and 10 g/d of TiO_2 via a gelatin capsule and a balling gun. Feed and fecal samples were collected from d 39 to 43 and 40 to 44, respectively. Fecal samples were collected by rectal grab at 0800, 1200 and 1600 h, and composited within heifer using 2 samples/d (2s; 0800 and 1600 h only) or 3 samples/d (3s; all samples). Data were analyzed as a split-split plot design with the whole plot testing forage treatment effect, the split plot testing the fecal collection schedule (2s vs. 3s) and the split-split plot testing the marker (Cr_2O_3 vs. TiO_2) using heifer as the experimental unit. No effect of treatment was found ($P > 0.05$) for DM, OM, NDF or ADF digestibility of winter forages. Across forage treatments, mean apparent nutrient digestibility in the total tract were 59 ± 5.9%, 62 ± 5.8%, 48 ± 9.9%, and 27 ± 14.7% for DM, OM, NDF, and ADF, respectively. No effect of marker, sampling schedule, or marker x sampling schedule interaction was found for nutrient digestibility ($P > 0.05$). In conclusion, collecting fecal samples at 0800 and 1600 h was sufficient for measuring digestibility in winter forages. Both Cr_2O_3 and TiO_2 may be used indistinctively to estimate digestibility of winter forages, however standard errors of the mean reported, especially for digestibility of fiber fractions may be of concern. The use of digestibility markers that associate more intimately with the forage (e.g., internal markers) should be tested in future studies.

Key Words: digestibility, winter forages, markers

T112 Estimating crude protein and fiber contents in Tifton-85 bermudagrass swards with a new portable chlorophyll meter.

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Traditional methods for determining the nutritional value are costly and time consuming, so several indirect methods are under study. This study aimed to evaluate the performance of a new model of portable chlorophyll meter as a fast and inexpensive procedure for the assessment of nutritional attributes of Tifton 85 bermudagrass (*Cynodon* spp. 'Tifton 85'). Data were obtained from a field trial where treatments consisted of 3 levels of soil N availability: low (native soil N); medium (75 kg N/ha/cutting), and high (150 kg N/ha/cutting). Measurements were performed in 2 successive regrowth periods, with duration of 28 and 29 d, respectively, in the rainy season. Chlorophyll meter readings (FCI values - Falker chlorophyll index) were taken in the uppermost fully expanded leaf. Correlation analysis showed significant relationships between FCI values and acetone 80% extractable–total chlorophyll ($r = 0.83$; $P < 0.0001$); crude protein (CP) contents that oscillated between

100.2 and 183.5 g/kg DM also showed significant relationships (r = 0.85; $P < 0.0001$); neutral detergent fiber (NDF) and acid detergent fiber (ADF) contents whereas lignin contents did not showed consistent associations. Crude protein contents were determined from N-Kjeldahl analysis, and the NDF, ADF and lignins by the method of Van Soest et al. (1991), in dried and ground samples. The results obtained were first subjected to standard normal distribution tests and after processed for variance analysis (F test, $P \leq 0,05$). The averages were compared through SNK test (a = 0,05) for the N variables and cut period, respectively. The programs used for data analysis were SAEG v.9.1 (UFV, 2007) and Graph Prism 5.0. Taken together, these preliminary results showed the feasibility of using this new chlorophyll meter to predict CP and ADF contents in Tifton 85 bermudagrass. However, there is need of more research to validate the use of a chlorophyll meter with other fibrous fractions.

Key Words: *Cynodon* spp., total chlorophyll, fibrous fractions

T113 Mixed silage of potato residue and corn straw affects growth performance and blood biochemical parameters in mutton sheep.

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This study was conducted to determine the effects of mixed silage with potato residue and corn straw on growth performance and blood biochemical parameters in mutton sheep. A total of 40 healthy White-Suffolk cross sheep within initial body weight (47.45 ± 6.38 kg) were randomly allocated into 4 treatments with 10 replicates per treatment and 1 sheep per replicate. The feeding trial lasted for 70 d. Four treatments included: 1) control group(Ctrl), 40% basal diet + 60% corn silage; 2) test group 1 (S25), 40% basal diet + 45% corn silage + 15% mixed silage; 3) test group 2 (S50), 40% basal diet + 30% corn silage + 30% mixed silage; 4) test group 3 (S75), 40% basal diet + 15% corn silage + 45% mixed silage. Data were analyzed using MIXED procedures of SAS (SAS Institute, 2001). The ADG of S75 group was increased by 14.29% compared with Ctrl group ($P < 0.05$). There was no difference in the dry matter intake (DMI) ($P > 0.05$). The ammonia-N content in S25, S50 and S75 groups was significantly lower than that in Ctrl group by 18.92% ($P < 0.01$), 30.17% ($P < 0.01$) and 33.03% ($P < 0.01$), respectively. No remarkable differences were observed in acetate content, propionate content, butyrate content, acetate percentage, propionate percentage, butyrate percentage, the ratio of acetate to propionate and the ratio of acetate to propionate and butyrate ($P > 0.05$). There was no significant difference in serum total protein ($P > 0.05$). On the sixtieth day of the trial, serum urea nitrogen content was greater in S25 and S75 groups than that in S50 and Ctrl group($P < 0.05$) and serum glucose contents of S75 group was improved compared with the other 3 groups ($P < 0.05$). In conclusion, the mixed silage with potato residue and corn straw can increase ADG, serum urea nitrogen content, serum glucose contents and decrease the ammonia-N content of mutton sheep. Therefore, the study suggests that the mixed silage with potato residue and corn straw can account for 75% of corn silage in the mutton sheep diet.

Key Words: potato residue, fermentation quality, blood biochemical parameters

T114 Effect of different fat protected sources on milk yield and composition in goats fed on corn silage as based diet in dairy goats.

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High quality milk and dairy products are nutritious and healthy foods that are frequently consumed by people who desire healthy products. In ruminant, fats are the major source of CLA in the human food. Canola and Safflower oil has the highest source of polyunsaturated fatty acids (PUFA) than that found in any other type of vegetable oil (i.e., almost 79% PUFA). The available evidence suggested that increase the intake of 18:2n-6 in high-forage diets could be used as a nutritional strategy for enhancing the supply of *cis*-9,*trans*-11-CLA available for absorption. The objective of the present study was to determine the milk yield and milk composition in dairy goats, supplemented with different fat protected sources, Canola calcium soap (CS), Safflower calcium soap (SFS) or lactomilk (LM) rich in 16:0 fatty acid. Three lactating dairy French alpine goats (BW 54 ± 2 Kg) in 3 × 3 Latin square design were used. Goats were housed in an individual metabolic cages, and fed at 0800 and 1600 h, with free water access and milked daily at 0800 h. Diets (14% CP, 2.8 Mcal MEm) were formulated with corn maize silage ad libitum, supplemented with a concentrate based on corn grain (50%), barley hay (21%), soybean meal (20%) and minerals (3%) plus one fat protected source (6%). Each 20 d as experimental period consisted for 14 d for adaptation and ended with 6 d of samples collection. Individual intake and daily milk yield were recorded daily. Milk fat, true protein, SNF, was determined for infrared Milko-Scan 133B analyzer® (Foss Electric, Hillerød, Denmark). Data of each period was analyzed using proc GLM in SAS; LS means are reported in Table 1. Milk yield was higher ($P = 0.009$) in SFS versus with CS and LM, while fat content (g/d) was lower ($P = 0.001$) in CS versus SFS and LM; and true protein content (g/d) was also higher ($P = 0.003$) in SFS followed by LM and CS. Total solids and SNF (g/d) was higher ($P = 0.005$) in SFS compared with the other treatments. According to the present study SFS treatment increase milk yield and chemical composition versus CS and LM.

Table 1. Effect of different fat protected sources on milk yield (kg/d) and composition (g/d, %) in dairy goats

Item	CS	SFS	LM	SEM	*P*-value
Milk yield (kg/d)	0.949^a	1.105^b	0.883^a	0.87	0.009
Fat (g/d)	32.3^a	35.0^b	34.3^b	0.56	0.002
Fat (%)	3.5^b	3.3^b	4.1^a	0.52	0.001
True protein (g/d)	29.8^a	37.7^b	34.6^c	0.48	0.003
True protein (%)	3.3^b	3.5^b	4.1^a	0.57	0.003
Total solids	111.3^a	127.9^b	113.6^a	0.85	0.005
Total solids (%)	12.2^a	12.0^b	13.6^a	1.75	0.049
SNF (g/d)	78.9^a	100.5^b	78.9^a	0.96	0.002
SNF (%)	8.6^a	9.5^a	9.4^a	0.91	0.002

Key Words: goats, safflower soap, sunflower soap

T115 Effect of oil palm (*Eleais guineensis*) effluent plus supplement in the feeding of pigs (Duroc x Pietrain) in the finishing phase during dry season. I. Espinoza,* R. Vivas, D. Zambrano, B. Montenegro, G. Muñoz, M. Romero, H. Medina, R. Soria, M. Medina, L. Godoy, and E. Torres, *Universidad Técnica Estatal de Quevedo, Quevedo, Los Ríos, Ecuador.*

This investigation was carried out at the "El Recuerdo" pig farm, located at one and a half mile at the Valencia - La Mana highway, province of Los Ríos, Ecuador. Its geographical location is 01° 6′ 20'' south latitude and 79° 29′ 23'' west longitude at 120 m above sea level and was conducted between August and October of 2010, lasting 56 d, including the period of adaptation. The effect of oil palm (*Eleaeis guineensis*) effluent (agro-industrial waste) plus supplement in the diet of pigs (Duroc × Pietrain) in the finishing stage during the dry season, along with the productivity indices (weight gain, feed intake, feed conversion, carcass yield and backfat) and cost/benefit ratio of the treatments under study were determined, assuming that with the implementation of one of the treatments under study production rates will be improved. Through an economic analysis of the treatments under study it was determined which of them improved the benefit / cost ratio. The treatments under study were 2 (T1: 2.5 kg of balanced feed plus 1 kg of oil palm effluent and T2: 2.5 kg of balanced feed plus 2 kg of oil palm effluent) compared with a control (2.5 kg of finishing phase balanced feed). A complete randomized block design was used in this study with 3 treatments and 6 replications. The highest feed intake in T2 ($P < 0.05$) and T1 in relation to the control, were because the pigs were influenced directly by the increased availability of food offered since the rations were larger in both cases. The total weight gains were similar ($P < 0.05$) in both treatments under study. However, there was a greater weight gain in the treatment supplemented with 1 kg of oil palm effluent surpassing the control with 3.67 kg. Besides a better feed conversion at 28 d in T1 ($P < 0.05$) was observed. In the variables carcass yield and backfat, no significant influences were observed when supplementing the diet of the pigs with oil palm effluent. The best cost / benefit ratio was achieved by T1 with 0.27.

Key Words: oil palm affluent, pig, supplement

T116 Planting date and crop harvest phenological stage effects on biomass and nutritive value of non-photosensitive forage soybean lines in Puerto Rico. A. Aponte, E. Valencia,* and J. Beaver, *University of Puerto Rico, Mayaguez, Mayaguez, PR.*

Forage soybean [*Glycine max* L. (Merr.)] has high potential for biomass production in the tropics, because, in a short period of time high quality hay can be produced for animal feed. However, in the tropics information on soybean for forage or grain is non-existent. Information of the effects of planting dates and crop harvest phenological stage (CHPS) on dry matter yield (DMY) of non-photosensitive soybeans are needed. This research assessed biomass production (Mg ha-1), crude protein (CP), neutral detergent fiber (NDF), and acid detergent fiber (ADF)] % of 10 non-photosensitive soybean lines at 2 CHPS and 2 planting dates on an Oxisol (Cotito series) at Isabela, Puerto Rico. The field design was a complete block with 4 replications in a split-plot arrangement of 10 forage soybean lines and 2 CHPS (R2 and R5.4); 100% flowering and 75% grain physiological filling, respectively. Planting dates were September 2010 and January 2011. For each planting date and CHPS, a 1.2 m^2 area was harvested from the main plot and fresh weight and a sub-sample (500g) taken. Subsamples were oven-air-dried to determine % dry matter (DM). Nitrogen % (Kjeldahl), NDF and ADF (Van Soest procedure) were determined in a commercial laboratory. The data was analyzed using the Statistical Package, INFOSTAT. Unlike planting date, CHPS had a significant effect ($P < 0.05$) on the DMY. Soybean forage DM produced on average between 5.4 and 6.5 Mg/ha when harvested at the R2 (8 weeks) and R5.4 (12 weeks) stages of development, respectively. Maximum biomass was obtained at the R5.4 harvest with an increase in DM of 1.0 Mg/ha in 28 d. There was an interaction ($P < 0.05$) between the lines x CHPS for CP ranging from 29.6% to 33.6% for R2 harvest, while samples for the R5.4 harvest ranged from 23.0 to 26.7%. NDF in R2 stage ranged from 33.3 to 34.6, and increased in the R5.4 stage from 38.1% to 44.8%, while ADF for R2 ranged from 21.0% to 25.6%, whereas ADF increased from 26.2% to 33.2% for the R5.4 stage. These results indicate that biomass for soybean lines did not differ ($P > 0.05$) between planting date, but there was a marked effect of CHPS on DM yield. Forage soybeans harvested at the R5.4 versus the R2 stage of development had 60% more biomass, and higher nutritional value. Fiber values were similar to alfalfa and can satisfy the nutritional requirement of ruminants in the tropics.

Key Words: forage soybeans, phenological stages, nutritive value

T117 Nutritional characterization of pastures used in Colombian dairies with emphasis on fatty acid profile. E. A. De La Vega,* J. E. Parales, C. A. Mendoza, M. M. Knowles, G. J. Díaz, M. L. Pabón, and J. E. Carulla, *Universidad Nacional de Colombia, Bogotá, Cundinamarca, Colombia.*

Fatty acid profile of different pastures used in Colombian dairy farms and their relationship with grazing management strategies and altitude (meters over sea level; mosl) were examined. Forage samples of pastures were taken from 115 dairy farms in 5 dairy regions. Pasture type and management were characterized for each farm. Samples were oven-dried and analyzed for DM, NDF, ADF, CP, total fat and ash. Fatty acid profiles of the samples were determined using GC. The data were subjected to multivariate statistical analysis using the 2-stage cluster procedure. To define homogeneous clusters, we followed the Bayesian Information Criterion Schwarz including continuous and discrete variables. None of the variables measures related to grazing management were included as main grouping criteria. Five clusters were identified which main grouping criteria were the altitude and type of pasture. Cluster 1: lowland ($\mu \pm SD$; 442 ± 99 mosl) native pastures; cluster 2: medium altitude ($\mu \pm SD$; 874 ± 444 mosl) pastures composed mainly of *Brachiaria* spp.; cluster 3: upland pastures ($\mu \pm SD$; 2711 ± 144 mosl) composed mainly of *Lolium* spp. pastures and mixed pastures of *Pennisetum clandestinum* with *Trifolium pratense*; cluster 4: upland grasslands ($\mu \pm SD$; 2597 ± 88 mosl) consisting of monocultures of *Pennisetum clandestinum* and cluster 5: upland pastures ($\mu \pm SD$; 2605 ± 83 mosl) composed of mixtures of *Pennisetum clandestinum* and *Lolium* spp. Lipids of low land and medium altitude pastures had lower content of linolenic acid ($\mu \pm SD$; 20.1 ± 7.5 vs 35.6 ± 9.4 g/100 g FA) and higher in saturated fatty acids ($\mu \pm SD$; 59.8 ± 8.2 vs 45.4 ± 8.4 g/100 g FA) than upland pastures ($P < 0.05$). Most variable fatty acids in forage lipids were linolenic and palmitic acid. Degree of saturation was mainly explained by an increase in palmitic acid and a reduction in linolenic acid ($r^2 = 0.73$; $P \leq 0.001$). Low land and medium altitude pastures had higher levels of DM (17.5 vs. 24.7 g/100 g DM), NDF (56.8 vs 67.7 g/100 g DM), ADF (26.6 vs 36.6 g/100 g DM) than high altitude pastures ($P \leq 0.05$). Differing pasture species combinations at various altitudes resulted in variable nutritional quality and lipid profiles for dairy pastures in Colombia.

Key Words: fatty acids, forages, linolenic acid

T118 Effect of sowing density and planting date on the establishment of *Pennisetum purpureum* 'CT-115' in a semiarid region of northern Mexico. E. Gutierrez Ornelas*[1,3], J. J. Nava Cabello[1], R. Herrera[2,3], H. Bernal Barragan[1,3], E. Treviño Ramirez[1], and E. Olivares Saenz[1], [1]*Universidad Autónoma de Nuevo León, San Nicolás de los Garza, Nuevo León, México,* [2]*Instituto de Ciencia Animal, San José de Las Lajas, Habana, Cuba,* [3]*Red Internacional de Nutición y Alimentación en Rumiantes, México.*

The objective of the experiment was to evaluate the effect of 2 sowing densities ((D1 = 17,850 and D2 = 11,350 plants/ha) and 4 planting dates of King Grass, *Pennisetum purpureum* cv. CT-115 according to a completely random block design with a 4 × 2 factorial arrangement of treatments, where each planting date (July, August, September, and October 2009) was done under an area of 900 m^2, including 2 replications per density. Seven plants were randomly sampled in each of the 16 experimental units to estimate the interest variables. Basic climatic factors affecting establishment of non irrigated forages were registered. Forage establishment variables were measured during May 2010. On January 2010 lowest temperatures were recorded (−6°C) during 2 consecutive days without affecting viability of plants after re-growing conditions were present on April 2010. Sowing density only affected ($P \leq 0.05$) the proportion of senescence material (D1 = 15.8 vs. D2 = 11.4%) and dry matter production (D1 = 6.1 vs. D2 = 4.3 ton/ha). Dry matter percentage was affected ($P \leq 0.05$) by the planting time, having lower content than those plants planting on July and August. Leaf proportion was higher ($P \leq 0.05$) in July and August (57.7 and 58.5%, respectively) compared with September and October (44.6 and 43.7%, respectively). Leaf/stem ratio and the number of stems/plant were higher ($P \leq 0.05$) in the 2 first months of planting. It can be concluded that the better sowing density was D1. The lowest temperatures registered during January 2010 did not affect the establishment of *Pennisetum purpureum* 'CT-115' planted from July to October at the region of Marin Nuevo León, México.

Key Words: *Pennisetum purpureum*, cultivar CT-115, sowing density

T119 Effect of plant density over the productive performance of gliricidia. E. N. Muniz*[1], J. H. A. Rangel[1], D. O. Santos[1], C. O. Sá[1], and J. L. Sá[2], [1]*Embrapa Tabuleiros Costeiros, Aracaju, Sergipe, Brazil,* [2]*Embrapa Semi* Árido, *Petrolina, Pernambuco, Brazil.*

Gliricidia sepium (Jacq.) Walp. is a forage tree species very well adapted to water stress conditions, with high protein content in its leaves make it a low cost strategy for ruminant diets during drought periods. In northeast Brazil, gliricídia has been used as cattle and sheep food in silvopastoral systems, and also as silage or hay providing good dry matter productivity of high quality and good acceptance by animals. The present work aimed to evaluate the effect of different plant densities over the biomass and dry matter productivity of gliricídia. The trial was carried out without irrigation in a randomized block design with 4 replications in the Pedro Arle Experimental Station belonging to Embrapa Tabuleiros Costeiros at Frei Paulo County, Sergipe, Brazil. The densities of 10,000; 20,000; 30,000; and 40,000 plants/ha were tested. Fresh biomass and dry matter productivity of 6 harvests were evaluated for the growth period between 05/22/2009 and 03/22/2011. Cuts were done at 09/02/2009, 03/16/2010, 05/26/2010, 08/24/2010, 12/09/2010 and 03/22/2011. Mean values of cuts for total biomass, stem biomass, leaves biomass, leaves percentage and total dry matter per cut were presented in Table 1. Values of biomass productivity increased with the increase of plant density after the density of 20,000 plant/ha. Based on the results, it is recommended the density of 40,000 plants/ha of gliricidia for that condition.

Table 1. Means of biomass productivity of gliricidia at different plant densities

Treatment	Total biomass/ cut (t)	Stem biomass/ cut (t)	Leaves biomass/ cut (t)	Leaves (%)	Leaves DM/ cut(t)	Total leaves DM (t) 6 cuts
10000	21.54^{b}	7.12^{b}	14.41^{b}	67.98^{a}	3.02^{b}	18.14^{b}
20000	20.72^{b}	6.56^{b}	14.16^{b}	68.49^{a}	2.92^{b}	17.53^{b}
30000	25.19^{ab}	8.05^{ab}	17.15^{ab}	69.05^{a}	3.46^{ab}	20.78^{ab}
40000	27.28^{a}	9.13^{a}	18.15^{a}	67.13^{a}	3.75^{a}	22.49^{a}

^{a,b}Means followed by the same letter in columns are not different by Tukey test ($P < 0.05$).

Key Words: dry matter, gliricidia

T120 Assessment of the socio-economic value of goods and services from Manitoba grasslands. S. Kulshreshtha[1], M. Undi*[2], J. Zhang[1], M. Ghorbani[1], K. M. Wittenberg[2], A. A. Stewart[3], E. Salvano[4], E. Kebreab[5], and K. H. Ominski[2], [1]*Dept of Bioresource Policy, Business and Economics, University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Department of Animal Science & National Centre for Livestock and the Environment, University of Manitoba, Winnipeg, MB, Canada,* [3]*Shur-Gro Farm Services Ltd., Waskada, MB, Canada,* [4]*Manitoba Agriculture, Food, and Rural Initiatives, Winnipeg, MB, Canada,* [5]*Dept of Animal Science, University of California, Davis.*

Grasslands in Manitoba occupy 2.4 million ha and provide goods and services (G & S) that have direct and indirect monetary value. The objectives of this study were to a) provide a framework for comparing the value of G & S from grasslands by utilizing direct and indirect assessment, b) assess the value of Manitoba grasslands and the variables influencing value, and c) identify gaps in knowledge thereby improving estimates of grassland contribution to socio-economic well-being. Methods of valuation employed in the study were specific to the type of G & S examined. Market price was utilized to value grassland G & S where transactions occur in the marketplace while the benefit transfer method was used to infer non-market values of those G & S that are not typically sold through the marketplace. A total of 18 grassland G & S were identified for Manitoba grasslands, but only perennial forage production, carbon storage, nutrient cycling, water regulation, waste treatment, soil formation, erosion control, wildlife habitat, and recreation were included in the valuation. Genetic, medicinal, and ornamental resources, water supply (including filtration), nursery function, biological value, and many cultural services, while important, could not be assigned monetary value due to lack of data. The socio-economic value of grasslands in Manitoba was estimated to be \$936 million yr^{-1} (equivalent to \$390 ha^{-1} on average) with a range of \$702 million to \$2,518 million yr^{-1}. The 2 most highly valued G & S in Manitoba grasslands were carbon storage and forage production. More research will be required to further quantify carbon storage in Manitoba grasslands as well as assess the value of G & S not included in the above total value of grasslands.

Key Words: grassland, goods and services, socio-economic value

Growth and Development II

T121 Effect of residual feed intake on hypothalamic gene expression and meat quality in heat-stressed Angus-sired cattle.

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Residual feed intake (RFI) is a heritable feed efficiency measure. The relationship between RFI, heat stress and meat quality is unknown. To address these issues, 48 Angus-sired steers were trained to the Calan Gate (Northwood, NH) system. Daily feed intake and RFI were assessed during a 70 d feeding trial conducted July through September. The test diet was 50% balage consisting of a winter annual mix, 50% grain (2.9 Mcal ME/kg DM). Feed intake was recorded daily while body weights and hip heights were recorded at 14 d intervals. Ultrasound measurements of rib eye area (REA) and backfat (BF) were recorded initially and before slaughter. RFI was calculated for each animal as the difference between actual dry matter intake and the expected intake to create 2 divergent cohorts consisting of High (H) and Low (L) RFI individuals. At slaughter, hypothalamic tissue samples were collected to facilitate gene studies into the mechanisms underlying variation in RFI. After chilling for 24 h post harvest, carcass characteristics were measured. Carcass and growth data were analyzed using a mixed model with RFI level (L, H) as the independent variable (SAS, 2002). Means were separated using lsmeans at a significance level of $P < 0.05$. The lsmeans for RFI were −1.2 and 0.99 respectively for the L and H cohorts ($P < 0.0001$) and were greater than 2 standard deviations apart. As expected dry matter intake was higher for the H individuals versus the L steers ($P < 0.0001$) while on-test gain was not different between groups. Marbling score was greater in L than H steers ($P < 0.05$). However there were no differences in objective color measures L*, a*, and b*, adjusted back fat, ribeye area or yield grade between L and H cohorts. Real-time PCR studies in the arcuate nucleus indicate that neuropeptide Y (NPY) and agouti related protein (AgRP) mRNA were expressed 2.8-fold and 1.85-fold greater while Pro-opiomelanocortin (POMC) mRNA was expressed 1.6-fold lesser in L than H animals. These data suggest there is no relationship between RFI and meat quality while surprisingly the mRNA expression of neuropeptides that stimulate feed intake were increased in efficient animals during heat-stressed conditions.

Key Words: RFI, meat quality, heat stress

T122 Effect of residual feed intake on meat quality and hypothalamic gene expression in Angus-sired cattle.

S. D. Perkins,* C. N. Key, C. F. Garrett, C. D. Foradori, C. L. Bratcher, L. A. Kriese-Anderson, and T. D. Brandebourg, *Auburn University, Auburn, AL.*

Residual feed intake (RFI) is a heritable feed efficiency measure. Mechanisms underlying RFI are poorly understood while the relationship between RFI and meat quality is unknown. To address these issues, 48 Angus-sired steers were trained to the Calan Gate (Northwood, NH) system. Daily feed intake and RFI were assessed during a 70 d feeding trial. The test diet was 50% sorghum-sudan silage, 50% grain (2.9 Mcal ME/kg DM). Feed intake was recorded daily while body weights and hip heights were recorded at 14 d intervals. Ultrasound measurements of rib eye area (REA) and backfat (BF) were recorded initially and before slaughter. RFI was calculated for each animal as the difference between actual dry matter intake and the expected intake to create 2 divergent cohorts consisting of High (H) and Low (L) RFI individuals. Steers were humanely harvested and hypothalamic tissue (HT) samples were collected to facilitate gene studies into the mechanisms underlying variation in RFI. After chilling for 24 h post harvest, carcass characteristics were measured. Carcass and growth data were analyzed using a mixed model with RFI level (L, H) as the independent variable (SAS, 2002). Means were separated using lsmeans at a significance level of $P < 0.05$. The lsmeans for RFI were −1.3 and 1.5 respectively for the L and H cohorts ($P < 0.001$) and were greater than 2 standard deviations apart. As expected dry matter intake was higher for the H individuals versus the L steers ($P < 0.001$) while on test gain was not different between the 2 groups. There were no differences in marbling score, objective color measures L*, a*, and b*, adjusted back fat, ribeye area or yield grade between L and H cohorts suggesting there is no relationship between RFI and meat quality. Initial targeted gene expression studies in the arcuate nucleus indicate that neuropeptide Y (NPY) mRNA is expressed 2.7-fold lower and pro-opiomelanocortin (POMC) mRNA is expressed 3.6-fold higher in L than H animals. This suggests differences in neuropeptide expression in part underlie differences in feed efficiency observed in growing cattle during conditions of thermoneutrality.

Key Words: RFI, meat quality, neuropeptide Y

T123 Serum IGFI and hepatic *IGFI* mRNA levels in feedlot cattle infected with bovine respiratory disease.

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Bovine respiratory disease (BRD) is a leading cause of feedlot morbidity and mortality. Calves treated for BRD exhibit decreased growth, but mechanisms responsible for BRD-induced impaired growth are still unknown. The objectives of these studies were to evaluate serum IGFI and hepatic *IGFI* mRNA levels in BRD-infected calves. In study 1, serum samples were collected from control calves (CONT1; n = 5) and calves receiving a single treatment for BRD (1TRT1; n = 5) at arrival, at time of treatment, and on d 33, and serum IGFI levels were quantified via RIA. Serum IGFI or relative fold change of *IGFI* mRNA was tested against treatment, day, and treatment × day using the GLM procedure of SAS and means were separated using PDIFF when appropriate. There was not a treatment x day interaction ($P > 0.10$), but overall means of IGFI were greater ($P < 0.05$) for CONT1 (100.1 ± 8.6 ng/mL) than 1TRT1 (55.6 ± 9.4 ng/mL). Serum IGFI was low at arrival (39.6 ± 3.4 ng/mL) and increased ($P < 0.05$) to 152.7 ± 12.4 ng/mL on d 33 for both groups. In study 2, serum and peripheral blood leukocytes (PBL) were collected from calves chronically infected with BRD (CHRON; n = 6) and controls (CONT2; n = 6). Serum IGFI levels decreased ($P < 0.05$) in CHRON (65.3 ± 46.0 ng/mL) compared with CONT2 (236.5 ± 46.0). In PBL, *IGFI* mRNA was present but similar ($P > 0.10$) in CHRON and CONT2. In study 3, hepatic mRNA was collected from controls (CONT3; n = 6), calves treated once for BRD (1TRT3; n = 6), calves treated twice (2TRT3; n = 5), and calves treated 3 times (3TRT3; n = 6). Relative abundance for *IGFI* mRNA was quantified, and, relative to CONT3, 1TRT3 exhibited similar ($P > 0.10$) *IGFI* mRNA levels. However, 2TRT3 and 3TRT3 *IGFI* levels were approximately 2.5-fold below CONT3 ($P < 0.05$). These results demonstrate that serum IGFI is reduced at time of arrival and in calves chronically infected with BRD. In calves treated once for BRD, reduced feed intake might account for a reduction in IGFI without affecting growth. However, calves treated multiple times for BRD exhibit alteration in hepatic synthesis of *IGFI* mRNA possibly leading to long-term growth suppression.

Key Words: bovine respiratory disease, IGFI, growth

T124 Relationship between carcass traits and tenderness with residual feed intake and residual average daily gain of Brahman steers. F. Rouquette Jr.*[1], R. Randel[1], J. Paschal[2], T. Machado[3], and C. Long[1], [1]*Texas AgriLife Research and Extension Center, Overton,* [2]*Texas AgriLife Extension Service, Corpus Christi,* [3]*Texas A&M University-Kingsville, Kingsville.*

Residual feed intake (RFI) and residual average daily gain (RADG) indices have been used to assess an efficiency rating to cattle. The objectives of this 3-year experiment were to determine the relationship between RFI and RADG groupings on carcass traits and tenderness. After weaning, yearling Brahman bulls were fed a growing ration via calan gates in drylot during 3 consecutive years, (2008, n = 56; 2009, n = 47; 2010, n = 34). Bulls were phenotyped for RFI and RADG and sorted into 4 efficiency groups: 1 = more than 0.5 standard deviation (SD) below the mean (most efficient); 2 = less than 0.5 SD below the mean; 3 = less than 0.5 SD above the mean; and 4 = more than 0.5 SD deviation above the mean (least efficient). Following the drylot period, bulls were stocked on bermudagrass pastures during the summer, castrated in the fall, and transported to a commercial feedlot for finishing to an approximate 1.0 cm backfat. After harvest, standard carcass traits were taken. Year was an independent variable and with an interaction for year and RFI and RADG, carcass trait relationships were assessed by year using Proc Mixed. Steers that were sorted into most efficient group had higher ($P < 0.05$) dressing % (2008, 2010), liveweight and hot carcass weights (2009), backfat (2010), and USDA Yield grade (2008, 2009, and 2010). Steers sorted into the least efficient group had higher ($P < 0.05$) marbling score (2009) and quality grade (2009). Steers harvested in 2010 were assessed for tenderness using Warner-Bratzler shear force. The shear force values for the 4 efficiency groupings were different when using either RFI ($P = 0.078$) or RADG ($P < 0.001$). For both efficiency rankings, the least efficient steers (group 4) had the highest scores (least tender) of 4.29 kg (RFI) and 4.33kg (RADG). These carcass traits indicated a general lack of relationship for either RFI or RADG groups. However, the most tender steaks were in Group 3 (RFI) and Group 2 (RADG).

Key Words: residual feed intake, residual average daily gain, carcass

T125 Adipocyte location and anabolic implant alter adipocyte transcriptome in steers. S. K. Duckett,* J. W. Long, M. D. Owens, S. E. Ellis, and S. L. Pratt, *Clemson University, Clemson, SC.*

The accumulation of excess fat results in economic loss in beef production. However, understanding how lipid is accumulated at different depots could lead to strategies reducing financial loss by targeting specific sites for lipid deposition. The objectives of this study were to: 1) determine if location of fat depot alters adipocyte gene expression and 2) evaluate the impact anabolic implants have on adipocyte's transcriptome in 2 separate adipose depots. Angus x Hereford steers (n = 24; BW = 488 kg) were randomly allotted to non-implant (CON) or implant (IMP) treatments. Steers were individually fed a high concentration diet for 72 d and IMP steers received a single Revalor-S (24 mg estradiol, 124 mg trenbolone acetate) at time of allotment. At slaughter, adipose tissue samples were collected from subcutaneous (SQ) and mesenteric (MS) depots, flash-frozen, and stored at −80°C for RNA extraction. Total cellular RNA was isolated using the mirVana miRNA Isolation Kit (Ambion, Austin, TX). The cleared homogenate was loaded on to the binding matrix by vacuum and the column washing and elution of bound tcRNA were performed per manufacturer's protocol. Four pools of tcRNA were generated for SQ-CON, SQ-IMP, MS-CON and MS-IMP. The samples were subjected to RNA sequencing (LC Sciences, Houston, TX) using the Illumina high-throughput sequencing technology. Data were analyzed by LC Sciences using Bowtie, Tophat, and Cufflinks statistical analysis software systems. The number of mappable reads ranged from 87,387,760 to 91,927,097 for all tissue-treatment combinations. This resulted in 32,493 to 35,030 predicted messenger RNA transcripts for all tissue-treatment combinations. Gene expression differences were compared between data sets of MS-CON vs MS-IMP, MS-CON vs SQ-CON, MS-IMP vs SQ-IMP, and SQ-CON vs SQ-IMP. Of differentially expressed genes identified, 95 were differentially expressed due to adipose depot ($P < 0.05$) and 36 were differentially expressed due to IMP ($P < 0.05$). Therefore, adipocyte gene expression is impacted by both location and anabolic steroid treatment, which suggests that strategies/treatments could be developed to adjust lipid accumulation based on location and exogenous hormonal treatment.

Key Words: beef, implants, gene expression

T126 Subcutaneous adipose tissue gene expression in bulls fed ergot alkaloid-containing fescue seed. T. A. Burns,* M. C. Miller, H. M. Stowe, S. M. Calcatera, S. L. Pratt, J. G. Andrae, and S. K. Duckett, *Clemson University, Clemson, SC.*

Grazing toxic endophyte-infected tall fescue (E+) is a common practice in the southeastern US and is associated with decreased performance and adipose tissue necrosis. The objective of this study was to determine the effects of E+ on male adipose tissue gene expression. In addition, isolation of adipose tissue is inherently difficult due to the abundance of lipid; therefore, a secondary objective of this work was to identify a RNA isolation method that efficiently isolated RNA of good quality. Eight beef bulls approximately 12 to 16 mo of age were stratified by breed, weight, and BCS and then assigned to 1 of 2 treatment groups receiving 4.2 g/kg of BW per day of E+ or endophyte-free fescue (E-) seed in a total mixed ration. After a feeding period of 126 d, bulls were slaughtered and tissues snap frozen for gene expression analysis. Four commercially available kits were used to isolate RNA according to manufacturer's instructions: mirVana miRNA Isolation Kit (Invitrogen; Grand Island, NY), Direct-zol RNA MiniPrep (Zymo Research; Irvine, CA), RNeasy Lipid Tissue Midi Kit (Qiagen; Valencia, CA), and PureYield RNA Midiprep System (Promega; Madison, WI). Data were analyzed using the Proc GLM procedure of SAS 9.2. Quality of RNA, assessed by 260/280 absorbance ratio, was acceptable for all isolation methods and was greatest ($P < 0.05$) for RNA isolated using Direct-zol, but only mirVana and RNeasy RNA had a consistently acceptable 18S/28S ribosomal band ratio. Efficiency of extraction (µg RNA/g tissue) was greatest ($P < 0.05$) for mirVana isolations. Therefore, real time PCR was performed on *stearoyl-CoA desaturase* (*SCD1*) and *cytochrome P450 subfamily 3A* (*CYP3A*) genes with reference gene *glyceraldehyde-3-phosphate dehydrogenase* from mirVana-isolated RNA. Subcutaneous adipose tissue of E+ bulls had downregulated expression ($P < 0.05$) of *SCD1* indicating a reduction in fatty acid desaturation compared with E-. Associated with animal metabolism of ergot alkaloids present in toxic fescue, *CYP3A* expression was not different ($P > 0.05$) in E+ compared with E- bulls. Therefore, expression of *SCD1* mRNA isolated from subcutaneous adipose tissue of bulls is affected by E+ fescue.

Key Words: bovine, fescue, RNA isolation

T127 Growth performance of Mahabadi goat kids fed different levels organic trivalent chromium. A. Emami, A. Zali, M. Ganjkhanlou,* A. Hojabri, and A. Akbari, *University of Tehran, Tehran, Iran.*

This study was carried out to determine the effects of supplementing chromium-methionine (Cr-Met) on performance in Mahabadi goat kids. Thirty-two male kids (average initial BW of 22 ± 2 kg, 4mo) were used in a completely randomized design with 4 treatments: 1) control (without Cr), 2) 0.5, 3) 1.0 and 4) 1.5 mg Cr as Cr-Met/animal/d. Diets were formulated to meet NRC requirements with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Diets were the same except for top-dress addition of Cr-Met and fed in 2 equal meals (0800 and 1600 h) and orts were collected before morning meal. Animals were kept in individual pens with self-mangers. Experimental period was 90 d. Animals were weighed at 21 d intervals. Feed conversion ratio (FCR) was calculated according to FCR = DMI (Dry matter intake) (kg)/Average daily gain (ADG) (kg). DMI, ADG and FCR data were analyzed using MIXED procedure of SAS 9.1. The Tukey test was used for comparison of treatment means. ADG was not affected by the Cr-Met ($P > 0.05$). Also DMI and FCR were not affected by the chromium supplementation ($P > 0.05$). These results indicated that dietary supplementation of Cr-Met failed to significantly affect growth performance of Mahabadi goat kids.

Table 1. DMI, ADG, and FCR of kids fed different levels of organic chromium

	Treatment (mg of Cr)				
Trait	Control	0.5	1.0	1.5	SEM
DMI(kg/d)	1.01	1.00	1.03	1.07	0.04
ADG	0.14	0.14	0.15	0.17	0.01
FCR	7.55	7.48	6.95	6.44	0.47

Key Words: feed intake, daily gain, feed conversion ratio

T128 Postweaning feed restriction effects on steer feedlot performance and carcass characteristics. R. L. Endecott*[1], B. L. Shipp[2], M. D. MacNeil[2], L. J. Alexander[2], and A. J. Roberts[2], [1]*Department of Animal and Range Sciences, Montana State University, Miles City,* [2]*USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.*

The objective was to evaluate effects of 2 levels of supplemental feed provided to cows during late gestation and 2 levels of feed provided to their sons during postweaning development on subsequent feedlot performance and carcass characteristics. Bull calves (n = 56 in 2010; n = 51 in 2011) were born from dams receiving adequate (1.8 kg/d) or marginal (1.2 kg/d) winter supplementation. After weaning, bulls were developed on ad-libitum (Control) or 27% less feed (Restricted) for ~140 d. Bulls were then band-castrated and placed on an 80% corn finishing diet ad libitum. Individual intakes were measured with a GrowSafe system for the final 100–150 d of the finishing period. Cattle were harvested at a commercial packing plant and carcass data were collected. Dam winter supplementation effects were not detected ($P \geq 0.22$). Postweaning phase ADG exhibited a postweaning treatment × year interaction ($P < 0.01$). Restricted calves had similar ADG in both years (0.64 vs 0.68 ± 0.03 kg/d) and gained less than Control calves. Control calves had greater ADG in 2010 than in 2011 (1.16 vs 1.03 ± 0.03 kg/d). Postweaning treatment did not affect feed intake during the finishing phase ($P = 0.29$; 13.0 vs 12.8 ± 0.22 kg/d for Restricted vs Control; as-fed basis). During the finishing phase, ADG exhibited a postweaning treatment × year interaction ($P < 0.01$). Restricted steers had similar ADG in both years (1.25 vs 1.27 ± 0.05 kg/d) and gained more than Control steers. Control steer ADG was less in 2010 than in 2011 (0.92 vs 1.13 ± 0.05 kg/d). Compared with Control steers, Restricted steers had lower ($P \leq 0.08$) final BW (603 vs 623 ± 9 kg), HCW (357 vs 373 ± 6 kg), and yield grade (2.71 vs 2.89 ± 0.10). However, back fat thickness (1.09 vs 1.14 ± 0.05 cm), ribeye area (85.4 vs 85.8 ± 0.98 cm^2), and marbling score (5.59 vs 5.50 ± 0.12) were not different ($P \geq 0.34$). Calves restricted during postweaning development gained more efficiently, and when harvested on a common date, had lower carcass weights and yield grade, but similar fat thickness, ribeye area and quality grade compared with their ad libitum-fed counterparts.

Key Words: postweaning development, uterine programming, finishing

T129 Stearoyl-CoA desaturase (SCD1) localization and intensity in bovine adipose and muscle tissues from implanted and non-implanted steers. M. Wilder, S. Safayi, S. E. Ellis, and S. K. Duckett,* *Clemson University, Clemson, SC.*

Anabolic steroids are commonly used during the finishing phase to increase weight gain and feed efficiency. The objective of this study is to assess the localization and relative amount of stearoyl-CoA desaturase (SCD1) in mesenteric adipose tissues (MS), subcutaneous adipose tissue (SC), and longissimus muscle (LM) of implanted and non-implanted steers. Stearoyl-CoA desaturase is the rate-limiting enzyme involved in fatty acid metabolism, which converts saturated fatty acid to monounsaturated fatty acid. In this experiment, 12 steers (448kg) were implanted with Revalor-S (24 mg estradiol, 124 mg trenbolone acetate) and 12 steers were not implanted. All steers were fed a high concentrate diet for 72 d before slaughter. Fat and muscle samples were removed at slaughter, immediately flash-frozen, and stored at −80°C for subsequent cyrosectioning and immunofluorescent staining. Cryosections were stained with POPO-1 iodide, a high-affinity blue nucleic acid stain, and green fluorescent phalloidin, an F-actin stain. Cryosections were also incubated overnight with SCD-1 antibody (4 μg/mL) and stained with AlexaFluor 594 secondary antibody. Micrographs were collected with the Nuance Multispectral imaging system using a consistent exposure and illumination protocol. SCD1 staining intensity was most obvious in the perinuclear region, but was also visible through the cytoplasm. SCD1 staining was visible in adipocytes, muscle cells, endothelial cells and schwann cells. Discrete cell populations were manually traced in each micrograph to assess the recorded fluorescent staining intensity in regions and cells of interest. Average intensities in each group of cells were analyzed to estimate the relative abundance of SCD1 protein. There was a tissue by treatment interaction ($P < 0.05$). Adipose tissues from SC and MS had greater SCD1 intensity than LM, regardless of treatment. The SCD1 staining intensity was reduced in MS from implanted steers relative to MS of non-implanted and SC of both non-implanted and implanted. Using immunofluorescent staining, we were able to visualize SCD-1 localization in various adipose tissues and determine changes in SCD-1 relative amounts due to implant treatment.

Key Words: beef, adipose tissues, SCD

T130 Body′s growth curve and shape of grazing young bulls, receiving concentrate supplementation with different protein profiles. H. J. Fernandes*[1,2], A. G. da Silva[2], M. F. Paulino[2], S. A. Lopes[2], L. O. Tedeschi[4], J. A. G. Azevêdo[3,2], and A. Aguiar[5], [1]*State University of Mato Grosso do Sul, Aquidauana, MS, Brazil,* [2]*Federal University of Viçosa, Viçosa, MG, Brazil,* [3]*State University of Santa Cruz, Ilhéus, BA, Brazil,* [4]*Texas A&M University, College Station,* [5]*University of Florida, Gainesville.*

The objectives of this study were to analyze and compare full body weight (FBW) and body measurements (BM) growth of crossbred bulls grazing *Brachiaria decumbens* Stapf. pastures over 430 d. Twenty bulls with initial FBW of 129 ± 28.1 kg, were divided in 4 groups, receiving either mineral supplement *ad libtum* (control) or 0.5% of FBW of one of the concentrate supplementation rations (26.7% CP), identified as T1 (high urea level), T2 (low urea level), and T3 (no urea). The FBW and the BM were recorded every 28 d. The BM included hooks width (HW), pins width (PW), pelvic girdle length, rump height (HeR), abdomen width, body length (BL), height at withers (HeW), and rib depth (RiD). The first and the second canonical variables were estimated using all BM by PROC CANDISC of SAS. A growth multiphase model with 3 phases was adjusted using PROC NLIN of SAS. The phases of the model corresponded to a first rainy season, a dry season (the feed restriction season in the year to grazing animals) and a second rainy season. Growth models and their parameters were compared using a dummy variable. The main BM to describe the differences between animal body shape (explaining 73.1% of the differences) were RiD, PW, HeR, and HeW. Animals in control group tend to be shorter and wider. There were no differences ($P > 0.05$) in the growth curves of FBW between the concentrate supplemented treatments. The growth curves of FBW of the control and the supplemented animals differs in days in the experiment at which the animals respond to feed restriction in dry season (82 and 113.3 d, $P = 0.047$), in the growth rate during this phase (0.141 and 0.328 kg/d, $P = 0.006$), and in days in the experiment at which the animals respond to the end of this phase (314 and 292 d, $P = 0.006$). These parameters could explain the greater mature weight ($P = 0.003$) of the supplemented animals. The main differences ($P < 0.05$) between the supplemented and the control animals in the growth curves of BM were the greater mature HeW, HeR, RiD, and BL in the supplemented group. The protein patterns of the concentrate affected ($P < 0.05$) the growth of the HeW, RiD, and HW.

Key Words: biometrics, cattle, modeling

T131 Mathematical models to describe growth of grazing beef cattle.

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The objective of this study was to evaluate the use of different mathematical models to describe growth of grazing beef cattle. Ten Nellore castrated males and 10 females, with initial age and weight of 16 ± 1.27 mo and 224 ± 18.5 kg, respectively, were grazing *Brachiaria decumbens* Stapf. pasture and received mineral supplement ad libitum, for 16 mo. Every 28 d, animals were weighed and biometric measures (including hook width, pin width, pelvic girdle length, rump depth, rump height, abdomen width, body length, height at withers, rib depth, and girth circumference) were taken to develop growth curves of the animals. Six mathematical models were evaluated to describe animal growth: multiphase (with 3 phases), linear, quadratic, exponential, monomolecular, and Richards. Assessment of adequacy of the models was performed using coefficient of determination (R^2), simultaneous F-test for identity of parameters, concordance correlation coefficient (CCC), and partition of the mean square error of prediction (MSEP). The analysis of paired mean square error of prediction and delta information criterion of Akaike were used to compare the models for accuracy and precision. Based on the simultaneous F-test for identity of parameters, monomolecular and Richards models produced estimates different ($P < 0.05$) of the observed growth data. Linear and exponential models presented low R^2 (49.3 and 52.6%) and CCC <0.800. The quadratic model had R^2 = 70.0% and CCC = 0.826 and partitioning of the MSEP of this model showed more than 99% of deviations observed were attributed to the random errors. The best fit was the multiphase model (R^2 = 82.5% and CCC = 0.906), and it was the most ($P < 0.05$) accurate and precise model. Best performance of the multiphase model can be attributed to the fact that this model is able to separate animal growth in 3 phases, best describing the seasonal environmental changes that grazing animals are subject to during the year.

Key Words: modeling, Nellore, tropical environment

T132 Dietary fat content and fiber type influence adiposity, lipid oxidative genes and cecal volatile fatty acid concentrations in pigs.

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The interactive effect of fat level and dietary fiber type on performance, backfat thickness and expression of key transcripts involved in energy metabolism was evaluated. Growing pigs (n = 32, initial BW = 10.2 ± 0.15 kg) were allocated randomly to 4 treatments with 2 dietary fat levels; low fat (LF, 3%) and high fat (HF, 17.5%) swine grease as fat source and 2 fiber types (inulin and solka floc, 4% inclusion) in a 2 X 2 factorial design. There were 2 replicates per treatment and 4 pigs per replicate. Pigs were fed ad libitum for 6 wks. At slaughter, liver and mesenteric adipose tissues were collected for gene expression quantification of peroxisome proliferator-activated receptorγ co-activator (PGC1α), peroxisome proliferator-activated receptor α (PPARα), acyl-coA oxidase (ACO) and carnitine palmitoyltransferase 1(CPT1α) via real time PCR. Fecal samples were analyzed for the concentration of key volatile fatty acids. Gene expression data are expressed as normalized values to 18s. There were no interactions between fat level and fiber type for final BW, ADG and G:F ($P > 0.05$). There was an increase in ADG and G:F and a trend ($P = 0.06$) toward increased final BW in HF- than LF-treated pigs. However, no effect of fiber type was found ($P > 0.05$). Pigs fed HF diet had greater ($P < 0.01$) backfat thickness than LF-treated pigs. Inulin reduced the subcutaneous fat deposit in the HF diet pigs ($P < 0.05$). High fat diet also resulted in lower ($P < 0.05$) concentrations of acetate, butyrate and propionate. Inulin tended ($P < 0.07$) to increase propionate concentration compared with cellulose. Expression of PGC1α and PPARα in liver was unaffected by fat level and fiber type ($P > 0.05$). In the liver, Inulin led to increased ($P = 0.04$) expression of ACO expression compared with solka floc (1.53 ± 0.22 vs. 1.10 ± 0.23, respectively). However, no effect of fat level was observed ($P > 0.05$). Pigs fed HF diet had greater ($P = 0.002$) expression of CPT1α in liver tissue than LF diet (1.65 ± 0.20 vs. 0.83 ± 0.18, respectively). High dietary fat level led to a tendency ($P = 0.07$) toward increased CPT1α mRNA abundance in mesenteric fat compared with LF-treated pigs (1.55 ± 0.25 vs. 1.03 ± 0.24, respectively), whereas no effect of fiber type was detected ($P > 0.05$). This study shows that dietary fatty acid and fiber type have a profound influence on adiposity and level of fermentation end products in the hind gut which may affect fatty acid oxidation in distant organs such as the liver.

Key Words: dietary fat, fiber, oxidation

T133 Factors affecting serum IGF-1 and triiodothyronine concentrations as related to fat deposition in feedlot lambs.

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To identify factors affecting serum IGF-1 and T3 concentrations after weaning and their relationship to fat deposition, 115 F_1 lambs (males and females) weaned at 90 d (BW = 17 ± 3.7 kg), sired by Charollais (CH), Dorper (DP), Hampshire (HM), Suffolk (SF) and Texel (TX) rams bred to estrus synchronized-Pelibuey (PB) and Blackbelly (BB) ewes, were utilized. Lambs were individually fed an ad libitum mixed ration in 80 pens (1.25 × 2.45 m) and 35 stalls (0.5 × 1.45 m) and weighed every 14 d until they reached a minimum BW of 42 kg for males and 40 kg for females. Serum concentrations of IGF-1 and T3 at d 14, 42, and 70 of the feeding trial were quantified by RIA. Log-transformed hormone concentrations were analyzed with PROC MIXED of SAS, fitting a linear model with fixed effects of breed of sire (SB), breed of dam (DB), sex, number weaned, management (pen *vs* stall), day of blood sampling, 2-way interactions, and BW at sampling as first and second order covariates. Sire within SB was fitted as a random effect and repeated measures within animal were assumed correlated with an ARH(1) covariance structure. There were management and sex by day and SB by DB interactions ($P < 0.05$) for IGF-1. IGF-1 concentrations were greater ($P < 0.05$) for lambs in pens than for lambs in stalls later on the trial and increased ($P < 0.05$) with time for males but not for females. Lambs from the CH × PB cross had the lowest ($P < 0.05$) IGF-1 concentrations. Pearson correlations ($P < 0.05$) for IGF-1 at d 14, 42, and 70 were −0.42, −0.47 and −0.42 with back fat; −0.54, −0.65 and −0.51 with kidney fat (KF); and −0.36, −0.43 and −0.26 with percent of total carcass fat (PTCF). There were day main effects and sex by management and sex by SB interactions effects ($P < 0.05$) for T3. Mean was greatest ($P < 0.05$) at d 70 and was greater ($P < 0.05$) in females than in males in stalls but not in pens. Also, T3 concentrations were greater ($P < 0.05$) in females than in males for the CH, DP and SF sired breeds, but not for HM and TX. Pearson correlations for T3 were important ($P < 0.05$) only at d 70 with KF (0.23) and at d 14 and 70 with PTCF (−0.40 and −0.21). Serum IGF-1 concentrations in lambs, more than T3, are related to fat deposition as affected by sex, breed, management and days on feed.

Key Words: IGF-1, triiodothyronine, sheep breeds

Lactation Biology II

T134 Effects of feed restriction and prolactin-release inhibition at drying-off on milk production, metabolism and mammary gland involution.

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The risk of acquiring a new intramammary infection during the dry period increases with milk production at drying-off and decreases as mammary gland involution progresses. A method commonly used to reduce milk production is a drastic reduction in feed supply in the days that precede drying-off. Our recent work has shown that milk production can also be reduced by an inhibition of the lactogenic signal driven by prolactin (PRL). To compare these 2 drying-off procedures, 24 Holstein cows in late lactation were assigned to 3 treatments based on milk yield, SCC and parity. They were fed 1) a lactation diet until drying-off (Control), 2) only dry hay the last 5 d before drying-off (Hay), or 3) as Control cows, but received twice daily i.m. injection of quinagolide (4 mg per injection), a specific inhibitor of PRL-release, from 5 d before drying-off to 13 d after (Quin). Cows from Control and Hay treatments received water injections. Blood and mammary secretion samples were collected on the last 7 d before and 1, 3, 5, 7, 10, and 14 d after the last milking. Quinagolide induced a sharp decrease ($P < 0.001$) in basal serum PRL concentrations on all the injection days. Interestingly, PRL was also depressed in Hay cows before drying-off. Both Quin and Hay treatments induced a drop ($P < 0.001$) in milk production, which averaged 17.9 and 10.1 kg/d, respectively, at drying-off compared with 24.8 kg/d for Control cows. Feeding dry hay decreased blood concentrations of glucose ($P < 0.001$) and most aminoacids (12 / 19; $P < 0.05$), and increased blood concentrations of β-hydoxybutyrate and Nonesterified fatty acids significantly ($P < 0.001$), whereas quinagolide did not affect these metabolites. Mammary secretion SCC was greater at d 1 of the dry period in the Hay ($P < 0.001$) and at d 5 in the Quin ($P < 0.05$) than in the Control cows. The BSA concentration increased faster ($P < 0.05$) in the mammary secretion of both Hay and Quin than that of Control cows, whereas the citrate:lactoferrin ratio, another indicator of involution rate, decreased faster ($P < 0.001$). In conclusion, this experiment shows that PRL-release inhibition could be a new alternative to reduce milk production before the drying-off and to hasten mammary gland involution without disturbing the metabolism of the cow. This strategy may reduced the incidence of new intramammary infection at drying-off.

Key Words: quinagolide, dry period, prolactin

T135 Effects of recombinant bovine somatotropin on blood flow to the mammary gland in early lactating Holstein cows.

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Doppler and B-mode ultrasound were used to evaluate the effects of recombinant bovine somatotropin (rBST) administration on mammary gland (MG) blood flow volume (BFV), Resistance Index (RI) and vessel diameter in cycling, lactating Holstein cows. The rBST (n = 4; 500 mg) was administered once at 42 d postpartum, while Control cows (n = 4) received 1.75 mL of saline solution. Ultrasound and temperature recordings were taken at d −7, −5, −2, 0, 1, 2, 5, 7, 9, 12, 14, 16, and 19 and the periods before and after treatment (d 0) were compared. The MG perfusion was characterized by the BFV and RI of the left and right pudendoepigastric trunk arteries (PETA). Additionally, both PETA diameters, posterior skin temperatures (ST) of the MG, and rectal temperatures (RT) were recorded. No differences were observed between the right and left PETA ($P > 0.05$); therefore, both values were combined for further analysis. Administration of rBST increased BFV ($P < 0.001$; 2837.73 ± 99 and 3107 ± 73 mL/min before and after, respectively) and decreased RI ($P < 0.001$; 0.46 ± 0.02 and 0.40 ± 0.01 before and after, respectively). In Control cows, a general decrease in BFV ($P < 0.001$; 3032.47 ± 95 and 2660.60 ± 56 mL/min before and after, respectively) and increase in RI ($P < 0.001$; 0.44 ± 0.02 and 0.51 ± 0.01 before and after, respectively) were observed through the sampling period. The PETA diameters were greatest in rBST treated than in Control cows ($P < 0.01$; 20.29 ± 0.02 and 19.71 ± 0.02 mm, respectively). A positive correlation was observed between the PETA diameter and BFV in Control (r = 0.18; $P < 0.01$) and rBST (r = 0.29; $P < 0.001$) cows, respectively. The ST variability of the MG was increased ($P < 0.05$) by rBST administration. However, RT and milk yield were not affected ($P > 0.05$) by treatment. These preliminary findings suggest that Doppler ultrasound may represent a feasible technique for the study of the vascular perfusion changes in the MG associated with rBST administration. Further studies in later stages of lactation are required to clarify the trends observed in RT and milk yield.

Key Words: mammary gland blood flow, Doppler ultrasound, dairy cows

T136 Effects of colostrum versus formula feeding on hepatic glucocorticoid and α_1- and β_2-adrenergic receptors in neonatal calves.

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Colostrum feeding affects glucose metabolism and the endocrine status in neonatal calves. Cortisol and catecholamines stimulate glycogen degradation and gluconeogenic enzyme activities in liver via glucocorticoid receptors (GR) and α_1- and β_2-adrenergic receptors (AR). We have tested the hypothesis that the number of GR as well as α_1- and β_2-AR in neonatal calves depends on colostrum feeding. We used 14 male German Holstein calves, fed either colostrum or formula for 4 d (group C and F, respectively) twice daily. Nutrients in formula based on milk protein (lactalbumin, casein), lactose, and coconut fat in same amounts as in colostrum milking, but formula contained no biologically active substances such as hormones and growth factors. Amounts (per meal) fed were 4% of BW on d 1 and 5% of BW on d 2 to d 4. On d 4 blood samples were taken to measure plasma concentrations of glucose and cortisol and liver samples were harvested 2 h after feeding. For AR measurements, liver membrane suspensions (2 mg protein/ml) were prepared and saturation binding assays were performed with increasing concentrations of (^{3}H)-prazosin and (^{3}H)-CGP-12177 for determination of α_1- and β_2-AR, respectively. For GR measurements the cytosol fraction (8 mg protein /ml) was incubated with increasing concentrations of (^{3}H)-dexamethasone. Maximal binding capacity (B_{max}) and binding affinity (K_D) were calculated by computer program. Data were analyzed by General Linear Model of SAS with feeding as fixed effect. Plasma

glucose concentrations were higher ($P < 0.05$) in C than F, but plasma cortisol concentrations did not differ between groups. For GR, B_{max} was higher ($P < 0.05$) in C than F, whereas K_D indicated no differences. B_{max} of α_1-AR tended to be higher ($P < 0.1$) in C than F, but K_D of α_1-AR as well as B_{max} and K_D of β_2-AR were not affected by feeding in a significant manner. Results indicated dependence of GR and α_1-AR on milk feeding immediately after birth and pointed at possible involvement of GR and α_1-AR in regulation of neonatal glucose metabolism in calves. Supported by DFG, Germany.

Key Words: calves, colostrum feeding, glucocorticoid and adrenergic receptors

T137 Fitness of lactation curve functions to daily and monthly test-day milk data in an Ethiopian dairy cattle population. G. Gebreyohannes[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], *[1]Kasetsart University, Bangkok, Thailand, [2]University of Florida, Gainesville.*

The objective of this research was to identify a lactation curve function that best fit daily (DD) and monthly test-day milk (MD) data in an Ethiopian dairy cattle population. Three functions were compared: an incomplete gamma (IG), a modified incomplete gamma (MIG; b = 1) and an inverse polynomial (IP). Analysis used 6,707 lactation milk records of 2,066 cows collected from 1979 to 2010 in the Bako, Holetta and Debre Zeit research centers. Breed groups were Horro (H), Boran (B), B-Friesian, H-Friesian, B-Simmental, H-Simmetal, B-Jersey and H-Jersey. The MIG and IG were first log-transformed to linear form before fitting. Goodness of fit of IG, MIG, and IP were compared using R-squared values. Factors affecting R-squared values were analyzed using a model that contained herd-year-season, parity, data type (DD and MD), breed group, lactation curve function and the interaction between data type and lactation curve function as fixed effects, and residual as a random effect. All factors in the model affected R-squared values ($P < 0.001$). Least squares means of R-squared values (LSMR2) were compared among subclasses of each factor. Milk data from cows in later parities (>4 parities; range 0.84 to 0.85) showed significantly higher LSMR2 ($P < 0.001$) than first parity cows (0.80 ± 0.002). The LSMR2 of functions fitted to MD data (0.88 ± 0.001) was higher ($P < 0.001$) than the one for DD data (0.79 ± 0.001). Horro cows had higher LSMR2 (0.86 ± 0.003) than other breed groups (0.77 to 0.85; $P < 0.001$). The MIG (0.90 ± 0.002) and IP (0.90 ± 0.002) functions had similar LSMR2, but both MIG and IP were significantly different from IG (0.71 ± 0.002; $P < 0.001$). The MIG function had the highest LSMR2 for DD data (0.88 ± 0.002), while the IP function had the highest LSMR2 for MD data (0.94 ± 0.002). The MIG and IP functions can be recommended for describing lactation patterns of Ethiopian dairy cattle using daily and test-day milk data, respectively.

Key Words: cattle, lactation curve function, test-day

T138 Effect of rearing intensity on growth performance and on mammary tissue in Holstein yearling heifers. V. Lollivier*[2,1], F. Dessauge[1,2], M. Boutinaud[1,2], and Y. le Cozler[2,1], *[1]INRA, UMR1348 Pegase, Saint-Gilles, France, [2]Agrocampus Ouest, UMR1348 Pegase, Rennes, France.*

Intensive growth during the first months of life influence the shaping animal's final body weight, but if excessive, it may alter the mammary gland development and subsequent milk yield, at least during lactation one. A long-term experiment aimed at studying the effect of growth intensity from birth to insemination in Holstein dairy heifers, combined to a targeted age at first calving of 22 or 24 mo, is being conducted and includes each year 60 to 70 heifers. Preliminary results indicate that the effect of intensive growth on lactation performance could be limited. Moreover, the effect on mammary development remains to be studied. In October 2011, 3 heifers which followed the routine rearing procedure (SP) and 4 heifers which were reared according to the intensive growth program (HP) were slaughtered at one year of age. Body composition and mammary gland weight were measured and mammary tissue morphology was investigated. Average daily gain from birth to slaughter was 874 and 968 g/d for SP and HP heifers, respectively. This corresponded to an average body weight of 358 and 389 kg at 360 and 355 d of age respectively. Mammary gland weight was not significantly affected by the treatment (2.22 vs 2.02 kg for SP and HP heifers, respectively). Impact of growth intensity on lobulo-alveolar mammogenesis was studied through histological analysis of mammary tissue. Results may have implications for understanding control mechanisms that regulate parenchymal development in Holstein heifers.

Key Words: mammogenesis, growth intensity, heifer

T139 Obesity and parity affect the mammary gland serotonin (5-HT) system. K. E. Merriman,* J. LaPorta, and L. L. Hernandez, *University of Wisconsin, Madison.*

5-Hydroxytryptamine (5-HT) is synthesized and secreted by the mammary gland as well as a homeostatic regulator. 5-HT was recently determined to be involved in the mammary gland's response to consumption of high-fat diet (HFD) in rats. The objective of our study was to determine the effects of HFD and a HFD plus vertical sleeve gastrectomy (HFD+VSG) on the mammary gland serotonergic system compared with low-fat diet animals (LFD). We conducted qPCR analysis for the following mRNA in the mammary gland: tryptophan hydroxylase 1 (TPH1), the rate-limiting enzyme in 5-HT synthesis, serotonin reuptake transporter (SERT), responsible for the 5-HT reuptake into the cell for degradation, and the 5-HT 7 receptor subtype (HTR7), responsible for regulating mammary gland involution. We determined that LFD primparous rats had similar expression for TPH1, SERT and HTR7 as nulliparous rats, while multiparous rats had significantly increased TPH1 (30-fold), SERT (700-fold) and HTR7 (6-fold) ($P < 0.05$) expression. In nulliparous HFD and HFD+VSG rats, there was a significant increase in mRNA expression for TPH1 (20, 60-fold, respectively), SERT (325, 75-fold, respectively) and HTR7 (6, 2-fold, respectively) compared with LFD rats ($P < 0.05$). In primparous HFD and HFD+VSG rats there was also a significant increase in mRNA expression for TPH1 (25, 255-fold, respectively), SERT (25, 990-fold, respectively) and HTR7 (70, 12-fold, respectively) compared with LFD rats ($P < 0.05$). There was no difference in the expression of TPH1, SERT and HTR7 compared with LFD rats ($P > 0.05$) in multiparous HFD and HFD+VSG. These results show that LFD rats have increased serotonergic components with increasing parity. Additionally, it is demonstrated that the serotonergic signaling system is over-stimulated in HFD and HFD+VSG rats that are nulliparous and primiparous relative to LFD. This suggests in normal weight animals, as parity increases there is an increase of 5-HT synthesis in the mammary gland that is necessary to maintain mammary gland homeostasis. In obese animals, there is an over-production of 5-HT and signaling within the mammary gland that could lead to issues with mammary gland homeostasis.

Key Words: 5-hydroxytryptamine, obesity, parity

T140 Cooling of heat-stressed cows during the dry period alters lymphocyte but not mammary gland gene expression. S. Tao*[1], E. E. Connor[2], J. W. Bubolz[1], I. M. Thompson[1], B. C. do Amaral[1], M. J. Hayen[1], and G. E. Dahl[1], [1]*University of Florida, Gainesville,* [2]*USDA-ARS, Beltsville, MD.*

Heat stress (HT) during the dry period compromises mammary gland development, decreases future milk production, and impairs immune status of dairy cows. Our objective was to evaluate the effects of cooling heat-stressed cows during the dry period on gene expression of the mammary gland and lymphocytes. Cows were dried off 46 d before their expected calving date and assigned to 2 treatments, HT or cooling (CL). Average temperature-humidity index during treatment was 76.6 for all cows. CL cows were cooled with sprinklers and fans that came on when ambient temperature exceeded 21.1°C, whereas HT cows were not. Rectal temperature (RT) was measured twice daily and respiration rates (RR) recorded thrice weekly during the dry period. After parturition, all cows were housed in a free-stall barn with cooling. Lymphocytes were isolated at dry-off, −20, 2, and 20 d relative to calving from a subset of cows (HT, n = 9; CL, n = 10) and mammary biopsies were taken at the same intervals (HT, n = 7; CL, n = 6) for RNA extraction. Gene expression was assessed using a custom multiplex expression assay based on traditional reverse transcription-PCR. Genes involved in prolactin (PRL) signaling (*PRLR-L*, *PRLR-S*, *SOCS2* and *3*, *IGFII*, *IGFBP5*, and *Cyclin D1*), fatty acid (FA) metabolism (*ACC* and *LPL*) and *IGFI* were evaluated in mammary tissue, and genes related to FA metabolism (*ACC*, *FASN*, and *LPL*), cytokine production (*IL6*, *IL8*, and *TNFα*) and *IGFI* were evaluated in lymphocytes. Data was analyzed by the PROC MIXED procedure of SAS. Compared with HT, CL cows had lower ($P < 0.01$) RT (39.4 vs. 39.0°C) and RR (78 vs. 46 breath/min) in the afternoon before calving. No differences ($P > 0.15$) were observed in PRL signaling or FA metabolism gene expression in the mammary gland. In lymphocytes, HT cows had higher ($P \leq 0.05$) *IGFI* and *TNFα* mRNA expression during the transition period relative to CL and upregulated ($P < 0.05$) *IL8* and downregulated ($P = 0.01$) *FASN* mRNA expression at 2 d relative to calving. We conclude that cooling HT cows during the dry period alters cytokine production and lipid metabolism in lymphocytes.

Key Words: heat stress, lymphocyte, mammary gland

T141 Identification and quantification of milk synthesis and secretion related proteins in bovine milk using a proteomics approach. J. Lu*[1,2], S. Boeren[2], J. Vervoort[2], H. van Valenberg[1], S. de Vries[2], J. van Arendonk[3], T. van Hooijdonk[1,4], and K. Hettinga[1], [1]*Dairy Science and Technology Group, Wageningen University, Wageningen, the Netherlands,* [2]*Laboratory of Biochemistry, Wageningen University, Wageningen, the Netherlands,* [3]*Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands,* [4]*FrieslandCampina, Amersfoort, the Netherlands.*

Lactation physiology is a process that is still partly understood. Proteomics techniques have shown to be useful to help advance the knowledge on lactation physiology in human and rodent species but is rarely used for dairy cows, except for mastitis. In fact, many aspects in bovine milk secretion still need to be investigated in detail and advanced proteomics techniques can help to improve this knowledge. Filter-aided sample preparation (FASP) and NanoLC-Orbitrap-MS/MS were applied to milk fat globule membrane and serum fractions, which were isolated from bovine tank milk samples (65 Holstein cows). This resulted in the identification of 246 proteins. Most proteins were low in abundance. Many of these low abundant proteins were for the first time found in bovine milk. The identified proteins in milk were similar to previous reports on the proteome of cells from mammary gland biopsies. The identified proteins were categorized according to their function description in Uniprot (www.uniprot.org). Sixty-three proteins were found to be directly related to milk component synthesis and secretion. These proteins are mainly enzymes and transporters. Thirteen enzymes which are part of the central metabolic pathway were identified. Eleven enzymes catalyze steps in lipid synthesis, including acetyl-CoA synthetase, fatty acid synthase, glycerol-3-phosphate acyltransferase. Forty-three transporters were identified. These transporters are involved in intracellular transport of lipids, proteins, minerals and vitamins, as well as secretion of these compounds. Butyrophlin, adipophilin, and XDH, which are essential proteins for lipid droplet secretion from epithelial cell, were all found in milk. Besides identification of proteins, dimethyl-labeling was tested to perform relative quantification of the proteins and was shown to give accurate results. The proteins identified to be involved in milk synthesis and secretion suggests that milk may be used rather than more intrusive tissue biopsies in the study of milk synthesis and secretion. These proteomic techniques can be used to solve different biological questions to increase our knowledge of lactation.

Key Words: proteomics, lactation physiology, milk synthesis and secretion

T142 Physiological state but not gestational photoperiod affects weights of liver and thymus in mice. P. A. Bentley* and T. B. McFadden, *University of Alberta, Edmonton, Alberta, Canada.*

Exposing dairy cows to short day photoperiod during gestation increased milk yield by 3 kg/d in the subsequent lactation. Although the mechanisms responsible for this effect are unknown, recent studies in other mammals have shown effects of altered photoperiod on peripheral tissues; such changes could influence milk yield. In this experiment, mice were used to investigate the effects of gestational photoperiod on lactation and development of mammary gland and other organs. We hypothesized that altering photoperiod during gestation would elicit physiological changes causing differences in milk production. Mice (n = 6/treatment x time) were exposed to long (16L:8D), normal (12L:12D) or short (8L:16D) day photoperiod treatment during gestation. Two groups of mice/treatment were sacrificed on d 17 and 19 of gestation. The remaining mice were allowed to pup and after parturition were placed on 12L:12D and litter size was standardized. For all mice, organ weights were determined immediately after sacrifice on d 17 and 19 of gestation and d 5 and 10 of lactation. For lactating mice, litter weight gain was measured daily to estimate milk yield. Data were analyzed for main effects and interaction of photoperiod and time using Proc GLM of SAS. There was no significant effect of photoperiod on litter weight gain during the first 10 d of lactation, nor on organ weights. However, litter weights of dams exposed to long or short day photoperiod were numerically greater after d 5 of lactation than those exposed to normal day length. Dam weight did not vary by photoperiod treatment and was used to normalize organ weights. Liver weights were greater ($P < 0.05$) on d 10 of lactation than during gestation, corresponding to the increased metabolic demand of lactation. Thymus weights decreased ($P < 0.01$) from d 17 to d 19 of gestation but increased ($P < 0.0001$) from d 5 to d 10 of lactation. Differences in thymus weight may reflect altered immune activity during the periparturient period. These data indicate some physiological adaptations to pregnancy and lactation in mice that may provide targets for studying molecular mechanisms involved in similar adaptations in dairy cows.

Key Words: photoperiod, gestation, metabolism

Meat Science and Muscle Biology II

T143 Pearson correlation coefficients of multiple methods for measuring water-holding capacity in two pork muscles. J. W. Rickard[1], Z. D. Callahan*[1], T. A. Wilmoth[2], C. S. Perkins[1], M. E. Wilson[2], and B. R. Wiegand[1], *[1]University of Missouri, Columbia, [2]West Virginia University, Morgantown.*

Water holding capacity is an economically important aspect of fresh and further processed pork. The ability to retain or take up added water contributes to consumer acceptance and the overall eating experience of pork products. The objective of this experiment was to estimate the relationship, via Pearson correlation coefficients, of multiple accepted methods of water holding capacity determination currently employed in academic and industry laboratories. Longissimus dorsi (LD) and lumbar lean (LL) were sampled using a 2.54 cm coring device on 24 h chilled carcasses from 40 individually fed market barrows of the same genetic line. Samples were subject to duplicate determination of water holding capacity using 24 h drip loss (DL), Carver Press method (CPM), vacuum package purge(VPP), and centrifugation (CENT)(1000 x g for 10 min). Additionally, we evaluated the relationship between LD muscle fiber type and diameter, pH 24hr, and various measures of water holding capacity of fresh muscle. Within LD muscle samples, a significant correlation existed for DL and CENT ($P = 0.003$, r = 0.454). Within LL muscle samples, a significant correlation existed for CENT and VPP ($P = 0.003$, r = 0.451). LD VPP was positively correlated to LD primary fiber number ($P = 0.008$, r = 0.523), but negatively correlated to LD secondary fiber number ($P = 0.014$, r = - 0.387). For LD and LL samples subject to CENT, there was a significant and negative correlation to pH 24hr ($P = 0.035$, r = - 0.337 and $P = 0.05$, r = - 0.312, respectively). Finally, in the current study, CPM measures of water holding capacity did not have a significant relationship to any other variable of interest ($P > 0.55$). These results indicate that muscle morphology is related to downstream water holding characteristics of fresh pork muscles. Additionally, the less invasive and less time consuming method of centrifugation (which requires approximately 15 min from sampling to result) might have merit in predicting water holding characteristics of LD and LL from pork carcasses.

Key Words: pork, water-holding capacity, Pearson correlations

T144 Carcass and muscle fiber characteristics of ractopamine fed market pigs with a genetic propensity to deposit significant subcutaneous carcass fat. C. S. Perkins*[1], T. A. Wilmoth[2], Z. E. Kerley[1], Z. D. Callahan[1], M. E. Wilson[2], and B. R. Wiegand[1], *[1]University of Missouri, Columbia, [2]West Virginia University, Morgantown.*

Ractopamine hydrochloride (Paylean) functions as a potent repartitioning agent in growing-finishing pigs with respect to muscle and fat deposition. The objective of this experiment was to assess the extent of fat and lean partitioning in pigs with a propensity to deposit high levels of subcutaneous carcass fat. Additionally, we investigated the change in primary and secondary muscle fiber size and number in this pig model when Paylean was fed at 7.4 ppm for the final 30 d of finishing. Following an approved animal care and use protocol, individually penned, growing (42 kg) barrows (n = 40) were fed a commercial corn-soy diet until they reached 91 kg body weight. Then, barrows were equally and randomly assigned to a diet containing 0 (CON) or 7.4 ppm Paylean (PAY) until they reached 121 kg final wt. Carcass measurements of hot carcass weight (HCW), loin muscle area (LMA), tenth rib fat (TRF), and last rib fat (LRF) were made. Longissimus dorsi (LD) and semitendonosus samples were removed after a 24hr carcass chill. Samples were fixed and used to determine diameter and number of primary and secondary fibers. As expected, PAY diets increased ($P < 0.005$) HCW (86.8 kg vs 94.5 kg) and increased ($P < 0.0001$) LMA (38.45 cm2 vs. 47.22 cm2). However, TRF and LRF were not changed with PAY inclusion ($P = 0.17$ and $P = 0.96$, respectively). Primary muscle fiber diameter was lower ($P = 0.03$) in the LD and tended to be lower ($P = 0.06$) in secondary muscle fibers of the LD for PAY fed pigs. Additionally, primary muscle cell number tended to be lower ($P = 0.63$), but did not differ ($P = 0.42$) for secondary muscle fiber number of the LD for PAY fed pigs. Measures of 24hr drip loss and pH in the LD did not differ ($P > 0.05$), because of treatment. These data indicate that a typical PAY feeding program (7.4 ppm for 30 d) increased muscle mass, but did not decrease subcutaneous fat depth at the tenth and last rib for a genetic line of pigs with a propensity to deposit greater than average subcutaneous carcass fat. Dietary PAY appears to alter some morphological aspects of muscle fiber types in the longissimus muscle.

Key Words: subcutaneous fat, ractopamine, muscle fiber

T145 Shelf stability and quality of fresh ground pork and pork sausage from pigs fed a combination of dried distillers grains with solubles, ractopamine hydrochloride, and conjugated linoleic acid. B. R. Wiegand,* H. L. Evans, Z. D. Callahan, and C. S. Perkins, *University of Missouri, Columbia.*

This experiment evaluated the effects of ractopamine (RAC), conjugated linoleic acid (CLA) and distillers dried grains with solubles (DDGS) on fatty quality and shelf stability of ground pork. Picnic shoulders (n = 72) were selected from pigs fed one of 8 dietary treatments, consisting of 2 levels of DDGS inclusion (0 or 20% DDGS), 2 levels of RAC (0 and 7.4 mg/kg), and 2 levels of CLA (0 and 0.6%). Picnic shoulder trim from each animal was divided into 3 sections and each was assigned to 1 of 3 processing treatments: A) ground pork, B) fresh pork sausage, or C) fresh pork sausage + rosemary extract. Samples were analyzed for fatty acid profiles, TBARS, and color during retail display. Higher IV were seen with DDGS ($P < 0.0001$) and RAC ($P = 0.004$) inclusion and lower IV with CLA ($P < 0.0001$). A significant interaction between RAC and CLA was observed for TBARS (mg malonaldehyde / kg sample) values ($P = 0.03$). In non-RAC fed pigs, CLA decreased TBARS when compared with non CLA fed pigs (0.654 vs. 0.831). Moreover, in non-CLA fed pigs, RAC decreased TBARS from 0.831 to 0.559, indicating that RAC was more effective at lowering TBARS than CLA, but no additive effect was seen on TBARS when both RAC and CLA were fed ($P > 0.05$). Within each processing treatment, RAC inclusion led to decreased ($P < 0.05$) TBARS. In non-RAC fed pigs, processing treatment B resulted in lower TBAR than A; however, processing treatment C had lower TBARS than both A and B. In RAC-fed pigs, no difference existed between process A and B or process B and C ($P > 0.05$); however, TBARS for ground pork (process A) were significantly higher than for pork sausage (process B). Dietary DDGS inclusion did not affect TBARS values ($P = 0.78$). Minolta L* (lightness) reflectance values were lower for DDGS-fed pigs over the entire display period (52.97 vs. 53.87; $P = 0.02$). Additionally, an interaction was observed between RAC and processing treatment for L* values ($P = 0.01$). Within processing treatments B and C, RAC inclusion led to lower L* reflectance values when compared with non-RAC fed pigs. Dietary fat source influences pork meat fatty acid profile and shelf-life can be extended with addition of rosemary as an antioxidant in pork sausage.

Key Words: pork, fat quality, shelf life

T146 Effects of genotype and dietary oil supplementation in pigs. 2. Pork quality and fatty acid composition.

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A 42 d study was carried out to evaluate the effect of genotype (GEN): terminal sire line Duroc × F1 (DC×F1); terminal sire line Embrapa MS115 × F1 (MS115×F1); and MS115 × Moura (MS115×MO) and 3 dietary oils (DIET): 3% soybean oil (SBO); 3% canola oil (CAN); and 1.5% canola oil + 1.5% flax oil (CAN+FLX), on pork quality and fatty acid composition. Ninety animals (45 barrows and 45 gilts) averaging 130.7 ± 3 d of age were utilized, 15 barrows and 15 gilts of each GEN per diet. The progeny of MS-115 sire line showed higher ($P < 0.05$) pH values at 45 min and 24 h post slaughter than DC×F1 pigs. The DCxF1 pigs had lower ($P < 0.05$) a* values and higher ($P < 0.05$) L* values than the other GEN. The highest ($P < 0.05$) content of intramuscular fat (IMF) was observed in DC×F1 pigs, followed by MS115×MO and MS115×F1 with the lowest values. Shear force was higher ($P < 0.01$) in MS115×F1 pigs, followed by DC×F1 and the lowest values observed in the MS115×MO. DIET did not affect meat quality, except marbling, which was higher ($P < 0.05$) in pigs fed CAN compared with CAN+FLX. DC×F1 pigs showed the highest values ($P < 0.01$) of C14:0, C16:0, C18:0, C16:1, and C18:1 fatty acids (FA), while MS115×F1 pigs had the highest ($P < 0.01$) content of C18:2, C18:3, C20:2, and C20:4 and the lowest ($P < 0.001$) content of C14:0, C16:0, and C18:1 in the loin. CAN or CAN+FLX oils provided higher ($P < 0.01$) content of C18:1 and lower ($P < 0.01$) content of C18:2 and C20:2. C18:3 was higher ($P < 0.01$) in the loin of pigs fed CAN+FLX and in the backfat of pigs fed CAN or CAN+FLX. The n-6/n-3 ratio was 14.61, 11.30, and 6.46 in the loin and 8.89, 6.68 and 3.77 in the backfat, for SBO, CAN and CAN+FLX oils, respectively. In conclusion, MS-115 sire line positively influenced meat color, but when crossed with F1 females reduced tenderness and IMF. Duroc sire line positively influenced the IMF. Moura breed positively influenced meat tenderness and IMF. Supplementing the diet with CAN or CAN+FLX oils provided higher monounsaturated and C18:3 and lower C18:2 FA, reducing the n-6/n-3 ratio, than supplementing SBO oil. CAN+FLX DIET provided the best n-6/n-3 ratio.

Key Words: canola oil, flax oil, soybean oil

T147 Effects of antibiotics on growth performance, plasma biochemical index and meat quality of growing-finishing pigs.

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To investigate the effects of antibiotics on growth performance, plasma biochemical index and meat quality of growing-finishing pigs, 1010 weaned piglets (average weight of 6.5 ± 1.5 kg) were chosen and grouped into 2 groups: control group (antibiotic-free group, 350 piglets) and antibiotics group (660 piglets), and fed with the same base diet. The diet in the antibiotics group supplemented with antibiotics (aureomycin 800 ppm, olaquindox 100 ppm and colistin 800 ppm) from d 28 to 120 (first stage), while the control group didn′t use any antibiotics. On d 120 and 180, 6 piglets from each treatment were selected randomly and slaughtered for tissue sampling, respectively. The results showed that mortality of pigs in the first stage was lower in the antibiotics group ($P < 0.05$), and the ADG and AIDF tended to be higher; however, ADFI and ADG tended to be lower in the second stage. Compared with the antibiotic-free diet, antibiotics tended to increase plasma IgG and IgM in the first stage, while decrease in the second stage; blood glucose had a similar change. Antibiotics decreased plasma urea in the first stage ($P < 0.05$), however, plasma urea tended to be higher in the second stage. Plasma cholesterol was lower in the control group in the second stage ($P < 0.05$). It is interesting that antibiotics resulted in a significant decrease in plasma Fe in the first stage ($P < 0.05$), and plasma Total Iron Binding in the antibiotic-free group was higher ($P < 0.05$). The result from the evaluation of meat quality showed that brightness of the meat from the antibiotic-free group had a decreasing trend, and red scale had an increasing trend. These data suggest that the use of antibiotics postweaning decreased feed efficiency in a extended period, and also decreased meat quality.

Key Words: antibiotics, meat quality, pig

T148 Effects of level of feeding and breed on fatty acid profile of meat from Brazilian native goats.

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Goat meat is an important protein source for Brazilian semi-arid's population. The meat composition can be affected by breed, age, gender and nutrition. The aim of this study was to evaluate the effects of 3 breed groups (Canindé, Moxotó and F1 Boer × nondescript breed) and 3 feeding levels on fatty acid profile of goat meat, using a 3 × 3 factorial design. Forty-five goats (15 of each breed group), with average initial body weight of 15 kg were used. Five goats of each breed group were randomly allocated to one of the following treatments: ad libitum intake, restricted fed at 75% of the ad libitum intake and restricted fed at 50% of the ad libitum intake. The diet consisted of 40% of Elephant grass and 60% of concentrate. Animals were kept in individual stalls, partially shaded, in the middle of a native Caatinga area, to simulate the semi-arid environment. After 90 d on feed, all animal were slaughtered and the carcasses were dissected into meat and bone. The meat was then ground and sampled. The fatty acid profile was accessed by gas chromatography. There was no interaction between level of feeding and breed group ($P > 0.10$). The polyunsaturated fatty acid concentration was higher ($P < 0.05$) in Moxotó than in F1 Boer group. The n-3 content in F1 Boer was greater ($P < 0.05$) than in Moxotó. There were no differences ($P > 0.05$) among breeds for the other fatty acids. For the levels of consumption, the ad libitum treatment had higher ($P < 0.05$) concentration of oleic (C18:1 c9), conjugated linoleic acids (C18:2 c9t11), unsaturated and monounsaturated fatty acids and lower ($P < 0.05$) levels of saturated fatty acids than the restricted fed treatments. The n-3 concentration was higher ($P < 0.05$) in the treatment with 50% restriction. As a conclusion, breed has a small effect on meat fatty acid profile, but the level of consumption affects the fatty acid profile of goat meat. Funded by FAPEMIG and CNPq.

Key Words: CLA, fat, intake

T149 Effect of dietary organic chromium on meat quality of Mahabadi goat kids.

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The objective of this study was to evaluate the possible effect of different levels of dietary chromium from chromium-methionine (Cr-Met) on meat quality of Mahabadi goat kids. Thirty-two male kids (BW = 22 ± 2 kg, 4 Mo) were used in a completely randomized design with 4 treatments: 1) control (without Cr), 2) 0.5, 3) 1.0 and 4) 1.5 mg Cr as Cr-Met/animal/d. Diets were formulated for NRC requirements with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Diets were the same, except for top-dress addition of Cr-Met fed in 2 equal meals (0800 and 1600 h). Experimental period was 90 d. At the end of the trial, kids were weighed and slaughtered following 16-h fasting. Meat samples were taken from the longissimus dorsi muscle (LDM). Color (lightness (L*), redness (a*) and yellowness (b*)), and pH of LDM were measured at 24 h after slaughter. Some of the LDM were immediately stored at −20°C for assessing moisture, intramuscular fat and crude protein content. Cooking loss (CL) was determined by weighing the samples before and directly after cooking in a water bath at 70°C for 1 h. Percentage of CL was calculated. Data were analyzed by the GLM procedure of SAS 9.1 and Tukey test ($P \leq 0.05$). PH, lightness, moisture (%), intramuscular fat (%), crude protein content (%) and CL percentage were not affected by Cr supplementation ($P > 0.05$). However, chromium supplementation decreased redness ($P = 0.02$) and yellowness ($P = 0.01$) of LDM. These results suggest that supplementing diet with Cr-Met did not influence the meat quality but decreased redness and yellowness of LDM in Iranian Mahabadi goat kids.

Table 1. Meat quality of kids fed different levels of Cr-Met

	Treatment (mg of CR)				
Trait	Control	0.5	1.0	1.5	SEM
pH	5.74	5.83	5.74	5.84	0.06
L*	49.15	44.91	48.95	48.56	1.57
A*	14.52^{a}	14.27^{a}	13.97^{ab}	13.15^{b}	0.32
b*	10.55^{a}	10.01^{a}	10.65^{a}	8.92^{b}	0.30
CK%	22.93	23.49	26.22	21.68	2.04
Fat%	1.91	1.96	2.42	2.15	0.69
Moisture%	71.32	68.89	72.99	75.11	2.73

^{a,b}Means in each row with different superscripts were statistically different ($P > 0.05$).

Key Words: meat quality, intramuscular fat, cooking loss

T150 Influence of dietary zilpaterol hydrochloride on finishing performance, carcass characteristics and meat quality of castrated male goats.

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The effects of β-2 agonist zilpaterol hydrochloride (ZH) supplementing on growth performance, carcass characteristics, longissimus muscle (LM) composition and meat quality characteristics (cooking loss and Warner-Bratzler shear force (WBSF)) in male goats were investigated. Sixteen Mahabadi castrated male goats (6 mo old and 23 ± 4.4 kg live body weight) were fed with the finishing diet based on 2.35 Mcal ME and 15.23%CP for 93 d (feedlot period). The goats were assigned to 2 treatment (ZH and control) arrangements in a completely randomized design. After 60 d of feedlot period, 8 castrated goats were treated to 0.2 mg/kg live body weight ZH for 30 d with 3 d as the withdrawn period. Then, all the goats (n = 16) were harvested and, their carcasses were stored at 0–2°C for 48h. The meat composition and quality were determined by standard procedures of the AOAC (1990) and AMSA (1995), respectively. The data collected from dry matter intake, total live body weight, postmortem aging for WBSF and cooking loss were analyzed by MIXED procedure, and the data obtained from other studied parameters were analyzed by GLM procedure of SAS software. Results showed that ZH decreased ($P < 0.01$) dry matter intake and increased total live body weight in the end of feedlot period ($P = 0.02$). These parameters improved feed efficiency ($P < 0.01$) and average daily gain ($P = 0.02$). After slaughter, it was clearly observed that ZH increased ($P < 0.01$) hot carcass weight and LM area and decreased back fat thickness and improved carcass dressing yield ($P < 0.01$). ZH led to increased WBSF values, cooking loss percentage, protein and moisture contents ($P < 0.01$), whereas it decreased fat content in LM ($P = 0.02$). Likewise, the postmortem aging decreased WBSF value in the LM muscle of ZH and control ($P < 0.01$). These results indicate that ZH has positive effects on enhancing feedlot performance and carcass efficiency, and improves some chemical compounds in castrated male goat meat. However, supplementation of this β-2 agonist can adversely affect meat quality characteristics.

Key Words: zilpaterol hydrochloride, meat quality, carcass characteristics

T151 Effect of diet linseed supplementation in ewes during gestation and lactation on fatty acid profile of suckling lamb meat.

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The polyunsaturated n-3 fatty acids (PUFA n3) contained in the human diet are essential for regular growth and development. Thus the increase of PUFA n3 content in meat represents a primary task in applied animal science. In this work, the effect of α-linolenic acid (ALA) diet supplementation of dairy ewes during pregnancy and early lactation on ALA conversion into longer-chain PUFA (C20:5, EPA; C22:5, DPA; C22:6, DHA) in muscle of 28 suckling lambs was investigated. Twenty-eight Sarda dairy ewes were divided in 4 groups and fed one of the dietary treatment from approximately the last 8 weeks of gestation to the first 4 weeks of lactation. A control diet (CONT) and an ALA enriched diet by adding lineseed (LIN) were used. The 4 dietary treatments consisted of gestation/lactation feeding of ewes to give CONT/CONT, CONT/LIN, LIN/LIN or LIN/CONT lambs. Lambs were slaughtered at 4 weeks of age. After 24 h at 4°C, the longissimus dorsi muscle was dissected from each right half-carcass. Fatty acid composition of intramuscular fat was determined by gas-chromatography. The effect of ALA supplementation during gestation, lactation or both on PUFAn3 was tested by one way ANOVA using dietary treatment as the main effect. The LIN/LIN treatment resulted in a significantly higher content of ALA (almost 3-fold; $P < 0.01$) and EPA (2-fold; $P < 0.01$) compared with the CONT/CONT. The LIN supplementation only during gestation (LIN/CON) decrease the ALA and EPA concentration compared with LIN/LIN group. Feeding the LIN only during lactation determined lower values for EPA (−50%; $P < 0.01$) and ALA (−24%; $P = 0.07$) compared with LIN/LIN group. These results evidenced that a continuous linseed supplementation during gestation and lactation resulted in an increase in muscle ALA concentration and in a conversion to its longer-chain metabolite EPA but not in DHA. From a nutritional point of view, the lineseed supplementation during all experimental periods resulted in a increase of PUFA n3 in lamb meat of 74%. Research supported by Cargill - Animal Nutrition Division, Milan, Italy.

Key Words: lamb meat, PUFA n-3, maternal linseed diet

T152 The influences of intermittent feeding zilpaterol hydrochloride during two last week finishing period on growth performance in Japanese quails. A. Towhidi,* M. Mohammadi Arekhlo, H. Moravej, and A. Zare Shahneh, *Department of Animal Science, College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran.*

Zilpaterol hydrochloride is a β-adrenergic agonist which has been shown to increase lean muscle and decrease fat deposition. The objective of this study was to determine the effect of intermittent feeding of zilpaterol hydrochloride (ZH) on growth performance of Japanese quails. 128 male quails at 33 d of age were divided into 4 treatments. Each treatment consisted of 4 replicates of 8 birds. Diets were based on corn and soybean meal during the finisher period (24% CP and 2.9 Mcal/kg of ME). The birds intermittently (2 d on, 2 d off) received different levels of ZH including 0, 0.2, 0.225, or 0.25 mg/kg of live weight. The treatment diets were fed until 47 d of age and then ZH was withdrawn 3 d before slaughter at d 50. Data were analyzed using the GLM procedure in SAS. Results showed that ZH supplementation improved weight gain ($P < 0.05$), and feed efficiency ($P < 0.01$) in treated groups compared with control diet, but did not affect feed intake. The highest feed efficiency belonged to the 0.225 mg/kg live weight treatment. Quails fed zilpaterol hydrochloride had lower abdominal and subcutaneous fat ($P < 0.05$) compared with the control. Dietary zilpaterol hydrochloride did not affect carcass, thigh, breast and liver weight. It was concluded that intermittent feeding of zilpaterol hydrochloride improved growth performance in Japanese quail.

Key Words: β2-agonist, body weight, Japanese quail

Nonruminant Nutrition: Feed Ingredients

T153 Dietary *Aspilia africana* leaf on nutrients digestibility and physio-chemical properties of intestinal segments in quails. O. O. K. Oko,* E. A. Agiang, and I. E. Iso, *University of Calabar, University of Calabar, Calabar, Cross River State, Nigeria.*

The prohibition of most synthetic growth promoters is steering increasing interest in phytobiotics as possible alternatives. Phytobiotics are heterogeneous groups of feed additives originating from fruits, herbs and spices. This study evaluated the effects of *Aspilia africana* leaf (AaL) products on nutrients digestibility and physio-chemical properties of intestinal segments in quails. A total of 420, 1-wk-old quails were assigned to 14 treatments; representing supplementation with 0% (control), 2.5, 5.0, 7.5 or 10% of either meal, aqueous or ethanolic extract of AaL, or 0.02 g/kg terramycin (antibiotic) to a corn and soybean meal based-diet for 42 d (n = 30 chicks per treatment). Each treatment had 3 pens of 10 chicks/pen. On d 36, a digestibility trial involving 12 quails per treatment was initiated. Feed and fecal samples were collected for 4 d and the apparent nutrient digestibility for crude protein, fat, fiber and ash were analyzed. On d 42, quails were euthanized and their intestinal tracts were excised and segmented. The weight, length and density of each segment were measured and 1 mL of digesta was obtained for pH determination. Data were subjected to a 2-way ANOVA. Results indicated that, compared with the control, 5 to 7.5% AaL and antibiotic improved ($P \geq 0.05$) nutrient digestibility in quails; values were higher in quails fed 5 to 7.5% AaL than those on the antibiotic for digestible protein (2.84% v 0.50%), fat (4.82% v 1.42%) and fiber (4.15% v 3.48%). Intestinal length and densities were not affected ($P \geq 0.05$) by dietary treatments. Intestinal weights were reduced ($P \leq 0.05$) by an average of 22.21% and 32.64% in quails fed AaL and terramycin diets, respectively. Also, the pH of contents from the cecum and jejunum were reduced ($P \leq 0.05$) by 0.88 and 0.50 units, respectively, in AaL-fed quails. Comparatively, the aqueous extract exerted higher phytogenic effects on the physio-chemical properties of the intestinal segments in quails than the meal or ethanolic extract. These findings indicate that dietary supplementation with 5 to 7.5% aqueous extract of *Aspilia africana* leaf could modulate the intestinal characteristics of quails, thus enhancing nutrient digestion.

Key Words: quail, phytobiotics, digestion enhancer

T154 Effects of egg by-product supplementation on the egg production, nutrient digestibility, egg quality, blood profiles, and fecal noxious gas emission in laying hens. L. Yan,* J. P. Wang, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choongnam, South Korea.*

A total of 288 42-week-old ISA-brown laying hens were used in a 5-week feeding trial to investigate the effects of egg by-product supplementation on the egg production, nutrient digestibility, egg quality, blood profiles, and fecal noxious gas emission. Hens were randomly allotted into 4 treatments with 12 replications (6 layers per replication) per treatment according to their initial BW. Dietary treatments were: 1) CON (basal diet); 2) EP1 (basal diet + 1% egg by-product); 3) EP2 (basal diet + 2% egg by-product); 4) EP3 (basal diet + 3% egg by-product). Egg by-product used in this trial consisted of 44.01% DM and 15.86% CP (feed basis). All diets were formulated to meet or exceed the NRC (1994) requirements for laying hens. Hens were individually caged and provided with 16 h of light daily. All cages were equipped with nipple drinkers and common trough feeders, experimental feed and water were provided ad libitum throughout the experimental period. The hens were housed in a windowless laying house at approximately 21°C. All statistical analyses were conducted in accordance with a randomized complete block design, using the GLM procedures of SAS software package (1996). Overall, administration of egg by-product led to a higher ($P < 0.05$) egg production and egg weight compared with the CON group. However, the nutrient digestibility, blood profiles, and fecal noxious gas emission were not affected ($P > 0.05$) by dietary egg by-product supplementation throughout the experimental period. The inclusion of egg by-product increased ($P < 0.05$) yolk height, yolk color, and egg gravity compared with the CON group. Hens fed the egg by-product supplemented diets led to a higher ($P < 0.05$) eggshell thickness and egg shell strength compared with the CON group. No difference was observed ($P > 0.05$) in the haugh unit throughout the experiment. In conclusion, results indicated that egg by-product could be used as a good material in laying hens to improve egg production and egg quality.

Key Words: laying hen, egg by-product, egg quality

T155 Economic evaluation of increasing levels of acerola meal replacing corn in the diet of broilers. V. C. da Cruz*[1], L. H. Zanetti[1], G. do Valle Polycarpo[2], R. F. de Oliveira[1], A. L. C. Brichi[1], L. C. Carvalho[1], O. J. Sabbag[1], and C. C. do Valle Polycarpo[3], *[1]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil, [2]University of São Paulo, Pirassunununga Campus, Pirassununga, São Paulo, Brazil, [3]São Paulo State University, São José do Rio Preto Campus, São José do Rio Preto, São Paulo, Brazil.*

The aim of this study was evaluate economically the different additions of acerola meal (AM) replacing corn (C) in diets of broilers from 1 to 42-d-old. Nine hundred eighty 1-d-old male Cobb chicks were allotted in a completely randomized design with 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 per experimental unit. AM addition was performed in relation to the percentage of corn inclusion in diet. The nutritional composition of AM was: 89.15% (DM), 8.36% (CP), 4.57% (EE), 3.19% (MM), 46.27% (CF), 50.86% (NDF), and 41.33% (ADF). An increase in the cost of the rations was observed at levels above 5% inclusion of AM replacing C. Diet with inclusion of 5% of AM showed better cost of feed (US$912.61) with a value similar to the control diet (US$913.87). Diets with higher inclusion levels (10 and 15% replacing C) had higher costs (US$1,008.17 and US$1,014.46, respectively), probably by the greater inclusion of soybean oil to keep the diets isocaloric. Because it is an ingredient with low-energy (756 kcal/kg AMEn), the AM (US$ 0.598/kg) used in diets for broilers, must be accompanied by the addition of soybean oil, therefore not causing an effective reduction in the cost per kg of ration. It was observed better value for operating profit, profitability index and final cost/bird for the treatment with 10% inclusion of AM, possibly because this diet provided lower mortality in the experiment; thus, making it more viable economically. The use of AM in diets for broilers can be advantageous in off-season periods, when the price of corn and soybeans are high. The use of alternative ingredients is directly related to the price of traditional feedstock such as corn and soybean meal, as well as the cost of possible supplementation to maintain adequate nutritional levels to animal performance. Thus, the experimental diet with 5% inclusion of AM has lower total cost. However, observing operating profit and profitability index, better values are found in treatment with 10% inclusion of AM.

Key Words: poultry, economic viability, residue byproducts

T156 Effects of egg by-product supplementation on growth performance, nutrient digestibility, blood profiles, relative organ weights, and meat quality in broiler. H. Y. Baek,* Z. F. Zhang, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choongnam, South Korea.*

A total of six hundred sixty 1-d-old ROSS 308 broilers (BW = 39.2 ± 0.1 g) were used in a 35-d experiment to evaluate the effect of egg by-product on growth performance, apparent total tract digestibility (ATTD), blood profiles, relative organ weight, and meat quality. Broilers were randomly assigned to 4 dietary treatments with 11 replicate pens per treatment and 15 broilers per pen. Treatments were: 1) CON, basal diet; 2) EP1, CON + 1% egg by-product; 3) EP2, CON + 2% egg by-product, and 4) EP3, CON + 3% egg by-product. During d 1–12, feed conversion rate (FCR) was lower ($P < 0.05$) in EP3 treatment than that in CON treatment, though BWG and FI were not affected ($P > 0.05$) by dietary treatments. During d 12–26, BWG and FCR were improved ($P < 0.05$) in EP3 treatment relative to CON and EP1 treatments. During d 26–36, no differences ($P > 0.05$) were noted in BWG, FI and FCR among treatments. Overall, BWG was higher ($P < 0.05$) in EP3 treatment than that in CON treatment, and FCR was lower ($P < 0.05$) in EP3 treatment than CON, EP1 and EP2 treatments. The ATTD of energy was higher ($P < 0.05$) in EP2 and EP3 treatments compared with CON treatment, but no differences ($P > 0.05$) were noted in the ATTD of DM and N among treatments. The concentration of leukocytes was higher ($P < 0.05$) in EP3 treatment than that in CON and EP2 treatments on d 35 of the experiment. Relative organ weight was not affected ($P > 0.05$) by supplementation of egg by-product. Drip loss was lower ($P < 0.05$) in EP2 and EP3 treatments than that in CON treatment. In conclusion, dietary supplementation with 3% egg by-product may improve growth performance, nutrient digestibility, and increase the concentration of leukocytes in broilers.

Key Words: egg by-product, growth performance, broilers

T157 A survey of free and conjugated deoxynivalenol in European feedstuffs. S.-T. Tran* and T. K. Smith, *Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Deoxynivalenol (DON, vomitoxin), produced by many *Fusarium* species, is one of the most widely distributed mycotoxins globally and is found as a contaminant of cereal grains such as corn, wheat, barley and triticale. Recent studies have described the presence of conjugated forms of DON which are produced by the plant after invasion by the fungus. The aim of the current study was, therefore, to investigate the natural occurrence of free and conjugated DON in European feedstuffs. Free and conjugated DON were determined in 118 feed samples collected in 2011 from Denmark, France, the Netherlands and Russia. Free DON was absent in 26 samples. Levels of free DON ranged from 0.10 to 10.80 µg/g. The highest levels of free DON were found in French samples while Dutch and Russian samples were much less contaminated and French samples contained the highest average free DON concentrations. Conjugated DON was detected in 36%, 38%, 52% and 70% of contaminated samples from Denmark, France, the Netherlands and Russia, respectively. High levels of conjugated DON (>20%) were detected in the majority of Russian samples (17 of 21) and French samples (4 of 12) but no significant differences between concentrations of free DON and total DON content were observed within each country. Samples highly contaminated with DON did not necessarily show a high concentration of conjugated DON. The current survey of free and conjugated DON in European feedstuffs emphasizes the potential challenges in understanding the hazard posed by DON concentration. Although much research has been carried out since the original discovery of free and conjugated DON, the significance of these mycotoxins for animal health remains to be determined.

Key Words: deoxynivalenol, conjugated, feedstuffs

T158 Effects of sorghum particle size on growth performance and carcass characteristics in finishing pigs. C. B. Paulk,* J. D. Hancock, A. C. Fahrenholz, J. M. Wilson, L. J. McKinney, and K. C. Behnke, *Kansas State University, Manhattan.*

A total of 200 finishing pigs (PIC TR4 × 1050; initially 54 kg) were used in a 69-d growth assay to determine the effects of sorghum particle size on growth performance and carcass characteristics. Pigs were sorted by sex, ancestry, and BW with 5 pigs per pen and 10 pens per treatment. Treatments were a corn-soybean meal-based control with the corn milled to a target particle size of 600 µm and sorghum milled to target particle sizes of 800, 600, and 400 µm. Actual mean particle sizes were 555 µm for corn and 724, 573, and 319 µm for sorghum. Pigs were slaughtered (average final BW of 123 kg) at a commercial abattoir and hot carcass weight (HCW) was used as a covariate for analyses of backfat thickness, loin depth, and percentage fat free lean index (FFLI). Pigs fed the sorghum-based treatments were not different ($P > 0.12$) in growth performance, HCW, backfat thickness, loin depth, or FFLI compared with those fed the corn control; however, there was a tendency for pigs fed sorghum based treatments to have improved ($P < 0.07$) dressing percentage. As particle size of sorghum was reduced from 724 to 319 µm, ADG was not affected ($P > 0.39$) but G:F increased (linear effect, $P < 0.01$). Reducing particle size of sorghum had no effect ($P > 0.15$) on HCW, backfat thickness, loin depth, or FFLI, but dressing percentage tended to improve ($P < 0.06$). Regression analysis indicated that sorghum ground to 515 µm supported G:F equal to that of corn ground to 555 µm. In conclusion, linear improvements in G:F were demonstrated with reduction of sorghum particle size from 724 to 319 µm. Moreover, our data suggest that when ground 50 µm finer than corn, sorghum-based diets will support growth performance and carcass measurements equal to corn-based diets.

Table 1.

Item	Corn, 555 µm	Sorghum, 724 µm	Sorghum, 573 µm	Sorghum, 319 µm	SE
ADG, g	1,078	1,128	1,103	1,100	23
ADFI, kg	2.90	3.10	2.99	2.91	0.07
G:F, g/kg	372	365	369	379	4
HCW, kg	88.1	90.6	89.7	90.0	1.8
Dress, %	72.5	72.7	73.0	73.2	0.2
Backfat thickness, mm	22.7	22.1	22.1	22.4	0.9
Loin depth, mm	59.7	60.9	59.9	59.4	0.9
FFLI, %	49.2	49.7	49.5	49.3	0.6

Key Words: sorghum, particle size, finishing pigs

T159 Chemical composition of canola meal, 00-rapeseed meal, and 00-rapeseed expellers. T. Maison* and H. H. Stein, *University of Illinois, Urbana.*

The objective of this work was to compare the chemical composition of canola meal, 00-rapeseed meal, and 00-rapeseed expellers. Eleven samples of canola meal were collected from crushing plants in North America, and 10 samples of 00-rapeseed meal and 5 samples of 00-rapeseed expellers were collected from crushing plants in Europe. All samples were analyzed for GE, DM, CP, AA, ash, acid hydrolyzed ether extract (AEE), crude fiber, ADF, NDF, ADL, glucose, fructose, maltose, sucrose, raffinose, stachyose, verbascose, starch, Ca, K, Mg, Na, P, S, Co, Cr, Cu, Fe, Mn, Mo, Se, Zn, phytic acid, and glucosinolates. Concentrations of these components in canola meals were compared with those in 00-rapeseed meals, and 00-rapeseed meals were compared with 00-rapeseed expellers. Results indicated that concentrations of sucrose, P, K, Zn, and glucosinolates are greater ($P < 0.05$) in 00-rapeseed meal than in canola meal. Concentrations of GE and AEE are greater ($P < 0.05$) in 00-rapeseed expellers than in 00-rapeseed meal, but concentrations of CP, Thr, ash, sucrose, crude fiber, NDF, ADL, Ca, K, Mg, P, S, and Mo, are greater ($P < 0.05$) in 00-rapeseed meal than in 00-rapeseed expellers. For canola meal, concentrations of CP, Ca, Fe, and Mn are greater than values published by NRC (1998), but concentrations of most other nutrients in canola meal are in good agreement with NRC (1998) values. In conclusion, the concentration of glucosinolates is much less in canola meal than in 00-rapeseed meal, and concentrations of AEE and GE are greater in 00-rapeseed expellers than in 00-rapeseed meal. However, concentrations of most other nutrients are greater in 00-rapeseed mal than in 00-rapeseed expellers.

Table 1. Composition of canola meal (CM), 00-rapeseed meal (RSM), and 00 rapeseed expellers (RSE), DM-basis

Item	CM	RSM	RSE
GE,[1] kcal/kg	4,708	4,734	5,143
CP,[2] %	41.4	40.7	38.8
Fat,[1] %	4.3	4.1	12.6
NDF,[2] %	33.6	33.8	27.0
Ash,[2] %	7.9	7.8	6.8
Glucosinolates[3], μmol/g	3.6	11.3	14.5

[1] 00-rapeseed expellers greater than 00-rapeseed meal ($P < 0.05$).
[2] 00-rapeseed meal greater than 00-rapeseed expellers ($P < 0.05$).
[3] Canola meal greater than 00-rapeseed meal ($P < 0.05$).

Key Words: canola meal, composition, rapeseed meal

T160 Comparison of growth performance of pigs fed cull chickpeas high in fiber.

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The objective of this experiment was to determine the effect of substituting high-fiber (11.3% crude fiber, CF) cull chickpeas for soybean meal and corn on growth performance in pigs. Forty-eight pigs (BW = 32.158 ± 1.148 kg; Large White × Landrace × Large White × Pietrain) in groups of 4 were placed in 12 concrete floor pens (1.5 × 6 m). In a complete randomized experimental design, pigs received one of 3 diets: 1) diet with 17.8% CP, 3.27 Mcal of ME/kg, 0.99% Lys and CF 3.47%; containing 71.5% corn, 26% soybean meal and 2.5% premix (CONT); 2) diet with 17.8% CP and 3.23 Mcal of ME/kg, 1.01% Lys, 5.95% CF, with 47.2% corn, 35% cull chickpeas, 13% soybean meal, 2.3% vegetable oil and 2.5% premix (CHP35), and 3) diet with 17.5% CP and 3.20 Mcal of ME/kg, 1.03% Lys, 8.42% CF, with 22.5% corn, 70% cull chickpeas, 5.0% vegetable oil and 2.5% premix (CHP70). Pigs were weighed at d 0 and 42 of the experiment and feed intake was recorded daily. Average daily gain and feed intake/gain ratio were calculated from these data. Body weight at d 42 was reduced ($P = 0.01$) in pigs fed diets containing cull chickpeas, being 69.8, 58.5 and 47.1 kg for CONT, CHP35 and CHP70, respectively. Average daily gain (0.837 CONT, 0.623 CHP35, and 0.358 kg CHP70) was also reduced ($P = 0.01$) by treatments containing cull chickpeas. Feed intake (2.088, 1.656 and 1.154 kg) was reduced in pigs fed cull chickpeas ($P = 0.01$). Feed/gain ratios (2.687, 2.663 and 3.289) were similar ($P = 0.16$) across treatments. Thus, we concluded that high-fiber cull chickpeas fed at 35% or more of the diet negatively affects growth performance of growing pigs.

Key Words: chickpeas, growth performance, pigs

T161 Standardized ileal digestibility of Illinois bundleflower, low-oligosaccharide soybean meal and conventional soybean meal.

J. A. Jendza* and S. K. Baidoo, *University of Minnesota, Waseca.*

Twenty-four growing pigs were fitted with ileal T-cannula, housed in individual metabolism crates, and used to determine the standardized ieal digestibility (SID) of low-oligosaccharide soybean meal (LOSBM), conventional soybean meal (SBM) and Illinois bundleflower (IBF). The lower fiber content of LOSBM results in higher analyzed concentration of CP and amino acid when compared with SBM. The reduced fiber content in LOSBM was also expected to improve SID of protein and amino acids as compared with SBM. Illinois bundleflower is a relatively novel, high-protein feedstuff for which little nutritional data are available. Treatments consisted of 3 diets formulated to supply all protein from a single source and a fourth N-free diet made primarily from cornstarch and sucrose. Diet 1 contained 33.6% IBF, and supplied 12% CP and 3,600 kcal/kg of DE. Diet 2 contained 25.3% SBM, and supplied 12% CP and 3,725 kcal/kg of DE. Diet 3 contained 22.6% LOSBM, and supplied 12% CP and 3,770 kcal/kg of DE. Diet 4 contained no source of protein, supplied 3,791 kcal/kg of DE, and was used to calculated basal endogenous losses. Digestibility results were compared across treatments using a multiple comparison test, the Tukey adjustment, and with $\alpha = 0.05$. Generally, SID of amino acids were numerically greater for LOSBM than SBM (between 0.54 to 12.13 percentage points higher), but the differences were not significant. On the other hand, the SID of most amino acids in IBF were 20 to 40 percentage points lower than that of SBM ($P < 0.05$). The SID of lysine, methionine, and threonine for SBM were 91.9, 87.8, and 83.2%, respectively. The SID of lysine, methionine, and threonine for LOSBM were 92.4, 88.8, and 86.2%, respectively. The SID of lysine, methionine and threonine for IBF were 73.3, 58.1, and 49.2%, respectively. In conclusion, LOSBM is at least as good a source of SID amino acids as SBM, but the protein value of IBF is much lower.

Key Words: swine, standardized digestibility, ileal cannula

T162 Resistant starch content of cereal grains common utilized for pig nutrition.

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Resistant starch (RS) has been defined as the portion of starch that is not hydrolyzed by the enzymes in the small intestine. Therefore it passes to the large bowel, where can be principally fermented to short-chain fatty acids. In pigs, diets containing starch with a high level of RS were associated with a greater digesta mass that may benefit the diversity and population of gut bacteria and may improve the production of short-chain fatty acids, including butyrate. However, high-RS diets may affect digestion of nutrient, were associated with a lower in vivo starch digestibility and feed efficiency and can exacerbate the expression of swine dysentery. Currently, limited information is available about the RS content of single cereal grains commonly employed in pig nutrition. Consequently a set of 42 raw samples (6 maize, 6 dehulled barley, 6 triticale, 6 rice, 6 high moisture corn or HMC, 6 wheat and 6 sorghum) randomly collected from international feed companies was evaluated for the RS content with a 2-steps in vitro method simulating gastric and pancreatic phases. Following Englyst classification of starch fractions, RS was measured considering the starch not hydrolyzed after 120 min of enzymatic incubation. Data were subject to one-way ANOVA and significance were declared at $P < 0.05$. Minimum significant difference (MSD) was generated from Tukey′s test and was used as the basis of the multiple comparisons among means. Cereals were characterized by a wide range of RS content ($P < 0.05$) and the MSD was 53 g/kg DM. In particular, sorghum had the highest RS content (262 ± 31 g/kg DM; $P < 0.05$), whereas wheat the lowest (53 ± 27 g/kg DM; $P < 0.05$). Intermediate RS values were recorded for dehulled barley (133 ± 31 g/kg DM), triticale (138 ± 40 g/kg DM), HMC (142 ± 25 g/kg DM), rice (165 ± 29 g/kg DM) and corn (191 ± 22 g/kg DM) samples. A proper evaluation of the RS content of cereal grains could be important for a complete feed evaluation. However, more research is warranted to increase knowledge about the role of RS on metabolic and productive responses in pigs.

Key Words: resistant starch, in vitro method, pig

T163 Effects of molasses supplementation on the growth performance, nutrient digestibility, blood characteristics, fecal moisture, and fecal noxious gas emission in growing pigs.

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A total of 120 growing pigs [(Landrace × Yorkshire) × Duroc, BW = 22.81 ± 1.21 kg] were used in a 5-week feeding trial to evaluate the effects of dietary administration of molasses on growth performance, apparent total tract digestibility (ATTD), blood characteristics, fecal moisture, and fecal noxious gas emission. Pigs were randomly distributed into 1 of 3 dietary treatments on the basis of BW. Each treatment had 10 replicate pens with 4 pigs per pen. Dietary treatments were: CON, basal diet; T1, CON + 2.5% molasses; T2, CON + 5.0% molasses. The cane molasses used in this trail contained 4.12% CP and 9.234 MJ/kg ME (feed basis). All diets were formulated to meet or exceed the NRC requirements for growing pigs. All pigs were housed in an environmentally controlled room with a full slatted plastic floor. Each pen was equipped with a one-sided, stainless steel self-feeder and a nipple drinker, pigs were allowed ad libitum access to feed and water. No differences ($P > 0.05$) were observed in ADG, ADFI, or G:F among dietary treatments. There were no differences ($P > 0.05$) in the ATTD of DM, N, and energy among dietary treatments. No effects ($P > 0.05$) were observed on the concentrations of RBC, WBC, and lymphocyte percentage. The fecal moisture was not affected ($P > 0.05$) by the supplementation of molasses. The fecal acetic acid emission in T2 treatment was lower ($P < 0.05$) than that in CON treatment on d 3, 5 and 7, but no difference ($P > 0.05$) was observed in the ammonia (NH_3) emission among treatments. This study indicated that the supplementation with 5% molasses in growing pig diets reduced the fecal acetic acid emission, without negative effects on the growth performance of growing pigs.

Key Words: growing pigs, growth performance, molasses

T164 Effects of fermented corn by *Bacillus subtilis* on the growth performance, nutrient digestibility, fecal microbial shedding, and fecal noxious gas emission in growing pigs.

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A total of 160 growing pigs [(Landrace × Yorkshire) × Duroc, BW = 27.3 ± 0.47 kg] were used in a 6-week growth experiment to investigate the effects of fermented corn by *Bacillus subtilis* on growth performance, nutrient digestibility, fecal microbial shedding, and fecal noxious gas emission. Pigs were allotted to 1 of 5 dietary treatments (8 replicate pens per treatment with 4 pigs per pen) based on their initial BW using a randomized complete block design. All the pigs were housed in an environmentally controlled room with a slatted plastic floor. Each pen was equipped with a 1-sided self-feeder and a nipple drinker, pigs were allowed *ad libitum* access to feed and water throughout the experimental period. Dietary treatments were: 1) CON (basal diet); 2) FC3, CON + 3% fermented corn; 3) FC6, CON + 6% fermented corn; 4) FC9, CON + 9% fermented corn; 5) FC12, CON + 12% fermented corn. Common corn was fermented by *Bacillus subtilis* 2–19cx for 48 h (35–40°C). The counts of *Bacillus subtilis* in fermented corn are 10^9 cfu/gram. An adjustment period with same corn-soybean meal was provided 3 d before the experiment. Pigs fed the FC6 and FC9 diets led to a greater ($P < 0.05$) ADG than those fed the CON and FC3 diets. FC6 treatment significantly increased ($P < 0.05$) G:F compared with CON treatment. No difference ($P > 0.05$) was observed in the nutrient digestibility throughout the experiment. The inclusion of fermented corn did not affect ($P > 0.05$) the fecal *Lactobacillus* and *E. coli* population. No difference was noted in fecal ammonia, H_2S, total mercaptans, and acetic acid emission. In conclusion, fermented corn could be used as a good feed material for growing pigs, with its optimal supplementation level at 6%. The inclusion of fermented corn did not affect the fecal microbial shedding, and fecal noxious gas emission in the current study.

Key Words: *Bacillus subtilis*, fermented corn, growing pig

T165 Apparent dry matter digestibility and nitrogen balance in pigs fed high fiber diets.

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The current study was conducted to investigate the effects of feeding high fiber diet on apparent total tract dry matter digestibility and nitrogen balance in growing pigs. Sixteen barrows averaging 16.4 kg were randomly assigned to 1 of 4 diets after metabolic crate assignments with individual pig serving as experimental unit. Diets included a corn-soybean meal basal diet as the control (CON), and 3 antibiotic-free, high-fiber diets (D1, D2 and D3) each containing 5% sugar beet pulp plus one of the following: 1:2, 1:1, and 2:1 oat to barley ratios. Diets were formulated to contain similar amounts of protein (18% CP) and energy (3.415 Mcal DE/ kg) and were supplemented with minerals and vitamins to meet NRC nutrient recommendations. However, the fiber content of the CON diet was much lower than the average of the 3 high-fiber diets (8.38% vs. 22.40% NDF). Pigs had free access to water, but feed allowance was limited to 10% of average initial body weight and fed twice daily. The study period was divided into a 10 d adjustment period and a 5 d collection of urine and feces. Data were analyzed using SAS procedures where animals were considered random effects, and diet means were used to compare treatment effects. Results of the study indicated that DM and N intakes in pigs fed D2 and D3 were higher ($P < 0.05$) than CON or D1-fed pigs. However, there was no significant difference in DM and N intakes between D2 and D3, or between CON and D1-fed pigs. The lowest ($P < 0.05$) apparent dry matter digestibility coefficient determined was for D1-fed pigs, with no significant differences among the rest of the treatment groups. The averages for total and fecal N losses in pigs fed high-fiber diets were higher ($P < 0.05$) than CON-fed pigs. Relatively higher fecal and lower urinary N losses were observed as oat to barley ratios increased, but differences observed were not statistically significant. It seems therefore, N-excretion had shifted from urine to feces indicating that microbial mass in feces increases as the amount of fiber in the diet increases.

Key Words: dietary fiber, oats, nitrogen loss

T166 Effects of supplemental zinc amino acid complex on physiology and performance in heat-stressed growing pigs. M. V. Sanz-Fernandez*[1], S. C. Pearce[1], L. R. Long[1], N. K. Gabler[1], J. F. Patience[1], M. E. Wilson[2], M. T. Socha[2], R. P. Rhoads[3], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Zinpro Corporation, Eden Prairie, MN, [3]Virginia Polytechnic Institute and State University, Blacksburg.*

Heat stress (HS) reduces livestock productivity and this may in part be caused by leaky gut. We have recently demonstrated that supplementing Zn amino acid complex (ZnAA) improves intestinal barrier function in HS pigs (Sanz-Fernandez et al., 2012). Consequently, we hypothesized that ZnAA would improve pig performance during HS. Crossbred gilts (n = 59; 43 ± 6 kg BW) were subjected to 3 experimental periods (P). During P-1 (20 d), pigs were housed in groups in thermo-neutral (TN) conditions (19°C, 61% RH) and ad libitum fed 1 of 3 diets: 1) control (120 ppm of Zn from $ZnSO_4$; n = 29), 2) control + 100 ppm ZnAA from Availa Zn (Zinpro Corporation; Zn220; n = 14), and 3) control + 200 ppm ZnAA from Availa Zn (Zn320; n = 16). Pigs remained on their diets throughout the whole experiment. During P1 (5 d), pigs were moved into individual pens in TN conditions. During P2, half of the controls (n = 13), and all the Zn220 and Zn320-fed pigs were exposed to constant HS conditions (36°C, 50% RH) and fed ad libitum; the other half of the control pigs (n = 16) remained in TN conditions and were pair-fed (PF) with the HS pigs to eliminate the confounding effects of dissimilar feed intake (FI). Pigs were sacrificed at d 1 or 7. As expected, there were no treatment differences in rectal temperature (Tr) or respiration rates (RR) during P1. During P2, HS pigs had increased Tr ($P \leq 0.01$; 40.23 vs. 38.37°C) and RR (114 vs. 37 bpm) compared with PF pigs. Within the HS groups, Tr linearly increased ($P \leq 0.05$) with increasing levels of ZnAA (40.6 vs. 40.31°C). Heat stress markedly reduced FI ($P \leq 0.01$; 60%), and ZnAA did not ameliorate this decrease. There were no treatment differences in ADG during P-1, but during P1 there was a quadratic response ($P \leq 0.05$) as Zn220-fed pigs outgained (8.5%) controls and Zn320-fed pigs. On d 1 of P2, pigs in all treatments lost a similar amount of BW (3.24 kg). By d 7, the PF pigs tended ($P \leq 0.10$) to lose more BW than the HS pigs (3.63 vs. 0.02 kg), but feeding ZnAA did not improve BW loss. Data from this small experiment indicate that supplementing ZnAA did not prevent reduced performance during severe HS.

Key Words: heat stress, zinc amino acid complex, pig

T167 Evaluation of the antioxidative capacity of *Lactobacillus plantarum* in vitro and its antioxidative effect on weaned pigs. H. F. Ji,* J. Wang, L. Hou, S. X. Wang, D. Y. Zhang, H. Liu, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China.*

This study was conducted to evaluate the antioxidative capacity of *Lactobacillus plantarum* and its effects on antioxidant enzyme levels in weaned pigs. The strain of *Lactobacillus plantarum* was originally isolated from the gastrointestinal tract of healthy weaned pigs in our laboratory and strains were identified by the China Center of Industrial Culture Collection. The antioxidant capacity of *Lactobacillus plantarum* was analyzed in vitro. Resistance of this strain to reactive oxygen species (ROS), such as hydrogen peroxide, superoxide anions, hydroxyl radicals, and DPPH (1,1-diphenyl-2-picrylhydraxyl) was determined. The result showed that over 90% of *Lactobacillus plantarum* cells were viable after 240 min of incubation in the presence of 1.0 mmol/L hydrogen peroxide. The free radical scavenging activity of *Lactobacillus plantarum* against superoxide anions, hydroxyl radicals, and DPPH increased along with the increase of *Lactobacillus plantarum* concentration. Subsequently, 48 piglets weaned at 28 d of age (8.02 ± 0.49 kg BW), were divided into 3 dietary treatments comprising of a basal diet or the basal diet supplemented with chlortetracycline at 50 mg/kg or 5.1×10^7 *Lactobacillus plantarum* cfu/g diet. The experiment lasted 4 weeks. Data were analyzed statistically by using ANOVA procedures of SAS (SAS 1996). The results showed that the supplementation of *Lactobacillus plantarum* had higher average daily gain compared with basal diet control (505 vs. 463 g/d; $P < 0.05$) and lower feed conversion ratio compared with basal diet and antibiotic control (1.62 vs. 1.78, 1.71; $P < 0.05$). Supplementation of *Lactobacillus plantarum* increased serum superoxide dismutase (127.6 U/ml; $P < 0.05$) and glutathione peroxidase (478.4 U/ml; $P < 0.05$), while malondialdehyde levels decreased (4.10 nmol/ml; $P < 0.01$) in serum of weaned pigs. In general, *Lactobacillus plantarum* had high antioxidant capacity and its supplementation improved the antioxidant status of weaned pigs, and it could be used to alleviate oxidative stress and increase growth performance of weaned pigs.

Key Words: *Lactobacillus plantarum*, antioxidative capacity, weaned pig

T168 Evaluation of Oleobiotec in the diet of broilers challenged with *Clostridium perfringens* compared with an antibiotic administered continuously in feed. V. Noirot, P. Etienne, M. Champagnac, and D. Eclache,* *Laboratoires Phodé, Terssac, France.*

The product Oleobiotec (Laboratoires Phodé, France), a formulation of plant active principles among which spices extracts and characterized essential oils, was tested on male broiler chickens challenged with *Clostridium perfringens* on a Canadian experimental farm. Three hundred 1-d-old Ross × Ross broiler chickens were divided into 2 groups of 6 replicate pens of 25 birds. They were slaughtered at 38 d at a minimum weight of 2.5 kg. The control group was fed basal diet supplemented with 55 ppm of bacitracin methylene disalicylate (BMD-110). The treated group received the same basal diet supplemented with Oleobiotec (200, 150 and 100 ppm in starter, grower and finisher feeds, respectively). Contamination of the litter was carried out by dispersing the litter of clostridia infected flocks. Microbial pressure was increased by high dose (× 40) of a live anticoccidial vaccine (Coccivac) at 9 d and by a diet rich in wheat. The chickens did not receive any in-feed anticoccidials. The chickens were weighed individually at 0, 7, 17, 30, and 38 d. Feed intake and feed conversion ratio were evaluated for each pen and group at weighing time. Dead birds were recorded daily. Contamination of the litters was checked by pen at 21 and 38 d using the most probable number (MPN) method using McGrady′s probability table and was not significantly different between treatments (J21: 39 vs. 195 MPN of spores/g; J38: 47 vs. 70 MPN of spores/g for control and Oleobiotec respectively, $P > 0.05$). Death rate was lower with Oleobiotec (3.4%) than with BMD (6.0%), but the difference was not significant ($P > 0.05$). Body weight at 30 d of age was reduced with Oleobiotec (1831 g vs. 1881 g for the control, $P < 0.05$). Oleobiotec produced similar results on average daily gain and feed conversion ratio to BMD ($P > 0.05$). In this study, Oleobiotec enabled us to obtain similar performances on broilers challenged with *Clostridium perfringens* to bacitracin zinc.

Key Words: plant extract, broiler chicken, *Clostridium perfringens*

T169 Ingestion of a novel galactoglucomannan oligosaccharide-arabinoxylan (GGMO-AX) complex affected growth performance and fermentative and immunological characteristics of broiler chicks challenged with *Salmonella typhimurium*. T. A. Faber*[1], R. N. Dilger[1], M. Iakiviak[1], A. C. Hopkins[2], N. P. Price[3], and G. C. Fahey Jr.[1], *[1]University of Illinois, Urbana, [2]Temple-Inland, Diboll, TX, [3]National Center for Agricultural Utilization Research (NCAUR), ARS-USDA, Peoria, IL.*

Fermentable carbohydrates may enhance the ability of the gastrointestinal tract to defend against a pathogenic infection. We hypothesized that a galactoglucomannan oligosaccharide-arabinoxylan (GGMO-AX) complex would positively affect immune status and prevent colonization and shedding in *Salmonella typhimurium* (ST)-infected chicks. Using a completely randomized design, one day old commercial broiler chicks (n = 240; 4 replications/treatment; 5 chicks/replication) were assigned to 1 of 6 dietary treatments differing in concentration of GGMO-AX (0, 1, 2, or 4%) or containing 2% Safmannan (Saf) or 2% short-chain fructooligosaccharides (scFOS). Cellulose was used to make diets iso-total dietary fiber (TDF). On d 10 post-hatch, an equal number of chicks on each diet were inoculated with either phosphate buffered saline (sham control) or ST (1×10^8 cfu). All birds were euthanized on d 10 post-inoculation (PI) for collection of intestinal contents and select tissues. Overall, body weight gain and feed intake of chicks was greater ($P < 0.05$) in infected chicks PI, except for weight gain on d 0–3 PI. Gain:feed was affected ($P < 0.05$) by diet, with Saf-fed chicks having the highest G:F. The GGMO-AX substrate demonstrated prebiotic-like effects as indicated by increased cecal short-chain fatty acid concentrations, decreased cecal pH, and increased populations of *Lactobacillus* spp. and *Bifidobacteria* spp. as dietary GGMO-AX concentration increased. Excreta ST populations on d 5 and 10 PI, and ileal and cecal ST populations, tended to be affected ($P < 0.10$) by diet. Messenger RNA expression of IFN-γ in the cecal tonsils was the only cytokine independently affected by infection and diet ($P < 0.01$). Chicks fed 2 and 4% GGMO-AX had similar expressions of IFN-γ and IL-1β, regardless of infection, suggesting that ST virulence was suppressed. Dietary supplementation with GGMO-AX resulted in prebiotic-like effects, but did not limit ST intestinal colonization or shedding, but possibly decreased the virulence of ST within the digestive tract.

Key Words: chick, galactoglucomannan oligosaccharide (GGMO), *Salmonella typhimurium*

T170 Effects of oligosaccharides in a soybean meal-based diet on fermentative and immune responses in broiler chicks challenged with *Eimeria acervulina*. T. A. Faber*[1], R. N. Dilger[1], A. C. Hopkins[2], N. P. Price[3], and G. C. Fahey Jr.[1], *[1]University of Illinois, Urbana, [2]Temple-Inland, Diboll, TX, [3]National Center for Agricultural Utilization Research (NCAUR), ARS-USDA, Peoria, IL.*

Fermentable oligosaccharides, particularly those found in soybean meal (SBM), may modulate fermentation in the ceca, thus affecting intestinal immune responses to intestinal pathogens. We hypothesized that fermentable oligosaccharides found in SBM would positively affect cecal fermentation and intestinal immune status in chicks challenged with an acute coccidiosis (*Eimeria acervulina*) infection and fed either a SBM-based diet or a semi-purified soy protein isolate- (SPI) based diet. Using a completely randomized design, day-old broiler chicks (n = 200; 5 replications/treatment; 5 chicks/replication) were assigned to one of 4 SBM- or SPI-based diets containing either dietary cellulose (4%) or a fermentable carbohydrate, galactoglucomannan oligosaccharide-arabinoxylan (GGMO-AX) complex (4%). On d 9 post-hatch, an equal number of chicks on each diet were inoculated with either distilled water (sham control) or *E. acervulina* ($1\text{x}10^6$ oocysts) and then euthanized on d 7 post-inoculation (PI). Overall, body weight gain and feed intake were greater ($P < 0.01$) for SBM-fed chicks, regardless of infection status. Gain:feed ratio was greater ($P \leq 0.05$) for SPI-fed chicks except during d 3–7 PI. Infection status, but not fiber source, affected propionate, isobutyrate, isovalerate, and total BCFA concentrations ($P \leq 0.02$). Soybean meal-based diets resulted in greater ($P \leq 0.04$) SCFA and BCFA concentrations than SPI-based diets. Messenger RNA fold changes of all duodenal cytokines were greater ($P \leq 0.01$) for infected chicks, and SBM-fed chicks had greater ($P < 0.01$) IFN-γ and IL-12β expression compared with SPI-fed chicks. Cecal tonsil cytokine expression was also affected ($P \leq 0.02$) by infection; however, protein source only affected ($P < 0.01$) IL-1β expression in this tissue. Overall, a SBM-based diet, compared with a semi-purified SPI-based diet, resulted in greater weight gain, feed intake, and SCFA production regardless of infection status, and also greater duodenal cytokine expression in *E. acervulina*- infected chicks, which is hypothesized to be related to the oligosaccharides found in SBM.

Key Words: chick, coccidiosis, galactoglucomannan oligosaccharide (GGMO)

T171 Effect of *Lactobacillus gasseri* from chicken origin on the production performance, intestinal flora, and immune function of broiler chickens. X.-H. Teng,* X. Li, and J. Li, *College of Animal Science and Technology, Northeast Agricultural University, Harbin, Heilongjiang, China.*

Many studies have shown that *Lactobacillus* dominates in normal animal intestinal tract and it is very important to maintain a healthy body. The objective of this research was to determine the effect of *L. gasseri*, which was separated, filtrated and prepared from chicken cecum in our laboratory, on production performance, intestinal flora and immune function of broiler chickens. A total of 150 AA broiler chickens at 1 d of age were randomly divided into 5 groups by sex and body weight, with 3 replicates per group and 10 chickens (5 female and 5 male) per replicate. The test data was analyzed by SPSS 16.0. A control group received the basal diet, while groups 1, 2, 3 and 4 received the basal diet supplemented with 1) 5mg/kg Flavomycin, 2) 1% lactobacillus of plant origin (as control group using a commodity product), 3) 0.73% *L. gasseri*, and 4) 0.73% *L. gasseri* plus 0.02% xylooligosaccharide, respectively. The results showed that average daily gain and average daily feed intake of 6-week-old broiler chickens in control group was lower ($P < 0.05$) than in groups of 1, 3 and 4. There was no difference ($P < 0.05$) in feed/gain ratio between control and treatment groups. For the intestinal flora, the number of *Lactobacillus* in the control group was lower ($P < 0.05$) than in groups of 2,3 and 4, but the number of *E. coli* in the control group was higher ($P < 0.05$) than in groups of 2, 3 and 4. Concentrations of IgA and IgG, weights of the thymus and bursa of Fabricius, and spleen index scores in the control group were lower ($P < 0.05$) than in groups of 3 and 4. Additionally, spleen index scores in group 1 was higher ($P < 0.05$) than in control group. There were no significant differences ($P > 0.05$) for other response variables in group of 1 compared with control group. The results suggested that addition of *L. gasseri* to diets could improve production performance and may alter intestinal flora and immune function of broiler chickens compared with a flavomycin-containing diet.

Key Words: *Lactobacillus gasseri*, production performance, immune function

T172 Effect of supplementing curcumin as feed additive on the performance, biochemical profile, immune response and carcass characteristics in broilers. M. Pavani[1], Y. Ramana-Reddy*[1], P. Gopal-Reddy[2], S. R. Sakunthala-Devi[1], T. Monika[1], M. Sudhakar-Reddy[1], and A. Gopal-Reddy[1], *[1]S.V. Veterinary University, Tirupati, Andhra Pradesh, India, [2]Tuskegee University, Tuskegee, AL.*

An experiment was designed to study the effect of curcumin at 0.0, 0.1, 0.2 and 0.3% level in the feed on the performance, serum biochemical profile, immune response and carcass characteristics in broilers. One hundred sixty broiler chicks (vencobb strain) were randomly divided into 4 equal groups having 8 replicates of 5 each and fed the experimental diets (starter 0–3 wk; finisher 4–6 wk) for 6 weeks with 0.0, 0.1, 0.2 and 0.3% curcumin. Sera samples were collected for biochemical profile on d 42. All the biochemical parameters studied were estimated by commercially available kits (M/S Qualigens India Ltd.). Cell medaited (PHA-P response) and humoral (SRBC titers) responses were observed by Corrier and Deloach, (1990) and Wegmann and Simthies, (1966) methods, respectively. Eight birds from each treatment were slaughtered at the end of the experiment for studying the carcass characteristics. The experimental data was analyzed by completely randomized design (CRD). The average daily gain (g), feed intake (g/d) and feed efficiency (kg/kg gain) in broilers were not affected by the curcumin levels in the diet. Serum glucose, total protein, albumin, triglycerides, creatinine, urea (mg/dl), SGOT, SGPT and alkaline phosphatase (IU/L) were also not influenced by the level of curcumin in the diet. However, cholesterol level (mg/dL) was significantly ($P < 0.01$) lower in broilers fed diets with different levels of curcumin compared with those fed control diet. Further, humoral and cell mediated responses were significantly ($P < 0.01$) higher in broilers fed diets with different levels of curcumin compared with control but the responses were not significantly different among the broilers fed diets with 0.1, 0.2 and 0.3% level curcumin. Dressing percentage and vital organs weight (g/kg carcass wt) such as liver, heart and gizzard were similar among the broilers fed experimental diets. Weights of the lymphoid organs (g/kg carcass wt), spleen, bursa and thymus was significantly ($P < 0.05$) higher in broilers fed curcumin supplemented diets but among the different levels of curcumin, the values were not significantly different.

Key Words: curcumin, broilers, performance

T173 Effect of a mixture of turmeric and capsicum oleoresins on performance and oocyst excretion of broilers challenged with coccidiosis. C. Oguey*[1], V. Brito[2], A. Casarin[3], and M. Forat[3], *[1]Pancosma, Geneva, Switzerland, [2]Euronutec, Queretaro, Mexico, [3]Instituto Internacional de Investigacion Animal, Queretaro, Mexico.*

Capsicum and turmeric are known to stimulate innate immunity. So combining these 2 plant extracts should improve performance of birds infected by *Eimeria*. The objective of this trial was to evaluate the effect of a mixture of capsicum and turmeric oleoresins (XT, XTRACT 6986, Pancosma) on performance and oocyst excretion of broilers challenged with coccidiosis. One day old male broilers were randomly allocated for 52 d to 1 the 2 following treatments (48 birds * 12 cages / treatment): PC = 50 ppm Roxarsone + 110 ppm Monensin + 7.5 ppm Avilamycine, and XT = 50 ppm Roxarsone + 110 ppm Monensin + 100 ppm XT. All birds were challenged to Eimeria spp. via litter spray at d14. FI, BW, BWG, FCR and oocyst excretion (expressed as log10) were recorded. Data were analyzed using GLM procedure of SAS. Before challenge, no oocysts were excreted and FI, BWG and FCR were similar between PC and XT ($P > 0.37$), showing the positive effect of XT on performance in the absence of infection. After challenge, final BW, BWG and FCR were also similar between PC and XT ($P > 0.25$). This demonstrated that the substitution of avilamycine with XT can maintain the performance of challenged birds. Oocyst excretions of E. acervulina and E. maxima were similar between the 2 treatments ($P > 0.32$). For E. tenella, birds in XT excreted the same amount of oocysts after 14 and 21 d of infection compared with PC (respectively 0.97 vs. 1.69 log after 14 d, $P = 0.25$ and 3.62 vs. 4.04 log after 21 d, $P = 0.12$) but excreted more oocysts 28 d after challenge (3.354 vs. 2.608 log, $P = 0.02$). This suggests that XT did not have the same effect as avilamycine on oocysts shedding. However, XT could be used to substitute this drug with no negative effect on performance of broilers challenged with coccidiosis.

Key Words: phytonutrients, poultry, coccidiosis

T174 Preventive supplementation with L-arginine and glutamine improved self-renewing of intestinal mucosa in LPS-injected rats. X. Wu[1,2], C. Zhang[1,2], Z. Ruan[2], Z. Deng[1], and Y. Yin*[1,2], *[1]State Key Laboratory of Food Science and Technology and College of Life Science and Food Engineering, Nanchang University, China, [2]Institute of Subtropical Agriculture, Chinese Academy of Sciences, China.*

To evaluate the effect of preventive supplementation with L-arginine and glutamine on self-renewing of intestinal mucosa in lipopolysaccharide (LPS)-injected rats, 40 Sprague Dawley rats (average weight of 185 ± 15 g) were randomly divided into 5 treatment groups: control groups A (CA) and B (CB), both receiving daily oral supplementation with 0.9% saline, 300 mg/kg per day arginine (Arg), 300 mg/kg per day glutamine (Gln), or 150 mg/kg per day each of Arg plus Glu (AG). At 10:00am on d 15, animals were injected with 4 mg/kg LPS (groups CB, Arg, Gln, and AG) or sterile saline (group CA) after oral supplementation. Four hours later, all animals were killed for blood and intestinal mucosa collection. Real-time PCR was used to detect mRNA abundance of β-catenin, proliferating cell nuclear antigen (PCNA), vascular endothelial growth factor (VEGF), and hepatocyte growth factor (HGF) in intestinal mucosa. Data were analyzed as a one-way ANOVA. The results showed that plasma amino acids in the AG group tended to be similar with the control group. The combination of Arg and Gln supplementation mitigated morphology impairment (lower villus height, $P < 0.05$) in jejunum induced by LPS. Overall, LPS administration resulted in a significant increase in VEGF and HGF mRNA abundance in jejunum ($P < 0.05$). The combination of Arg and Gln increased PCNA mRNA abundance in both jejunum and ileum ($P < 0.05$), while they also increased β-catenin and decreased VEGF in ileum ($P < 0.05$). There were no differences in mRNA expression of these genes between the Arg and Glu groups ($P > 0.05$). Arg only increased PCNA mRNA abundance in jejunum and Gln decreased VEGF mRNA in jejunum ($P < 0.05$). These results suggest combined oral supply of Arg and Gln has more favorable effects on proliferation and differentiation of stimulated intestinal epithelium cells in LPS-induced rats compared with Arg or Gln alone.

Key Words: arginine, glutamine, intestinal epithelium cells

T175 Effects of different levels of dihydromyricetin from *Ampelopsis grossedentata* in feed on growth performance, immune and antioxidantive activities in *Sarotherodon* sp. X. Shu[1], l. C. Cai[1,2], and Y. L. Yin*[1], *[1]Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, Hunan, China, [2]Institute of Biological Resources, Jiangxi Academy of Science, Jiangxi, Nanchang, China.*

The experiment was conducted to study effects of adding dihydromyricetin (DMY), natural herb extract from *Ampelopsis grossedentata* in feed on growth performance, immune and antioxidantive activities in fish. In this experiment, a total of 720 *Sarotherodon* sp. with average body weight of 13.57 g was randomly allocated to 24 glass tanks and assigned to 6 treatments: 5 levels of DMY (0.1%, 0.2%, 0.4%, 0.8% and 1.6%) and one control (basal diet). Feed was offered to the fish twice daily during the 8-week trial. Feed intake (FI) and survival rate were recorded daily, and live weight gain (WG), average daily gain (ADG) and feed efficiency were calculated. At 4 and 8 wk of age, 5 fish from each group were randomly selected to collect blood into sterile centrifuge tubes for further analysis. Data was analyzed as a complete randomized design by the one-way ANOVA using SPSS, and Duncan multiple range test was used to compare treatment means. The results suggested that treatment with 0.1%, 0.2%, 0.4% and 0.8% DMY were not different ($P > 0.05$) from the control, but 1.6% DMY enhanced ($P < 0.05$) body weight gain and decreased ($P < 0.05$) feed conversion. The serum content of total protein increased ($P < 0.05$) and the activities of serum lysozyme (LSZ), superoxide dismutase (SOD) and catalase (CAT) were improved ($P < 0.05$) in all treatments containing DMY. Fish survival rate was also improved with DMY addition compared with the control treatment, with survival being highest for the 0.4% DMY treatment. In conclusion, dietary supplementation of 0.1% to 1.6% DMY can improve *Sarotherodon* sp. performance, survival, and serum indices.

Key Words: fish, nutrition, growth

Physiology and Endocrinology II

T176 Effects of mild heat stress on growth and carcass characteristics in broiler chickens. E. Sucu[1,2], M. V. Sanz-Fernandez[1], S. C. Pearce[1], A. Nayeri[1], G. P. Murugesan[1], R. R. Rhoads[3], M. E. Persia[1], and L. H. Baumgard*[1], *[1]Department of Animal Science, Iowa State University, Ames, [2]Department of Animal Science, Uludag University, Bursa, Turkey, [3]Department of Animal Science, Virginia Polytechnic Institute and State University, Blacksburg.*

Heat stress (HS) markedly alters bioenergetics in a variety of farm animals but how HS affects growth, carcass characteristics, and metabolic responses in broiler chickens has not been thoroughly evaluated. Thirty-six Ross male chickens, 28 d of age (1120 ± 20 g BW) were housed in climate chambers at the Iowa State University Zumwalt Station and exposed to one of 2 environmental conditions: 1) thermal neutral (TN) conditions (constant 25°C) with ad libitum water and feed intake (n = 15) or 2) mild HS conditions (constant 35°C) and ad libitum water and feed intake (n = 21). A blood sample was collected via cardiac puncture, and liver, abdominal fat pad and breast muscle were immediately weighed following sacrifice at 24 h, 3 d or 7 d of environmental exposure. All animals were feed restricted for 6 h before sacrifice. All data were analyzed using the PROC MIXED procedure of SAS (SAS Inst. Inc. Cary NC). The statistical analysis included the effects of environmental treatment, day of sacrifice and their interaction. Overall, HS birds had an increased rectal temperature compared with TN birds ($P < 0.05$, 41.7 ± 0.07 vs. 41.2 ± 0.08°C) and this temperature difference tended ($P = 0.13$) to become less pronounced with time. There was a treatment by time interaction ($P < 0.05$) on body weight gain as ADG was decreased by 77, 40 and 22% in HS compared with TN birds at d 1, 3 and 7, respectively. The temperature and ADG data indicate the birds were acclimating to the mild heat strain. Overall, compared with TN birds, actual liver weight and liver weight as a percentage of BW were decreased ($P < 0.05$) in HS birds (15 and 9%, respectively), but liver lipid content (4.22%) and liver dry matter (25.5%) did not differ between environmental treatments. The abdominal fat pad (22.6 g), breast muscle (137.5 g) and plasma insulin (1.3 ng/ml) levels did not differ between environments. Results of this study indicate that a mild but constant heat strain markedly reduces productivity and alters liver weight in broiler chickens. Reasons why HS affected liver weight are unknown but are of bioenergetic interest.

Key Words: heat stress, broiler chicken, metabolism

T177 Effect of season on copper concentration in blood serum from goats in different reproductive status. R. Rojo, B. Albarrán-Portillo, A. García-Martínez, J. Cedillo-Monroy, and J. F. Vázquez-Armijo,* *Centro Universitario UAEM Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, México, Mexico.*

The effect of season (rainy: RS, and dry: DS) on copper (Cu) concentration in blood serum of crossbred goats were studied. Blood samples from 40 crossbred goats were taken each season. The goats were clustered into 5 different groups considering their reproductive status, as follows: pubertal goats, anestrous adult goats, cyclic adult goats, pregnant goats, and kidded goats. Concentration of Cu in blood serum (mg/L) were assayed using atomic absorption. Data were analyzed for a completely randomized design with a factorial arrangement with 8 replicates. Blood serum concentration of Cu were 1.15, and were affected by reproductive status, season, and their interaction. Blood serum concentration of Cu were lower in RS (0.92) than DS (1.37) ($P < 0.05$). Overall, kidded goats had the highest ($P < 0.01$) Cu concentration (RS: 0.98 ± 0.07; DS: 1.95 ± 0.06) than other animals in both seasons. Adult goats showed a deficiency of Cu concentration in blood serum, especially during RS (0.88 ± 0.09). However, the lowest value obtained was to Pubertal goats in RS (0.69 ± 0.07). The results reflect the different requirements imposed by reproductive status and season interaction on goats.

Key Words: copper, blood serum, goats

T178 Effects of the beta-2 adrenergic agonist zilpaterol hydrochloride in castrated male goats: Plasma insulin, cortisol, thyroids, triglyceride, and glucose concentrations. A. Hatefi*[1], A. Towhidi[1], A. Zail[1], M. Ganjkhanlou[1], and A. Plascencia[2], *[1]Department of Animal Science, University of Tehran, Karaj, Alborz, Islamic Republic of Iran, [2]Instituto de Investigaciones en Ciencias Veterinarias, Universidad Autónoma de Baja, California Mexicali, Baja California, México.*

To evaluate the influence of zilpaterol hydrochloride (Zilmax, Intervet, South Africa) supplementation on blood insulin, cortisol, T3 and T4 (as thyroid hormones) and the metabolites glucose and triglyceride, 16 Mahabadi castrated male goats were individually fed a dry-rolled barley-based finishing diet with or without zilpaterol hydrochloride supplementation dosed at 0.20 mg/kg BW/d for finishing 30 d of 90 d feedlot period. Blood samples were taken at first and end of supplementing period and plasma was stored at –20°C until analysis. These samples were quantified by spectrophotometry procedure for glucose and triglyceride, by RIA for insulin and cortisol and triiodothyronine (T3) and thyroxin (T4) were determined according to standard ELISA methods. Obtained data were analyzed MIXED procedure of SAS software according to a completely randomized design. A P-value < 0.05 was considered statistically significant. Results showed that ZH supplementing has significant effect on metabolic hormones at d 90; as caused to increase insulin (108.02 vs. 100.56 ng/mL and $P < 0.01$), T3 (0.75 vs. 0.65 ng/mL and $P < 0.01$), T4 (25.41 vs. 21.99 ng/mL and $P < 0.01$) and decrease cortisol (20.78 vs. 28.55 ng/mL and $P < 0.01$) concentrations compare with control and d 60. Following to expressed hormonal changes at d 90, this β-agonist significantly influenced on blood metabolites as caused to decrease glucose (104.55 vs. 119.43 mg/dL and $P < 0.01$) and triglyceride (43.25 vs. 49.42 43mg/dL and $P = 0.02$) than control and d 60. Our study indicated zilpaterol hydrochloride supplementation of 0.20 mg/kg BW/d on castrated male goats at end of feedlot period has significant effects on blood metabolic hormones and metabolites at end of supplementing period.

Key Words: zilpaterol hydrochloride, metabolic hormones, castrated male goat

T179 Effect of water deprivation on the thermoregulatory system of desert goats (*Capra hircus*). A. Al-Haidary* and E. Samara, *King Saud University, Riyadh, Saudi Arabia.*

This study was conducted during summer season to investigate the effect of water deprivation under heat stress conditions on the thermophysiology of desert goat. The experiment was conducted on 4 stages (euhydration, dehydration, rehydration, d 10 of rehydration). The first 3 stages were lasted for 72 h each, while the last stage lasted for 24 h. A telemetry system was used for continuous measurement of goat's core body temperature. Results revealed that desert goat had showed a distinguished circadian rhythm of core body temperature during euhydration. The rhythm minimum and maximum were attained early in the morning and at the end of the day, respectively with 0.79°C oscillation range. Water deprivation that coincided with high ambient temperature of summer season has affected goat's core body temperature. The range of oscillation of core body temperature increased during dehydration stage to 1.78°C, then decreased to 88°C during rehydration stage, and further decreased to 0.72°C at d 10 of rehydration. The observed increase in core body temperature due to water deprivation indicates thermo-labile characteristics of desert goat. Goat's body heat storage was significantly ($P < 0.05$) increased during dehydration stage. Furthermore, dehydration had significantly ($P < 0.05$) increased daily averages of respiration rate, heart rate, skin, coat, and rectal temperatures of desert goat. Dehydration had also significantly ($P < 0.05$) decreased overall means of daily feed intake, dry matter intake, feces water content, and body weight. Ten days of rehydration has been approved sufficient for all measured thermo-physiological parameters to recover from the effect of water deprivation. These results demonstrate the capability of desert goat to ameliorate the stressful effects of water deprivation under heat stress conditions.

Key Words: core body temperature, gaot, dehydration

T180 Comparison of the morphological characters of ovulated follicular waves during synchronized and normal estrous cycle in dairy cattle. M. Poorhamdollah*[1], H. Kohram[1,2], A. Z. Shahneh[1], and A. Sadeghi-Sefidmazgi[3], *[1]University of Tehran, Karaj, Tehran, Iran, [2]Shahid Chamran University, Ahvaz, Iran, [3]Isfahan University of Technology, Isfahan, Iran.*

The objective of this study was to compare the morphological characteristics of follicular waves during a synchronized estrous cycle to those of a normal estrous cycle in dairy cattle. A total of 10 Holstein dairy cows were selected and divided into 2 groups (n1 = n2 = 5). In group 1, the estrous cycles were synchronized by 2 successive injections of $PGF_{2\alpha}$ (Vetglan, cloprostenol, Aburaihan, Iran), 14 d apart; and the characteristics of ovulated follicular waves were evaluated. In group 2, the ovulated waves during a natural estrous cycle for each cow were served as controls. Ovaries of all cows were examined daily by transrectal ultrasound (B mode; Pie medical, Falco 100, 8 MHz). *t*-test was used to assess the significance of difference between morphological characteristics of follicular waves in synchronized and normal estrous cycles. The results showed that there were no significant differences ($P > 0.05$) between morphological characteristics in terms of the maximum size of the largest follicle (F1); (15.60 ± 1.12 vs 13.60 ± 0.42; mm), maximum size of the second largest follicle (F2); (10.20 ± 1.01 vs 8.72 ± 0.59; mm), mean large size of subordinate follicles (6.04 ± 1.06 vs 6.03 ± 0.34; mm), mean size of F1 at deviation (8.80 ± 1.15 vs 7.64 ± 0.46; mm), mean days of emergence to deviation of F1 (4.00 ± 0.70 vs 3.48 ± 0.32), mean number of emergent follicles (11.00 ± 1.57 vs 7.44 ± 0.46) and mean size of F1 at growth and static phase (3.85 ± 0.63 vs 4.16 ± 0.67 and 2.72 ± 0.40 vs 2.44 ± 0.50; mm, respectively) as well as daily growth rates of F1 (1.04 ± 0.15 vs 1.38 ± 0.04) of follicular waves in synchronized estrous cycle versus normal estrous cycle in dairy cattle, respectively. In conclusion, there were no significant differences between morphological characters of follicular waves in synchronized estrous cycle and normal estrous cycle in dairy cattle.

Key Words: cattle, follicular wave, $PGF_{2\alpha}$

T181 Effect of methionine supplementation during postpartum period in dairy cows. II: Embryo quality. A. H. Souza*[1], P. D. Carvalho[1], A. R. Dresch[1], L. M. Vieira[1,2], K. S. Hackbart[1], D. Luchini[3], S. Bertics[1], N. Betzold[4], M. C. Wiltbank[1], and R. D. Shaver[1], *[1]University of Wisconsin-Madison, Madsion, [2]University of Sao Paulo-VRA, Brazil, [3]Adisseo, Alpharetta, GA, [4]U.S. Dairy Forage Research Farm, Prairie du Sac, WI.*

Objectives of this study were to evaluate the effects of supplementing methionine in the postpartum period on embryo quality in dairy cows. Holstein cows (n = 72), receiving same basic TMR (NRC 2001), were milked twice a day and were kept in tie-stalls. Animals were blocked by parity and calving date and randomly assigned to 2 treatments differing in level of dietary methionine: 1) Methionine (MET); diet composed of (%DM) corn silage (39.7), alfalfa silage (21.8), HMSC (17.2), roasted soybeans (8.6), grass hay (4.6), canola meal (4.0), mineral-vitamin mix (2.7) and ProVAAl Ultra (w/Smartamine, 1.4), formulated to deliver 2875 g MP with 6.8 Lys %MP and 2.43 Met %MP; 2) Control (CON); cows fed the same basal diet but replacing ProVAAl Ultra by ProVAAL Advantage (no added Smartamine), formulated to deliver 2875 gr MP with 6.8 Lys %MP and 1.89 Met %MP. Data was analyzed with the proc GLIMMIX of SAS and cows treated as a random experimental unit. Cows were superovulated with a modified 5d-Double Ovsynch with 4 d of decreasing FSH (Folltropin, 400mg/cow) doses and flushed 6 d after synchronized ovulations. A single batch of FSH and frozen semen (single ejaculates 15x106 sptz/straw) of 2 sires were used. In addition, a single treatment-blinded technician graded all embryos. There were no differences between groups in CL number, fertilization, or embryo quality. Surprisingly, % of structures recovered/CL was greater for MET than CON. Thus, most ova/embryo properties did not differ between groups; however, potential effects of MET on embryo development after the first week of pregnancy need to be investigated. Supported by Adisseo, Accelerated Genetics, USDA Grant 2010–85122–20612.

Table 1.

	MET	CON	
n	35	37	*P*-value
CL number	17.0±1.3	17.7±1.5	0.90
Total ova/embryos recovered	9.1±1.4	6.8±1.0	0.18
% Ova/embryos recovered per CL	49.5±4.9	35.8±4.4	0.05
Number of fertilized ova	6.5±1.1	5.5±0.9	0.56
% Fertilized ova	74.7±5.6	82.2±3.8	0.27
Number of transferable embryos	5.0±0.9	4.3±0.1	0.57
% Transferable embryos of fertilized	59.7±6.5	62.4±6.0	0.55
Number of degenerate embryos	1.5±0.4	1.3±0.4	0.75
% Degenerate of fertilized	25.1±5.8	27.5±6.0	0.74

Key Words: methionine, embryo quality, dairy cow

T182 Lactation and physiological performance in Holstein dairy cows managed under summer heat stress conditions in northwest Mexico. P. Luna-Nevarez*[1], C. Leyva-Corona[1], F. Rivera-Acuña[1], J. F. Medrano[2], G. Rincon[2], G. A. Silver[3], D. M. Hallford[3], R. L. Ashley[3], and M. G. Thomas[4], *[1]Instituto Tecnologico de Sonora, Ciudad Obregon, Sonora, Mexico, [2]University of California, Davis, [3]New Mexico State University, Las Cruces, [4]Colorado State University, Fort Collins.*

Milk production is challenging for Holstein dairy cows managed under severe high temperature and humidity weather conditions common to northwest Mexico during summer, such that a cooling system is recommended to alleviate heat stress. Thus, the objective of this study was to evaluate the effect of a low-pressure cooling system on milk production and physiological responses indicative of heat stress during summer in dairy cows milked in Sonora. Twenty-eight multiparous Holstein cows with ~150 d in milk, that received bovine somatropin every 14 d during lactation, were randomly assigned in 2 groups, cooling (CL, n = 14) and heat stress (HS, n = 14), from May 7 to July 23, 2011. All cows were maintained in shaded holding pens. Cows in the CL group received a cooling program in the waiting parlor, which included 4 series of shower (5 min) alternated with forced ventilation (10 min) 6 times per day (0700, 0900, 1100, 1300, 1500 and 1700). Heat-stressed cows were cooled only before milking (0700 and 1700). Milk production was recorded daily using an electronic system. Blood samples were collected once per week to measure serum levels of prolactin and IGF1. Rectal temperature and respiratory frequency were measured twice the day before bleeding. Ambient temperature and humidity values were collected from a nearby climatic station. Data were analyzed in SAS (2009) using a mixed model procedure with repeated measures. Cows in the CL group had higher ($P < 0.05$) milk production (22.6 vs. 21.6 ± 0.5 kg/day) and serum concentrations of prolactin (35.1 vs. 29.4 ± 1.2 ng/mL) and IGF1 (295.8 vs. 269.6 ± 15.7 ng/mL) relative to HS cows. Conversely, relative to CL cows, HS cows had a higher ($P < 0.05$) rectal temperature (38.4 vs. 38.2 ± 0.1°C) and respiratory frequency (70.5 vs. 66.6 ± 1.2 breath/min). We conclude that reduced serum levels of prolactin and IGF1 in dairy cows during summer are a consequence of heat stress, which is remedied by cooling to maintain an acceptable level of lactional performance in Holstein dairy cows.

Key Words: cooling, heat stress, prolactin

T183 Relative quantification of mRNA abundance for LH receptor, angiogenin and p450scc, and determination of hormone levels in dominant follicles and follicular cysts from dairy cows.

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Follicular cysts are nonovulatory structures that contribute to prolong the calving interval in dairy cattle. The objective was to compare the expression of mRNA encoding LH receptor (LHCGR), angiogenin (Ang) and cytochrome P450 side-chain cleavage enzyme (CYP11A1) in granulose cells and the hormonal level in dominant follicles (DF) and follicular cysts (FC). We obtained follicular structures (DF, n = 16; and FC, n = 16) from dairy cows slaughtered at a local abattoir. The follicular fluid was subjected to ELISA to determine estradiol 17β (E2), progesterone (P4) and IGF-1 (intraassay coefficient of variation was 5.58, 7.02, and 10.30% for E2, P4, and IGF-1, respectively). Abundance of target genes mRNA relative to GAPDH was quantified by real-time PCR. The experiment was conducted using a completely randomized design, with the fixed effect of type (DF or FC). Correlation among gene expression and hormones levels were also calculated. There were no difference ($P > 0.05$) between DF and FC for the expression (fold change) of LHCGR (8.18 ± 0.54 vs 7.16 ± 0.28), Ang (1.79 ± 0.20 vs 1.78 ± 0.21), CYP11A1 (3.50 ± 0.24 vs 3.42 ± 0.24) and the concentrations of E2 and P4 (1384.64 ± 1.82 vs 1142.11 ± 1.82, and 13.10 ± 1.41 vs 18.63 ± 1.41 ng/ml, respectively). The concentrations of IGF-1 in FC was higher ($P < 0.05$) than in DF (132.78 ± 1.18 and 78.21 ± 1.18 ng/ml, respectively). Positive correlations ($P < 0.05$) between LHCGR with CYP11A1 (r = 0.74), LHCGR with E2 (r = 0.95), and CYP11A1 with E2 (r = 0.69) were detected in DF. In FC there was a positive correlation ($P < 0.05$) between LHCGR with E2 (r = 0.82), and a negative correlation between CYP11A1 with IGF-1 (r = −0.70) and follicular diameter (r = −0.59). The results provide evidence for IGF-1 to be involved in the growth and extended lifespan of follicular cysts

Key Words: follicular cysts, gene expression, IGF-1

T184 Hormonal regulation of the hedgehog system in ovarian granulosa and theca cells of cattle.

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Although expression of Indian and Desert hedgehog (Hh) proteins, as well as their receptor Patched 1, dramatically decrease during follicular atresia in rodents, little is known about the hormonal regulation of these Hh system proteins in cattle. Therefore, in vitro experiments were conducted to study the effects of gonadotropins, steroids, transforming growth factor-β superfamily proteins, wingless-type MMTV integration site family member 3A (WNT3A), and IGF1 on components of the Hh system. Gene expression of Indian hedgehog (*IHH*), Desert hedgehog (*DHH*) and its type 1 receptor, Patched 1 (*PTCH1*), were quantified by real-time RT-PCR in cultured bovine granulosa (GC) of small (1–5 mm) follicles or theca (TC) cells of large (5–20 mm) follicles collected from bovine ovaries. In cultured GC, 24-h treatment with 300 ng/mL of E2 increased ($P < 0.05$) *IHH* mRNA abundance in the presence of FSH as well as in the presence of 30 ng/mL of IGF1 ($P < 0.05$). Alone IGF1 suppressed GC IHH mRNA abundance by 78% ($P < 0.05$). In IGF1-treated GC, cortisol (300 ng/mL) and WNT3A (300 ng/mL) increased ($P < 0.05$) GC *IHH* mRNA by 1.9- and 5.5-fold, respectively, whereas 300 ng/mL of prostaglandin E2 (PGE2) or angiogenin had no effect ($P > 0.10$). Relative expression of *DHH* mRNA was 20-fold less than that of *IHH* mRNA in small follicle GC treated with WNT3A. In cultured TC, 24-h treatment with 30 ng/mL of IGF1 and LH decreased ($P < 0.05$) *PTCH1* mRNA expression by 50% and 40%, respectively. The combined treatment of IGF1 and LH was less inhibitory (i.e., 20% suppression) on *PTCH1* expression than either treatment alone. Treatment of TC with bone morphogenetic protein 4 (BMP4; 30 ng/mL) reduced ($P < 0.05$) *PTCH1* mRNA abundance by 50%, whereas treatment with growth differentiation factor 9 (GDF9; 250 ng/mL) or activin (25 ng/mL) was without effect ($P > 0.10$). We conclude that the ovarian Hh system in cattle is controlled by several hormones including IGF1 and FSH, and that these effects are regulated by estradiol and other intra-ovarian factors such as WNT3A and BMP4. We hypothesize that as follicles grow and develop, increased free IGF1 may suppress production of IHH by GC and PTCH1 by TC.

Key Words: hedgehog proteins, granulosa, theca

T185 Pregnancy per AI of conventional versus sex sorted semen in dairy heifers subjected to a modified CIDR-PGF2α-GnRH timed-AI protocol.

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The 5-d CIDR-CoSynch is an effective timed-AI protocol in heifers. Sexed sSorted (SS) yields lower fertility than conventional semen (CS), and thus, there is less room for technical error when SS semen is used in timed-AI protocols. The objectives of this study were to evaluate the effect of GnRH at CIDR insertion on pregnancy per AI (P/AI) in a 5-d CIDR-CoSynch protocol and to compare the P/AI of CS versus SS in dairy heifers subjected to timed-AI. In a 2 × 2 factorial design, 477 Holstein replacement heifers, received a CIDR insert on d 0 (start of treatment). Subsequently, heifers were paired by age and assigned randomly to receive either 100 μg of GnRH (GnRH-CIDR, n = 241) or no GnRH treatment (CIDR5, n = 236). On d 5, the CIDR was removed and all heifers received 25 mg PGF2α. Seventy-two hours after CIDR removal all heifers received GnRH (100 μg, i.m.) and were randomly assigned to be inseminated with CS (n = 234) or SS semen (n = 243). Estrus activity was monitored using tail chalk methods from d 5 to d 8. Pregnancy status was determined via ultrasound and by PSPB analysis (bioPRYN) on d 32 and 45 after AI. P/AI data were analyzed by logistical regression. P/AI was marginally ($P = 0.06$) different between treatments (GnRH-CIDR 45.8% vs. CIDR5 50.2%). P/AI was greater ($P < 0.01$) for CS compared with SS semen (59.5% vs. 37.0%), however there was no treatment by semen effect. Regardless of semen type and across both treatments, P/AI was greater ($P < 0.01$) in heifers detected in heat then not observed in heat (54.5% vs. 32.1%). Pregnancy detection did not differ between ultrasound and bioPRYN. The results of this experiment indicate that GnRH administration at CIDR insertion does not improve P/AI in heifers subjected to 5-d CIDR-CoSynch protocol, and the use of sex-sorted semen should be limited to use in heifers detected in estrus.

Key Words: dairy heifers, timed AI, sex-sorted semen

T186 Insulin action on hepatic gene expression in dairy cows with different fat mobilization during early lactation.

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Changes in insulin action around calving contribute to metabolic adaptation in dairy cows during the transition from pregnancy to lactation. Insulin action may be affected by the physiological status and body fat mobilization. The objective of this study was to investigate insulin effects on hepatic gene expression of factors involved in energy metabolism in cows with variable liver fat concentration (LFC) after calving. German Holstein cows (>10,000 kg milk/305 d; ≥ 2nd lactation) were classified by LFC postpartum (pp) in low (L; < 240 mg fat/g DM; n = 9) and high (H; > 240 mg fat/g DM; n = 10). Euglycemic-hyperinsulinemic clamps (6 mU/kg BW × min insulin for 6 h) were performed in wk 5 ante partum (ap) and wk 3 pp and liver biopsies were taken before and at the end of the clamp to measure LFC and mRNA concentrations of pyruvate carboxylase (PC), cytosolic and mitochondrial phosphoenolpyruvate carboxykinase (PEPCKc, PEPCKm), propionyl-CoA-carboxylase (PCCA), carnitine palmitoyl-transferase 1A (CPT1A), glucose transporter GLUT2 and GLUT4, IGF-I, and glucocorticoid, growth hormone, and insulin receptors (GR, GHR1A, InsR). Phosphoglycerate kinase 1 was usesd as reference gene and data were analyzed by Mixed Model of SAS with LFC, time, and insulin as fixed effects. LFC differed between cows ($P < 0.01$) (H: 306 ± 0.2 mg/g; L: 195 ± 0.1 mg/g). PC mRNA concentrations increased ($P < 0.05$), but mRNA of GLUT2, GLUT4, IGF1, GHR1A and GR decreased ($P < 0.05$) from ap to pp. Insulin decreased ($P < 0.05$) mRNA concentrations of PC, PEPCKc, PEPCKm, PCCA, CPT1, and InsR, but increased mRNA of IGF-I and GLUT4 ap and pp. Insulin increased GHR1A mRNA only pp and PEPCKc mRNA decreased from ap to pp only without insulin (time × insulin: $P < 0.05$, respectively). PEPCKc mRNA tended to be lower ($P = 0.1$), but expression of GLUT4 and GR were higher ($P < 0.05$) in L than in H. Hepatic gene expression depended partly on time, but was less affected by LFC. Insulin strongly inhibited enzymes involved in hepatic glucose production and fat oxidation, but stimulated parameters of the somatotropic axis and GLUT4. Supported by DFG, Germany.

Key Words: dairy cow, insulin action, hepatic gene expression

T187 Modulation of the metabolic response to an endotoxin challenge in Brahman heifers through OmniGen-AF supplementation.

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This study examined the effect of feeding OmniGen-AF (OG; Prince Agri Products) on the metabolic response of newly-weaned heifers to an endotoxin (lipopolysaccharide; LPS) challenge. Brahman heifers (n = 24; 183 ± 5 kg) from the Texas AgriLife Research Center in Overton, TX were separated into 2 treatment groups at weaning: 1) Control (C; n = 12) and 2) OG (n = 12; fed at 4 g per 45.4 kg BW) and fed for 69 d. On d 39, heifers were transported from Overton to New Deal, TX. On d 40, heifers were fitted with indwelling jugular catheters and moved into a barn with individual stalls. On d 41 heifers were challenged with LPS (0.25 μg/kg BW i.v.) and blood samples were collected at 0.5 h intervals from −2 to 8 h and again at 24 h relative to LPS challenge (0 h). Serum was isolated and stored at −80°C until analyzed for glucose, insulin, nonesterified fatty acids (NEFA), and blood urea nitrogen (BUN). Heifer weight was also recorded at various intervals throughout the study. Heifer BW increased throughout the study ($P < 0.01$) and was not affected by treatment ($P > 0.21$). Pre-LPS glucose concentration was greater in OG (255.7 ± 6.6 mg/dL) than C heifers (227.8 ± 6.6 mg/dL; $P < 0.01$). Glucose concentration increased post LPS ($P < 0.01$), but was not affected by treatment with OG ($P = 0.36$). Insulin concentration pre- and post-LPS was not affected by treatment with OG ($P = 0.84$ and 0.89). Post-LPS insulin concentration increased ($P < 0.01$) and peaked at 2 h post LPS. Pre- and post-LPS NEFA concentration was greater in C (0.19 ± 0.01 and 0.39 ± 0.01 mmol/L) than OG heifers (0.16 ± 0.01 and 0.31 ± 0.01 mmol/L; $P < 0.05$), with NEFA concentration increasing post LPS ($P < 0.01$). Pre- and post-LPS BUN concentration was also greater in C (10.2 ± 0.2 and 10.5 ± 0.1 mg/dL) than OG heifers (8.5 ± 0.3 and 9.3 ± 0.1 mg/dL; $P < 0.03$), with BUN concentration increasing post LPS ($P < 0.01$). These data suggest that supplementing heifers with OG altered their metabolic response by increasing available glucose before the LPS challenge and reducing the need for OG heifers to mobilize energy through lipolysis and proteolysis, which may have allowed for a more acute response to the challenge.

Key Words: cattle, metabolism, OmniGen-AF

T188 Ultrasound body composition traits response to an endotoxin challenge in Brahman heifers supplemented with OmniGen-AF.

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This study examined the effect of feeding OmniGen-AF (OG; Prince Agri Products) on body composition response of newly weaned heifers to an endotoxin (lipopolysaccharide; LPS) challenge. OmniGen-AF is a yeast-based product and our hypothesis was that this yeast based product would provide a level of stress/immunological protection that would allow for nutrient sparing during times of stress. Brahman heifers (n = 24; 183 ± 5 kg) from the Texas AgriLife Research Center in Overton, TX were separated into 2 treatment groups at weaning: 1) Control (C; n = 12) and 2) OG (n = 12; fed at 4 g per 45.4 kg BW) and fed for 69 d. On d 39, heifers were transported from Overton to New Deal, Texas.

On d 40, heifers were fitted with indwelling jugular catheters and moved into a barn with individual stalls. On d 41, heifers were challenged with LPS (0.25 µg/kg BW i.v.) and blood samples were collected at 0.5 h intervals from −2 to 8 h and again at 24 h relative to LPS challenge (0 h). Ultrasound body composition traits for longissimus muscle area, rib fat, percent intramuscular fat and rump fat were collected at weaning (d 0), d 39, 44 and 69. Data were analyzed using the PROC Mixed procedure of SAS specific for repeated measures. Heifer BW increased throughout the study ($P < 0.001$) and was not affected by treatment ($P > 0.68$). Ultrasound body composition traits for longissimus muscle area, percent intramuscular fat, rib fat and rump fat increased ($P < 0.0001$) throughout the study. However, there were no effects ($P > 0.20$) of feeding treatment on ultrasound body composition traits throughout the study. There were tendencies ($P < 0.09$) for the OG group to have more stable rib fat and percent intramuscular fat measurements after transport and an endotoxin challenge. While no significant differences between treatments were observed in this study, the data suggest that OG supplementation before transport and LPS challenge may have preserved energy stores in Brahman heifers.

Key Words: cattle, ultrasound, OmniGen-AF

T189 Hepatic expression of mitochondrial respiratory complex genes of pure and crossbred beef cows grazing different herbage allowances of native pastures. M. Veyga, A. L. Astessiano, A. Kaitazoff, V. Bassaizteguy, A. I. Trujillo, and M. Carriquiry,* *School of Agronomy, UdelaR, Montevideo, Uruguay.*

Hepatic expression of genes encoding proteins of the mitochondrial respiratory complexes has been related to mitochondrial function and feed efficiency, which in turn may depend on nutritional plane and animal genotype. Adult cows (n = 24) in a factorial arrangement of herbage allowances throughout the year (2.5 vs. 4 kgDM/kgBW; LO vs. HI) and cow genotype (purebred: Angus and Hereford vs. F1 crossbred; PB vs. CB) were used in a complete randomized block design to evaluate hepatic expression of 9 genes encoding proteins of the mitochondrial respiratory complexes. Cows were maintained in the herbage allowance treatment since May 2007 and gestated and lactated one calf every year from 2007 to 2009. At the end of the third year, cows were slaughter at 190 ± 15 d postpartum and liver mass was recorded and samples were collected to measure gene expression by SYBR-Green real time PCR using HPRT and β-actin as endogenous control genes (which expression did not differ among cow groups by microarray analysis). Data were analyzed using a mixed model and means were considered to differ when $P < 0.05$. Liver mass did not differ between HI than LO cows but was less in PB than CB cows (45.9 vs. 49.6 ± 1.26 g/kgPV0.75). Expression of SDHA and SDHD (complex II), UQCRC1 (complex III) mRNA did not differ due to herbage allowances or cow genotype. However, hepatic expression of NDFUS4 (complex I, 0.90 vs. 1.51 ± 0.24), CYC1 (complex III, 0.68 vs. 1.05 ± 0.13), and ATP5B and ATP5O (complex V, 0.72 vs. 1.08 ± 0.16 and 0.56 vs. 1.02 ± 0.16, respectively) mRNA tended ($P \leq 0.094$) to be less in HI than LO cows. Hepatic expression of ATP5B and ATP5O and CYC1 and COX5B (complex IV) mRNA were greater in PB than CB cows (1.10 vs. 0.7 ± 0.17; 1.08 vs. 0.5 ± 0.16; 1.04 vs. 0.69 ± 0.13 and 1.28 vs. 0.97 ± 0.13, respectively). However, ATP50 mRNA tended ($P = 0.066$) to be affected by the interaction between herbage allowance and cow genotype as its expression was greater in LO-PB cows than the other groups. Results suggest that increased mitochondrial gene expression may compensate reduced liver size in PB than CB cows and could indicate a higher feed efficiency of cows grazing low vs. high herbage allowance of native pastures.

Key Words: liver, respiratory chain, mRNA

T190 Expression of adipokines and their receptors in adipose tissue of pure and crossbred beef cows grazing different herbage allowances of native pastures. A. Kaitazoff,* A. Casal, A. L. Astessiano, M. Veyga, A. I. Trujillo, and M. Carriquiry, *Facultad de Agronomía, UdelaR, Montevideo, Uruguay.*

Adipose tissue metabolism plays an important role during periods of negative energy balance or feed restriction and adipokines secreted by adipose tissue participated in regulating energy homeostasis. Pure and crossbred adult beef cows (n = 10) were used in a complete randomized block design to evaluate the effects of herbage allowances throughout the year (2.5 vs. 4 kgDM/kgBW; LO vs. HI) on adipokines and their receptors mRNA expression in mesenteric adipose tissue. Cows were maintained in the same herbage allowance treatment since May 2007 and gestated and lactated one calf every year from 2007 to 2009. At the end of the third year, cows were slaughter at 190 ± 15 d postpartum, mesenteric adipose tissue was dissected and weighed and samples were collected to measure gene expression by SYBR-Green real time PCR using HPRT and Î^{2}-actin as endogenous control genes. Data were analyzed using a mixed model and means were considered to differ when $P \leq 0.05$. Cow BW at slaughter did not differ between HI and LO cows (436 ± 16 kg). However, mesenteric adipose tissue mass was less for HI than LO cows (25.1 vs. 28.3 ± 2.6 g/kgPM). Adipose adiponectin (ADIPO) and its receptor-1 (ADIPOR1) mRNA expression were not affected by herbage allowance but ADIPOR2 mRNA tended ($P = 0.13$) to be greater for HI than LO cows (1.04 vs.0.57 ± 0.23). Expression of leptin and its receptor-b (LEPRb) mRNA, as well as insulin receptor (INSR) mRNA in adipose tissue did not differ between herbage allowances but LEPR-a was less in HI than LO cows (0.90 vs. 2.23 ± 0.69). Adipose angiopoietin-like protein 4 (ANGLP4) mRNA was greater in HI than LO cows (1.19 vs. 0.09 ± 0.65). Expression of adipokine receptors (ADIPOR2 and LEPR-a) as well as ANGPL4 mRNA in mesenteric adipose tissue could be mediating differences in energy metabolism in rangeland beef cows grazing different herbage allowances.

Key Words: beef cattle, grazing, adipokines

T191 Hepatokines in periparturient dairy cows with different extent of body fat mobilization. C. Schäff, T. Laeger, H. M. Hammon, M. Röntgen, and B. Kuhla,* *Nutritional Physiology "Oskar Kellner," Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Adropin and the fibroblast growth factor-21 (FGF21) are 2 hepatokines linking feed intake with energy homeostasis and lipid metabolism. While adropin acts to reduce feed intake and hepatic fat synthesis, FGF21 increases hepatic ketogenesis and feed intake/kg BW in rodents. Thus we investigated whether adropin and FGF21 are regulated during the periparturient period of dairy cows and if their expression/secretion is associated with the postpartum (pp) liver fat content (LFC). German Holstein cows (>10,000 kg milk/305 d; >2nd lactation) were grouped retrospectively according to the mean LFC pp in low (L; <24% total fat/DM; n = 9) and high (H; LFC > 24.4% total fat /DM; n = 10). Cows were fed TMR ad libitum and frequent blood samples were withdrawn to analyze the concentration of FGF21, nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHBA). Liver biopsies were taken at d −34, −17, 3, 18, 30 relative to parturition and at slaughter (d 40 pp) to measure LFC and mRNA concentrations of the hepatokines and the non-regulated house-keeping gene phosphoglycerate kinase 1 (PGK1) via real-time RT-PCR. Data were evaluated by Mixed Model of SAS with LFC and time as fixed effects and pairwise comparisons (multiple *t*-test). Daily dry matter intake (DMI) varied with time ($P < 0.001$) with a continuous rise after calving in both groups. The DMI/kg BW increased also with time

($P < 0.001$) and was lower in H than in L cows ($P < 0.01$). LFC peaked at d 18 pp and was higher in H than in L cows (H: 41.3%; L: 24.5%; $P < 0.001$). Pairwise comparison revealed that at d 30 pp, mRNA expression of adropin was higher in H than in L cows ($P < 0.05$). Expression of FGF21 was not different between groups. Plasma concentrations of FGF21 decreased from ante partum by d 3 pp and re-increased thereafter ($P < 0.01$) whereas NEFA and BHBA (each $P < 0.001$) were higher in H than in L cows pp. Higher expression of adropin in H cows after the LFC peak pp may contribute to the depletion of liver fat but also to the lower feed intake pp in H as compared with L cows. Hepatic FGF21 mRNA expression is not paralleled by FGF21 plasma concentration. Supported by DFG, Germany.

Key Words: dairy cow, adropin, FGF21

T192 Glucose and epinephrine tolerance tests in steers categorized as residual feed intake efficient versus inefficient.

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Two experiments were performed to examine peripheral glucose and insulin dynamics in feedlot steers classified as residual feed intake efficient (–RFI) vs. inefficient (+RFI). Crossbred Angus steers were used in experiment one (n = 72; initial weight 333 ± 8.5 kg) and 2 (n = 60; initial weight 355 ± 7.3 kg). All steers were fed for a total of 70 d and had access to the same diet (87% corn, 8% corn distiller's grains, 1% blood meal, 1.6% feather meal, and 2.5% mineral and vitamins). Residual feed intake was calculated based on the regression of dry matter intake (DMI) onto metabolic body weight (BW0.75) and average daily gain (ADG). In experiment one, 2 –RFI and 2 +RFI steers were selected for a glucose tolerance test (GTT1) and in experiment 2, 4 –RFI and 4 +RFI steers were selected for a glucose tolerance test (GTT2) and an epinephrine tolerance test (ETT). Therefore, as planned, body weight and ADG did not differ ($P > 0.05$) between treatments for all tolerance tests, yet DMI and RFI differed ($P < 0.05$) between treatments for all tolerance tests, which allowed us to have 2 distinct groups of animals to perform our experiments. For GTT1, each steer was injected with 150 mg/kg BW of glucose via jugular catheter and 20 min later given 30 mU/kg BW of insulin. For GTT2, each steer was injected with 150 mg/kg BW of glucose via jugular catheter, but no insulin followed. For ETT, each steer was injected with 1 ug/kg BW of epinephrine via jugular catheter. Frequent blood samples were collected before and after injection of glucose for all tests. Serum was assayed for glucose and insulin. Basal, peak, area under the curve, clearance rate (%/min) and half-life's of glucose and insulin did not differ between treatments for GTT1 and GTT2. In addition, results for ETT did not show any difference ($P > 0,05$) for basal, peak, area under the curve, clearance rate (%/min) and half-life's of glucose and insulin. We conclude that peripheral glucose and insulin dynamics do not differ according to RFI classification of feedlot steers.

Key Words: RFI, glucose, epinephrine

T193 Insertion of used CIDRs on day 3 to 5 post-insemination in heifers to improve pregnancy rate.

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Increasing progesterone (P_4) concentrations from d 3 to 5 of the estrous cycle improves pregnancy rates in repeat-breeder beef cattle. This study was designed to determine if increasing P_4 on d 3 to 5 post-insemination improves pregnancy rates in beef heifers. A total of 92 beef heifers were used in 2 replicates during this experiment. All heifers were synchronized using the Co-Synch + CIDR protocol and were timed AI (TAI) at 56 h following $PGF_{2\alpha}$ administration and CIDR removal. They were administered 100 µg of GnRH at TAI and on d 3 to 5 post-GnRH all treated heifers received a used CIDR from the prior synchronization and control heifers received insertion of the empty CIDR gun. Jugular blood samples were collected from all heifers in replicate 2 (n = 60). Plasma P_4 concentrations were determined via radioimmunoassay, and ~30 post-TAI heifers were tested for pregnancy using ultrasonography. Statistical analysis was performed in SAS using a proc glm with a tukey's chi-squared and proc glimmix with lsmeans post-hoc tests. In replicate one, significantly more ($P < 0.05$) treated heifers were pregnant (12/16, 75%) compared with control heifers (5/16, 31%). In replicate 2, there was no difference in pregnancy rates for treated (12/30, 40%) and control (12/30, 40%) heifers. The mean pregnancy rates between replicates were different ($P < 0.05$); therefore, they were not combined. In replicate 2, all heifers in the control group with plasma P_4 below 1 ng/ml (on consecutive blood samples from d 3 to 5) were removed from further P_4 analysis. Plasma P_4 was significantly higher in pregnant vs. control heifers on d 4 (1.25 ± 0.09 ng/ml vs. 0.85 ± 0.21) and d 5 (1.89 ± 0.18 ng/ml vs. 1.40 ± 0.11). The pregnancy rate among the heifers, with >1ng/ml of P_4, was 12/21 (57%). Use of used CIDRs on d 3 to 5 produced variable pregnancy rates due possibly to differences in P_4 remaining within the CIDR. However, supplementing P_4 at this time may improve pregnancy rates as pregnant heifers had significantly higher P_4 concentrations during this time compared with open heifers.

Key Words: progesterone, heifer, supplementation

T194 Effect of phase of estrous cycle and fixed-timed insemination on fertility of Criollo cows after a norgestomet or progesterone based treatment.

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Phase of estrous cycle and time of insemination were examined for their influence on fertility of 86 cycling mature Criollo (Corriente) cows after a 9-d norgestomet (Crestar; n = 28) or a 7-d progesterone (CIDR; n = 58) synchronization. Cyclicity was assumed if serum progesterone (P4) concentrations were ≥ 1 ng/mL in either one of 2 samples taken 8 d apart, being the second sample taken the same day of onset of synchronization treatment for phase of estrous cycle determination as well (follicular = P4 ≥ 1 ng / mL in first sample and < 1 ng/mL in second sample, and luteal P4 <1 ng/mL in first sample and ≥1 ng/mL in second sample). Cows were randomly inseminated at 48 or 60 h after the progestin or progesterone device withdrawal along with an injection of 100 µg of GnRH analog. Fertility (pregnancy rate as dependent variable and norgestomet or progesterone, phase of cycle and time of insemination as well as their interactions as independent variables) was analyzed using Proc Logistic of SAS. Synchronization method (Crestar and CIDR) had no effect on pregnancy rate (39.2% and 34.4%, respectively; $P > 0.1$). Also, cows with ovaries in follicular phase had similar pregnancy rate to those with ovaries in luteal phase (34.1% and 37.7%, respectively: $P > 0.1$). Pregnancy rate was higher in cows inseminated at 60 h than those at 48 h after progestin or progesterone removal (53.1% and 15.3%, respectively; $P < 0.01$). Follicular or luteal phase of estrous cycle at start of treatment did not have an effect on pregnancy of Criollo cows after insemination. Furthermore, the higher pregnancy rate of cows inseminated 60 h after the end of progestin or progesterone treatment might indicate that, in Criollo cows, ovulation may occur at a longer time interval after synchronization treatment than other cattle breeds and/or that the dominant follicle and its oocyte present after synchronization require specific conditions that may include a longer period of time to be successfully ovulated.

Key Words: Criollo cattle, ovulation, artificial insemination

T195 Injection site does not alter effectiveness of beef cattle synchronization. C. L. Pickworth*[1,2], D. H. Poole[2], and W. Greene[1], *[1]The Ohio State University, Wooster, [2]North Carolina State University, Raleigh.*

Quality assurance programs are valuable assets to the beef cattle industry for improving meat product quality and consumer acceptance. A key area in beef quality assurance programs is to reduce injection site blemishes in valuable meat cuts by administering all intramuscular injections in the neck. A common belief among cattle producers utilizing estrus synchronization is that the drugs are more effective when administered in the rump compared with the neck. The objective of this study was to compare the effectiveness of injection site of prostaglandin (PGF2α) on first service conception rates following estrus synchronization. One hundred and 5 beef cows and heifers were blocked by breed and stratified by parity before being randomly assigned to 1 of 2 treatments. The 2 treatments were: intramuscular PGF2α administration in the neck or in the rump. Cows and heifers were synchronized using a combination of a 7 d intravaginal progesterone implant (CIDR) and PGF2α injection followed by estrus detection and breeding either on observed heats or timed insemination. Days pregnant was determined by a veterinarian using ultrasonography approximately 70 d post-insemination. Data were analyzed as a randomized complete block design in Proc Mixed with animal as the experimental unit. Differences are declared significant at $P < 0.05$ and means are reported as LS means. Site of PGF2α injection did not affect ($P > 0.05$) overall conception rates in response to artificial insemination at 57.5 and 55.6% conception after first service for cattle receiving injections in the neck and rump, respectively. Nor did injection site affect ($P > 0.05$) whether cattle were bred based on estrus detection or timed insemination. Parity and breed of cattle did not affect ($P > 0.05$) pregnancy rates, nor were there any interactions ($P > 0.05$) with site of injection. Overall conception rate at the end of the breeding season was 86.6%. Administering PGF2α intramuscularly in the neck does not alter conception rates or effectiveness of the synchronization protocols as is misconceived by producers. Therefore, all producers should follow beef quality assurance protocols when administering intramuscular injections during estrus synchronization.

Key Words: beef production, estrus synchronization, quality assurance

T196 Presynchronizing $PGF_{2α}$ injection before a fixed time artificial insemination (TAI) CO-Synch + CIDR program. S. L. Hill*[1], S. L. Pulley[1], H. I. Mellieon Jr.[1], K. C. Olson[1], J. R. Jaeger[1], R. M. Breiner[1], G. A. Perry[2], G. C. Lamb[3], and J. S. Stevenson[1], *[1]Kansas State University, Manhattan, [2]South Dakota State University, Brookings, [3]University of Florida, Marianna.*

We hypothesized that follicular wave synchronization may be improved by inducing luteal regression before initiating a TAI program. The objective of the current study was to determine if injecting $PGF_{2α}$ (PG) 3 d before initiating CO-Synch + CIDR program would: 1) increase uniformity of follicles; and 2) improve pregnancy outcomes. Suckled beef cows at 9 locations (n = 1,537) were assigned randomly to 2 treatments after stratification of cows based on breed, parity, and days postpartum: 1) PG-CO-Synch + CIDR: PG (25 mg i.m.) on d −-13, GnRH-1 (100 μg i.m.) and insertion of a CIDR insert on d −10, PG (25 mg i.m.) and CIDR insert removal on d −-3; or 2) control: same as PG-CO-Synch + CIDR without the initial PG injection. All cows were inseminated at 72 h after CIDR removal and GnRH-2 (100 μg i.m.) was administered after TAI. Blood was collected on d −23, −13, −10, −3, and 0 for later progesterone analyses. Cows treated with PG on d −13 were more likely ($P < 0.05$) to have luteolysis after d −13 than control cows (83 vs. 29%) and reduced ($P < 0.05$) serum progesterone (0.55 vs. 1.40 ng/mL) on d −10. PG-CO-Synch + CIDR cows had larger ($P < 0.05$) follicles (12.5 vs. 10.8 ± 0.4 mm) on d −10 and more ($P < 0.05$) ovulated after GnRH-1 than controls (60.6 vs. 36.5%); however, follicle diameters on d 0 were not more uniform in PG-CO-Synch + CIDR cows. Multiparous cows treated with PG on d −13 had a greater ($P < 0.05$) incidence of estrus between d −13 and −10 than multiparous controls and all treated and control primiparous cows (32.3 vs. 15.4, 16.8 and 16.2%, respectively). Incidence of estrus between d −3 and 0 after PG on d −3 was likewise greater ($P < 0.05$) for treated multiparous cows vs. other treatment-parity groups (74.1 vs. 64.3, 58.6, and 59.1%, respectively). Pregnancy rates at d 35 did not differ between treatments but were greater ($P < 0.001$) at d 35 (60.0 vs. 47.7%) and at the end of the breeding season (96.2 vs. 92.3%) for multiparous vs. primiparous cows, respectively. In summary, more multiparous cows in the PG-CO-Synch + CIDR treatment exhibited estrus and had greater pregnancy outcomes than primiparous cows, but no overall treatment advantage was detected compared with the control.

Key Words: timed AI, luteolysis, follicle diameter

T197 Effects of pregnancy on endometrial gene expression related to amino acid, fatty acid and glucose metabolism in dairy cattle. R. L. A. Cerri*[1,2], I. M. Thompson[1], I. H. Kim[3], A. D. Ealy[1], P. J. Hansen[1], C. R. Staples[1], J. L. Li[1], and W. W. Thatcher[1], *[1]University of Florida, Gainesville, [2]University of British Columbia, Vancouver, BC, Canada, [3]Chungbuk National University, South Korea.*

Objectives were to determine effects of pregnancy on endometrial gene expression related to amino acid, fatty acid and glucose metabolism on d 17 of the estrous cycle and pregnancy. Heifers (n = 33) were assigned randomly after parturition to lactating (L, n = 17) or nonlactating (NL, n = 16) groups. Cows were subjected to an ovulation synchronization program for a timed artificial insemination (TAI); 10 cows in L and 12 in NL were inseminated. Slaughter occurred 17 d after the day equivalent to TAI, and conceptus and intercaruncular endometrial tissues collected. Only pregnant (L, n = 8; NL, n = 6) and non-inseminated cyclic (L, n = 7; NL, n = 4) cows were analyzed. Microarray analysis used the bovine Affymetrix platform. Data were analyzed using Bioconductor GCRMA and Limma methods. Differentially expressed genes were selected with P-value <0.01 and fold differences >1.5. Analyses detected 697 genes differentially expressed for pregnancy (406 downregulated and 291 upregulated). Gene ontology (GO) analyses of downregulated genes during pregnancy revealed several terms related to amino acid, fatty acid or glucose metabolism. Genes upregulated in pregnant cows were associated with 89 GO terms, among them terms related to amino acid metabolism (amino acid and derivative metabolic processes, GO:0006519; translation, GO:0006412), fatty acid metabolism (monocarboxylic acid metabolic processes, GO:0032787), and glucose metabolism (carboxylic acid metabolic process, GO:0019752). Several genes such as ASL, ARG2, SLC27A5, CRAT, FBP1, PCK2, SLC2A1 were upregulated in pregnancy and are candidate targets for interventions aiming for improvement in fertility of dairy cows. New insights into changes that occur in the endometrium during the period of corpus luteum maintenance identify several upregulated metabolic genes that may contribute to countering sub-fertility observed in lactating dairy cows.

Key Words: endometrium, gene expression, pregnancy

T198 Use of bovine pregnancy-associated glycoproteins (bPAGs) to diagnose pregnancy in postpartum Nelore beef cows.

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Although accurate pregnancy diagnosis is a critical factor affecting reproductive management success, relatively few beef operations utilize the technology. Binucleate trophoblast cells constitute 15 to 20% of the ruminant placenta trophoblast population, appear around d 19 to 20 of gestation in cattle and secrete bPAG. Bovine PAG are commonly used to diagnose pregnancy success in *Bos taurus* breeds and are a marker of placental function; however, much less is known about the efficacy of bPAG for pregnancy diagnosis in *Bos indicus* breeds. The objective was to measure serum concentrations of bPAG to detect the presence of an embryo/fetus on d 30 after artificial insemination (AI; d 0) in *Bos indicus* (Nelore) beef cows. In experiment 1, postpartum Nelore beef cows (n = 56) were AIed at a fixed time following synchronization of ovulation. Serum samples were collected on d 0, d 21, d 24, d 27, and d 30. Real-time ultrasonography for diagnosis of pregnancy was performed on d 30 with 39% confirmed pregnant (n = 22). The first increase ($P < 0.0001$) in serum bPAG occurred on d 24 and there was no relationship ($P = 0.44$) between ovulatory follicle diameter and bPAG concentrations at d 30; which is similar to *Bos taurus* breeds. In experiment 2, ovulation was synchronized in postpartum Nelore beef cows (n = 720). Pregnancy diagnosis and blood sample collection occurred between d 29 and 33 post insemination. Pregnancy rate at d 30 was 54% (n = 386) and average serum concentration of bPAG was 15.11 ± 9.92 ng/mL (mean ± SD). Serum concentrations of bPAG accurately detected pregnancy in 97% of all cows compared with real-time ultrasonography and none of the nonpregnant cows had a serum bPAG concentration that exceeded the threshold level for pregnancy detection. Serum concentrations of bPAG were higher ($P < 0.03$) in primiparous cows (n = 55; 20.45 ng/mL ± 1.80 ng/mL; mean ± SEM) compared with multiparous cows (n = 331; 14.23 ng/mL ± 0.49 ng/mL; mean ± SEM). In summary, bPAG first increased in Nelore beef cows on d 24 following insemination and a single serum sample on d 29–33 post-insemination was 97% accurate in diagnosing pregnancy.

Key Words: cattle, pregnancy, placenta

T199 Fetal to maternal transplacental DNA transfer in female beef cattle.

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Exchange of DNA between mother and fetus has been well documented in humans but only limited reports exist for beef cattle. Our objective was to determine if we could detect male fetal DNA in the maternal blood after parturition. Whole blood was collected within 48 h after parturition from multiparous (n = 48) and primiparous (n = 54) bovine females having single (n = 75) or twin (n = 27) births. Real-time PCR analysis was performed on genomic DNA, extracted from the blood sample, using male-specific primers that target the Y chromosome. Male genomic DNA isolated from whole blood was also included in each assay as a positive control. No dams (n = 30) giving birth to only female offspring were positive for the Y PCR test. However, of the dams that gave birth to a male calf (n = 72), a total of 9 were positive for the Y PCR test. Common characteristics of those 9 females included 8 primiparous and 1 multiparous (second parturition) dams that birthed either a single male calf (n = 4) or twins (n = 5) that included at least 1 male. In addition, 3 of the 4 single male births experienced dystocia requiring assistance with a calf jack, and the positive multiparous dam gave birth to a set of twins (1 male, 1 female) that were dead at birth due to dystocia. Samples that were positive for the Y PCR test were reassayed with the same primers as well as with additional Y-specific primers obtained from a bovine SNP beadchip assay to confirm results. Six of the 9 females that were positive for the original Y-PCR test were also positive for the additional Y SNP PCR tests. Results indicate that DNA can be transferred from the fetus to the dam and that it may be more likely to occur in younger females experiencing trauma at calving such as dystocia or birth of twins. USDA is an equal opportunity provider and employer.

Key Words: Y chromosome, parturition, transplacental DNA transfer

T200 Nutrient restriction during early pregnancy alters cotyledon arterial vascular reactivity in response to bradykinin in beef cows.

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It is hypothesized that altered uterine or umbilical blood flows in nutrient restricted cows would be due to changes in placental arterial sensitivity to bradykinin (BK). To examine the effects of maternal nutrient restriction on cotyledonary (COT) artery vasoactivity during early gestation, multiparous beef cows were randomly assigned to either 100% (CON; n = 6) or 60% NRC requirements (RES; n = 4) on d 30 of gestation. At d 85 of gestation cows were slaughtered and arteries that terminated into the fetal portion of the placentome (COT artery) were dissected to be used for in vitro vasoreactivity assays using wire myography. Arterial rings were placed into organ chambers of a wire myograph filled with 5 mL of physiological saline aerated with a mixture of 95% O_2 and 5% CO_2. The arterial rings were normalized by progressive stretching. The presence or absence of endothelium in the arterial rings was verified by testing the ability of BK (10–7 M) to produce endothelium-dependent relaxation in arteries pre-contracted with U46619 (10–6 M). Endothelium-intact rings were contracted with U46619 (10–6 M) and the dose response curve (DRC) to BK was obtained. In addition, a BK DRC was obtained for rings which were incubated for 30 min with inhibitors to: 1) BK2 receptor, HOE 140 (10–6); 2) Ca^{2+}-activated K+ channels, iberiotoxin (IBTx;10–7 M); and 3) endogenous nitric oxide synthase; N(omega)-L-arginine (NLA 10–5). Cotyledonary arteries from RES cows were more sensitive ($P < 0.01$) to a BK induced relaxation compared with CON cows. There was a treatment by dose interaction ($P = 0.02$) when arteries were incubated with HOE140, with COT arteries from CON cows contracting, and no change in vasoactivity observed in COT arteries from RES cows. CON cows were more sensitive ($P < 0.01$) to BK induced relaxation in the presence of IBTx compared with RES cows. There was no effect ($P = 0.56$) of maternal diet in the response to BK when COT arteries were in the presence of NLA, which blocked relaxation.

Alterations in placental vasoactivity may affect uterine-umbilical blood flows and nutrient availability to the developing calf.

Key Words: bradykinin, cow, placenta

T201 Assessment of serum IGF-1 and β-hydroxybutyrate concentrations on reproductive performance prior to calving and breeding in young beef cows grazing native range.

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Metabolites involved in the metabolic adaptation to negative energy balance may potentially contribute to regulation of reproductive success. Therefore, the objective of this 4-yr study was to determine the association of serum metabolites, cow BW, BCS, and calf performance on conception date in spring calving 2- and 3-yr-old beef cows (n = 381) grazing native range at the Fort Keogh Livestock and Range Research Laboratory. Cows were classified by subsequent calving date in a 55 ± 2 d breeding season as either conceiving early (EC; conceived in first 15 d of breeding) or late (LC; conceived during the remaining breeding season). Blood samples were collected in 2 periods 30 ± 1 d before calving and 14 ± 1 d before breeding to determine circulating concentrations of IGF-1 and β-hydroxybutyrate (BHB). Assignment to conception group resulted in a mean conception date that was 33 d earlier ($P < 0.01$) in EC than LC cows. Cow age × sample period × conception date interaction ($P < 0.01$) occurred for serum BHB concentrations. Serum BHB concentrations were similar ($P > 0.10$) for 2-yr-old cows regardless of their conception date classification and sampling period. However, pre-calving serum BHB concentrations were greater ($P < 0.01$) for LC than EC in 3-yr-old cows with no difference ($P = 0.86$) at pre-breeding. Serum IGF-1 concentrations were greater ($P < 0.01$) for EC cows relative to LC cows at pre-calving and pre-breeding sampling periods. Cow BW and BCS were not different ($P \geq 0.43$) at pre-calving or pre-breeding between EC and LC cows. Calf BW at birth was not different ($P = 0.25$) between EC and LC cows, but EC cows weaned lighter (205-d BW; $P < 0.01$) calves, suggesting more energy may have been diverted from milk production toward reproduction in EC cows. This study indicates that pre-calving serum concentrations of BHB and IGF-1 may be indicative of their capacity for subsequent rebreeding. Chute-side measurements of these factors may provide producers opportunity to manage cows differently to improve overall reproductive efficiency.

Key Words: beef cows, conception date, serum metabolites

T202 Sex comparison of white Fulani cattle blood profile in southwestern Nigeria.

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Sexual dimorphism has been established in the brain regions of farm animals and poultry, but for their blood, reports do not agree as to differences at the same age. While some reports show no differences except for pregnant and lactating females, others indicate otherwise. This study was carried out to investigate the blood of white fulani breed of cattle in southwestern Nigeria if there would differences at same matured age (4 yr). A total of 100 cattle was used consisting of 50 bulls and 50 cows. Full hematology was investigated using the Vet Auto hemoanalyser machine. Some serum metabolites were also investigated including Total Protein, Albumin and total cholesterol. Data obtained were subjected to one-way ANOVA (ANOVA). The results show that white blood cell count (WBC) was significantly ($P \leq 0.05$) higher in females (17.23 ± 1.08) than in males (12.25 ± 0.77). Mean corpuscular hemoglobin concentration (MCHC) also showed sex differences with females having higher and significant ($P \leq 0.05$) average value (33.8 ± 0.19) than males (32.6 ± 0.24). The results from Serum analysis show that bulls (with 37.8 ± 0.54) have higher and significant ($P \leq 0.05$) Albumin values than cows (34.9 ± 0.29). Though the results obtained in this study fall within normal ranges for this species, it however does not indicate any specific sex effect for this breed.

Key Words: cattle, blood, sex

T203 Maternal diet restriction effects on fetal organ weights in beef cows during early pregnancy.

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The objectives were to examine the effects of maternal nutrient restriction on fetal organ weights during early gestation. On d 30 of pregnancy, multiparous beef cows were randomly assigned to either 100% (CON; n = 6) or 60% NRC requirements (RES; n = 6). Cows were individually fed once daily in a Calan gate system at 1000 h. At d 85 of gestation cows were slaughtered and fetal organ tissues were collected and weighed. Fetal eviscerated weight (g) was greater ($P = 0.05$) in RES vs. CON. Absolute fetal organ or tissue weights (g) and fetal organ or tissue weights relative to fetal weight (g/kg) were not different ($P \geq 0.09$) between dietary treatmens for adrenals, kidneys, perirenal fat, spleen, or stomach complex. Fetal brain weight was not different ($P = 0.5$) between treatments, while brain weight relative to fetal weight was decreased ($P = 0.02$) in RES vs. CON. Fetal lung weight was not different ($P = 0.67$) between treatments, while lung weight relative to fetal weight was decreased ($P = 0.04$) in RES vs. CON. Heart weight was increased ($P = 0.001$) in RES vs. CON fetuses, while heart weight relative to fetal weight was not different ($P = 0.33$) between treatments. Fetal pancreas weight was increased ($P = 0.06$) in RES vs. CON, while pancreas weight relative to fetal weight was not different ($P = 0.17$) between treatments. Fetal omental and mesenteric fat weight and omental and mesenteric fat relative to fetal weight were increased ($P \leq 0.06$) in RES vs. CON. Maternal diet restriction during early pregnancy alters fetal organ weights. Interestingly, compensatory fetal intra-abdominal visceral fat deposition appears to occur when beef cows are nutrient restricted during early gestation.

Key Words: beef cows, fetal organs, nutrient restriction

T204 Maternal feed efficiency during gestation is correlated with offspring birth weight and girth in nutrient restricted and control-fed ewes.

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We hypothesized that some of the variation in offspring fetal and neonatal growth observed within a given gestational nutritional treatment (e.g., nutrient restriction) in developmental programming studies is related to differences in maternal metabolic efficiency and nutrient utilization. Thus, our objective was to investigate the relationship of maternal feed efficiency (G:F) during gestation with offspring birth and neonatal responses. Data from 2 studies with similar designs and dietary treatments were utilized. In both studies, primiparous ewes with singleton pregnancies received a pelleted diet providing either 100% (control; n = 24) or 60% (nutrient restricted; n = 24) of NRC recommendations for

gestation. Nutritional plane treatments began on d 40 to 50 of gestation and lasted until parturition. Ewes were fed individually, and G:F was calculated as ADG (g/d) divided by DMI (g/d). At birth, lambs were immediately removed from their dams for artificial rearing. Data were analyzed using the CORR procedure of SAS to determine the relationship of ewe G:F during gestation with lamb measures within each nutritional plane. For nutrient restricted ewes, gestational G:F (range: −0.12 to 0.10) was positively correlated with birth weight (r = 0.50; $P = 0.01$), curved crown rump length (CCR; r = 0.46; $P = 0.02$), and heart girth (r = 0.60; $P = 0.002$), as well as BW at 7 d (r = 0.46; $P = 0.03$) and 21 d (r = 0.42; $P = 0.04$). Despite this, G:F of nutrient restricted ewes was not correlated ($P = 0.59$) with lamb ADG from birth to 21 d. For control ewes, gestational G:F (range: 0.08 to 0.21) also was positively correlated with birth weight (r = 0.39; $P = 0.06$) and heart girth (r = 0.54; $P = 0.006$), but was not correlated ($P > 0.16$) with CCR, 7- or 21-d BW, or ADG to 21 d. These data indicate that ewe metabolic efficiency and nutrient utilization, as measured by G:F, are related to lamb weight and size at birth. This relationship is stronger in a nutrient restriction model, suggesting that more efficient dams are able to partition more nutrients for fetal growth when nutrients are limiting.

Key Words: developmental programming, feed efficiency, fetal growth

T205 Nutrient intake during lactation affects performance of beef cows and calf growth. K. J. McLean,* B. H. Boehmer, L. J. Spicer, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Fall calving cows grazing native grass pasture were used during 3 consecutive years (n = 44, n = 51 and n = 58, respectively) to evaluate the effects of nutritional supplementation during breeding and the first trimester of gestation on cow performance, plasma IGF-1, and subsequent postnatal growth of calves. Cows calved in Sept-Oct and were assigned to control (C, 1.82 kg/d of 38% CP supplement, approximately 100% of NRC requirements) or low (L, 0.2 kg/d of 8% CP supplement) from November 17 to March 20; supplement was individually fed in a stall barn. Cows were maintained on the same pasture and exposed to bulls for 60 d commencing Dec. 1. During lactation half of the cows on the C and L prenatal treatments were assigned to the C treatment the other half was assigned to the L treatment. The GLM procedure (SAS) was used to analyze BW, BCS and plasma IGF-1 of cows, and calf BW, as a 2X2 factorial ANOVA. Control cows lost less BW from Nov. to Jan. compared with L cows (37.8 ± 3.1 and 59.2 ± 3.1 kg, respectively, $P < 0.001$). Control cows were also heavier in May compared with L cows (566 ± 10 and 538 ± 10 kg, respectively, $P = 0.05$). However, BCS was not influenced ($P > 0.11$) by treatments. At breeding in Dec., C cows tended ($P = 0.06$) to have greater plasma concentrations of IGF-1 compared with L cows (26 ± 3 and 17 ± 3 ng/mL, respectively). Birth weight and postnatal growth of calves was not influenced ($P = 0.63$) by prenatal treatment. Calves on postnatal C cows had greater ADG from birth to Jan. compared with L calves (0.81 ± 0.03 and 0.74 ± 0.02 kg/d, $P = 0.05$). Weaning weight (205 d) was greater for calves on postnatal C versus L cows (188 ± 5 and 173 ± 4 kg, respectively, $P = 0.02$). Protein supplementation of beef cows during early gestation that caused greater BW loss, less BW gain of suckling calves, and reduced plasma concentrations of IGF-1, did not alter birth weight or postnatal growth of prenatally exposed calves.

Key Words: beef cows, gestation, nutrition

T206 Mineral supplementation associated with Megalac E and/or citrus pulp during timed AI synchronization programs in postpartum Nellore cows. M. V. Biehl*[1], A. V. Pires[2,1], I. Susin[2], D. D. Nepomuceno[2], J. R. S. Goncalves[3], R. Sartori[2], F. M. da Rocha[1], L. H. Cruppe[4], J. L. M. Vasconcelos[5], and M. L. Day[4], *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, PR, Brazil, [4]The Ohio State University, Columbus, [5]Sao Paulo State University, Botucatu, SP, Brazil.*

The objective of this study was to compare reproductive performance of Nellore cows (n = 215), synchronized with a 7 or 9-d CIDR + estradiol benzoate (EB) and 3 supplementation programs. Cows were blocked according to BW (428 ± 3.43), BCS (2.77 ± 0.03, scale 1–5) and DPP (81.9 ± 1.16) in a 2 × 3 factorial arrangement. The supplements were: mineral mixture (MM); MM + MegalacE + citrus pulp (CP) (MEG); MM + Kaolim + CP (KAO). Supplementation began 30 d before CIDR insertion and were terminated 30 d after timed AI. Blood samples for P4 analysis were collected 10 d before and at CIDR insertion to determine reproductive status. The CIDR was inserted with 2 mg of EB and it was removed either 7 or 9 d later. All cows received 25 mg PGF (Lutalyse) 48 h before CIDR removal, 300 IU eCG (Novormon) and 0.6 mg estradiol cipionate (ECP) at CIDR removal. Treatments were: 7dMM (n = 35; e.g., 7d CIDR and MM supplementation), 7dKAO (n = 34), 7dMEG (n = 36), 9dMM (n = 36), 9dKAO (n = 36), and 9dMEG (n = 38). Estrus was detected for 48 h and timed AI performed 50 h after CIDR withdrawal. Rebreeding with bulls 10 d after AI for period of 30 d. Pregnancy diagnosis was performed 30 and 60 d after AI. At CIDR insertion, 73.8% (158/215) of cows were anestrus. Estrus was detected in 77.7% (167/215) of the cows and time to estrus (41.2 ± 0.5 h) did not differ among CIDR and supplementation treatments. Timed AI pregnancy rates neither differed between the length of CIDR treatments nor among the supplementation programs (7dMM, 51.4%; 7dKAO, 50%; 7dMEG, 27.8%; 9dMM, 36.1%; 9dKAO, 38.9% and 9dMEG, 36.8%). Natural mating rebreeding pregnancy rate also did not differ between the length of CIDR treatments and among the supplementation programs. Final pregnancy rate was greater ($P < 0.05$) for the supplement KAO compared with the MEG (84.3 and 67.6%, respectively), and the MM group did not differ from any of the treatments. In conclusion, supplementation with Kaolim + CP or Megalac E + CP did not improve reproductive performance. In addition, timed AI pregnancy rates did not differ between 7-d and 9-d CIDR+EB programs.

Key Words: Megalac E, beef cows, timed AI

T207 Different luteolytic doses of PGF$_{2\alpha}$ in Nellore cows on days 5 and 7 of the estrous cycle. M. V. C. Ferraz Junior[1], A. V. Pires[2], R. Sartori[2], M. V. Biehl*[1], D. D. Nepomuceno[2], I. Susin[2], E. M. Ferreira[2], F. M. Rocha[1], J. R. S. Goncalves[3], L. H. Cruppe[4], and M. L. Day[4], *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, PR, Brazil, [4]The Ohio State University, Columbus.*

The aim of this study was to evaluate the luteolytic competence of different PGF2α (PGF) doses on d 5 and 7 of the estrous cycle. Nonlactating Nellore cows in random stages of the estrous cycle were treated with 25 mg PGF (Lutalyse) for synchronization purpose. Three hundred and 39 cows detected in estrus after PGF injection were divided into 2 groups to be treated on d 5 or d 7 of the subsequent estrous cycle. Treatments consisted of 3 different PGF doses (12.5, 25 and 50 mg) within target d of the cycle (d 5 and d 7). Treatments were defined as follow: 5d12.5PGF (n = 57); 5d25PGF (n = 58); 5d50PGF (n = 58); 7d12.5PGF (n = 56); 7d25PGF (n = 55) and 7d50PGF (n = 55). Blood samples for progesterone (P4) analysis were collected at 0, 24 and 48 h after PGF treatments to assess the incidence of luteal regression. The presence of a CL was defined as P4 concentration ≥1 ng/ml at the time of PGF and its regression defined as attainment of concentrations of P4 ≤ 1 ng/ml by 48 h after PGF. Detection of estrus was performed twice daily with the aid of teaser bull for 5 d after PGF. Serum P4 concentrations were quantified using a chemiluminescent immunoassay (Immulite 1000, Siemens Healthcare Diagnostics, Deerfield, IL, USA). Data were analyzed using the GLIMMIX and MIXED procedures of SAS. Estrus detection rate was greater ($P < 0.05$) in animals treated on d 7 compared with d 5 of the estrous cycle (48.8% and 32.4%, respectively). Furthermore, as dosage of PGF increased, the estrus detection rate increased ($P < 0.05$; 24.8%, 41.6% and 54.9% for the 12.5, 25 and 50 mg doses, respectively). Interactions of d of the estrous cycle and PGF dose were not detected for estrus detection rate. Incidence of luteolysis was greater ($P < 0.05$) on d 7 compared with d 5 of the estrous cycle (75.9% and 40.5%, respectively) and increased with dose of PGF (41.6%, 56.6% and 75.2% for 12.5, 25 and 50mg, respectively), with no day x dose interaction. In conclusion, in Nellore cows, the capacity of PGF to induce luteal regression increases between d 5 and 7 of the estrous cycle and as dose of PGF increases from 12.5 to 50 mg/dose.

Key Words: luteolysis, estrous cycle, beef cows

T208 Relationship of body condition with serum prolactin, antral follicle count, and calving rate of beef cows.

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Multiparous (mean age = 7.6 ± 2.1 yr; range 4 to 11 yr), Brahman-influenced beef cows were managed to achieve thin (BCS = 4.3 ± 0.6; BW = 462 ± 51 kg; n = 43) or good (BCS = 6.4 ± 0.8; BW = 582 ± 81 kg; n = 54) body condition (BC) beginning 164 d before breeding to determine the relationship of BC on serum prolactin, total antral follicle count, and calving rate. Cows grazed replicated (n = 4) common bermudagrass during a 60-d breeding season. Blood samples were collected at d 0, 30, and 60 of the breeding season, and serum concentrations of prolactin (PRL) were quantified; serum progesterone was determined on d −10 and 0 of the breeding season to determine luteal status at the beginning of breeding. Antral follicle count (AFC; total number of follicles >3 mm in diameter on both ovaries) was determined via ultrasonography at d 0 and 60 of the breeding season. Ovarian pairs were classified as low (<16 antral follicles), intermediate (16 to 24 antral follicles), or high (>24 antral follicles) AFC. Body weight and BCS were recorded during the breeding season (d 0, 30, and 60). Data were analyzed with ANOVA (model included BC, luteal status, and their interaction; pasture was used as a random effect), and CORR and chi-squared analyses of SAS. Seventy percent of cows were cyclic at the start of breeding. Thin cows gained more ($P < 0.001$) BW (76 ± 4 kg) and BC (1.0 ± 0.1 BCS units) than good-BC cows (51 ± 5 kg; 0.2 ± 0.1 BCS units) during the breeding season. Concentrations of serum PRL tended ($P < 0.12$) to be greater in cyclic cows (n = 68) than anestrous cows (n = 29) on d 30 and 60 of the breeding season. Cyclic cows had a decreased ($P < 0.02$) actual AFC on d 0 of the breeding season compared with anestrous cows (15.8 ± 1.4 vs. 21.7 ± 2.2 antral follicles, respectively). A luteal status × BC interaction tended ($P < 0.10$) to influence actual AFC on d 60 of the breeding season; anestrous, thin cows (21.3 ± 1.8 antral follicles) had increased actual AFC compared with all other groups (mean = 14.6 ± 2.1 antral follicles). More ($P < 0.05$) cyclic cows were classified as low AFC on d 0 than anestrous cows. Similarly, a greater ($P < 0.05$) number of cyclic cows than anestrous cows were classified as low or intermediate AFC on d 60. Body condition score on d 0 ($r = -0.29$; $P < 0.005$) and 60 ($r = -0.31$; $P < 0.003$) of the breeding season was inversely correlated with actual AFC on d 0. Calving rate was reduced ($P < 0.0001$) in thin cows (46%) compared with good-BC cows (87%). Calving rate of cows was similar ($P > 0.10$) among classifications of AFC at d 0 and 60 and averaged 76%. Luteal status tended to affect serum PRL during the breeding season. Further, presence of serum progesterone indicative of luteal activity as well as good BC appeared to negatively influence AFC in Brahman-influenced cows.

Key Words: antral follicle count, beef cow, prolactin

T209 Serum progesterone concentrations in Holstein and Nelore cows after the insertion of two different progesterone devices.

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The objective of this study was to compare the circulating progesterone (P4) profile for 2 different commercial devices for delivery of P4, CIDR (1.9 g, Pfizer) and Sincrogest (1.0 g, Ourofino) in Holstein and in Nelore cows. We hypothesized that independent of the P4 device inserted, the P4 concentrations would be lower in Holstein than in Nelore cows, possibly due to greater P4 metabolism in dairy than in beef cattle. Also, we hypothesized the lower content of P4 present in Sincrogest (1.0 g) would produce lower circulating P4 than CIDR (1.9g) in either Holstein or Nelore cows. Nonlactating, non-pregnant cows (n = 10 Holstein and n = 10 Nelore) were randomly assigned to 1 of 2 groups: CIDR or Sincrogest devices. Blood samples were taken from all cows at hour 0, 1, 6, 12, 24, and 48 after insertion of the devices to analyze P4 concentration by radioimmunoassay. Cows were fed a maintenance diet 14 h before device insertion and at 12, 24, and 48 h after device insertion (following blood sampling). Data were analyzed using generalized linear models, considering the heterogeneous first-order autoregressive covariance matrix, due to repeated measures on the same cow at different times. There was a significant effect of breed (1.18 vs. 2.24 ng/mL, Holstein vs. Nelore, $P = 0.0004$), type of P4 device (1.99 vs. 1.43, CIDR vs. Sincrogest, $P = 0.03$), time ($P < 0.05$), and an interaction of breed by time ($P = 0.0004$). Progesterone concentrations were different ($P < 0.01$) among Holstein and Nelore at hour 0, 1, 6, 12, 24, and 48. Circulating P4 differed or tended to differ for CIDR vs. Sincrogest at hour 1 ($P = 0.09$), 6 ($P = 0.07$), 12 ($P = 0.09$), 24 ($P = 0.05$), and 48 ($P = 0.01$) but not at hour 0 ($P = 0.83$). Thus, independent of the brand of P4 device utilized, P4 concentrations were about 90% greater in Nelore than in Holstein cows, probably due the higher P4 metabolism in Holsteins. Interestingly, the Sincrogest device with 47% less P4 than the CIDR device, produced circulating P4 that was only 28% lower than CIDR. Supported by FAPESP, CAPES and CNPq of Brazil.

Key Words: intravaginal progesterone device, *Bos taurus*, *Bos indicus*

Production, Management and the Environment: Beef, Swine, Sheep

T210 Management and facility factors that affect mortality in grow-finishing pigs. P. S. Agostini*[1,2], A. G. Fahey[2], E. G. Manzanilla[1], J. V. O'Doherty[2], C. de Blas[3], and J. Gasa[1], *[1]Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]University College Dublin, Belfield, Dublin, Ireland, [3]Universidad Politécnica de Madrid, Madrid, Spain.*

The objective of this study was to investigate the effect of some on-farm production and management factors on the mortality rate of grow-finishing pigs. In total 316 batches from 246 growing-finishing farms, including 459,148 pigs, using a Pietrain male finisher and belonging to 8 Spanish companies were used. All data were collected by survey during 2008 and 2009. Survey information included season of placement, sex segregation by pens, number of pig origins, frequency of antibiotic treatments, water source in the farm, initial and final body weight (IBW and FBW), percentage of the barn utilized, floor, feeder, ventilation and number of animals placed. A multivariate linear mixed regression model was used including factors that had a P-value <0.25 in a univariate regression model. These factors were then included in the multivariate model and the final model was determined using a stepwise selection method. The company was considered as a random factor but it was not significant ($P > 0.05$) and thus not included in the final model. The average rate of mortality was 4.13 ± 2.65%. There was a significant increase in mortality when: a) batches were placed between October and March ($P < 0.01$), b) pigs were obtained from multiple origins versus a unique origin ($P < 0.05$), c) pigs were treated ≥3 times with antibiotics versus those treated <3 times ($P < 0.01$), d) fed in a multi-space feeder compared with single-space ($P < 0.01$) and finally e) in farms with more than 800 pigs placed ($P < 0.05$). Moreover, a quadratic effect of IBW ($P < 0.05$) was observed showing that pigs with lower and higher IBW had higher mortality. An interaction between IBW and type of feeder was found ($P < 0.01$) and it showed that pigs fed through multi-space feeder and with IBW lower and higher than 21 kg presented higher and lower mortality, respectively, compared with single-space and single-space with drinker. Total variability of mortality explained by the model was 26%. This study indicates that farms may reduce mortality by improving some farm facilities and/or modifying some management practices.

Key Words: grow-finishing pigs, factors, mortality

T211 Housing and management factors that affect feed conversion ratio in grow-finishing pigs. P. S. Agostini*[1,2], A. G. Fahey[2], E. G. Manzanilla[1], J. V. O'Doherty[2], C. de Blas[3], and J. Gasa[1], *[1]Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]University College Dublin, Belfield, Dublin, Ireland, [3]Universidad Politécnica de Madrid, Madrid, Spain.*

The objective of this study was to investigate the effect of some on-farm production and management factors on the feed conversion ratio (FCR) of grow-finishing pigs. In total 316 batches from 246 growing-finishing farms, including 459,148 pigs, using a Pietrain male finisher and belonging to 8 Spanish companies were used. All data were collected by surveys during 2008 and 2009. Survey information included: season of placement, sex segregation by pens, number of pig origins, frequency of antibiotic treatments, water source in the farm, initial and final body weight (IBW and FBW), percentage of the barn utilized, floor, feeder, ventilation and number of animals placed. A multivariate linear mixed regression model was used that included factors that had a P-value <0.25 in a univariate model and then selected by stepwise procedure in the multivariate model. Company was considered as a random factor but it was not significant ($P > 0.05$) and thus not included in the final model. The mean FCR was 2.71 ± 0.15. Averages of FCR were lower when batches: a) were placed between April and September ($P < 0.01$), b) pigs were segregated by sex in pens (entire male versus female) ($P < 0.01$), c) the proportion of the floor covered by slats was reduced to less than 50% ($P < 0.05$), d) were fed in a single space feeder with an incorporated drinker ($P < 0.01$), e) treated 3 or more times with antibiotics than those treated less than 3 times ($P < 0.01$), f) pigs had a lower FBW at slaughtering ($P < 0.01$) and finally g) had a higher percentage of the barn utilized ($P < 0.01$). Moreover, a quadratic effect of IBW ($P < 0.01$) was observed showing that pigs with lower and higher IBW had higher FCR. An interaction between IBW and trimester of placement was also found ($P < 0.01$) and it showed that pigs placed between July and September and with IBW lower and higher than 19 kg had higher and lower FCR, respectively, compared with pigs placed in other months. Total variability of FCR explained by the model was 31%. This study indicates that farms may reduce FCR by improving some farm facilities and/or modifying some management practices.

Key Words: grow-finishing pigs, factors, feed conversion ratio

T212 Management and facility factors that affect the variability of average daily gain in grow-finishing pigs. P. S. Agostini*[1,2], A. G. Fahey[2], E. G. Manzanilla[1], J. V. O'Doherty[2], C. de Blas[3], and J. Gasa[1], *[1]Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]University College Dublin, Belfield, Dublin, Ireland, [3]Universidad Politécnica de Madrid, Madrid, Spain.*

The objective of this study was to investigate the effect of some on-farm production and management factors on the average daily gain (ADG) of grow-finishing pigs and explain the variability found between companies. Information from 275,936 pigs from Pietrain male finisher, distributed in 190 batches belonging to 5 Spanish companies (ranging from 19 to 59 batches for each company), was collected by survey during 2008 and 2009. ADG was defined as the total average weight gain per pig (kg) divided by the length of the grow-finishing period (days). A multivariate linear mixed regression model was used and factors were considered to have a significant effect when $P < 0.05$. The company was considered as a random factor and batch and herd effects as the residual factor. The mean ADG was 0.632 ± 0.048 kg. Animals placed from July to December had higher ADG than batches placed in other months ($P < 0.01$). Pigs fed in a single-space feeder with incorporated drinker had higher ADG than single and multi-space without drinker ($P < 0.05$). Small batches (less than 800 pigs placed) had higher ADG ($P < 0.01$) and pigs raised a higher final body weight (FBW) at slaughtering also had higher ADG ($P < 0.01$). An interaction between FBW and feeder was found ($P < 0.05$) showing that pigs fed through single-space feeder with drinker and with FBW lower and higher than 102 kg had lower and higher ADG respectively compared with other feeders. When no fixed effects were included in the model (null model), about 33% of the variability was registered between companies, meanwhile when fixed effects were included (full model), companies only explained 8% of the variance. The total variance explained by the full model was 26%. Companies may have important specific factors affecting the ADG which have not been considered in this study; among them some approaches of health status, biosecurity conditions or nutrition programs should be included in future studies.

Key Words: grow-finishing pigs, factors, average daily gain

T213 Effects of herb supplementation on growth performance, litter performance, and diarrhea occurrence in lactating sows and piglets.

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This study was conducted to evaluate the effects of herb supplementation on growth performance, litter performance, and diarrhea occurrence in lactating sows and piglets. A total of 30 sows (Landrace × Yorkshire) and their litters were employed in this study. Sows were allocated to 1 of 3 treatment groups. Dietary treatments included: 1) CON, basal diet, 2) A, basal diet + 0.01% (*Scutellaria baicalensis* + *Astragalus membranaceus*), and 3) B, basal diet +0.01% (*Codonopsis pilosula* + *Angelica gigas*). The experiment started 7 d before farrowing and lasted for 28 d. Within 24 h after parturition, numbers of piglets were adjusted equally per sow. Backfat thickness was evaluated at 3-d before farrowing and weaning day (21d). No differences ($P > 0.05$) were observed in ADFI and backfat thickness throughout the experimental period. However, backfat loss was lower ($P < 0.05$) in CON treatment than that in A and B treatments. No significant difference ($P > 0.05$) was found in the estrus interval and fecal moisture content among dietary treatments. No significant difference ($P > 0.05$) was observed in the birth BW, 14 d BW, and 21 d BW (weaning weight) of piglets among treatments. No difference ($P > 0.05$) was observed in diarrhea occurrence of sucking piglets by dietary supplementation with herb. No significant difference ($P > 0.05$) was noted in total number of piglets born, number of weaned piglets, and mortality of piglets. In conclusion, no effect of herbs was observed on the performance of lactating sows and diarrhea occurrence in piglets. Further studies should be conducted to confirm the positive effect of dietary supplementation with herbs in lactating sows.

Key Words: herb, piglet, sow

T214 Wood to feed: Diversifying income opportunities by increasing the livestock feeding value of woody plant species.

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The primary goal of this project is to develop the technology and knowledge base necessary to convert invasive woody biomass material into a viable ruminant feed ingredient. Woody species such as *Juniperus* and *Prosopis* occur on millions of acres of rangelands in the US and continue to increase at rapid rates, reducing forage productivity, water resources, wildlife habitat, and ecosystem health. Treatments to manage these woody species are generally not cost-effective. However, increasing the value of woody biomass through conversion to animal feed or biofuels will provide cost-effective management options, while concurrently increasing grass production and ecosystem health. Although not unique to the livestock industry, current drought and escalating fuel and fertilizer prices have drastically increased feed costs and interest in using nontraditional feeds. Use of woody biomass as feed is not a novel idea, with research conducted in the early 1920s and late 1950s evaluated the feeding value of sawdust and mesquite wood in cattle diets. Limited adoption of mesquite as livestock feed probably occurred because of the relative costs of traditional feed ingredients was not great enough to justify the risk of using a novel feed and conversion of wood to feed was not very efficient. However, both of these conditions have changed. Thus, Texas AgriLife Research faculty, colleagues, and industry collaborators have renewed "wood to feed" efforts and have been successfully incorporating ground woody material into ruminant livestock diets. A recent study from our laboratory showed that ground juniper can replace ground oat hay in lamb feedlot diets without negatively affecting DMI, ADG, or G:F ($P > 0.05$). Even though a renewed interest in "wood to feed" has surfaced, livestock producers are reluctant to move forward because many questions still remain about how to integrate individual systems components into a profitable and sustainable operation. Therefore, to increase the adoption of technologies to cost-effectively harvest and utilize woody biomass as ruminant feeds, we are creating a web-based "Wood to Feed" Center where multidisciplinary scientists work directly with ranchers, landowners, and industry representatives to integrate expertise and novel ideas.

Key Words: woody plants, roughage, natural resources

T215 Effect of body size on feed intake and methane emissions from ewes offered fresh ryegrass.

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Sheep production in the UK is stratified into systems that utilize smaller, hardier breeds in the hills, their crossbreds in the uplands, and heavier, more productive breeds and their crossbreds in the lowlands. This experiment tested the hypothesis that body mass and associated allometric relationships, rather than breed type, determines enteric methane production in sheep. Methane emission measurements were made on mature, barren ewes of 4 different breed types: Welsh Mountain (WMO), Scottish Blackface (SBF), Welsh Mule (WMU), and Texel (TEX) (n = 8 per breed). The mean live weights for the different breeds were 46 (±2.9), 62 (±6.2), 71 (±4.4) and 78 (±3.8) kg, respectively. Following a 3-week adaptation period, the ewes were housed in methane chambers and zero-grazed on herbage cut from an intensively managed perennial ryegrass sward. They were fed on an ad libitum basis, with 2 equal portions offered at 0900 and 1600 h. Data were collected for 3 consecutive days for each animal. There was a significant treatment effect of breed type on voluntary intake, with mean DM intake recorded as 1.08, 1.02, 1.30 and 1.55 for WMO, SBF, WMU, and TEX respectively (SED = 0.111 kg; $P < 0.001$). However, there was a relatively poor relationship between metabolic body weight (BW) and DM intake ($R^2 = 0.30$); consequently body mass was a poor indicator of methane emissions ($R^2 = 0.17$). There was a stronger correlation between DM intake (g/d) and methane emitted ($R^2 = 0.57$). In conclusion, BW was a relatively poor indicator of DM intake and therefore a poor predictor of methane emissions from sheep of different breed sizes when offered fresh ryegrass.

Key Words: breed size, methane, sheep

T216 Fifty years of the Wyoming ram test: How have sheep changed?

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Production characteristics of white-faced rams have been systematically evaluated over a 140 d test for gain and wool characteristics in the

Wyoming white-faced ram test since 1961. Records from this test are predominantly from Rambouillet rams but records from other breeds such as Columbia and Targhee are included. Individual production traits from test records (n = 3941) from 1961 through 2010 were analyzed to determine how sheep have changed over the last 50 years. Although age of rams on test has remained stable at 354 ± 0.6 d, both weight-on and -off test have increased linearly ($P < 0.001$) since 1961 with weight-off test increasing 22.7 kg over this time frame. This larger body size likely contributed to a linear increase ($P < 0.001$) in clean fleece weight. Rate of gain also increased linearly ($P < 0.001$) with rams gaining approximately 0.23 ± 0.01 kg/d in the early years to a current rate of gain of 0.39 ± 0.01 kg/d. Although wool characteristics remain an important component to the test index, spinning count, a measure of wool diameter, did not change in a linear manner ($P > 0.05$), and has remained stable at a 62 spinning count. Market forces may influence breed characteristics over time, and thus correlates to market prices were determined with a 0, 2 and 5 yr time lag. Average daily gain was strongly correlated (r >0.6) with feeder lamb price, and had the strongest correlation with a 2 year (r = 0.76) time lag. Sheep inventory negatively correlated (r = 0.87) with average daily gain but correlated similarly with a 0, 2 or 5 year time lag. Wool price did not correlate (r <0.1; $P \geq 0.5$) with spinning count at any of the time lags. Rambouillet rams have increased in size over the last 50 years with an increase in efficiency of production. Although clean fleece weight has increased proportionally to ram size, fiber diameter has remained largely unchanged and did not correlate to market wool price. This suggests that market influences on white-faced ram selection have largely affected growth traits while avoiding any negative effect on wool quality.

Key Words: ram, production, wool

T217 The environmental and economic impact of removing growth-enhancing technologies from United States beef production. J. L. Capper[1] and D. J. Hayes*[2], [1]*Washington State University, Pullman,* [2]*Iowa State University, Ames.*

This study quantified the environmental and economic impact of withdrawing growth-enhancing technologies (GET) from the US beef production system. A deterministic model based on the metabolism and nutrient requirements of the beef population was used to quantify resource inputs and waste outputs per 454 × 10^6 kg of beef. System boundaries extended from manufacture of cropping inputs to delivery of live animals at the slaughterhouse. Two production systems were compared – one using GET (steroid implants, in-feed ionophores, in-feed hormones and β-adrenergic agonists) where approved by the FDA at current adoption rates; the other without GET use. Both systems were modeled using characteristic management practices, population dynamics and production data from US beef systems. The economic impact and global trade and carbon implications of GET withdrawal were calculated based on feed savings from the environmental model. Withdrawing GET from US beef production reduced productivity (growth rate and slaughter weight) and increased the population size required to produce 454 × 10^6 kg beef by 385 × 10^3 animals. Feedstuff and land use were increased by 2,830 × 10^3 t and 265 × 10^3 ha respectively by GET withdrawal, with 20,139 × 10^6 more liters of water being required to maintain beef production. Manure output increased by 1,799 × 10^3 t as a result of GET withdrawal, with an increase in carbon emissions of 714,515 t per 454 × 10^6 kg beef. The projected increased costs of US beef produced without GET resulted in the effective implementation of an 8.2% tax on beef production, leading to reduced global trade and competitiveness. To compensate for the increase in US beef prices and maintain worldwide beef supply it would be necessary to increase beef production in other regions, with a projected cumulative increase in global carbon emissions of 3,147 × 10^6 t of CO2-equivalent from 2009 to 2023. It is clear that withdrawing GET from US beef production would reduce both the economic and environmental sustainability of the industry.

Key Words: productivity, carbon footprint, growth-enhancing technology

T218 Drought management: Replacing hay with a field pea/co-product supplement fed daily or on alternate days. D. G. Landblom*[1] and S. Senturklu[2], [1]*North Dakota State University-Dickinson Research Extension Center, Dickinson,* [2]*Canakkale Onsekiz Mart Universitesi, BMYO, Canakkale, Turkey.*

One hundred seven, 3- to 10-yr-old, third trimester to early-lactation cows were randomized to treatment and weight blocks, in a 110.5 d study to evaluate a 25% hay reduction and a blended RDP-RUP supplement replacement for hay fed either daily (C) or on alternated days (Alt-D) as a drought management strategy. Cows were fed an all mixed hay control diet (Alfalfa-Bromegrass; 10.2% CP) (C) or a mixed hay and wheat straw (4.7% CP) diet in which the amount of hay fed per cow was reduced 25% and replaced with a field pea/co-product supplement (22.8% CP) that was fed either daily (D) at 0.25% of initial BW or 0.50% of initial BW on alternate days (Alt-D). The 0.635 cm pelleted supplement contained a blend of RDP and RUP from field peas (70.0% RDP), distillers dried grains with solubles (65.0% RUP), and barley malt sprouts (64.0% RDP). Data were analyzed using MIXED procedures of SAS. Unsupplemented C cows were fed an average 16.5 kg of mixed hay daily compared with supplemented cows that were fed 9.57 kg of hay, 1.5 kg wheat straw, and 1.52 kg of the pea/co-product supplement totaling 12.66 kg daily (as-fed). Using the blended RDP-RUP supplement as a replacement for hay, fed either D or on Alt-D, did not affect ending cow weight ($P = 0.89$), body condition score ($P = 0.19$), 12th rib fat depth ($P = 0.19$), or pre-breeding estrous cyclicity ($P = 0.68$). Subsequently, hay conserving strategies did not affect fall calf weaning weight ($P = 0.63$), gain ($P = 0.62$), or ADG ($P = 0.64$). Daily cost per cow was $1.13, $1.19, and $1.185 for the C, D and Alt-D methods, respectively. The data suggest that blending the selected RDP and RUP ingredient sources supplied sufficient ammonia nitrogen to the rumen on the non-supplementation day and appeared to provide adequate nutrient flow when fed on alternate days; and proved to be an effective drought management strategy. Conversely, when hay is plentiful the conservation strategy would be a cost effective method for stockpiling hay as a hedge against drought or to make hay available as a cash crop.

Key Words: beef cattle, field pea, RDP-RUP

T219 Effect of grazing stockpiled perennial forages on beef cow performance, nutrient intake and soil nutrients. H. A. Lardner*[1,2] and D. Damiran[1,2], [1]*Western Beef Development Centre, Humboldt, Saskatchewan, Canada,* [2]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Saskatchewan, Canada.*

An experiment was conducted to evaluate the effects of grazing stockpiled perennial forages in field paddocks or round bale hay fed in drylot pens on beef cow performance, estimated dry matter intake (DMI), nutrient intake and soil nutrient levels. Winter feeding systems were (i) field grazing [meadow bromegrass (*B. riparius*)-alfalfa (*M. sativa*)] stockpiled perennial forage (SPF) (TDN = 55.4%; CP = 11.6%) and (ii) similar grass-legume round bale hay fed in drylot pens (DL) (TDN = 56.9%; CP = 11.7%). Dry, pregnant Black Angus cows (n = 60; mean

BW = 620 ± 1.1 kg) were randomly allocated to one of 2 replicated (n = 3) winter feeding systems. In SPF, cows were allocated swathed forage in field paddocks on a 3 d basis and supplemented (rolled barley grain+ wheat dried distillers grains with solubles; TDN = 84.0%, CP = 18.4%) at 0.2% of BW. Soil nutrient levels were determined on each treatment site following winter grazing. The DMI was measured for each treatment using the herbage weight disappearance method. Cow BW, body condition score, and rib and rump fat were measured at start and end of the experiment. Statistical analysis was conducted as a one way ANOVA using the Proc Mixed Model procedure of SAS. Measured forage biomass was not different ($P > 0.05$) between DL and SPF systems, 4341 and 4910 ± 200 kg/ha, respectively. Forage utilization was lower ($P < 0.05$) in SPF than in DL (57.8% vs. 93.0%) system. Cows on SPF consumed less ($P < 0.05$) DM (8.8 vs. 12.5 kg/d), CP (1.04 vs. 1.47 kg/d), and ME (17.7 vs. 25.7 Mcal/d) from stockpiled forages than cows fed hay in DL. However, total DMI (forage + supplement) and corresponding nutrients were not different ($P > 0.05$) between systems. Cow BW (634.9 and 634.7 ± 1.5 kg), rib fat (3.3 and 3.4 ± 0.4 mm), rump fat (3.7 and 3.5 ± 0.4 mm) and calf birth weight (40.1 and 39.9 ± 0.9 kg) were similar ($P > 0.05$) between DL and SPF systems, respectively. Soil nutrient levels at the 0–60 cm depth were similar ($P > 0.05$) on the feeding sites, except SO_4 which tended to be lower ($P = 0.06$) on SPF (35.9 kg/ha) compared with DL sites (422.3 kg/ha). These results suggest it is possible to manage beef cows grazing stockpiled perennial forages during winter in western Canada.

Key Words: stockpiled forage, winter grazing, beef cow

T220 The environmental, economic and social implications of improving yield and average daily gain in beef production.

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A deterministic model of the US beef industry was developed to quantify changes in environmental impact (EI), profitability and social acceptability resulting from either increasing average daily gain (ADG) by 15% or increasing yield per animal by 15%, with the goal of producing 1 billion kg of beef. Both treatments were compared with a baseline scenario representative of the average growth rate (0.69 - 0.8 kg/d for stockers and 1.22–1.37 kg/d for finishers) and finishing weight (544 kg for heifers and 635 kg for steers) in the US beef industry. Metrics for EI included land, water and feedstuff use, as well as greenhouse gas (GHG) emissions and manure production with system boundaries extending from cropping inputs to animal slaughter. Profitability was calculated by enterprise budgets for current cattle and feed prices sourced from the National Agricultural Statistics Service. The consumer perception of the value (price-dependent) received from purchasing beef was the metric of social acceptability. When ADG increased, land, water and feed use per billion kg of beef were reduced by 2%, 13% and 4%, respectively and GHG emissions and manure production per billion kg of beef were reduced by 7% and 4%. Increased ADG increased whole-industry profitability by 7% which subsequently led to a 5% improvement in consumer's perceived value of purchased beef. Increased yield also reduced EI: land, water and feed use per billion kg of beef were reduced by 3%, 16% and 9%, respectively compared with controls, and GHG emissions and manure production per billion kg of beef were reduced by 10% and 8%. Industry profitability increased by 13.5%, resulting in a 15.8% improvement in consumer's perceived value of beef purchased. Given that sustainability is an environmental, economic and social construct, these conclusions suggest that the sustainability of beef production can be achieved by either increasing yield or increasing ADG. This research supports the assertion that, within the beef industry, management practices centered on improving efficiency will also improve sustainability.

Key Words: beef, sustainability, environmental impact

T221 Body development and endocrine relations at puberty in crossbred heifers.

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The objective of this study was to determine the age and liveweight at puberty of crossbreed heifers from various Nelore (N)-Hereford (H) genetic groups (GG) (25%N-75%H; 37.5%N-63.5%H; 43.7%N-56.3H%; 50%N-50%H; 75%N-25%H) submitted to 4 average daily gains (ADG; kg/d) from weaning to puberty: 0.5 (L; n = 32), 0.75 (M; n = 32), 1.00 (H; n = 29) and 1.25 (VH; n = 27). Puberty was defined as estrus followed by formation of a corpus luteum. Backfat thickness (BF = mm) at the start and at the end of the experimental period was determined by ultrasound. Mean age and liveweight at puberty (LWP) were 388.0 ± 1.9 d and 331.4 ± 1.3 kg, respectively. Heifers with higher post weaning average daily gain were heavier at first estrous and had a lower age at puberty ($P = 0.028$). However, there was an interaction ($P = 0.012$) between growth rates and breed composition. The 75% Nelore were heavier, older and taller at puberty than 25%, 37.5%, and 43.5% N heifers ($P = 0.034$). The phenotypic correlation between body condition score, backfat thickness and puberty age were −0.37 and −0.58, respectively ($P = 0.041$). A linear effect ($P = 0.011$) was observed between the ratio weight:height at 11 mo of age (WH11) and age at puberty (AP). Heifers submitted to higher ADG showed the greater follicle diameter at 10 mo age ($P = 0.031$) and were younger at puberty ($P = 0.033$). The IGF-I blood serum levels were 206, 234, 308 and 312 ng/ml at puberty for L, M, H, and VH ADG, respectively. The IGF-I levels were associated ($P = 0.019$) with AP in heifers because they influenced follicular growth (FG) at 10 mo of the age. There was no multicollinearity among the variables evaluated in the model. A multiple regression analysis found a linear model ($P = 0.017$) to estimate puberty: AP = 437.96 - FG10 × 1.66 + GG × 0.46 + LWP × 0.71-WH11 × 42.67 -BF × 9.95-ADG × 47.59-LW11 × 0.35 ($r^2 = 0.87$). Variables related to body development were better than endocrine predictors of puberty in beef heifers.

Key Words: puberty, beef heifers, follicular growth

T222 Effects of prepartum grouping strategy on health, reproductive, and productive parameters of dairy cows.

P. R. B. Silva*[1,2], J. G. N. Moraes[1,2], L. G. D. Mendonça[1], A. A. Scanavez[1], G. Nakagawa[1], M. I. Endres[2], J. Fetrow[1], and R. C. Chebel[1], [1]*Department of Veterinary Population Medicine, University of Minnesota, St Paul,* [2]*Department of Animal Science, University of Minnesota, St Paul.*

Objectives were to evaluate the effect of an "all-in-all-out" (AIAO) prepartum grouping strategy on health, productive, and reproductive parameters of Jersey cows. Cows (254 ± 7 d of gestation) were paired by gestation length and assigned randomly to AIAO or control treatments. In the AIAO (n = 259) treatment groups of 44 cows were moved into a pen where they remained for 5 wk, whereas in the control treatment (n = 308) approximately 10 cows were moved into a pen weekly to maintain stocking density (44 cows/48 headlocks). Pens were identical in size and design and each of the pens received each treatment a total of 3 times, totaling 6 replicates. Cows were examined at enrollment, calving (d0), d28, and d56 for lameness and on d 1, 4, 7, 10, and 14 for retained fetal membranes (RFM) and metritis. Cows were observed daily for displacement of abomasum (DA) and mastitis until d60. Cows were examined by ultrasound for detection of corpus luteum (CL) on d 39 and 56. Cows were observed daily for estrus starting on d 50 and pregnancy exam was conducted 38 and 66 d after AI. Milk production and components were measured monthly and energy corrected milk yield was calculated for the first 3 tests. Data were analyzed by MIXED procedure and the fixed effect was treatment (AIAO vs control) and the random effect was treatment within pen and replicate. Treatment had no effect on incidence of lameness on d 0 ($P = 0.75$), 28 ($P = 0.45$), and 56 ($P = 0.35$). Similarly, treatment had no effect on incidence of RFM ($P = 0.84$), metritis ($P = 0.35$), acute metritis ($P = 0.54$), DA ($P = 0.92$), and mastitis ($P = 0.47$). Percentage of cows with a CL on d 39 ($P = 0.17$) and 56 ($P = 0.96$) were not affected by treatment. Similarly, percentage of cows inseminated in estrus ($P = 0.52$) and percentage of cows pregnant after first AI ($P = 0.47$) were not affected by treatment. Finally, treatment had no effect on milk ($P = 0.82$) or energy-corrected milk ($P = 0.66$) yield and on linear somatic cell score ($P = 0.28$). In conclusion, AIAO grouping strategy did not reduce incidence of peripartum diseases and did not improve reproductive and productive performance.

Key Words: prepartum cow, grouping strategy, performance

T223 Effects of prepartum grouping strategy on body condition score and metabolic parameters of peripartum dairy cows.

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Objectives were to evaluate the effect of an "all-in-all-out" (AIAO) prepartum grouping strategy on body condition score (BCS) and metabolic parameters of peripartum Jersey cows. Cows (254 ± 7 d of gestation) were paired by gestation length and assigned randomly to AIAO or control treatments. In the AIAO treatment (n = 259) groups of 44 cows were moved into a pen where they remained for 5 wk, whereas in the control treatment (n = 308) groups of approximately 10 cows were moved into a pen weekly to maintain stocking density (44 cows/48 headlocks). Pens were identical in size and design and each of the pens received each treatment a total of 3 times, totaling 6 replicates. Cows received a BCS at enrollment, calving (d0), d28, and d56. Blood samples were collected from all cows on d −21, −14, −7, 0, 7, 14, and 21 for determination of nonesterified fatty acid (NEFA) concentration. Blood was sampled weekly from d-14 to d 14 from a subgroup of cows (n = 34/treatment) to determine concentration of glucose. Cows were classified according to NEFA concentration as above or below 0.10 mmol/L on wk 3 and as above or below 0.18 mmol/L on the week preceding calving, because, based on the data from the current study, these were the criteria that predicted occurrence of displacement of abomasum with the best sensitivity and specificity. Data were analyzed by MIXED procedure and the fixed effect was treatment (AIAO vs control) and the random effect was treatment within pen and replicate. Treatment did not affect BCS on d −21 ($P = 0.67$), 0 ($P = 0.64$), 28 ($P = 0.59$), and 56 ($P = 0.90$). Glucose concentration was not affected by treatment ($P = 0.28$) or by the interaction between treatment and day ($P = 0.11$). Similarly, treatment ($P = 0.17$) and the interaction between treatment and day ($P = 0.11$) did not affect NEFA concentration. Percentage of cows with NEFA >0.10 mmol/l on wk 3 before calving ($P = 0.19$) and percentage of cows with NEFA >0.18 mmol/l on wk 1 before calving ($P = 0.99$) were not affected by treatment. In conclusion, AIAO prepartum grouping strategy did not improve metabolic parameters of peripartum dairy cows compared with a conventional grouping strategy.

Key Words: prepartum dairy cow, grouping strategy, metabolic parameter

T224 Heterosis of productivity rates in the breeding cycle of pure and crossbred Hereford and Angus cattle grazing native pastures at low and high allowances.

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Uruguayan extensive cow-calf systems are based in native pastures with low offers of dry matter (DM), especially in the winter. Hereford cows represent 70% of the genetic resources of Uruguayan herds. Productivity of the breeding cycle in these systems is extremely dependent on weather conditions, reaching about 70 kg of calf weaning weight per breeding female per year. The objective of this experiment was to study the productivity of heterosis of crossed (F1; reciprocal F1) and purebred (PB) Hereford and Angus cattle, for 3 breeding cycles (2007 to 2009) in native pastures offered high (H) and low (L) forage allowances (2.5 and 4 kg DM/kg BW, respectively). Animals (n = 120-year) were located in 2 blocks with 4 plots each one (treatments): F1 cows in High allowance (HF1) or Low allowance (LF1), and Pure breed in High (HPB) and low (LPB) allowance. Productivity rate (PR) was estimated as the weight (kg) of a 4th month old weaned calf weaned per breeding female per year (WW) x weaning rate (WR; number of calves weaned/female exposed in the breeding season). Mixed models with cow nested in treatment were used to analyze WW and WR. Weaning rate was higher ($P < 0.05$) in F1 than PB cows (individual heterosis). Weaning weight was greater ($P < 0.05$) for calves of F1-H cows with 128 ± 3.4 kg, whereas F1-L, and PB-H and -L did not differ significantly (112, 115 and 107 ± 3.5 kg, respectively). Consequently, PR was superior in F1-H and inferior in PB-L treatments, weaning 111 kg and 81 kg of calf per breeding cow per year, respectively. The PR did not differ between PB-H and F1-L with 93 kg and 92 kg, respectively, per breeding cow per year. The management of forage allowance and genetic resources can lead to improved productivity of cow-calf systems based on grazing of native pastures.

Key Words: forage allowance, heterosis, productivity

T225 Effects of dried distillers grains fed for programmed rate of body weight gain in beef heifers grazing native rangelands prior to breeding on growth and reproductive performance.

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The objective of this study was to evaluate effects of dried distillers grains plus solubles (DDGS) on growth and reproductive performance of beef heifers fed at a programmed rate of BW gain. Eighty-two beef heifers (initial BW = 249 ± 3.2 kg) grazing native range (2 pastures per treatment; 4% CP, 42% NDF, DM basis) were used in a completely randomize designed experiment and assigned to 1 of 3 treatments 49 d before breeding. Treatments were: 1) high level of DDGS (1.81 kg/heifer daily) to provide gain at (0.36 kg/d) for 28 d and then fed (0.68 kg/heifer daily) to achieve a low rate of gain (0.18 kg/d) up to breeding (HL); 2) a low rate of gain for the first 28 d and the high rate of gain up to breeding (LH); 3) moderate rate of gain (0.27 kg/d) throughout the feeding period by feeding (1.13 kg/heifer daily) (MOD). Heifers were weighed every 14 d, at which time blood was collected via coccygeal venipuncture and serum progesterone concentrations were determined. Heifers were synchronized at the end of the feeding period using the CO-Synch + CIDR (progesterone insert) with fixed-time AI. Heifers received an injection of GnRH (100 µg, i.m.) and a CIDR was inserted at d −7 relative to timed AI. At d 0, CIDR was removed and heifers received 25 mg of PGF $_{2\alpha}$. Heifers were observed for estrus and bred 12 h after observation of estrus. All heifers not bred by 54 h after CIDR removal were given GnRH (100 µg, i.m.) and AI. Heifers were joined with bulls for 60 d. No difference ($P = 0.11$) in ADG was noted in the first 28 d of supplementation, however, ADG was greater ($P = 0.01$) for HL and MOD groups during the second period of the experiment. Days to reach puberty tended to be less ($P = 0.08$) for the LH treatment compared with the MOD and HL treatment. The LH treatment also tended to have a greater ($P = 0.06$) percentage of pubertal heifers at breeding compared with MOD. Treatment did not affect ($P = 0.35$) overall pregnancy rates. Despite the fact that HL and MOD treatments had greater ADG, the LH growth program increased the percentage of heifers that were pubertal at breeding.

Key Words: heifers, puberty, reproduction

T226 Beef heifer growth and reproductive performance responses to stockpiled fall forage allowances.

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The objective of this study was to compare heifer growth and reproductive performance following 2 patterns of gain during the fall 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 and contained cool-season grass-legume mixtures. Spring born heifers (year 1, n = 71; year 2, n = 64) of primarily Angus background and 248 kg mean BW were allocated to 2 grazing treatments each replicated 3 times per year (11 hd/replicate of a treatment) for 193 and 188 d in years 1 and 2, respectively. The fall grazing treatment consisted of daily herbage dry matter (DM) allocation of 3.5 (LOW) or 7.0 (HIGH) % of BW. During the winter feeding period haylage (6.5 kg DM/hd/d, yr 1; 5.4 kg DM/hd/d, yr 2) and soybean hulls (1.7 kg DM/hd/d, yr 1; 1.5 kg DM/hd/d, yr 2) were fed. Heifers were grazed continuously (as one group) throughout the spring during both years. Individual BW and blood samples were collected. In both years, heifers were synchronized and artificially inseminated (AI) utilizing a single sire. A cleanup bull was used for 35 d. Mean ADG was greater for HIGH heifers (0.45 kg/d) than LOW heifers (0.16 kg/d) during the fall grazing period ($P < 0.05$). During the winter feeding period, ADG were 0.03 kg/d and 0.36 kg/d ($P < 0.05$) for LOW vs HIGH heifers. During the spring grazing period, ADG were 1.6 kg/d and 1.5 kg/d ($P = 0.05$) for LOW vs HIGH heifers. Proportion of heifers that reached puberty at the onset of the breeding season did not differ (42% and 44%, $P = 0.81$ for LOW vs HIGH), although LOW heifers had lower BW at the time of breeding (345 kg vs 362 kg, $P < 0.05$ for LOW vs HIGH). No treatment differences occurred for overall pregnancy rates by AI (28% vs 37%, $P = 0.34$), bull (42% vs 38%, $P = 0.70$), or overall (70% vs 75%, $P = 0.56$) for LOW vs HIGH heifers. 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

T227 Effects of climate and moon illumination on grazing activity of weaned beef calves during early summer.

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How environmental conditions influence day and nighttime grazing behavior may be beneficial to intensive grazing management and understanding the dynamics of foraging behavior. The objective of this study was to examine the effects of climate and moon illumination on the grazing activity of weaned beef calves during early summer. Seven calves were equipped with 3-axis accelerometer dataloggers. Logger activity was recorded for 35d beginning June 13, 2011. Logger x, y, and z tilt positions differed by activity (Wilks $P < 0.001$). Activity (grazing, lying, and standing/walking) was predicted using linear discriminant analysis based on 2, 3h observation periods. A random sample representing 50% of observed activity was used for model training. Prediction based on a single model among calves did not differ from predictions based on within calf models ($P = 0.50$). Model sensitivity and specificity was 0.79 and 0.94, respectively. Hourly climate measurements [temperature (T), relative humidity, rainfall, and solar radiation] were recorded from a weather station located on the research facility. Relative humidity was calculated at T above 26.7 C. Moon illumination data (MOON) was downloaded from the US Naval Observatory. Grazing activity was separated into periods of day (DG) and night (NG) as determined by weather station solar measurements. Days (n = 3) with rainfall exceeding 1 cm over multiple h was removed. Dependent variables examined included the proportion of NG to DG, the number of grazing events during DG and NG, mean event duration, and NG:DG ratio for events and durations. NG was estimated at 37.9% (SE 0.01%). Proportion NG was correlated with average daytime T (0.57, $P < 0.01$) and heat index (0.42, $P < 0.01$) but not solar radiation (0.006, $P = 0.93$). NG was also correlated with MOON (0.23, $P < 0.01$). Number of NG events was not correlated with daytime T (−0.02, $P = 0.72$). However, mean duration per NG event was correlated (0.25, $P < 0.001$). Ratios of NG to DG duration >1 were associated with lower daytime T [30.8 vs 32.3 (SE 0.27); $P = 0.02$] but 6.7% (SE 2.8%) greater humidity ($P = 0.02$) and no difference in moon illumination ($P = 0.24$). These results suggest weather may be more of a determinant of NG activity than moon illumination.

Key Words: beef cattle, grazing activity, weather

T228 Riparian management practices in the Manitoba landscape: Off-stream watering systems for beef cattle.

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Livestock are attracted to riparian areas as they offer shade, forage, and water. However, their presence can be detrimental to these sensitive ecosystems. This study aims to determine the impact of off-stream waterers and natural barriers on animal performance and distribution. The study was replicated at 2 experimental locations in Manitoba, Killarney and Souris, with each site being replicated in 2 grazing seasons. At each location the pasture was divided into 3 treatments: no off-stream waterer or barriers (CON), off-stream waterer with barriers along the river band to deter cattle from watering at the river (BAR), and off-stream waterer without barriers (NOBAR). Cows and calves (25 pairs/treatment) were weighed on the first and last day of each 28-d period. Visual observations were recorded at 5 min intervals from dawn until dusk for 4-d of each period to determine the preferred drinking location of cows in BAR and NOBAR. Treatment had no significant effect (*P*

> 0.05) on cow and calf weights averaged over the summer periods, with the exception of calf weights in Souris in 2010 ($P < 0.0001$). The average weight of cows in Souris was 612.3 ± 26.7kg and the average weight of calves is 131.4 ± 6.0kg, considering both years. Likewise the average weight of cows at the Killarney location was 509.5 ± 22.3kg and the average weight of calves is 122.7 ± 5.6kg, again considering both years. From visual observations in Killarney, the recorded usage of off-stream waterer varied between 100% in Period 1, 93% in Period 2, and 100% in Period 3 in BAR, and from 50% in Period 1, 38% in Period 2, and 40% in Period 3 in NOBAR. In Souris, the recorded usage of off-stream waterer varied between 85% in Period 1, 31% in Period 2, and 7% in Period 3 in BAR, and from 44% in Period 1, 33% in Period 2, and 0% in Period 3 in NOBAR. These results indicate that the presence of off-stream waterers do not create significant differences in weights among cows and calves. Furthermore, cattle did not drink exclusively from the off-stream waterers, however, they will use when available, possibly attracting them away from the riparian area.

Key Words: riparian areas, off-stream waterer, animal performance

T229 Effects of injectable trace minerals on the humoral immune response to porcine red blood cell challenge and fertility in beef heifers. P. Moriel[1], P. G. M. A. Martins*[1], G. C. Lamb[2], L. J. Havenga[3], and J. D. Arthington[1], [1]*University of Florida, Range Cattle Research and Education Center, Ona,* [2]*University of Florida, North Florida Research and Education Center, Marianna,* [3]*MultiMin USA Inc., Fort Collins, CO.*

Our objective was to evaluate the effects of injectable trace minerals (ITM; MultiMin 90, MultiMin USA Inc., Fort Collins, CO) on mineral status, humoral immune response, and measures of performance in Brahman × British beef heifers (n = 33; age = 296 ± 22 d) grazing established limpograss pastures. Heifers were randomly allotted to 1 of 2 treatments; (1) ITM (n = 17); 3.0 mL s.c., containing 90, 10, 15, and 5 mg/mL of Zn, Mn, Cu, and Se, on d 0, 51, 83, and 127, and (2) Control (n = 16); 3.0 mL of sterile saline s.c. on the same days. Heifer shrunk BW was determined on the beginning (d 0) and end of the study (d 177). Plasma P4 concentrations were assessed monthly in blood samples collected on a 10 d interval for determination of puberty. All heifers received an i.m. injection of a 25% porcine red blood cell (PRBC) solution on d 51 and neutralizing antibody titers were measured in blood samples collected on d 0, 3, 7, 14, and 21, relative to PRBC injection. Liver biopsy samples were collected on d 177 from 24 heifers (12/treatment) for determination of trace mineral status. Throughout the study, heifers remained in a single group, were provided free-choice access to salt with no supplemental minerals and were exposed to a single Angus bull from d 83 to 177. Heifer BW did not differ at the beginning (208 ± 8.0 kg) and end of the study (259 ± 8.4 kg), but ADG was greater ($P < 0.06$) for ITM compared with saline-injected heifers (0.31 vs. 0.26 kg, respectively; SEM = 0.018). Heifers receiving ITM had greater ($P < 0.06$) PRBC neutralizing antibody titers on d 7, 14, and 21 following challenge, compared with saline-injected heifers. Liver concentrations of Se were greater ($P < 0.01$) in ITM heifers vs. saline-injected heifers at the end of the study (d 177; 0.88 vs. 0.48; SEM = 0.06). Liver concentrations of Cu, Zn, and Mn were adequate for all heifers and did not differ between treatments ($P > 0.25$). There were no differences in age at puberty or overall pregnancy rate (average = 427 ± 49 d and 57.6%, respectively). These results demonstrate that ITM may increase BW gain, humoral immune responses, and Se status in growing heifers reared on pastures without access to supplemental trace minerals.

Key Words: heifer, immunity, trace minerals

T230 Effect of propionate salt inclusion in postpartum supplementation on young cow reproductive performance. J. A. Walker,* G. A. Perry, and K. C. Olson, *South Dakota State University, Brookings.*

Two-year-old cows were supplemented with propionate salt to evaluate animal and reproductive performance. Sixty cows were allocated to one of 3 treatments at calving. Propionate salt was incorporated in a protein supplement (30% CP, 73% TDN) at rates of 0, 80 or 160 g/d of propionate salt (Ca-propionate). Cows were individually supplemented twice weekly at 1.14 kg/d. Cows had access to a native range pasture (121.4 ha). Blood was collected weekly to determine postpartum anestrous interval based on serum progesterone (≥1 ng /ml). Body weight and BCS were determined at calving, end of supplementation, start of breeding season, and weaning. No differences in cow BW ($P = 0.28$) and BCS ($P = 0.77$) were found between treatments. Cow BW changed throughout the study ($P < 0.01$; 379 ± 5.2, 361 ± 5.2, 397 ± 5.2 and 444 ± 5.2 kg for calving, end of supplementation, start of breeding season and weaning, respectively). Cow ADG differed by period ($P < 0.01$): cows lost weight from calving to end of supplementation (−0.32 ± 0.14 kg/d), and gained from end of supplementation to breeding (5.11 ± 0.14 kg/d) and breeding to weaning (0.38 ± 0.14 kg/d). Cow BCS changed throughout the study ($P < 0.01$; 3.94 ± 0.06, 4.11 ± 0.06, 4.10 ± 0.06, and 4.66 ± 0.06 for calving, end of supplementation, start of breeding season and weaning, respectively). Calf BW was not different ($P = 0.98$) between treatments. Calf BW increased throughout the study ($P < 0.01$; 35.6 ± 2.2, 91.8 ± 2.2, and 197.9 ± 2.2 kg at birth, start of breeding season, and weaning, respectively). Postpartum anestrous interval ($P = 0.70$), percentage of cows initiating estrous cycles before the breeding season ($P = 0.54$), conception rate to AI ($P = 0.68$), and season long pregnancy rates ($P = 0.87$) were not different between treatments. Propionate salt did not influence cow BW, cow BCS, calf BW, or cow reproductive performance.

Key Words: propionate salt, young beef cows

T231 Metabolizable protein supply alters pregnancy and subsequent retention rate during heifer development while grazing dormant winter forage. J. T. Mulliniks*[1], D. E. Hawkins[2], K. K. Kane[1], S. H. Cox[1], L. A. Torell[1], E. J. Scholljegerdes[1], and M. K. Petersen[3], [1]*New Mexico State University, Las ,* [2]*West Texas A&M University, Canyon,* [3]*USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.*

Type of heifer development system can have major effect on the future productivity and retention rate of the cowherd. Therefore, the objective of this experiment was to determine growth, reproductive performance, retention rate, and economic efficiency of heifer's developed in a range raised (with 2 CP treatments) or high input (feedlot developed) heifer development system. Spring-born, crossbred heifers (n = 191) were stratified to 1 of 3 treatments at weaning: (1) 0.9 kg/d of a 36% CP supplement containing 64% RDP (CSM), (2) 0.9 kg/d of a 36% CP supplement containing 50% RDP (RUP), or (3) a concentrate diet fed in dry lot (CONC) to gain 0.68 kg/d. Supplementation was initiated in February and terminated at the onset of a 45-d breeding season in May. Heifer BW and hip height (HH) were taken monthly from initiation of supplementation until breeding and again at weaning. Females were removed from the herd for failure to reproduce or wean a calf. Percent of heifers becoming pregnant and remaining in the herd at start of each breeding season was recorded to determine retention rate throughout their 3rd calf crop. Breeding BW was greater ($P < 0.01$) for the CONC than CSM or RUP developed heifers. Hip height at breeding was greater ($P < 0.01$) in RUP and CSM relative to CONC heifers. However, palpation BW and HH was similar ($P \geq 0.24$) for all heifer development treatments. At breeding, RUP and CSM heifers reached 51% of mature BW ($P < 0.01$) compared with CONC heifers at 58% of mature BW. Pregnancy rates were 94, 88, and 84% for RUP, CSM and CONC heifers ($P = 0.10$). Net return was $99.71 and $87.18 per developed heifer greater for RUP and CSM heifers, respectively compared with CONC heifers due to differences in pregnancy and development costs. Retention rate at age 4 was greatest ($P < 0.01$) for RUP heifers. This study indicates that range developed heifers can be as reproductively successful as heifers developed in a dry lot, while improving future productivity. Furthermore, metabolizable protein supply improves reproduction in heifers developed on dormant native range.

Key Words: beef heifers, heifer development, retention rate

T232 Winter growing rate of gain on subsequent growth of beef steers grazing a subtropical pasture in summer. J. I. Arroquy*[1,3], A. E. Fumagalli[1], D. Kuckseva[2], and P. Vispo[2], *[1]INTA EEA Santiago del Estero, Santiago del Estero, Argentina, [2]INTA EEA Colonia Benitez, Resistencia, Chaco, Argentina, [3]CONICET, Santiago del Estero, Argentina, [4]FAyA-UNSE, Santiago del Estero, Argentina.*

Eighty Braford steers (initial BW: 149.5 ± 3.0 kg; initial hip-height: 110.5 ± 0.3cm; 6 mo old) were allotted by BW to one of 4 growing-phase diets (4 pens/treatment) to evaluate the effect of winter animal performance on summer growing rate grazing Guineagrass. Diets were: 1) ad libitum access to low-quality Guineagrass hay plus protein supplementation (GHPS); 2) same as treatment 1 plus energy supplementation (GHPG); 3) limit fed high concentrate diet to achieve a gain of 0.7 kg/d (LFHC); and 4) ad libitum corn-silage diet (CS). Immediately after winter phase (130 d), steers grazed Guineagrass pasture for 123 d. Winter feeding treatments and grazing summer steers were evaluated by average daily gain (ADG), hip-height (cm), 12th-rib fat (mm) and ribeye area (cm2; ultrasonic evaluations). In winter growing phase, ADG was significantly greater in CS diet than the others ($P < 0.01$), LFHC had greater ADG than GHPS and GHPG ($P < 0.05$), and GHPS and GHPG did not differ. ADG for winter growing phase were: 257, 298, 438, and 647 g/d for GHPS, GHPG, LFHG and CS, respectively. ADG in summer did not differ among treatments (494, 568, 600, and 496 g/d for GHPS, GHPG, LFHG and CS, respectively). Hip-height had similar response to feeding treatment as ADG. CS fed steers were taller than other treatments ($P < 0.05$). Final summer BW was higher in CS and LFHC than GHPS and GHPG ($P < 0.05$). Final fat thickness for winter growth was superior in LFHC and CS (2.05 and 2.15 mm, respectively) compared with GHPS and GHPG ($P < 0.05$; 1.66 and 1.70, respectively), whereas fat thickness at the end of summer period did not differ among treatments (2.33 ± 0.13 mm). Ribeye area was larger for CS and LFHC than the others ($P < 0.05$) at the end of winter and summer period. In conclusion, even though compensatory growth in summer reduced differences among winter feeding treatments, moderate winter ADG increased final summer liveweight, hip-height as well as ribeye area.

Key Words: winter growing phase, guineagrass, summer growing phase

T233 Effects of weaning age and winter development environment on heifer performance. N. L. Hojer*[1], M. B. Hubert[2], P. S. Johnson[2], M. H. Price[3], and K. C. Olson[2], *[1]South Dakota State University, Brookings, [2]South Dakota State University, Rapid City, [3]South Dakota School of Mines & Technology, Rapid City.*

Our objective was to determine if early weaning (about 125 d) versus normal weaning (about 250 d) and wintering replacement heifers in drylot versus rangeland affected heifer growth and reproductive performance. Heifer calves from the 2009 and 2010 calf crops (n = 104 and 73, respectively) were allocated to the 2 weaning treatments and then stratified by age into the 2 winter development treatments forming a 2 by 2 factorial of treatments. Heifers wintered in drylot received mixed grass and alfalfa hay (yr 1: 11.6% CP, 52.5% TDN; yr 2: 12.3% CP, 53.4% TDN) plus 1.8 kg of a dried distiller's grain (DDGS)-based supplement/hd/d (yr 1: 22.7% CP, 75.8% TDN; yr 2: 25.4% CP, 76.7% TDN). Heifers wintered on rangeland also received 1.8 kg/hd/d of the same supplement. Over the winter, each treatment was allocated to a separate pen or pasture. After estrus synchronization and timed AI, all heifers were placed on rangeland to graze through the summer. During the summer of yr 1 heifers were allocated by winter treatment to 2 pastures, and in yr 2 all 4 treatment combinations were allocated to separate pastures. Responses measured were BW, ADG, puberty at initiation of estrus synchronization, and pregnancy detection. Pubertal status was indicated by serum progesterone ≥1 ng/ml. A winter by weaning treatment interaction affected ($P < 0.001$) BW and ADG both years. During the winter months, range heifers were lighter and grew slower than drylot, but BW did not differ due to winter treatments by the end of the summer. However, early weaned heifers remained lighter than normal weaned heifers at the end of the summer. Weaning treatment affected ($P = 0.03$) fall pregnancy rate (93.2% ± 4.0 and 74.7% ± 7.98 for early- and normal-weaning, respectively) in yr 2. In yr 1, there was a difference ($P = 0.006$) between drylot and range heifers (92.7% ± 3.52 and 72.8% ± 6.47, respectively) in the proportion that obtained puberty before estrus synchronization. In conclusion, a producer needs to consider important interactions between weaning and winter management practices when establishing a replacement heifer development program that best fits the goals of their operation.

Key Words: beef heifer development, weaning, heifer performance

T234 Blended byproduct feeds in finishing rations on performance, carcass, and fecal characteristics of yearling heifers. B. T. Johnson,* C. L. Maxwell, B. K. Wilson, J. J. Wagner, S. L. Roberts, B. W. Woolfolk, C. J. Richards, and C. R. Krehbiel, *Oklahoma State University, Department of Animal Science, Stillwater.*

This study compared inclusion levels of a 1:1 blend of Sweet Bran (SB) and dried distiller′s grains (DDGS) byproducts in a dry-rolled corn feedlot ration on performance, carcass merit, and fecal characteristics. Heifers (n = 108; initial BW = 324 ± 13.6 kg) were blocked by BW, randomized to treatment, and fed for 142 d. Treatments were control (CONT, 8% DDGS), intermediate with 22% SB and 22% DDGS (INTER), and all byproduct with 44% SB and 44% DDGS (ALL). During d 28 to 55, a time of severe environmental heat with an average Temperature Humidity Index (THI) value of 80, ALL increased ADG and G:F ($P < 0.02$) by 12.2% and 16%, respectively. Average daily gains were similar for all other periods. There was a trend ($P = 0.09$) for increased overall G:F with ALL using live final BW, and increased ($P < 0.01$) G:F on a carcass adjusted final BW basis. Heifers fed ALL had a 1.81% increase ($P < 0.05$) in dressing percentage. There was a trend ($P = 0.08$) for increases in HCW for the INTER (3.5%) and ALL (2.5%) compared with CONT, with no other differences in carcass characteristics. These data indicate that replacing dry-rolled corn in a finishing diet with a 1:1 blend of SB and DDGS increases feed efficiency and HCW without altering ADG. Rectal fecal samples were taken every weigh period for pH, fecal scoring, and DM content. Further analysis by treatment was compared by taking concrete bunk pad samples at every weigh period and determining sample DM and density. Fecal pH and scores increased ($P < 0.05$) throughout the study for ALL, indicating a more viscous structure. A linear decrease in fecal DM was noted as level of byproduct inclusion increased ($P < 0.05$) for each sampling period. Pad sample DM decreased linearly ($P \leq 0.05$) on d 56, 112, and 142. Data indicate replacing corn with a 1:1 blend of SB and DDGS also increases fecal pH, fecal score and decreases fecal DM and DM of the pad (more water in manure on the pad/pens). During high temperatures, the ALL diet may have additional performance benefits.

Key Words: byproduct, performance, fecal characteristics

T235 Transit effects on fecal *E. coli* O157:H7 prevalence and coliform concentrations in feedlot cattle.

C. C. Aperce,* C. A. Alvarado, C. L. Van Bibber, K. A. Miller, and J. S. Drouillard, *Kansas State University, Animal Sciences and Industry, Manhattan.*

Our objective was to evaluate effects of transportation on fecal shedding of *E. coli* 4 and 24 h after hauling. The study was a randomized complete block with 20 steers per block (10/treatment), 3 blocks (days), and 2 treatments: a non-transported group, and transported steers that were placed in a trailer, hauled for 1 h, and subsequently allowed to rest. Fecal samples were taken pre-transport, and at 5 and 29 h post-transport. Fecal samples were collected from both groups at h 0, 5, and 29 from freshly voided fecal pats. One gram of feces was transferred to a PBS tube, serially diluted, and plated on Petrifilm for enumeration of total coliforms, and another sample (1 g) was added to gram-negative broth with cefixime, cefsulodin, and vancomycin, and subjected to immunomagnetic separation. Resulting beads were plated onto MacConkey agar with sorbitol, cefixime, and tellurite. Non-sorbitol fermenting colonies were picked and tested for indole production and O157 antigen agglutination. Results were confirmed by API 20E kit. Prevalence of *E. coli* O157 was transient across replications ($P = 0.002$). *E. coli* O157 occurrence in the transported group was constant across the 3 sampling times (10, 3.3, and 16.7%, for h 0, 5, and 29, respectively; $P = 0.43$); however, a significant increase in its prevalence was observed in the control group at h 5 (33%) compared with h 0 (17%, $P = 0.06$) and 29 (13%, $P < 0.02$). Numbers of coliforms remained constant across sampling day ($P > 0.1$). There were no significant correlations between prevalence of *E. coli* O157 and coliform concentrations. Coliform concentrations of control steers remained stable from 0 to 29 h post-transit. Transported animals had lower coliform concentrations at hour 5 (3.2 log cfu/gram; $P < 0.02$), but returned to pre-transport levels of 4.5 log cfu at h 29. Results suggest that shedding patterns are influenced by transportation, and that shedding can vary greatly within a period of 29 h. Additional post-transit sampling times may be useful to determine more precisely the pathogen shedding patterns associated with transportation.

Key Words: *E. coli* O157:H7, hauling

T236 Cattle anthelmintic resistance testing and training in North Carolina.

N. C. Whitley[1], M. L. Alley[2], R. M. Kaplan[3], S. Howell[3], K. Moulton[1], R. A. Franco*[1], and A. E. Cooper[1], [1]*North Carolina A&T State University, Greensboro,* [2]*North Carolina State University, Raleigh,* [3]*University of Georgia, Athens.*

The objective was to investigate the presence of anthelmintic resistance in gastrointestinal nematodes (GIN) on cattle farms while providing parasite management training to agricultural professionals. Fecal egg count reduction testing was used as a training tool on 3 beef cattle farms using no treatment (CON) or labeled doses of moxidectin (Cydectin; pour on—CPO, 3 farms; injectable—CI, 1 farm), fenbendazole (Safeguard; SAFE; 3 farms), CPO and SAFE combined (CS; 1 farm) or levamisole (Prohibit; P; 1 farm) with a total of 346 calves used at weaning. Fecal samples were collected from calves 1 to 2 weeks before the start of the study, on d0 (d of treatment) and d14. A Modified McMasters technique was used to determine fecal egg counts (FEC; eggs per gram, epg) with a sensitivity of 4 or 8 epg. Fecal co—proculture for GIN speciation was conducted on d14 fecal samples collected randomly from calves in each treatment group. Animals were assigned to treatment groups for similar mean preliminary BW and FEC. Percentage reduction (RED) of FEC was calculated as: [1 – (mean d-14 treatment FEC/mean d-14 CON FEC)] × 100%. Only calves with a minimum d0 FEC of 40 epg were used in RED calculations (17/trt for Farm 1; 28 to 30/trt for Farm 2; 25 to 32/trt for Farm 3). Statistical means and standard errors were calculated using SAS Proc Means. Mean d0 FEC for Farm 1, 2 and 3 were 62 ± 7, 204 ± 12 and 222 ± 13 epg, respectively. Farm 1 RED were 84.9% for CPO and 99.3% for SAFE. Farm 2 RED for CPO, SAFE, CS and P were 91.4, 96.9, 99.8 and 95.8%, respectively. Farm 3 RED for CPO, CI and SAFE were 16.5, 39.6 and 99.8%, respectively. Larvae from CON fecal cultures on all farms were primarily *Cooperia* with *Ostertagia ostertagi* also present at 40% for Farm 1 and Hemonchus in very low numbers on all 3 farms. For those treatments not considered effective, *Cooperia oncophora* and *Cooperia* spp. were the predominant GIN, except for P (*O. ostertagi*). These findings indicate that anthelmintic resistance in GIN of cattle is present in NC; 10 professionals were trained and the awareness of more NC agents and producers to this potential problem has increased.

Key Words: anthelmintic, cattle, resistance

T237 Effects of temperament on physiological responses, feedlot performance, and carcass characteristics of Nelore steers.

C. L. Francisco[1,4], A. M. Jorge*[1], F. D. Rezende[2], A. Schmidek[2], J. M. B. Benatti[3], M. H. Faria[2], E. Oba[1], and R. F. Cooke[4], [1]*Universidade Estadual Paulista - FMVZ, Botucatu, SP, Brazil,* [2]*APTA, Colina, SP, Brazil,* [3]*Universidade Estadual Paulista - FCAV, Jaboticabal, SP, Brazil,* [4]*Oregon State University, EOARC, Burns.*

The objective of this experiment was to evaluate the effect of temperament on plasma hormones, performance, and carcass traits of Nelore (*Bos indicus*) feedlot steers. Forty-four steers were evaluated for BW and temperament at feedlot entry (d 0). Temperament was assessed by chute score and exit velocity. Further, individual exit score was calculated by dividing exit velocity results into quintiles and assigning steers with a score from 1 to 5 (exit score: 1 = slowest steers; 5 = fastest steers). Temperament scores were calculated by averaging chute score and exit score. Steers were also classified for temperament type according to temperament score [≤3 = adequate temperament (ADQ) or >3 = aggressive temperament (AGR)]. Shrunk BW was recorded on d 0 and 109, whereas blood samples were collected on d 0, 67, and 109 for analysis of plasma cortisol and insulin. Total DMI was recorded daily (d 0 to 109). Steers were slaughtered on d 109, and carcasses were evaluated for backfat thickness, LM area, carcass pH, and incidence of hematomas. Samples from the LM were collected and analyzed for Warner-Bratzler shear force. Plasma cortisol was greater ($P = 0.04$) whereas plasma insulin tended to be reduced ($P = 0.06$) in AGR vs. ADQ steers (19.6 vs. 16.7 ng/mL of cortisol, and 12.7 vs. 19.4 IU/mL of insulin). Feedlot BW gain was reduced ($P = 0.02$) in AGR vs. ADQ steers (1.05 vs. 1.30 kg/d). Total DMI tended to be reduced ($P = 0.14$) whereas G:F was reduced ($P = 0.03$) in AGR vs. ADQ steers (8.8 vs. 9.4 kg/d of DMI, and 119 vs. 138 g/kg of G:F). Carcasses from AGR steers had greater ($P = 0.05$) incidence of hematomas compared with ADQ carcasses (1.3 vs. 0.6 hematomas/carcass). No differences between ADQ and AGR steers were detected for the remaining carcass traits. In conclusion, aggressive steers had greater plasma cortisol during handling, decreased feedlot performance, and impaired carcass quality compared with cohorts with adequate temperament.

Key Words: Nelore steers, feedlot performance, temperament

T238 Skin temperature differentials in relation to residual feed intake in beef cattle using infrared thermography. L. S. Martello*[1], P. R. Leme[1], S. da Luz e Silva[1], R. da Costa Gomes[2], C. A. Zotti[1], C. L. Oliveira[1], and T. F. Canata[1], [1]*Faculdade de Zootecnia e Engenharia de Alimentos, Universidade de São Paulo, Pirassununga, SP, Brazil,* [2]*Faculdade de Zootecnia, Universidade Estadual de Londrina, Londrina, PR, Brazil.*

Infrared thermography (IRT) has been studied as an alternative for indirect measuring of the residual feed intake (RFI) because of its association with body heat dissipation and consequently with skin temperature. Moreover, different areas of the body have distinct relationships with heat dissipation and should be considered for analyses. Therefore the aim of this study was to evaluate the skin temperature measured by IRT on different body areas, in low and high RFI cattle under feedlot conditions. Residual feed intake of Nellore steers (n = 40) and bulls (n = 40) fed high concentrate diets (85% of concentrate) was determined after 70d feeding. Nine calves classified as high and 9 as low RFI were then allotted to individual pens with free access to shadow and sunlight and had the IRT determined for 10 consecutive days. The IRT of 8 body regions were measured at 7h, 12h and 16h with the infrared camera Fluke® TI 20. The evaluated regions were 2 spots on frontal head (FH1 and FH2), eye, cheek, flank, ribs, rump and front feet. The rectal temperature (RT) was also measured. The effect of efficiency group on IRT was evaluated by ANOVA using SAS software. The mean air temperature (AT) during the trial was 24.4°C ranging from 14.4°C to 30.7°C indicating a stressful environmental for cattle during hottest hours. The IRT temperatures showed a linear association ($P < 0.01$) with AT whereas RT showed a quadratic effect ($P < 0.05$) on AT. The IRT temperatures measured at eye, cheek, flank, ribs, rump and front feet were not affected by RFI group. However, IRT on FH1 and FH2 for high RFI cattle (31.4°C and 30.3°C, respectively) were lower ($P < 0.01$) than for low RFI cattle (31.8°C and 30.7°C, respectively). Conversely, lower RT was observed for low RFI (38.3°C) than for high RFI group (38.4°C; $P < 0.01$). The higher skin temperature, measured by IRT, for calves of low RFI group may be related with an improved efficiency of thermoregulatory mechanisms, because the RT remained lower in the Low RFI group. The IRT of frontal head (FH1 and FH2) is a promising body location for studies related to RFI in beef cattle

Key Words: infrared image, skin temperature, cattle

Ruminant Nutrition: Beef: Co-products

T239 Microbial community shifts during anaerobic digestion of finishing cattle manure with and without distillers grains in the diet. S. C. Fernando, A. K. Watson, Y. A. Wanniarachchi, T. J. Klopfenstein, G. E. Erickson, J. L. Harding, A. L. Shreck,* C. J. Johnson, and M. M. Klosterman, *University of Nebraska, Lincoln.*

Two diets were fed to finishing cattle and the manure was used to monitor methane production and microbial communities associated with anaerobic digestion of feedlot manure. Diet 1 contained 82.5% dry rolled corn (CONT) and diet 2 contained 40% wet distillers grains plus solubles (DM basis) replacing dry rolled corn (WDGS). Manure (feces and urine) was collected and frozen until used in anaerobic digesters. Continuously stirred anaerobic digesters (n = 7, 1 L capacity) were maintained for 5 mo to reach steady-state. Upon reaching steady-state, 50 mL of effluent was removed and replaced with 50 mL of manure/water slurry (9% DM) collected from CONT (n = 4) or WDGS (n = 3) fed animals on a daily basis. After a 35 d adaptation, samples were collected at 3-d intervals for microbial community analysis. The concentration of methane was measured under constant flow of N2 gas and was 0.116 and 0.137 L/g OM fed into the digester ($P = 0.05$) from CONT and WDGS respectively. The microbial communities (Eubacterial and Archaeal) were identified using 454-pyrosequencing. An average of 10,000 and 3,000 sequences were generated from each sample to evaluate the Eubacteria and Archaea communities respectively. Community level analysis revealed structuring of microbial communities based on diet ($P < 0.001$). Bacteria belonging to the phylum *Chloroflexi* (65.7%) and *Bacteroidetes* (19.2%) dominated the microbial community in digesters receiving WDGS manure. Within phylum *Chloroflexi*, genus *Longilinea* (35.7%) and unclassified *Anaerolineaceae* (64.3%) accounted for most the sequences. In contrast, digesters receiving CONT manure was dominated by phylum *Bacteroidetes* (68.2%) and *Chloroflexi* (24.5%). Within phylum *Bacteroidetes*, genus *Proteniphilum* (50.6%) and unclassified *Porphyromonadaceae* (45.5%) accounted for a most of the sequences. These results suggest the microbial food chain that contributes toward methane production is greatly influenced by the diet fed to cattle, suggesting that dietary manipulation may provide opportunities to reduce (or increase if desirable) methane production from cattle manure.

Key Words: anaerobic digester, methane, microbial

T240 Effects of crude glycerin on in vitro gas production and VFA profiles in Nellore feedlot steers. E. H. C. B. van Cleef*[1,2], J. M. B. Ezequiel[2], A. P. D'Aurea[1,2], A. C. Homem Junior[1,3], F. B. O. Scarpino[1,4], R. M. P. Pardo[5], and E. M. Ferreira[6], *[1]São Paulo State University, Jaboticabal, São Paulo, Brazil, [2]FAPESP, [3]CAPES, [4]CNPq, [5]Sucre University, Sincelejo, Colombia, [6]University of São Paulo, Piracicaba, São Paulo, Brazil.*

Two studies were conducted to evaluate the effects of crude glycerin on in vitro gas production and VFA profiles in feedlot Nellore steers. Ruminal fluid was collected from 5 rumen-cannulated steers fed finishing diets (70% concentrate) composed by corn silage, corn grain, soybean hulls, sunflower meal, mineral supplement and one of 5 concentrations (0, 7.5, 15, 22.5, or 30%) of crude glycerin (84% glycerol). Samples of 125 mL of ruminal fluid were placed into 250-mL flasks equipped with pipe collectors coupled to gasometers made with PET bottles. Total mixed rations were added at 1.7 g DM/flask, and consisted of the same ingredient mixture fed to each donor steer. Gas production (CH_4 and CO_2) were determined after 12 h of incubation at 39°C and repeated for 5 d (periods). Study 2 used the same treatments and donor animals. To determine VFA profiles 25 mL were collected 1 h before feeding, 1, 2, 4, 6, and 8 h after feeding. Samples of 1.6 mL were centrifuged with 0.4 mL meta-phosphoric acid and formic acid solution, and 0.2 mL of 2-ethyl-butyric acid 100 mM. After centrifugation, 1.2 mL was analyzed for concentrations of VFA using a gas chromatograph. The statistical design used was a Latin square (5 × 5) and data were analyzed using the MIXED procedure of SAS, in which contrasts were used to determine linear and quadratic effects of crude glycerin, and control treatment vs. crude glycerin treatment. Adding crude glycerin decreased in vitro production of CH_4 ($P \leq 0.01$) and CO_2 ($P \leq 0.05$). VFA profiles were highly affected by addition of crude glycerin. Propionate, valerate and butyrate were increased ($P \leq 0.01$) and acetate concentration was decreased ($P \leq 0.01$) as well as acetate:propionate ratio ($P \leq 0.05$). These results suggest that the crude glycerin causes significant changes in VFA profile decreasing waste of energy by the animals, evidenced by the decrease in methane production.

Key Words: biodiesel, co-products, methane

T241 Effect of lipid sources addition on nutrient intake of steers finished at feedlot. G. Fiorentini*[1,2], I. P. C. Carvalho[1,2], J. F. Lage[1,2], R. C. Canesin[1,2], C. S. Ribeiro Junior[1,2], and T. T. Berchielli[1,3], *[1]Universidade Estadual Paulista (UNESP) - FCAV, Jaboticabal, SP, Brasil, [2]Fundaçao de Amparo à Pesquisa do Estado de Sao Paulo (FAPESP), Sao Paulo, SP, Brazil, [3]Instituto Nacional de Ciência e Tecnologia em Ciência Animal (INCT-CA), Brasília, DF, Brazil.*

The objective of this study was to evaluate the effect of different lipid sources on nutrient intake of steers finished at feedlot. Forty-five Nellore steers (initial average body weight of 423kg, with 16 mo age) were feed on 60% maize silage and 40% concentrate, with 7% of ether extract on total diet. The fat sources were soybean grain (SG), protected fat (Lactoplus®) (PF), linseed oil (LO) and palm oil (PO) plus a control (CO) treatment, without additional fat. The supplements were based in corn and soybean meal. The animals were housed on individual stalls, for 90 d (divided in 3 periods of 30 d). The leftovers were removed and weighed every day. The feed and leftovers were analyzed for nutrient composition dry matter (DM), neutral detergent fiber (NDF) and crude protein (CP). The animals were assigned to a completely randomized design, with 5 treatments and 9 replications. The effect of diet type, period and its interaction were analyzed by ANOVA. When significant, differences were analyzed by the Tukey test. The results showed that the lipid source affected significantly ($P < 0.001$) the nutrient intake, evaluated as dry matter (DMI), neutral detergent fiber (NDFI) and crude protein (CPI), expressed in kg/animal/d. The period also affected significantly ($P < 0.01$) the DMI and CPI. There was no significant interaction between diet and period. Generally, in first and second period animals that received CO and PF showed greater intake of DM (8.7, 8.1, 7.6 and 7.6), NDF (3.1, 2.8, 2.8 and 2.7) and CP (1.4, 1.3, 1.2 and 1.2), respectively, while animals that received PO had the lowest intake of nutrients (3.8 and 4.2 kg DM, 1.9 and 1.94 kg NDF and 0.5 and 0.6 kg CP), respectively to first and second period. However, in third period the diets CO, PF and SG had greater DMI and CPI than PO while NDFI did not differ among diets. These results suggest that the addition of lipid sources at the level of 7% in diet influences the nutrients intake of feedlot steers. Diets with

PF and SG or CO provides a greater nutrient intake while the presence PO in the diet decreases the voluntary intake due to low acceptability.

Key Words: beef cattle, palm oil, protected fat

T242 Feeding distillers grains as an energy source to gestating and lactating beef heifers: Impact on steer progeny longissimus muscle fatty acid profile. P. J. Gunn*[1], G. A. Bridges[2], R. P. Lemenager[1], and J. P. Schoonmaker[1], [1]*Department of Animal Sciences, Purdue University, Lafayette, IN,* [2]*North Central Research and Outreach Center, University of Minnesota, Grand Rapids.*

Angus-cross beef heifers pregnant to a single sire (n = 80) 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 LM fatty acid profile of the male progeny. From 192 d of gestation through 118 ± 0.2 d of lactation, dams were fed either a control diet of corn silage and haylage (CON; 10% CP prepartum; 11.8% CP postpartum) or corn stover and DDGS (DG; DDGS at 1.2% BW per d; 15.7% CP) diet. Due to bunk design, progeny access to diets was unable to be restricted. Male progeny (n = 36) were weaned, commingled, and started on a step-up diet at 186 ± 0.2 d of age. At 210 ± 0.2 d of age, steers were placed in individual pens and fed a finishing diet devoid of DDGS (12.7% CP, 1.36 kcal/kg NEg on DM basis), once daily for ad libitum consumption. Steers were harvested at a common 12th rib fat depth of 1.41 ± 0.22 cm. A LM sample from the 12–13th rib interface of the carcass was collected, ground, and extracted for analysis of fatty acid methyl esters. Data were analyzed using the MIXED procedures of SAS. Concentrations of myristoleic (14:1) and palmitoleic (16:1) acids tended to be greater ($P = 0.06$) in CON than DG progeny. Conversely, DG progeny had greater stearic (18:0; $P = 0.01$; 17.3 vs. 15.9 g/100 g) and eicosenoic acid (20:1 n-9; $P = 0.004$; 0.105 vs. 0.094 g/100 g) concentrations than CON progeny. All other fatty acids and classes of fatty acids (short chain, medium chain, long chain, saturated, monounsaturated, and polyunsaturated), as well as the proportion of omega 3 and omega 6 fatty acids did not differ due to maternal treatment ($P \geq 0.17$). In summary, feeding DDGS at 1.2% of BW per day to first-parity heifers marginally affected LM fatty acid profile in steer progeny.

Key Words: DDGS, developmental programming, steer

T243 Effect of distillers grain supplementation on fescue intake and utilization. C. A. Schaeffer,* E. S. Vanzant, J. W. Lehmkuler, and K. R. McLeod, *University of Kentucky, Lexington.*

This experiment was conducted to determine effects of increasing level of supplemented dried corn ethanol distillers grains with solubles (EDG; 29% CP, 5% EE, DM basis) on intake and utilization of moderate quality tall fescue hay (12% CP; DM basis). Ruminally cannulated steers (n = 18, initial BW = 247 ± 6 kg) were used in a randomized complete block design. EDG was fed daily at 0, 0.25, 0.5, 0.75, 1.0, or 1.25% BW (DM basis). Hay was offered at 125% of the previous 5-d mean intake. Steers were adapted to diets for 14d before 2 sequential 7-d periods for intake and digestion measurement and 2d for determining ruminal fermentation and kinetic responses. Forage OM intake (FOMI, %BW), responded quadratically to treatment ($P = 0.05$) with little change in FOMI up to 0.75% BW EDG and decreasing FOMI thereafter. Total and digestible OM intakes (%BW) responded quadratically ($P = 0.05$), increasing from 0 to 0.75% BW EDG and plateauing between 0.75% and 1.25% EDG. OM digestibility responded cubically ($P = 0.07$) and was maximal at 0.5% BW EDG. NDF digestibility decreased linearly ($P = 0.06$) with increasing EDG. All ruminal fermentation variables demonstrated time x treatment interactions ($P \leq 0.10$). Ammonia concentration peaked 3 h post feeding, was lowest at 9 h post feeding and generally increased linearly ($P < 0.10$) with increasing EDG. Pre-feeding ruminal pH increased linearly ($P < 0.01$) with increasing level of EDG. At all other sampling times, pH decreased linearly ($P \leq 0.02$) with increasing EDG. Increasing level of EDG had little impact ($P > 0.14$) on total VFA concentrations. Ratio of acetate to propionate responded cubically ($P \leq 0.07$) to treatment at most time points. However, the linear portion of the response explained most (≥78%) of the variation in A:P at all sampling times except 0h, when A:P decreased as EDG increased. Liquid dilution rate was not affected by treatment ($P \geq 0.24$) nor was rumen content of OM (%BW) either just before ($P \geq 0.26$) or 4 h post ($P \geq 0.15$) feeding. Results suggest that, with growing cattle grazing fescue, increased growth would be expected as EDG supplementation increased to about 0.75% BW, with higher levels of EDG having little effect on gain.

Key Words: distillers grains, forage, intake

T244 Effect of soybean hull level on diet digestibility and growth performance of beef calves. J. R. Russell,* M. S. Kerley, and W. J. Sexten, *University of Missouri, Columbia.*

The objective was to determine a breakpoint where the fiber:starch may benefit from exogenous methods to improve fiber digestion. Fiber digestibility should be greatest at a DM WSC intake of 0.4% BW (diet 80) and should decrease as fiber:starch changes. Five diets with increasing soybean hull (SH) to whole shelled corn (WSC) ratios (20, 60, 80, 90, and 100% SH) were fed to beef cattle to determine the effect of increasing fiber inclusion on digestibility of DM (DMd), NDF (NDFd), and ADF (ADFd) as well as DMI, ADG, and G:F. Cattle were blocked by sex and stratified by BW. The diets were distributed across 40 steers (347 ± 29 kg BW) and 50 heifers (374 ± 24 kg BW) and fed for 70 d. Titanium dioxide was included in the diet for the final 14 d with fecal samples collected on d 70. Diets were balanced for RDP and post-ruminal AA based on available ME. Individual DMI was measured using the Growsafe Feed Intake System. Means comparison was used to identify significance. Diet 20 and 80 did not differ ($P > 0.05$) in DMd, however 20 was greater ($P < 0.05$) than 60, 90, and 100. The DMd was not different ($P > 0.05$) between the 60, 80, 90, and 100 diets. Diet 80 had a tendency to be greater than 20 for NDFd ($P < 0.08$) and ADFd ($P < 0.06$), though neither 80 nor 20 differed ($P > 0.05$) from the other 3 diets. Diet 80 was greater ($P < 0.05$) for DMI than 60, 90, and 100 but did not differ ($P > 0.05$) from 20. There was no difference ($P > 0.05$) in DMI between 20, 60, 90, 100. Diet 20 was greatest ($P < 0.05$) for ADG. The ADG of diets 60 and 80 did not differ ($P > 0.05$) but 80 was greater ($P < 0.05$) than 90 and 100. Diets 60, 90, and 100 did not differ ($P > 0.05$) for ADG. Diet 20 had the greatest ($P < 0.05$) G:F while the other diets did not differ ($P > 0.05$). In this experiment SH had approximately 70% energy equivalence to WSC. Intake of WSC at 0.4% BW increased ADG but did not improve G:F. Methods are needed to improve fiber digestibility of SH to make animal performance on SH-based diets comparable to starch-based diets.

Key Words: digestibility, fiber, soybean hulls

T245 Ruminal fermentation and blood metabolites of Holstein steers fed diets differing in wheat processing and fat source. K. Erjaei, A. Zali, M. Ganjkhanlou,* and M. Dehghan-Banadaky, *University of Tehran, Tehran, Iran.*

To evaluate the effects of wheat processing and dietary fat source on ruminal fermentation and blood metabolites, Holstein steers (n = 28) averaging 296 ± 56 kg were randomly allotted in 4 treatment (7 steers each). An experiment was conducted in a 2 × 2 factorial arrangement (2 methods of wheat processing: steam flake and treatment with formaldehyde and fat source: roasted soybean and Rumifat) with completely randomized design. On the last days of experiment, from each steer, blood samples were collected from the coccygeal vein and samples of ruminal fluid were collected by stomach tube. There were no significantly differences among diets for ruminal pH, total volatile fatty acids (VFA) and ammonia nitrogen (NH_3-N) concentrations. Concentration of propionate was greater, in steers fed steam flake wheat ($P < 0.01$). Other VFA concentrations were not affected significantly by dietary treatments. Plasma cholesterol and triglyceride concentrations were significantly lower and higher respectively in steers fed roasted soybean ($P < 0.01$ and $P < 0.01$). Plasma glucose concentration was higher ($P < 0.01$) in steers fed wheat treatment with formaldehyde. Steers fed roasted soybean had lower blood urea nitrogen ($P < 0.01$). Plasma NEFA and total protein concentrations were unaffected by dietary treatments. Results of this study show that wheat treatment with formaldehyde might be expected to protect starch from rumen degradation. Also blood metabolites indicate that roasting of soybean may protect ether extract and protein from rumen degradation.

Key Words: wheat processing, roasted soybean, ruminal fermentation

T246 Feedlot performance and fatty acid composition of muscles from Holstein steers fed diets differing in wheat processing and fat source.

K. Erjaei, A. Zali, M. Ganjkhanlou,* and M. Dehghan-Banadaky, *University of Tehran, Tehran, Iran.*

To evaluate the effects of wheat processing and dietary fat source on performance and fatty acid composition of muscles, Holstein steers (n = 28) averaging 296 ± 56kg were randomly allocated in 4 treatment (7 steers each). An experiment was conducted in a 2 × 2 factorial arrangement (2 methods of wheat processing: steam flake and treatment with formaldehyde and fat source: roasted soybean (RSB) and Rumifat) with completely randomized design. The study lasted 98 d (14d adaption). Dry mater intake (DMI) and average daily gain (ADG) of calves were measured daily and monthly respectively. Following the final weighing at 85d, To measure the traits related with carcass characteristics 3 steers per treatment were slaughter. No significantly differences were detected for DMI, ADG and feed efficiency. Carcass traits were not affected by dietary treatments. The amount of C18:2, C18:3, C24:0 and polyunsaturated fatty acids were greater ($P < 0.01$) in muscles from steers fed RSB. Also the amount of C18:0 and conjugated linoleic acid were greater ($P < 0.02$) in muscles from steers fed RSB. In contrast the amount of C: 16 and saturated fatty acid were greater ($P < 0.01$ and $P < 0.05$, respectively) in muscles from steers fed Rumifat. It was concluded that no difference were detected in performance of steers by fed diets differing in wheat processing and fat source but the use of RSB in the diet improved the fatty acid composition of muscles in terms of human health.

Key Words: roasted soybean, fatty acids, Holstein steers

T247 Evaluation of the ruminal bacterial diversity of cattle fed diets containing citrus pulp pellets (CP) using bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP).

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The rumen microbial ecosystem has been extensively studied, but remains a mystery from a quantitative perspective. Dietary components and changes cause shifts in the ruminal microflora that can affect animal health and productivity, but the majority of these changes remain unknown. The objective of this study was to analyze the diversity of bacterial populations in the rumen of cattle fed various amounts of citrus pulp (CPP). Heifers (n = 18; 298.7 ± 5.1 kg) were fed a basal feedlot diet and randomly assigned to 1 of 3 diets (n = 6/diet). Diets containing CPP (0, 10, or 20%) were formulated to be exchanged with steam flaked corn on a 1:1 basis. Using bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP), the normal ruminal microbiota was examined to understand how different concentrations of a common by-product feedstuff affect ruminal microbial ecology. Bacteria in the genera of *Prevotella* and *Eubacterium* were found to be the predominate bacteria that populated the rumen comprising 34% and 6%, respectively, of the bacterial population. The Firmicutes:Bacteroidetes ratio tended to increase ($P = 0.07$) in animals fed CPP when compared with controls. Also, *Butyrivibrio* and *Carnobacterium* populations increased in number with increasing amounts of CPP in the feed ration. In contrast, a decline ($P = 0.009$) in the population of *Dialister*and *Catonella* occurred with increasing CPP. An increase ($P = 0.04$) in the proportion of Bacilli bacteria in the ruminal microflora was associated with increases in dietary CPP. Overall, there were relatively few changes observed in ruminal microbial populations highlighting the functional flexibility of the rumen and demonstrating that feeding CPP at rates up to 20% does not adversely affect ruminal microbial ecology. The lack of major changes in ruminal microflora may possibly be due to a lack of essential oils in the CPP which may play a greater role in the alteration of ruminal microbial populations and may also explain the lack of apparent effect seen in other studies.

Key Words: bacterial diversity, citrus pulp

T248 Rumen dynamics of neutral detergent fiber in grazing steers supplemented with lipid sources.

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This study was carried out to evaluate the effects of lipid sources in supplements on the flow kinetics of fibrous particles and neutral detergent fiber (NDF) degradation profile using Nellore steers on *Brachiaria brizantha* 'Xaraes' pasture. Ten fistulated Nellore steers with average live weight of 350 ± 9.5 kg were randomly assigned to a double 5 × 5 Latin square design. Different lipid sources (linseed oil, palm oil, soybean grain and calcium salts (Lactoplus) was added to the supplements (100 g/kg DM) and offered at 1.0% body weight. The control treatment was composed of a corn and soybean meal supplement with no additional fat. The transit kinetics of fibrous particles was done through a pulse dose of ytterbium mordant fiber. Fecal samples were collected at 0, 3, 6, 9, 12, 24, 36, 48, 72, 96 and 120 h after marker administration. In situ fiber incubation was carried out to estimate the rumen degradation parameters of NDF, with the incubation times corresponding to the fecal sampling. The transit kinetics parameters were estimated through adjustment of a gamma-2 time-dependent model to the ytterbium excretion profiles. All adjustments of non-linear models were performed according to the Gauss-Newton iterative algorithm. The effectively degraded fraction of potentially degradable NDF (EDF), discrete lag (LAG) and mean retention time in the rumen (MRTR) are secondary parameters, derived from the rumen flow of fibrous particles (γ) and common rate of lag and degradation (λ), therefore, not subject to statistical analyses. The potentially degradable and undegradable fraction of pasture NDF were 52.83 and 47.17g/Kg, respectively. The time of intestinal transit (τ) was not affect ($P > 0.05$) by lipid supplementation. Animals fed palm oil had a reduction on γ and λ ($P < 0.05$). EDF and LAG were also lower on palm oil diet. This results indicates that the inclusion of palm oil in the supplement of gazing animals impair fibrous substrates utilization.

Table 1. Estimated parameters of fibrous particles kinetics and neutral detergent fiber degradation profile according to lipid source supplementation

Treatment	γ (h−1)	λ (h−1)	τ (h)	EDF (%)	LAG (h)	MRTR (h)
Control	0.0319	0.060	5.75	72.19	4.70	62.70
Palm	0.0185	0.021	6.95	54.73	13.42	108.11
Linseed	0.0318	0.054	5.90	70.12	5.22	62.89
C. Salts	0.0234	0.056	6.74	79.93	5.03	85.47
Soybean G.	0.0330	0.058	6.47	67.73	4.86	60.61
P-value	<0.0001	<0.0001	0.8746	-	-	-

Key Words: beef cattle, degradation rate, oil

T249 Effects of supplementation with a pressed dried distillers grain block on beef cow performance and hay intake during late gestation.

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Multiparous crossbred beef cows (n = 72; BW = 600.2 ± 6.2 kg, BCS = 4.3 ± 0.4, age = 6.9 ± 0.1 yr) in late gestation were blocked by expected calving date and randomly allocated by BW to 1 of 3 treatments: ad libitum chopped grass hay (CON; 6.5% CP and 56.8% NDF, DM basis), CON hay with ad libitum access to a pressed dried distillers grain block (BLOCK; SweetPro 16; 16.0% CP and 5.0% fat), and CON hay with 0.57 kg/cow per day of a positive control supplement (POS; 57% corn and 43% DDGS; 16.0% CP and 6.0% fat). Each treatment had 6 replicates (n = 4/pen), and the trial consisted of 2 periods (period 1: d 1 to 41; period 2: d 42 to 70). Hay was weighed and fed twice daily and refusals weighed once weekly to determine pen hay intake. All CON and POS cows had ad libitum access to a trace mineralized salt, whereas macro and trace minerals were provided by the BLOCK supplement. Data were analyzed with treatment, block, and treatment x block as fixed effects in the model for performance measures. Week and week x treatment were also fixed effects in the model for hay intake. Means were separated using LSD and considered significant when $P \leq 0.10$ or tendencies when $P < 0.15$. Hay intake was affected ($P = 0.06$) by treatment, where cows receiving the BLOCK treatment consumed less ($P = 0.02$) hay than CON (15.07, 15.43, 15.26 ± 0.11 kg for BLOCK, CON, and POS, respectively). Although BW change was not affected ($P = 0.29$) by treatment during period 1, BLOCK and POS had greater BW change during period 2 ($P \leq 0.07$) and for the overall trial ($P = 0.005$). During period 1, cow BCS change tended to be affected ($P = 0.11$) by treatment, where BLOCK and POS had greater ($P \leq 0.09$) BCS change than CON. Body condition score change during period 2 and overall was unaffected ($P \geq 0.46$) by treatment. Additionally, treatment did not affect ($P \geq 0.35$) ultrasonic backfat thickness, LM depth, or marbling score. These data suggest that the ad libitum pressed dried distillers grain block used was not only able to improve cow performance in a similar manner to supplement fed daily, but also reduced hay intake compared with control.

Key Words: beef cows, gestation, supplementation

T250 Supplementing urea in beef finishing diets containing 25% modified distillers grains has no influence on cattle performance, but does decrease marbling in yearling steers.

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Finishing diets containing elevated levels of distillers grains may contain excessive concentrations of CP, yet still be deficient in degradable intake protein (DIP). To address this situation, finishing diets containing 25% modified distillers grains (MDGS), 40% dry rolled corn, 20% high moisture corn, 12% corn silage, and 3% dry supplement (DM basis) were supplemented with 0 (CON), 0.36 (Low-U), or 0.72% (High-U) urea. Diets contained 13.3 and 6.6, 14.2 and 7.6, and 15.2 and 8.5% CP and DIP for CON, Low-U, and High-U, respectively. Two hundred 51, predominately Angus yearling steers were blocked by source and randomly allotted to 24 pens. Steers in block 1 (n = 71; BW = 388 ± 41 kg) were housed in 9 partially roofed concrete-surfaced pens. Block 2 cattle (n = 180; BW = 375 ± 24 kg) were housed in 15 soil-surfaced dry lot pens. Cattle were fed for 98 and 144 d for blocks 1 and 2, respectively, before harvest at a commercial abattoir. Preplanned contrasts evaluated CON v supplemental urea, and Low-U v High-U, respectively. Calculated DIP requirements for microbial needs were 68 g/d deficient for CON, but in excess 33.7 and 132.6 g/d for Low-U and High-U ($P < 0.001$). Body weights, ADG, and G:F were not different between treatments ($P \geq 0.08$). Marbling score was increased ($P = 0.04$) in CON (524) steers compared with Low-U (495) and High-U (491). This resulted in 60.0% of carcasses in upper 2/3 Choice and Prime grades for CON compared with 40.6% for Low-U and 46.5% for High-U ($P = 0.05$). No other carcass trait differences were observed ($P \geq 0.28$). Results suggest that urea supplementation to finishing diets containing 25% MDGS does not improve feedlot performance, but can decrease quality grade yearling steers.

Key Words: feedlot, distillers grains, metabolizable protein

T251 Effects of alternate day feeding of dried distillers grains plus solubles on ruminal ammonia concentration, blood urea nitrogen, nonesterified fatty acids, and insulin-like growth factor I in forage-fed steers.

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Our objective was to examine the effects of feeding dried distiller′s grains plus solubles (DG) or grass hay on alternate days on ruminal ammonia (NH$_4$), blood urea nitrogen (BUN), nonesterified fatty acids (NEFA), and IGF$_1$ in forage-fed steers. Four ruminally, duodenally, and ileally cannulated Holstein steers (448.8 ± 7.3 kg BW) received each of 4 dietary treatments (TRT) in a 4 × 4 Latin square: 1) ad libitum hay only (CON); 2) hay and 0.4% BW DG daily (DG7); 3) hay daily and 0.8% BW DG on alternate days (DG3); and 4) hay only or 0.8% DG only on alternate days (DGA). Treatment periods consisted of 13 d of adaptation and 8 d of blood and ruminal sample collection. Supplemented days (SUP) and non-supplemented days (NSUP) were defined as days when DG3 and DGA did or did not receive DG, respectively. Ruminal ammonia was similar ($P > 0.10$) for all treatments at feeding on SUP.

Four h post-feeding on SUP, DG7 had greater (TRT × time; $P = 0.002$) NH_4 compared with CON and DGA whereas DG3 was intermediate. At feeding and 6 h post-feeding on NSUP DGA had increased (TRT × time; $P < 0.001$) NH_4 compared with all other treatments. At 4 and 6 h post-feeding on NSUP DGA had increased (TRT × time; $P < 0.001$) NH_4 compared with CON, DG7, and DG3. Steers fed DGA had less ($P < 0.01$) BUN on SUP compared with all other treatments (5.5, 7.9, 8.3, and 7.8 ± 0.4 for DGA, CON, DG7, and DG3, respectively). Similarly, BUN was greater ($P < 0.01$) for DGA on NSUP compared with CON, DG7, and DG3 (11.8, 8.1, 8.6, 8.9 ± 0.5 mmol/L for DGA, CON, DG7, and DG3, respectively). There were no differences ($P > 0.10$) in NEFA among treatments on SUP however, on NSUP DGA (209.5 ± 12.7 mmol/L) steers had increased ($P < 0.01$) NEFA compared with all other treatments (84.4, 88.0, and 77.7 ± 12.7 mmol/L for CON, DG7, and DG3, respectively). All treatments had similar ($P > 0.10$) concentrations of IGF_1 throughout the collection period (114.0, 126.3, 128.8, 128.9 ± 6.6 ng/mL for CON, DG7, DG3, and DGA, respectively). The feeding strategy DGA altered NH_4, BUN, and NEFA, but did not influence IGF_1.

Key Words: distillers grains, metabolism, supplementation frequency

T252 Carcass traits of steers finished in feedlot fed crude glycerin. J. F. Lage,* T. T. Berchielli, E. San Vito, A. F. Ribeiro, R. A. Silva, E. E. Dallantonia, L. M. Delevatti, B. O. Felipe, M. Machado, P. M. França, and R. A. Reis, *Universidade Estadual Paulista "Júlio de Mesquita Filho," Jaboticabal, São Paulo, Brazil.*

This trial aimed to evaluate the effects of feeding crude glycerin (CG) - 80% of glycerol - included on 10% of diet dry matter, replacing corn or soybean hulls in different concentrate levels (60:40 or 40:60) on carcass traits of steers finished in feedlot. Sixty intact male (Nellore), with 18 mo of age and 373.73 ± 24.67 initial body weight, were randomly assigned to 6 treatments, with 10 replicates in factorial arrangement (2 levels of concentrate x 3 feeding regimens). The diets were: control diet, without inclusion CG, containing corn in the concentrate (CN); diets with inclusion CG with high level of starch, containing corn in the concentrate (CGC) and diets with inclusion CG with low level of starch, containing soybean hulls in the concentrate (CGS). The diets were isonitrogenous and formulated to meet the requirements for maintenance and gain of the animals according to Brazilian recommendations. After 94 d on feed, the shrunk body weight (SBW) was recorded and the animals were slaughtered. The carcasses were weighed for obtained the hot carcass weight (HCW) and dressing percentage (DP). The carcass were refrigerated for 24 h at 0°C and then rib fat thickness (RFT) and ribeye area (REA) were measured in the region between 12 and 13 th rib. Data were analyzed using the GLM procedure of SAS and the effects of treatments were considered significant at $P < 0.05$. The interaction between concentrate levels and feeding regimens was not significant ($P > 0.05$). Differences were detected ($P < 0.05$) in the DP among the feeding regimens. The animals fed with the diet CGC had higher mean values for DP (57,23%) than the animals fed the diets CN (56,34%) and CGS (55,92%). No difference were detected ($P > 0.05$) for SBW, HCW, RFT and REA among the treatments, with mean values 498.36 kg, 281.57 kg, 5.13 mm and 76.11 cm^2, respectively. The variables evaluate were not altered ($P > 0.05$) by the concentrate allowance levels assessed (60:40 or 40:60). The inclusion of 10% of crude glycerin in diets with high starch increase the dressing percent, however, does not affect the shrunk body weight, hot carcass weight, ribeye area and rib fat thickness.

Key Words: beef cattle, glycerol, rib fat thickness

T253 Performance of Nellore steers receiving protected linseed oil during different periods of feedlot. W. Henrique*[1], V. G. Carvalho[2], T. M. Pivaro[2], J. L. V. Coutinho Filho[1], A. A. M. Sampaio[2], E. A. Oliveira[2,3], and B. L. Rosa[2], *[1]Sao Paulo Agency for Agribusiness Tecnhology, Sao Jose Rio Preto, Sao Paulo, Brazil, [2]FCAV/Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil, [3]FAPESP Post-doctorate fellowship, Sao Paulo, Sao Paulo, Brazil.*

The objective was to assess the use of linseed oil protected from ruminal degradation during different periods of confinement or linseed oil, as ingredients of the diet, for 35 Nellore steers. The animals were housed in individual pens for 105 d at the Sao Paulo Agency for Agribusiness Technology, in Sao Jose do Rio Preto, Brazil. In addition to the control diet and with linseed oil during all the feedlot, it was evaluated the addition of protected linseed oil during the last 35 d, the last 70 d or during all the feedlot. The roughage used was corn silage exclusively, in the proportion of 40% in dry matter diet. All diets were isonitrogenous and those with the addition of oil were also isoenergetic. The proportion of protected linseed oil was 4.0% and linseed oil 3.4% in dry matter diet. The feedstuffs and the leftovers were analyzed and the animals were weighed at the beginning and at the end of the experiment, preceded by total fasting for 15 h. The experimental design was a randomized block one, balanced by animal weight, and means were compared by Student's *t*-test at 5% of probability. There were no differences for initial (392.94 kg) and final body weight (522.72 kg), average daily gain (1.236 $kg.day^{-1}$), dry matter intake, per day (9.392 kg) or related to the body weight (2.05%), and feed efficiency (0.131 kg gain.kg DM $intake^{-1}$). The addition of protected linseed oil during different periods of confinement or linseed oil did not bring additional benefits for the performance of fattening cattle in feedlot.

Key Words: cattle, fattening, weight gain

T254 Performance of crossbred heifers and steers fed increasing linseed oil levels. W. Henrique*[1], B. L. Rosa[2], E. A. Oliveira[2,3], A. A. M. Sampaio[2], T. M. Pivaro[2], A. T. Andrade[2], and V. G. Carvalho[2], *[1]Sao Paulo Agency for Agribusiness Technology, Sao Jose Rio Preto, Sao Paulo, Brazil, [2]FCAV/Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil, [3]FAPESP Post-doctorate fellowship, Sao Paulo, Sao Paulo, Brazil.*

The objective was to assess the increasing linseed oil supplementation (1, 3.8 and 5.2% in DM diet) fed to crossbred cattle Nellore × Canchim and its influence on the average daily gain (ADG), slaughter weight (SW), feed efficiency (FE) and dry matter intake per day (DMI) and as a percentage of body weight (DMI%BW). Fifteen steers (427.80 ± 42.01 kg and 24 ± 2 mo old) and 14 heifers (400.57 ± 33.79 kg and 24 ± 2 mo old) were housed in individual pens at Jaboticabal, campus of Sao Paulo State University and fed diets with 80% concentrate in DM and sugarcane IAC 86–2480 as exclusive roughage source. The experiment was a randomized block design one, arranged in a 3 × 2 factorial scheme (oil ratios x sexual condition) and means were compared by Student's *t*-test at 5% of probability. After fattening period, the animals were slaughtered in a staggered way by blocks. There were no interactions ($P > 0.05$) between sexual conditions and oil levels for all variables. Steers showed higher ($P < 0.05$) SW (535.07 and 494.79 kg), ADG (0.982 and 0.857 kg/d) and DMI (9.098 and 8.070 kg/d) when compared with heifers, respectively. The FE and DM%BW did not showed difference ($P > 0.05$) for sexual condition. No difference ($P > 0.05$) was observed to ADG among diets (0.92 kg/d). Diets containing 1 and 3.8% presented higher values ($P < 0.05$) for DMI than 5.2% of oil (9.046, 8.764 and 8.040 kg/d, respectively). Similar results ($P < 0.05$) were observed for DMI%BW (1.93, 1.88 and 1.74%, respectively). Animals fed diets with 1 and 3.8% of oil were less efficient ($P < 0.05$) than animals fed diets with 5.2% of oil (0.094, 0.104 and 0.123 kg of ADG/kg of DMI, respectively). Increasing linseed oil in diets to crossbred beef cattle can improve feed efficiency by decreasing the dry matter intake and keeping the daily gain.

Key Words: feed efficiency, Nellore × Canchim, weight gain

T255 Performance of growing Nellore steers on pasture in the dry season fed crude glycerin. E. San Vito,* T. T. Berchielli, J. F. Lage, R. C. Canesin, R. A. Reis, C. S. R. Junior, L. M. Delevatti, M. Machado, E. E. Dallantonia, A. F. Ribeiro, and R. A. Silva, *Universidade Estadual Paulista "Julio de Mesquita Filho," Jaboticabal, São Paulo, Brazil.*

The aim of this work was to evaluate the effect of crude glycerin (CG) inclusion as a substitute to corn grain in the average daily gain (ADG) and shrunk body weight final of growing Nellore steers on pasture, supplemented in the dry season. The CG used was derived from soybean biodiesel production (80% glycerol). Fifty Nellore steers with initial shrunk body weight of 279.52 ± 16.31 kg were randomly assigned to 5 treatments, with 10 replicates. The animals were distributed in 10 paddocks, with 1.8 ha each (2 paddocks per treatment), of *Brachiaria brizantha* 'Xaraés'. Treatments were constituted by 5 levels of CG inclusion in the supplement: (0, 7, 14, 21 and 28% of CG based on dry matter) as a substitute to the corn grain. The animals were supplemented daily in a proportion of 0.7% of body weight, and it contained 40% of crude protein based on dry matter. The supplement was constituted of corn grain, soybean meal, urea, gluten meal and mineralized salt. The experiment was executed in 136 d, and the animals were weighed in the beginning and in the end of the experiment, after 14 h of solids and liquids shrunk to evaluate the average daily gain. Data was analyzed using the GLM procedure of SAS program and the effects of treatments (linear and quadratic) were considered significant at $P < 0.05$. There was an increased linear effect of glycerin levels ($P < 0.05$) on the final live weight ($r^2 = 0.73$) and daily average gain ($r^2 = 0.35$), and the following equations were adjusted: FW = 374.38 + 0.72 x % of CG in the supplement and ADG = 0.65 + 0.041 x % of CG in the supplement. Final shrunk body weight of animals was 375.4, 377.4, 381.8, 389.9 and 398.1 kg and the average daily gain was 0.704, 0.719, 0.752, 0.812 e 0.871 kg to the inclusion of 0, 7, 14, 21 and 28% of CG in the supplement, respectively. It is possible to conclude that an increase in crude glycerin levels (up to 28%) in the supplements of growing steers on pasture in the dry season can increase the average daily gain and final body weight of the animals.

Key Words: biodiesel, by-product, forage

T256 Palatability of post-extraction algal residue as a protein supplement for cattle. M. L. Drewery,* J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

Market value of post-extraction algal residue (PEAR) is driven by its ability to compete with commonly fed protein sources; for example cottonseed meal (CSM) and dried distillers' grains (DDG). An initial step in evaluating PEAR (20% CP, 59% OM) is to determine palatability when fed as a protein supplement. Accordingly, we evaluated the palatability of PEAR-containing supplements in cattle consuming a basal diet of Bermudagrass (13% CP, 76% NDF). Twelve steers were used in a 12 × 12 Latin square experiment consisting of 12 4-d periods. Each period included 3-d where steers were fed a test supplement and a 1-d washout where steers were fed DDG. Supplements were formulated with different carrier ingredients (DDG, CSM, or liquid supplement, LS) and different levels of PEAR inclusion (0, 20, 40, and 60% for DDG and CSM and 0, 33, 66, and 100% for LS). Intake and time required for consumption were recorded daily. A significant ($P < 0.05$) treatment × day interaction for g consumed per min (GPM) was observed. This interaction resulted from changing rates of consumption as cattle adapted to supplements. Supplements containing DDG had the greatest rates of consumption (177 – 187 GPM), followed by CSM supplements (148 – 166 GPM). Blends including PEAR and LS had slower rates of consumption (58 – 93 GPM). Supplement formulation significantly ($P < 0.05$) affected the amount of supplement consumed and time required for complete consumption. Supplements which contained DDG or CSM were consumed in less than 11 min; complete consumption was observed 92 – 100% of the time. Treatments containing LS required more time for complete consumption (21 – 33 min) and were finished 77 – 96% of the time. Our results suggest PEAR can be blended (up to 60%) with existing ingredients utilized in beef rations to create suitable protein supplements. However, PEAR is not palatable when offered alone (complete consumption of 100% PEAR occurred 77.5% of the time and required 31.5 min) or incorporated into LS. Additional research is necessary to determine the impact of PEAR on nutrient utilization in cattle.

Key Words: supplementation, post-extraction algal residue, dried distillers grains

T257 Protein sources and nitrogen associated with the residual biodiesel glycerin supplements to fattening cattle during the rainy season: performance productive. A. J. Neto[1], J. T. Zervoudakis[1], L. da Silva Cabral[1], L. K. H. Zervoudakis*[1], R. L. Galati[1], P. V. R. Paulino[2], L. C. R. P. Silva[1], R. P. da Silva[1], J. Q. Soares[1], and T. de Paulo Trindade[1], *[1]Universidade Federal de Mato Grosso, Cuiabá, Mato Grosso, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

The objective was to evaluate the effect of protein sources and nitrogen associated with the residual biodiesel glycerin in the diet of beef cattle grazing in the rainy season on performance. Twenty Nelore steers age and initial body weight average of 25 months and 422 kg were used, during the experimental period of 84 days. The area consisted of 4 paddocks of 1.6 ha each formed with *Brachiaria brizantha* 'Marandu', with a mass of forage and potentially digestible dry matter of 1552.71 and 1146.01 kg/ha, respectively. The experiment was structured in a completely randomized design to evaluate the following supplements: control (only mineral); GU – glycerin with urea; GFS - glycerin with soybean meal and GFA - glycerin with cottonseed meal as a function of the variables: gain total weight and average daily gain. The supplementation was provided daily at 10 a.m., with supply of 2.0 kg of supplement/animal. The productive performance of animals was 0.992; 1.095; 0.997 and 1.010 kg/animal/day for the supplements: MM, GU, GFA, and GFS. There was no difference ($P = 0.60$) between the levels of supplementation and the control group on average daily gain of animals. The combination of glycerin with protein sources and nitrogen promotes good animal performance under grazing.

Key Words: glycerol, pasture, weight gain

Ruminant Nutrition: Dairy II

T258 Oocyte and embryo quality of dairy cows fed omega 3 and 6 fatty acids sources in the transition period and early lactation. J. R. Gandra,* R. D. Mingoti, L. C. Verdurico, R. V. Barletta, J. E. Freitas Jr., C. S. Takiya, T. H. A. Vendramine, R. Gardinal, and F. P. Rennó, *1University of Sao Paulo, Sao Paulo, Brazil.*

The objective of this study was to evaluate the supplemental sources of omega 3 and 6 fatty acids and the effects in oocyte and embryo quality of dairy cows fed during the transition period and early lactation. Forty-eight Holstein cows were divided into 4 experimental groups in randomized design. The animals were randomly assigned to receive one of 4 treatments: 1) control (C; n = 12), without fat sources in the pre and postpartum, 2) flaxseed (FS; n = 12), in which cows were fed 60 and 80 g/kg of DM of flaxseed in the pre and postpartum, respectively; 3) whole raw soybeans (WS; n = 12), in which cows were fed 120 and 160 g/kg of DM of whole raw soybeans in the pre and postpartum; 4) calcium salts of unsaturated fatty acid (CSFA; n = 12; Megalac-E), in which cows were fed 24 and 32 g/kg of DM of calcium salts of unsaturated fatty acid in pre and postpartum. The experimental diets were fed from 35 d before the estimate calving, and provided until 84 d of lactation, formulated to meet the nutritional requirements of each period (pre and postpartum). The procedure for follicular aspiration (FA) was performed in 2 periods: 35 ± 7 d of lactation (FA1) and 60 ± 7 d of lactation (FA2). After FA the oocytes were classified grade I, II, III, atretic and degenerate. Only submitted in vitro fertilization (IVF) oocytes with grade I, II and III. Data were analyzed using PROC MIXED of SAS 9.1, with the effect of diet, aspiration (FA) and interaction as fixed effects, and animal has random effect. The data were analyzed by orthogonal contrasts (C vs. WS+CSFA+FS; WS vs. CSFA; and FS vs WS+CSFA. FA effect ($P < 0.05$) was observed for the number of degenerate and viable oocytes (3.00 vs 1.82) and (4.65 vs 8.70), respectively to FA1 and FA2. There was interaction ($P < 0.05$) between the fatty acids sources and FA in the number of viable embryos. Effect ($P < 0.05$) were observed for the contrast FS vs WS+CSFA, when analyzing the number of viable embryos (1.27 vs. 0.73), respectively. The oocyte and embryo quality of dairy cows fed omega 3 and 6 fatty acids sources in the transition period and early lactation influenced the oocyte and embryo quality in post-partum period.

Key Words: fat sources, follicular aspiration, transition period

T259 Effects of different PUFAs supplementation during the postpartum periods of early lactating dairy cows. I: Milk production and composition. E. Dirandeh[1], A. Towhidi*[1], M. Ganjkhanlou[1], S. Zeinoaldini[1], Z. Ansari Pirsaraei[2], and A. R. Zarenezhad[3], *[1]Department of Animal Science, Faculty of Agricultural Science and engineering, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, Faculty of Animal Science and Fishery, Sari University of Agricultural and Natural Resources, Sari, Mazandaran, Iran, [3]Mahdasht Dairy Farm, Sari, Mazandaran, Iran.*

The objectives were to determine the effect of diet enriched in α-linolenic acid (n-3), or linolenic acid (n-6) on milk production and composition in lactating dairy cows. Ninety high-yielding multiparous Holstein dairy cows with no over clinical illnesses were blocked according to calving date and parity. Cows were assigned randomly to be fed either 1-soybean whole roast (S, n = 30), or 2-linseed (L, n = 30), or 3-palm oil as a source of saturated fatty acid (C, n = 30) from calving until first heat after d 40 postpartum (dpp) and then half of the cows in each treatment group were switched to receive either linseed (L) or saturated fatty acid (C) from first heat after d 40 to 120 dpp. There was no difference between groups (mean ± SEM) in parity (3.0 ± 1.90) or BCS at calving (3.2 ± 0.07). Milk yield were recorded daily throughout the experiment. Milk samples were taken weekly (Monday and Thursday mornings) and analyzed for fat, protein and lactose contents by infrared analysis at the National Milk Records Laboratory, Sari, Iran, using AOAC reference method No. 972.16 (AOAC 1990). Data were analyzed with PROC MIXED of SAS. Result showed milk yield was not affected by diet ($P = 0.36$). Milk yield increased over time ($P < 0.001$), while no treatment × day interaction was detected ($P = 0.35$). Milk composition was similar among diets, except milk fat percentage that was lower in LL group than other groups ($P = 0.01$). Concentration and yield of milk fat did not change from wk 0 to 4 in cows fed linseed and soybean whole roast, whereas milk fat concentration declined from 3.54 to 3.20% ($P < 0.05$) and from 1.25 to 1.14 kg/d ($P < 0.05$), respectively, from wk 0 to 4 in cows fed palm oil. Milk protein percentage and yield did not differ between the dietary groups in our study. There was no difference in lactose, total solid and SNF in the milks.

Key Words: dairy cow, n-3 fatty acid, n-6 fatty acid

T260 Effects of lipid and propionic acid infusions on feed intake of lactating dairy cows. S. E. Stocks* and M. S. Allen, *Michigan State University, East Lansing.*

Propionic acid is more hypophagic when hepatic acetyl CoA concentration is elevated during early lactation. The objective of this experiment was to evaluate effects of intravenous lipid infusion and intraruminal propionic acid infusion on feed intake of lactating cows. Eight multiparous, ruminally cannulated, Holstein dairy cows (81 – 252 d in milk) were used in a replicated 4x4 Latin square experiment with a 2x2 factorial arrangement of treatments. One cow was removed because of an adverse reaction to the lipid infusion. Treatments were propionic acid (PR) infused intraruminally at 0.5 mol/h for 18 h starting 6 h before feeding or sham control (CO), and intravenous jugular infusion of lipid (TG, Intralipid 20%) or saline (SA, 0.9% NaCl) infused at 0.5 L/h for 24 h starting 12 h before feeding. Changes in plasma concentrations of metabolites and hormones and hepatic concentration of acetyl CoA from before infusion until the end of infusion were evaluated. No interactions of treatments were observed for DMI or changes in concentration for metabolites or hormones. Infusion of PR decreased DMI 15% (16.1 vs. 19.0 kg/12 h, $P = 0.02$) compared with CO but lipid infusion did not affect DMI over the 12 h infusion period. Infusion of PR tended to decrease hepatic acetyl CoA concentration (−5.7 vs. −2.4 nmol/g wet tissue, $P = 0.09$) compared with CO, consistent with PR decreasing DMI by stimulating oxidation of acetyl CoA. Contrary to our expectations, TG did not increase concentrations of NEFA ($P = 0.75$) or BHBA ($P = 0.48$) in plasma, or acetyl CoA in liver ($P = 0.65$), and did not increase milk fat yield ($P = 0.67$), suggesting that the infused TG was stored or oxidized by extrahepatic tissues. As a result, there was no interaction between PR and TG for DMI. While the effect of PR on DMI was consistent with our previous results, this model was not useful to evaluate the interaction between PR and TG related to control of feed intake by hepatic oxidation.

Key Words: hepatic oxidation, control of feed intake, propionate metabolism

T261 Relationships between ruminal volatile fatty acid concentrations, milk production, digestibility, and milk fatty acid composition in dairy cows. A. N. Hristov*[1], K. J. Shingfield[2], P. Huhtanen[3], J. L. Firkins[4], and K. Harvatine[1], [1]*The Pennsylvania State University, University Park,* [2]*MTT Agrifood Research Finland, Jokioinen, Finland,* [3]*Swedish University of Agricultural Sciences, Umeå, Sweden,* [4]*The Ohio State University, Columbus.*

The objective of this meta-analysis was to investigate the relationships between ruminal volatile fatty acids (VFA) concentrations (acetate, Ac; propionate, Pr, valerate, Va), their molar proportions, mol/100 mol (p), Ac:Pr ratio (AcPr), milk production, digestibility, and milk fatty acid (FA) composition in dairy cows as a potential on-farm tool for monitoring rumen function. The data set used in the analysis contained 496 individual cow data from 27 experiments conducted at 4 locations. Data were analyzed using the CORR and MIXED (with study as random effect) procedures of SAS. Average DMI and milk yield of the cows were: 22 (SD = 4.7) and 32 kg/d (SD = 10.3), respectively. The greatest correlation (all $P < 0.001$) for DMI was with Va and pVa (r = 0.38 and 0.34) and Pr (0.22). The greatest correlation for milk yield was with AcPr (−0.44), Pr and pPr (0.43 and 0.42), and Va (0.36). Best fit (based on the Akaike Information Criterion) models for milk yield and DMI included Pr and pVa and total VFA, respectively. Correlations of milk fat and protein contents with rumen VFA were weaker: −0.18 (Pr and pPr), 0.16 (AcPr), and 0.15 (pAc) and −0.11(Pr), respectively. Milk fat yield correlated with Va and pVa (0.19 and 0.16) and milk protein yield with AcPr (−0.40), Ac (−0.35), and Pr and pPr (0.37). Digestibility of NDF correlated with Va and pVa (−0.43 and −0.45), Ac (0.42), and Pr and pPr (−0.33 and −0.38). The greatest correlations between rumen VFA and milk FA were: for Ac with 18:1 (c11–18:1, −0.50; c16–18:1, 0.49; and c13–18:1, −0.46) and 22:4n-3 (−0.40); for pAc with 22:4n-3 (−0.67), t6–8-18:1 (−0.48), c9–10:1 (0.48), and t13–18:1 and 22:6n-3 (−0.47); for Pr with c9–10:1 (−0.42), c9–17:1 (0.42), and 22:6n-3 (0.39); for pPr with c11–18:1 (0.50), 22:4n3 (0.49), and c9–10:1 (−0.47); and for Va with c9-t1218:2 (0.59), total c18:2 (0.52), t9–14:1 (0.50), and c16–18:1 (−0.43). This analysis indicated that milk yield in dairy cows correlated positively with Pr and inversely with AcPr. The greatest correlations of VFA and milk FA were for Ac with c11–18:1 and for Va with c9-t1218:2.

Key Words: dairy cow, milk fatty acid, volatile fatty acid

T262 Occurrence and concentration of mycotoxins, molds and yeasts in total mixed rations from South Dakota and Minnesota dairy farms. F. Diaz-Royon*[1], A. Garcia[1], K. F. Kalscheur[1], K. A. Rosentrater[2], J. S. Jennings[3], and K. Mjoun[3], [1]*Dairy Science Department, South Dakota State University, Brookings,* [2]*Department of Agricultural and Biosystems Engineering, Iowa State University, Ames,* [3]*Alltech South Dakota, Brookings.*

Because of mycotoxin degradation in the rumen, dairy cattle can resist better than other livestock the adverse health effects associated with their exposure. At the same time though, dairy cattle are subjected to greater production stress which may increase their susceptibility to mycotoxins. Total mixed rations (TMR) from twenty-seven large dairy farms in eastern SD and western MN were collected during the summer and fall of 2011. Samples were screened for mycotoxins, molds, and yeasts to provide an overview of their prevalence in dairy diets. Ten subsamples of 0.5 kg each were taken from the feed bunk of high-production dairy cow pens. Subsamples were composited and later split in two 0.8-1.0 kg samples. After vacuum sealing, one sample was stored at −20°C for mycotoxin analyses and the second sample was stored at 4°C for mold and yeast analyses. Samples were quantitative analyzed for 18 different mycotoxins through high performance liquid chromatography (HPLC) and gas chromatography-mass spectrometry (GC-MS). Detection limit was 0.5 ppm except for fumonisin B1 and aflatoxin B1, which were 1.0 and 0.05 ppm, respectively. Molds and yeasts were counted by direct plate dilution. In addition, mold isolates were identified using the conventional microscopic tape method in samples with mold growth equal to or higher than 1,000 cfu/g. There were 26 TMR samples (96.3%) positive for vomitoxin, with a maximum concentration of 0.8 ppm. These samples contained fumonisin concentrations lower than U. S. Food and Drug Administration maximum acceptable limits for use in animal feeds. Other mycotoxins were not detected. Mold growth was lower than 1,000 cfu/g in 15 TMR samples (55.5% of the samples) and higher than 10,000 cfu/g in 7 samples (25.9%). *Aspergillus* and *Mucor* were the fungi genera most isolated. On average yeast content in TMR was 1.9×10^6 cfu/g with only one sample (3.7%) showing yeast counts below 1,000 cfu/g. In spite of vomitoxin being detected in 96.3% of the TMR samples analyzed during the summer and fall of 2011, its concentration was always below that considered a health hazard by the FDA.

Key Words: mycotoxins, dairy cows, total mixed ration

T263 Feed restriction, but not L-carnitine infusion, affects the liver transcriptome with an evident induction of gluconeogenesis and inhibition of energy production and sterol synthesis in mid-lactating dairy cows. H. Akbar,* M. Bionaz, D. B. Carlson, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Abomasal carnitine infusion during acute feed restriction has been shown to increase hepatic fatty acid oxidation and decrease liver lipid accumulation in dairy cows. Using mid-lactating dairy cows we studied the effects of abomasal L-carnitine (20 g/d) in combination with restricted dry matter intake (DMI; 50% of previous 5-d average) on the hepatic transcriptome. Eight lactating Holstein cows were used in a replicated 4 × 4 Latin square design with 14-d periods. A 2 × 2 factorial arrangement was used to determine the effects of water infusion + ad libitum DMI, water infusion + restricted DMI, carnitine infusion + ad libitum DMI, or carnitine infusion + restricted DMI. Liver biopsies were obtained to extract RNA for transcriptome profiling using a bovine microarray consisting of 7,872 cDNA. Analysis of variance (false discovery rate $P \leq 0.15$ for overall treatments effect; equivalent to uncorrected $P \leq 0.05$) identified significant changes in transcriptomics only for feed restricted cows without any carnitine effect, resulting in 312 (155 downregulated, 157 upregulated) differentially expressed genes. Quantitative PCR (qPCR) was performed to confirm array data and measure expression of additional genes not present on the array. The qPCR data confirmed the effect of feed-restriction but not of carnitine treatment. Feed restriction increased expression of GPX3, involved in the detoxification of hydrogen peroxide, and of genes associated with gluconeogenesis (PC, PDK4), inflammation (SAA3), and signaling (ADIPOR2); whereas, it downregulated BBOX, key for L-carnitine biosynthesis, and the transcription factor HNF4A. Functional analysis of microarray data was carried out using Ingenuity Pathway Analysis, DAVID, and the novel dynamic impact approach (DIA). The functional analysis of DEG by feed restriction uncovered as the most relevant and inhibited functions biosynthesis of cholesterol and energy generation by mitochondrial respiration. Associated with the decrease of energy production the data also indicated a decrease in glucose catabolism, particularly through the glycolysis/pyruvate/TCA cycle and pentose phosphate pathways. Data indicated a decrease in fatty acid oxidation and ketone body production by feed restriction. Microarray and qPCR results revealed that in mid-lactating cows feed restriction but not L-carnitine affects the liver transcriptome with an evident inhibition of cholesterol synthesis and energy production. In contrast, gluconeogenesis increased and glucose catabolism decreased. We interpreted those results as a likely response of liver to spare energy for the lactating mammary gland. This study provides new and unexpected insights on the effect of negative energy balance on liver transcriptome in mid-lactating cows.

Key Words: bioinformatics, microarray, negative energy balance

T264 A comparison of methods to analyze physical effective factor and physically effective NDF in TMR and orts. S. D. Ranathunga,* K. F. Kalscheur, and D. P. Casper, *Dairy Science Department, South Dakota State University, Brookings.*

The objectives were to compare available methods to measure physical effective factor (pef) and physically effective NDF (peNDF) in TMR and orts while using different forage and dried distillers grains with solubles (DG) concentrations. Four Holstein cows were assigned to a 4 × 4 Latin square in a 2 × 2 factorial arrangement of treatments. Diets contained either low forage (LF; 41% of diet DM) or high forage (HF; 60% of diet DM) with DG at 0 or 18% of diet DM. The pef and peNDF of TMR and orts were measured using 3 methods: 1) Dry sieving method using 12 screens (DS), 2) Penn State shaker box using top 3 screens (PS), and 3) Z-box (Z). Average pef and peNDF for all TMRs differed ($P < 0.05$) between the 3 methods (55.5, 79.7, and 52.6% and 16.0, 22.9, and 15.2%, for DS, PS, and Z, respectively). Average pef and peNDF of the orts were greater ($P < 0.05$) for PS (65.4, 82.4, and 63.6% and 22.2, 27.8, and 21.6%) compared with other methods. There was a forage × DG effect on pef of TMR and pef and peNDF of orts irrespective of the method. The peNDF of TMR was affected by forage and DG concentrations irrespective of the method. The results suggest that PS method overestimates pef and peNDF of TMR and orts and interpretation of data are different compared with the DS method. Estimates pef and peNDF values of TMR and orts by the Z method are closer and interpretation of data similar to that of the DS method.

Table 1.

	LF		HF		
Method	0DG	18DG	0DG	18DG	SEM
TMR-pef-DS	52.0^{c}	48.4^{c}	63.8^{a}	58.0^{b}	0.76
PS	77.2^{b}	74.1^{b}	84.9^{a}	82.6^{a}	
Z	45.0^{c}	44.0^{c}	63.2^{a}	58.1^{b}	
TMR-peNDF-DS	13.0^{b}	13.7^{b}	18.5^{a}	18.7^{a}	0.24
PS	19.3^{d}	21.0^{c}	24.6^{b}	26.7^{a}	
Z	11.2^{b}	12.5^{b}	18.3^{a}	18.8^{a}	
Orts-pef-DS	63.3^{b}	50.4^{c}	72.3^{ab}	75.6^{a}	2.36
PS	79.5^{ab}	72.7^{b}	90.1^{a}	87.2^{a}	
Z	59.5^{b}	47.0^{c}	75.8^{a}	71.9^{a}	
Orts-peNDF-DS	18.8^{b}	16.2^{b}	25.8^{a}	28.1^{a}	0.77
PS	23.6^{b}	23.3^{b}	31.9^{a}	32.3^{a}	
Z	17.7^{b}	15.1^{b}	26.9^{a}	26.7^{a}	

$^{a–d}$Means within a row with different superscripts differ ($P < 0.05$).

Key Words: forage, pef, peNDF

T265 Effect of post-ruminal supplementation of phytonutrients on bacterial diversity in feces of dairy cows. J. Oh*[1], A. N. Hristov[1], C. Lee[1], K. Heyler[1], T. Cassidy[1], S. Dowd[2], and D. Bravo[3], [1]*The Pennsylvania State University, University Park,* [2]*MR DNA Molecular, Shallowater, TX,* [3]*Pancosma, Geneva, Switzerland.*

The objective of this experiment was to investigate the effect of post-ruminal supplementation of phytonutrients on bacterial diversity in feces of lactating dairy cows. Eight ruminally cannulated Holstein cows (232 ± 34.1 DIM) were used in a replicated 4 × 4 Latin square design trial with 23-d periods. Treatments were control (CON) and 2 g/d of curcuma oleoresin (CU), garlic extract (GE), or capsicum oleoresin (CA). Treatments were dissolved in ethanol solution and pulse-dosed into the abomasum of the cows once daily, 2 h after feeding for 9 d during each experimental period. Fecal samples (8) were collected from the rectum on d 6 and 7 of phytonutrient supplementation and analyzed for bacterial diversity using 16S rDNA bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP). Predominant genera bacteria were *Clostridium*, *Eubacterium*, *Ruminococcus*, *Bacteroides*, *Oscillospira*, and *Odoribacter* (8 to 10% of the total population) and were not affected ($P > 0.11$) by treatment. Predominant species were *Eubacterium siraeum*, *Oscillospira guilliermondii*, and *Fecalibacterium prausnitzii* (7 to 10%) and were also not affected ($P > 0.11$) by treatment. Compared with CON, GE increased ($P < 0.04$) the proportion of bacteria of the genera *Thiococcus* (0.06 and 0.12%), *Borrelia* (0.01 and 0.06%), and *Lactococcus* (0.01 and 0.08%) and CU, GE, and CA decreased *Flexithrix* (0.05 vs. 0.02, 0.02, and 0.01%). Compared with CON, GE increased ($P < 0.03$) the proportion of *B. garinii* (0.01 and 0.06%) and *L. lactis* (0.01 and 0.07%). Relative to CON, CU and CA decreased ($P < 0.05$) *Prevotella multiformis* (0.06, 0.02, and 0.003%) and CU decreased ($P < 0.05$) *Clostridium stercorarium* (0.06 and 0.02%). The proportion of *F. dorotheae* was lower ($P < 0.04$) for CU, GE, and CA (0.02, 0.02, and 0.01 vs. 0.05% for CON). In conclusion, post-ruminal supplementation of phytonutrients did not alter the major bacterial species in feces of dairy cows, although some bacteria such as *Thiococcus*, *Borrelia*, and *Lactococcus* were enhanced by GE and species such as *Prevotella multiformis* and *F. dorotheae* were inhibited by the phytonutrients.

Key Words: phytonutrients, fecal bacteria, dairy cow

T266 Applicability of the plasma free amino acid dose response approach for determining lysine bioavailability of ruminally protected lysine products. N. L. Whitehouse*[1], E. S. Fletcher[1], A. F. Brito[1], and C. G. Schwab[2], [1]*University of New Hampshire, Durham,* [2]*Schwab Consulting LLC, Boscobel, WI.*

It has been long recognized that lysine (Lys) is a limiting AA for lactating dairy cows. As a result, several ruminally-protected Lys (RP-Lys) supplements are now available for increasing Lys concentrations in metabolizable protein (MP). However, there is no universally accepted procedure for obtaining estimates of efficacy of these products. To evaluate 4 different RP-Lys supplements, we examined the dose-response relationships between plasma free Lys concentrations and intestinally (Trial 1) or abomasally (Trials 2–4) infused Lys in lactating dairy cows. Four Latin square trials were conducted; 2 with basal diets formulated to have low concentrations of Lys in MP and 2 with high concentrations (according to NRC, 2001). At the start of the trials, DIM of cows were: 63–123 (Trial 1), 60–70 (Trial 2), 175–245 (Trial 3), and 90–130 (Trial 4). Blood samples collected from the tail vein were centrifuged, deproteinized, and composited by cow/d with plasma stored at −80°C until AA analysis. Our data (see table below) showed a linear response between plasma Lys concentrations and infused Lys, corroborating results from previous research. We also observed that expressing plasma Lys concentrations either as µg/mL or as µM, before expression as a percentage of total AA, resulted in relatively similar regression equation parameters as well as similar variation and bias estimations. It is concluded that the plasma free AA response approach can be utilized for determining Lys bioavailability of RP-Lys supplements.

Table 1. Regression parameters for incremental levels of infused lysine

Trial	MPLys, %	Infused Lys, g/d	Slope	Intercept	r^2	SE	RMSE
Lys, % Total AA (μ/mL)							
1	5.27	0, 16.5, 33, 49.5, 66	0.027	2.95	0.97	0.38	0.142
2	5.54	0, 8, 16, 24, 32	0.048	2.81	0.90	0.31	0.238
3	6.81	0, 14, 28, 42, 56, 70, 84	0.024	5.21	0.96	0.45	0.166
4	6.81	0, 30, 60	0.022	4.51	0.98	0.22	0.151
Lys, % Total AA (μM)							
1	5.27	0, 16.5, 33, 49.5, 66	0.024	2.49	0.97	0.32	0.122
2	5.54	0, 8, 16, 24, 32	0.037	2.45	0.84	0.27	0.236
3	6.81	0, 14, 28, 42, 56, 70, 84	0.022	4.81	0.84	0.38	0.315
4	6.81	0, 30, 60	0.018	3.79	0.97	0.19	0.134

Key Words: lysine, bioavailability technique, dose response

T267 Physiological variables associated with reproductive success in dairy cows with different prepartum feeding strategies. F. C. Cardoso,* N. V. L. Serão, and J. K. Drackley, *University of Illinois, Urbana.*

To investigate the association between physiological factors and reproductive performance (days to conception; DTC) in dairy cows fed different prepartal dietary energy regimens, cow-level data from 408 cows from 7 different experiments by our group from 1993 to 2010 were analyzed. Treatments were classified as controlled energy (CE; median NE_L intake = 13.7 Mcal/d) or high energy (HE; median NE_L intake = 22.1 Mcal/d) diets fed during far-off (FO) or close-up (CU) dry periods. Principal component (PC) analysis was conducted on 8 variables: glucose wk 3 (GLU3), glucose wk 4 (GLU4), β-hydroxybutyrate wk 1 (BHBA1), insulin wk 2 (INS2), nonesterified fatty acids wk −1 (NEFA-1), energy-corrected milk wk 4 (ECM4), fat corrected milk wk 4 (FCM4), and milk urea nitrogen wk 4 (MUN4). Prior to analyses, the multinormality of the variables was assessed. The effect of PCs was investigated using linear and logistic (LR) regressions. For LR analysis, animals were classified in 2 groups as high (>131) or low (<121) DTC. All analyses were carried out using SAS 9.2 (SAS Institute, Inc.). PCs with eigenvalues (λ) greater than 0.9 were extracted, and only loadings greater than 0.4 were discussed. PC scores (PCS) were generated for each extracted PC. Four PCs were extracted from the analysis, accounting for 80.1% of total variability. The PC loadings indicated that, for PC1, increased ECM4 and FCM4 were associated with decreased INS2, GLU3, and GLU4. PC2 represented animals with higher NEFA-1 and BHBA1. PC3 had higher values for ECM4, FCM4, GLU3, and GLU4, whereas PC4 had higher values for MUN4 and INS2. Regressing PCS of PC2 on PC1 indicated that the relation between these PCs differed between diets ($P < 0.01$). For increased values of PC1, HE cows had increased values of PC2, whereas those fed CE showed decreased values of PC2. Inclusion of PCs in a logistic model revealed that high values of PC2 result in increased DTC (OR = 1.604, $P = 0.09$). In conclusion, PCs explained and predicted reproductive success in dairy cows. These 8 variables might be used to predict reproductive success.

Key Words: principal component, transition period, reproductive performance

T268 Plasma responses to intra-ruminal or post-ruminal administration of 2-hydroxy-4-methylthio-butanoic acid and its isopropyl ester in dairy cattle to evaluate rumen escape. G. I. Zanton,* S. E. Bettis, and M. Vazquez-Anon, *Novus International, Inc., St. Charles, MO.*

Two experiments were conducted to evaluate the rumen escape of methionine precursors. In experiment 1, 4 rumen cannulated, Holstein steers (718 ± 16 kg) were bolus dosed intra-ruminally (R) or post-ruminally via the omasal canal (O) with 80 mg of DL 2-hydroxy-4-methylthio-butanoic acid (HMTBa as MFP)/kg BW at the time of normal feed distribution. Treatments were administered during 2, 7 d periods according to a crossover design. Plasma samples were prepared from blood taken from the coxygeal vein at 0, 1.5, 3, 6, 9, 12, 18, 24, 30, 36, and 48 h after treatment administration. Plasma was analyzed for concentration of DL HMTBa. In experiment 2, the model developed in experiment 1 was used to compare the rumen escape of HMTBa provided as MFP to the isopropyl ester of HMTBa (HMBi). Eight rumen cannulated Holstein steers (548 ± 27 kg) were blocked by weight and randomly assigned to 4 treatment sequences according to a replicated 4 × 4 Latin square design. Treatment administration, sampling, and analysis were conducted as in experiment 1. Mean responses in area under the curve (AUC) were analyzed in the mixed procedure of SAS with significance declared at $P < 0.05$. In experiment 1, steers consumed 12.5 kg of DM or 1.7% of BW. Plasma HMTBa AUC was greater for O than for R (151 vs 73 ± 6 mg/L). By comparing the plasma HMTBa AUC for R relative to O, it was determined that MFP had a rumen escape of 49%. For experiment 2, DMI was 12.5 kg/d and 2.3% of BW and not affected by treatment or site of administration. Plasma HMTBa AUC was higher for HMBi (O: 169, R: 99 mg/L) than MFP (O: 135, R: 54 mg/L) at both sites; there was no interaction. By comparing the plasma HMTBa AUC for R relative to O for both sources, it was determined that HMBi had a rumen escape of 60% and MFP had a rumen escape of 41%.

Key Words: dairy, HMTBa, methionine

T269 Casein and fatty acid fractions in milk are affected by parity and nutritional regulated body condition score at the beginning of the transition period in dairy cows under grazing conditions. V. Artegoitia*[1,2], A. Meikle[2], L. Olazabal[3], J. P. Damian[2], M. L. Adrien[1], D. A. Mattiauda[1], J. Bermudez[1], A. Torre[3], and M. Carriquiry[1], *[1]Facultad de Agronomía, Universidad de la República Oriental del Uruguay, Montevideo, Uruguay, [2]Facultad de Veterinaria, Universidad de la República Oriental del Uruguay, Montevideo, Uruguay, [3]Laboratorio Tecnológico del Uruguay, Montevideo, Uruguay.*

The study objective was to evaluate the effect of BCS [high (H) vs. low (L)] at 30 d before calving (−30 d) on milk casein and fatty acid (FA) fractions in primiparous (P; PH, n = 13; PL, n = 9) and multiparous (M; MH, n = 9; ML, n = 8) Holstein cows fed under grazing conditions. Cows were offered different planes of nutrition of long-term pastures from −100 to −30 d pre-calving, to generate 0.5 BCS unit differences between groups at the end of the period. Milk samples were collected at wk 2 and 8 of lactation (WOL). Means were considered to differ when $P \leq 0.05$. Milk, protein, and fat yields and somatic cell counts (SCC) were greater in M than P cows, and milk protein and fat yields decreased from WOL 2 to 8 in all cows. Casein content was greater in M than P cows, decreased from WOL 2 to 8, and it was greater for MH cows than the other groups at WOL 2. Milk β-casein was less and κ-casein was greater in M than P cows, which could be due to a greater degradation of β-casein by plasmin activity associated to greater SCC in M cows' milk. The κ-casein was greater in PL than in PH cows, consistent with higher insulin concentrations in the former cows at the end of the treatment.

The de novo (4:0 to 15:1) and mixed origin (16:0 to 16:1) FA in milk fat increased, whereas preformed FA (≥17:0) decreased from WOL 2 to 8, associated with the early (WOL 2) lipid mobilization for milk synthesis. Mixed origin FA tended to be affected by BCS ($P = 0.10$), as they were greater for ML than MH cows. Saturated FA tended to be greater ($P = 0.06$) and MUFA were less in milk fat of M than P cows. Milk PUFA, particularly n-3 FA, were greater in H than L cows at WOL 2 for M cows and WOL 8 for P cows suggesting a greater dry matter intake in these cows. Milk CLA was greater in H than L cows and decreased from WOL 2 to 8 only in PL cows. Results indicate that casein and fatty acid fractions in milk are affected by parity and by BCS at the beginning of the transition period in dairy cows on grazing conditions.

Key Words: body reserves, milk composition

T270 Arterial amino acid concentrations drives milk yield in postpartum transition dairy cows.

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Previous studies based on splanchnic amino acid fluxes and milk protein output showed that dairy cows mobilize close to 5 kg of essential amino acids in the first month postpartum. The present study aimed at investigating the effects of alleviating the protein deficiency in postpartum transition dairy cows on mammary uptake of amino acids. Eight Holstein cows (second lactation) were used in a complete randomized design with repeated measurements at 4, 15, and 29 d in milk (DIM). At the calving day, cows were assigned to either continuous abomasal infusion of casein (CAS) or water (CTRL). All cows were fed the same diet. Abomasal casein infusion was profiled as 360 g/d at 1 DIM, 720 g/d at 2 DIM, followed by daily reductions of 19.5 g/d ending at 194 g/d at 29 DIM. Arterial and mammary venous blood sample sets were obtained bihourly at sampling days. Data was analyzed using PROC MIXED in SAS with treatment, DIM, and the interaction as fixed effects. Cow was considered as random effect, and DIM within cow as repeated measurement. Dry matter intake was unaffected ($P = 0.36$) by treatment. Milk yield increased more rapidly after calving with CAS ($P < 0.01$) and averaged 43.8 ± 1.0 kg/d with CAS and 36.6 ± 1.0 kg/d with CTRL. Milk protein yield with CAS was 1,664 ± 39 g/d at 4 DIM compared with 1,212 ± 86 g/d for CTRL, whereas milk protein yield did not differ at 29 DIM (1383 ± 48 g/d; interaction: $P = 0.02$). The calculated utilization of infused casein to milk protein was 64% at 4 DIM and 60% at 29 DIM. Arterial concentrations and mammary venous—arterial concentration differences for essential amino acids (EAA) were higher at 4 DIM with CAS as compared with CTRL, but did not differ at 29 DIM (interactions: $P = 0.02$ and $P = 0.03$, respectively). Mammary extraction rate of EAA was unaffected by CAS ($P = 0.37$) and DIM ($P = 0.58$). Circulating levels of insulin and IGF-1 were unaffected by CAS ($P = 72$ and $P = 36$, respectively). In conclusion, these results suggest that mammary uptake of amino acid is driven by arterial supply during initiation of lactation, thus, extra metabolizable amino acids supplied to postpartum transition cows are efficiently used for milk protein production.

Key Words: transition dairy cows, protein requirement, amino acids

T271 Productive performance of dairy cows fed with omega 3 and 6 fatty acids sources in the transition period and early lactation.

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The objective of this study was to evaluate the supplemental sources of omega 3 and 6 fatty acids and the effects in the milk yield and composition of dairy cows fed during the transition period and early lactation. Forty 8 Holstein cows were divided into 4 experimental groups in randomized design. The animals were randomly assigned to receive one of 4 treatments: 1) Control (C; n = 12), without fat sources in the pre and postpartum, 2) Flaxseed (FS; n = 12), in which cows were fed 60 and 80g/kg of DM of flaxseed in the pre and postpartum, respectively; 3) Whole raw soybeans (WS; n = 12), in which cows were fed 120 and 160g/kg of DM of whole raw soybeans in the pre and postpartum ; 4) Calcium salts of unsaturated fatty acid (CSFA; n = 12, Megalac-E), in which cows were fed 24 and 32g/kg of DM of calcium salts of unsaturated fatty acid in pre and postpartum. The experimental diets were fed since 35 d before the estimate calving, and provided until 84 d of lactation, formulated to meet the nutritional requirements of each period (pre and postpartum). Milk yield was measured daily and samples for milk composition were collected weekly from the first to the 12th week of lactation. Data were analyzed using PROC MIXED of SAS 9.1, with the effect of diet, time and interaction has fixed effects, and animal has random effect. The data were analyzed by orthogonal contrasts (C vs. WS+CSFA+FS; WS vs. CSFA; and FS vs WS+CSFA). There was no effect of the fatty acids sources on the milk yield, FCM, protein and lactose (kg/d and %). The average milk yield was 32.27 kg/d, where diets C, FA, WS and CSFA were (31.80, 31.43, 31.81 and 33.57 kg / d), respectively. There was effect of lipid sources for milk fat (kg /d and %) and in the contrast WS vs CSFA (3.52% vs. 2.88%); (1.09 kg/d vs 0.92 kg/d) respectively. The productive performance of dairy cows fed with omega 3 and 6 fatty acids sources in the transition period and early lactation was only affected in the milk fat yield and percent.

Key Words: fat sources, productive performance, transition period

T272 Effects of 18-carbon fatty acids on triacylglycerol accumulation in bovine mammary epithelial cells in vitro.

R. L. Cui, J. Q. Wang,* H. Y. Wei, D. P. Bu, X. M. Nan, H. Hu, 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 investigate the effects of concentration and ratio change of stearic acid, oleic acid, linoleic acid and linolenic acid on triacylglycerol (TG) accumulation in bovine mammary epithelial cells, and to reveal their contribution to TG accumulation when the four 18-carbon fatty acids (18-C FA) existed in medium simultaneously. Bovine mammary epithelial cells from a 3-year old lactating (ca. 100 DIM) Chinese Holstein dairy cow were incubated at 38°C in DMEM/F12 medium containing 1 g/L fatty acid-free bovine serum albumin (BSA), 5 mg/L prolactin, 5 mg/mL insulin, 5 mg/mL Holo-transferrin, 5 mg/mL progesterone, 10^{-7} mol/L hydrocortisone, 10 ng/mL bovine epithelial growth factor and 5 mg/mL bovine estradiol. An orthogonal L_{16} (4^5) test was performed in this experiment, and the concentrations of 18-C FAs were all 25, 50, 75 and 100 μM. TG contents in cells and medium were tested by Triglyceride Quantitation Kit after different combination performed for 24 h. In addition, every treatment had 3 replicates in this experiment, and ANOVA of SAS was used to analyze the experimental data. The results showed that stearic acid was the most important determinant of TG accumulation when the four 18-C FAs existed in medium simultaneously, and TG accumulation tended to increase as stearic acid concentration increased. The combination of 100 μM stearic acid, 100 μM oleic acid, 50 μM linoleic acid, 75 μM linolenic acid was the the optimal combination for increasing TG accumulation in our experiment. In conclusion, stearic acid was the most important determinant of TG accumulation when the four 18-C FAs were all available.

Key Words: bovine mammary epithelial cells, 18-carbon fatty acids, triacylglycerol

T273 Effects of 18-carbon fatty acids on cell proliferation and triacylglycerol accumulation in bovine mammary epithelial cells in vitro. R. L. Cui, J. Q. Wang,* H. Y. Wei, D. P. Bu, X. M. Nan, H. Hu, 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 investigate the effects of 18-carbon fatty acids (18-C FAs) on cell proliferation and triacylglycerol (TG) accumulation in bovine mammary epithelial cells in vitro. Bovine mammary epithelial cells from a 3-year old lactating (ca. 100 DIM) Chinese Holstein dairy cow were incubated at 38°C in DMEM/F12 medium containing 1g/L fatty acid-free bovine serum albumin (BSA), 5mg/L prolactin, 5 mg/mL insulin, 5 mg/mL holo-transferrin, 5 mg/mL progesterone, 10^{-7} mol/L hydrocortisone, 10 ng/mL bovine epithelial growth factor and 5 mg/mL bovine estradiol. Epithelial cells were cultured with different concentration of stearic acid, oleic acid, linoleic acid and linolenic acid for 24 h, separately, and the cells cultured without any fatty acids served as control. Then the MTT experiment was performed and the TG contents in medium were detected by Triglyceride Quantitation Kit. In addition, every treatment had 3 replicates in this experiment, and ANOVA of SAS was used to analyze the experimental data. In MTT experiment, the concentrations of 4 18-C FAs were all 0, 0.78, 1.56, 3.125, 6.25, 12.5, 25, 50, 100, 200, 400 μmol/L, and the results showed that the cell proliferation was inhibited significantly when the cell cultured with 200 or 400 μmol/L stearic acid, oleic acid, linoleic acid or linolenic acid ($P < 0.05$). According to MTT results, the concentrations of 4 18-C FAs were 0, 25, 50, 100 μmol/L for detecting TG contents, and the results showed that TG contents in medium were increased in a concentration-dependent manner from 0 to 100 μmol/L ($P < 0.05$). In conclusion, high concentration (200 or 400 μmol/L) of 18C-FAs can inhibit the cell proliferation, and TG accumulation can be increased as the concentration of 18-C FAs increase.

Key Words: bovine mammary epithelial cells, 18-carbon fatty acids, cell proliferation

T274 Lipopolysaccharide-induced alterations in milk fatty acid composition and mRNA expression of genes related to fatty acid metabolism. Y. D. Zhang, J. Q. Wang,* D. P. Bu, T. Hu, X. M. Nan, H. Hu, R. L. Cui, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Two experiments were conducted to evaluate the effect of lipopolysaccharide (LPS) on milk fat production and fatty acid composition. Eight multiparous Holstein cows (185 ± 30 DIM) received external pudic arterial administration of LPS (*E. coli* O111:B4) at 0.01 μg/kg BW in 10 mL of sterile saline (0.9% NaCl; treatment) or saline only (control) according to a crossover design. The experiment consisted of a 7-d preliminary period and 2 7-d treatment periods. Milk samples were collected at 0, 6, 12, and 24 h after LPS infusion on d 1 and twice daily from d 2 to 7. In the second experiment, the expression of genes for fatty acid metabolism in dairy cows was studied by incubating mammary epithelial cells with LPS at 0, 0.1, or 10 ng/mL for 24 h using RT-qRCR. All data were analyzed using the MIXED procedure of SAS (SAS Institute Inc., 2001, Cary, NC). In the in vivo study, milk yield ($P = 0.19$), milk fat concentration ($P = 0.34$), and milk fat yield ($P = 0.56$) were not affected with LPS infusion. LPS altered the milk fatty acid composition, resulting in an increase in the proportion of unsaturated fatty acids and short-chain fatty acids (<16:0) and a decrease in the proportion of saturated fatty acids and long-chain fatty acids (>16:0). In the in vitro experiment, LPS did not affect fatty acid-binding protein FABP3 or FABP4 mRNA expression ($P > 0.05$), but increased transporter CD36 mRNA expression ($P < 0.01$). Treatment with 0.1 ng/mL LPS increased fatty acid synthesis enzyme FASN, ACACA, ACSS2 and fatty acid metabolism gene PPARG, PPARGC1A mRNA expression ($P > 0.05$) compared with the control. Differential regulations of fatty acid synthesis enzyme FASN, ACACA, ACSS2 and fatty acid metabolism gene PPARG, PPARGC1A mRNA expression were observed with 10 ng/mL LPS. LPS alters fatty acid metabolism, functioning as an important factor affecting milk fat synthesis.

Key Words: fatty acids metabolic-related gene, LPS, milk fat composition

T275 Hepatic expression of GH-IGF axis genes in Holstein cows with different nutritional managements during early lactation. A. L. Astessiano*[1], P. Chilibroste[2], M. Fajardo[2], J. Laporta[1], J. Gil[2], D. A. Mattiauda[1], A. Meikle[3], and M. Carriquiry[1], *[1]1School of Agronomy, UDELAR, Montevideo, Uruguay, [2]2School of Veterinary Medicine, UDELAR, Paysandú (EEMAC), Uruguay, [3]3School of Veterinary Medicine, UDELAR, Montevideo, Uruguay.*

Multiparous cows (n = 25) were used in a randomized block design to study the effects of nutrition during the first 60 d postpartum (DPP) on endocrine profiles and hepatic gene expression. Cows were assigned to 3 treatments (TREAT): TMR) total mixed rations (30 kg DM/d offered; 45% forage, 55% concentrate); G1) 50% pasture in one (am) grazing session (7 h; pasture allowance = 15kg DM/d) + 50% TMR (15kg DM/d offered) and G2) 50% pasture in 2 (am/pm) grazing sessions (11h; pasture allowance = 15 kg DM/d) + 50% TMR (15 kg DM/d offered). Blood and liver biopsies were obtained at −40, −20, 10 and 55 DPP to quantify insulin and IGF-I, and mRNA expression of GH-IGF axis by real time PCR. Means from a repeated measures analysis differed when $P < 0.05$. Cow BCS decreased during the postpartum and at 55 DPP was greater in TMR than G1 and G2 cows. Milk energy output did not differ among TREAT (27.8, 26.4 and 23.4 ± 1.4 Mcal/d for TMR, G1 and G2). Serum IGF-I decreased from pre to postpartum and did not differ among TREAT while serum insulin decreased from pre to postpartum in G1 and G2 remaining stable in TMR cows. Hepatic GHR and IGFBP4 mRNA were not affected by TREAT or DPP. Expression of GHR1A mRNA decreased from −20 to 55 DPP while IGF-I mRNA tended ($P < 0.10$) to decrease from −20 to 10 DPP and to increase at 55 DPP. The IGFBP2 mRNA increased from −20 to 10 DPP but decreased thereafter at 55 DPP, being its abundance at 55 DPP less in TMR than G1 and G2 cows. In contrast, IGFBP3 mRNA tended ($P < 0.10$) to decrease from −20 to 10 DPP and increased at 55 DPP, being the decrease at 10 DPP more evident In G1 and G2 cows. The IGFBP1 mRNA increased from −20 to 55 DPP while IGFBP5 and IGFBP6 mRNA increased from −40 or −20 to 10 DPP and remained elevated at 55 DPP. However, IGFBP6 mRNA tended ($P = 0.06$) to be greater in G2 than TMR and P1 cows. Decreased serum IGF-I in early lactation was associated to decreased IGF-I mRNA and to changes in hepatic IGFBP synthesis which modulate bioavailability and stability of circulating IGF-I. Cows fed TMR showed a better metabolic status (greater BCS, serum insulin, IGBP3/IGBP2 mRNA ratio) during early lactation

Key Words: nutrition, transition cow, somatotropic axis

T276 New discovery on bovine glutathione peroxidase 3. H. R. Khazanehei,* P. Eck, and J. C. Plaizier, *University of Manitoba, Winnipeg, MB, Canada.*

Due to a high-energy demand for milk production, high-yielding dairy cows often experience a negative energy balance during early lactation. As a consequence, lipid is mobilized from adipose tissues and transported to the liver to provide energy through β-oxidation. This process produces reactive oxygen species (ROS), which can cause many disorders and cell damages. An experiment was conducted to assess the liver gene expression pattern before and after parturition and at the initiation of lactation. Liver biopsies were obtained at wk −3, 1 and 4 relative to parturition. Differential gene expression was assessed by affymetrix microarray analysis and FlexArray 1.6.1. An FDR-adjusted P lower than or equal to 0.1 and a fold-change greater than 2 were considered as a cut-off point to indicate significant up- or downregulation of genes. Gene networks were assembled using Ingenuity Pathway Analysis (IPA). The most overexpressed gene (5.08 fold change) at wk 1 was glutathione peroxidase 3 (GPX3). This indicates its non-redundant function in situations of metabolic and oxidative stress, where it detoxifies hydrogen peroxide. A further database query revealed that the bovine glutathione peroxidase 3 gene has not been characterized. Therefore we combined information from genetic databases (NCBI Gene Bank, UniGene, UCSC, ENSMBL) to hand curate and annotate the genetic locus and transcript variants, using assemblies in Sequencher 4.8. We identified 5 exons, and based on EST alignments exon 2 can be skipped in a minority of transcripts. This seems to be a bovine specific splice variant, since this event is not observed in other species alignments (http://genome.ucsc.edu/cgi-bin/hgTracks).

Key Words: dairy cow, gene expression, glutathione peroxidase 3

Ruminant Nutrition: Dairy: Feed Additives II

T277 Effect of post-ruminal supplementation of phytonutrients on total-tract digestibility, nitrogen losses, and milk production and composition in dairy cows. J. Oh*[1], A. N. Hristov[1], C. Lee[1], K. Heyler[1], T. Cassidy[1], and D. Bravo[2], *[1]The Pennsylvania State University, University Park, [2]Pancosma, Geneva, Switzerland.*

The objective of this experiment was to investigate the effects of post-ruminal supplementation of phytonutrients on ruminal fermentation, apparent total-tract digestibility of nutrients, N utilization, and milk production and composition in lactating dairy cows. Eight ruminally cannulated Holstein cows (232 ± 34.1 d in milk) were used in a replicated 4×4 Latin square design trial with 23-d periods. Treatments were: (1) control (CON), (2) 2 g/d curcuma oleoresin (CU), (3) 2 g/d garlic extract (GE), and (4) 2 g/d capsicum oleoresin (CA). The phytonutrients were dissolved in ethanol solution and pulse-dosed into the abomasum of the cows once daily, 2 h after feeding for 9 d during each experimental period. Control cows received ethanol solution only. Ruminal pH and ammonia and volatile fatty acid concentrations were not affected ($P =$ 0.40 to 0.97) by treatment. Apparent total tract digestibility of nutrients (dry and organic matter, crude protein, and fiber fractions) was similar ($P = 0.34$ to 0.91) among treatments. Total urinary-N, urinary urea-N, fecal-N, and total-N excretions were also not affected ($P = 0.22$ to 0.91) by treatment. Relative to CON, GE decreased ($P = 0.04$) dry matter intake (DMI, 21.2 vs. 19.9 kg/d, respectively). Milk yield was decreased ($P = 0.04$) with GE and CA compared with CON (35.8, 35.2 and 37.4 kg/d, respectively). Treatments did not affect milk composition and somatic cell count, 4% fat-corrected milk yield, and milk fat and true protein yields. In conclusion, post-ruminal supplementation of phytonutrients had no effect on ruminal fermentation, nutrient digestibility, N utilization, and milk composition in dairy cows. The decreased DMI with GE resulted in decreased milk yield and CA decreased milk yield without affecting DMI. The production effects from this trial have to be interpreted with caution due to the short duration of the treatment and milk data collection periods (9 and 6 d, respectively).

Key Words: phytonutrients, digestibility, dairy cow

T278 Effects of plant extracts on microbial population, methane emission and ruminal fermentation characteristics in in vitro. E. T. Kim*[1], K.-S. Min[2], C.-H. Kim[2], S. C. Kim[1], and S. S. Lee[1], *[1]Division of Applied Life Science (BK21 Program), Gyeongsang National University, Jinju, Gyeongsangnamdo, Republic of Korea, [2]Hankyong National University, Anseong, Gyeonggido, Republic of Korea.*

This study was conducted to evaluate effects of plant extracts on methanogenesis and rumen microbial diversity in in vitro. Plant extracts (*Artemisia princeps* var. *orientalis*; wormwood, *Allium sativum* for. *Pekinense*; garlic, *Allium cepa*; onion, *Zingiber officinale*; ginger, *Citrus unshiu*; mandarin orange, *Lonicera japonica*; honeysuckle) were obtained from Plant Extract Bank at Korea Research Institute of Bioscience and Biotechnology. The rumen fluid was collected before morning feeding from a fistulated Holstein cow fed timothy and commercial concentrate (TDN; 73.5%, crude protein; 19%, crude fat; 3%, crude fiber; 12%, crude ash; 10%, Ca; 0.8%, P; 1.2%) in the ratio of 3 to 2. The 30 mL of mixture, comprising McDougall buffer and rumen liquor in the ratio of 4 to 1, was dispensed anaerobically into serum bottles containing 0.3 g of timothy substrate and plant extracts (1% of total volume, respectively) filled with O_2-free N_2 gas and capped with a rubber stopper. The serum bottles were held in a shaking incubator at 39°C for 24 h. Total gas productions in all added plant extracts were higher ($P < 0.05$) than that of control, and that of ginger extract was highest ($P < 0.05$). The methane emission was highest ($P < 0.05$) at control, but lowest ($P < 0.05$) at garlic extract which was reduced about 20% of methane (40.2 vs. 32.5 mL/g DM). Other plant extracts were also led to decrease methane emission (wormwood; 8%, onion; 16%, ginger; 16.7%, mandarin orange; 12%, honeysuckle; 12.2%). Total VFAs concentration and pH were not influenced by the addition of plant extracts. Acetate to propionate ratios of garlic and ginger extracts were lower ($P < 0.05$, 3.36 and 3.38 vs. 3.53) than that of the control. Real-time PCR indicted that all plant extracts affected to the decrease of the ciliated-associated methanogen population, while the fibrolytic bacteria population was increased. In particular, *F. succinogens* community was increased by wormwood, garlic, mandarin orange and honeysuckle extracts, while *R. flavefaciens* population was inhibited by wormwood and garlic extracts, and *R. albus* diversity was influenced by mandarin orange and honeysuckle extracts.

Key Words: methanogenesis, plant extracts, real-time PCR

T279 Adding plant oils to dairy goat diets: Changes in milk fatty acids with sampling time. A. L. Martínez Marín[1], P. Gómez-Cortés[2], G. Gómez Castro[1], M. Juarez[2], L. M. Pérez Alba[1], M. Pérez Hernández[1], and M. A. de la Fuente*[2], *[1]Universidad de Córdoba, Córdoba, Spain, [2]Instituto de Investigación en Ciencias de la Alimentación, Madrid, Spain.*

Knowing the time at which the responses to dietary plant oil addition are clear in milk fat could shorten experimental periods and give clues on rumen and mammary metabolism of fatty acids (FA). Our aim was to find out changes in milk fat FA composition from 1 h to 21 d after introducing 3 differently unsaturated plant oils in dairy goat diets. Twelve midlactation multiparous goats were randomly allocated to one of 4 dietary treatments: Control (basal diet, no added oil) or the same basal diet added with 48 g/d of either high oleic sunflower oil, regular sunflower oil (RSO), or linseed oil (LO). Basal diet was made of alfalfa hay (0.33) and pelleted concentrate (0.67). Milk samples were taken at 0 (covariate), 1, 12, 24, 72, 120, 192, 312 and 504 h. Milkings at 0, 1 and 12 h were stripped out by hand after an intravenous dose of oxytocin. Analysis of fatty acid methyl esters (FAME) was performed by gas chromatography. MIXED procedure of SAS was used to analyze milk fat FA contents (g/100 g total FAME). Seventy 2 FA were identified and quantified in milk fat. The same differences between Control and oil treatments found at 504 h were also observed at 312 h in 12 chosen relevant FA, 5 sums of FA (saturated, mono- and polyunsaturated, total trans-18:1 and total conjugated linoleic acid) and linoleic to α-linolenic acid ratio. Both vaccenic (VA) and rumenic acid (RA) contents with LO treatment started showing differences with Control at 12 h (1.65 vs. 0.61; $P < 0.001$ and 0.60 vs. 0.30; $P < 0.001$). Between RSO and Control, differences of VA contents started at 12 h (1.87 vs. 0.69; $P = 0.016$) and that of RA at 24 h (0.79 vs. 0.36; $P = 0.048$). Content of α-linolenic acid with LO was different of Control at 1 h (0.18 vs. 0.13; $P = 0.019$); this difference increased at 12 h (0.34 vs. 0.13; $P < 0.0001$) and kept growing until 504 h (0.73 vs. 0.17; $P < 0.0001$). Reliable results of milk FA changes can be obtained at sampling times lower than 21 d and these modifications can help in the study of rumen and mammary metabolism of dietary FA.

Key Words: dairy goat, plant oil, fatty acid

T280 Supplementing rumen-protected Met and Lys in low protein diets based on corn distillers grains fed to lactating dairy cows.

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Feeding rumen-protected Met (RPM) and Lys (RPL) may allow feeding lower CP diets to dairy cows, thereby increasing N efficiency and reducing environmental impact. Moreover, RPL supplementation may improve the value of corn distillers dried grains plus solubles (DDGS) because its RUP is limiting in Lys. A trial tested experimental preparations of RPM and RPL that provided 15 g/d of DL-Met and 26 g/d of L-Lys. Forty lactating Holstein cows were blocked by DIM and parity into 8 squares in a replicated 5 × 5 Latin square trial with 5 dietary treatments: 1) low CP control (14.9% CP) without supplement, diet 1) top-dressed with 2) RPM, 3) RPL, 4) RPM + RPL, and 5) high CP control (16.8% CP) without supplement. As fed, all diets contained (DM basis): 31% alfalfa silage, 31% corn silage, 7.7% DDGS, 2.4% mineral-vitamin premix and 31% NDF. Diets 1–4 contained 25% corn grain plus 3.3% solvent soybean meal (SBM); diet 5 contained 21% corn grain, 1.9% solvent SBM, 3.6% expeller SBM, and 1.9% corn gluten meal. Periods were 3-wk (total 15 wk); data from wk-3 were analyzed using Proc Mixed in SAS. Contrasts and LS-means are reported in the table. Relative to the low CP control, feeding higher CP increased DMI and yield of milk and protein, but also increased MUN. No RPM main effect was observed; however, the RPM*RPL interaction for milk yield was significant because RPM increased milk 1.2 kg/d but milk was unaltered on RPM + RPL. Feeding RPL reduced ECM/DMI because numerically greater DMI had no effect on ECM yield. In this trial, feeding RPM, but not RPL, increased milk yield on low CP diets containing SBM plus DDGS.

Table 1.

CP, %:	14.9	14.9	14.9	14.9	16.8				
RPM, g/d:	0	15	0	15	0	Contrasts			
RPL, g/d:	0	0	26	26	0	CP	RPM	RPL	RPM*RPL
Variable									
DMI, kg/d	24.2	24.4	25.0	24.2	25.5	<0.01	0.34	0.29	0.08
Milk, kg/d	38.0	39.2	38.7	38.0	40.2	<0.01	0.58	0.54	0.05
Milk/DMI	1.60	1.65	1.59	1.60	1.61	0.58	0.12	0.16	0.28
ECM, kg/d	35.1	35.6	35.0	34.2	36.9	0.07	0.72	0.25	0.31
ECM/DMI	1.47	1.48	1.42	1.42	1.46	0.87	0.80	0.04	0.86
Fat, kg/d	1.41	1.41	1.39	1.34	1.46	0.22	0.53	0.14	0.42
Protein, kg/d	1.09	1.11	1.10	1.09	1.16	0.02	0.92	0.72	0.37
MUN, mg/dL	9.8	10.1	10.2	10.4	13.6	<0.01	0.29	0.07	0.78

Key Words: corn distillers dried grains, rumen-protected methionine, rumen-protected lysine

T281 Performance and diet digestibility of dairy cows supplemented with *Bacillus subtilis* spores.

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This experiment evaluated the supplementation of dairy cows with *B. subtilis*. Trial 1 used 18 Holsteins (246 DIM) in a crossover design, with 39-d periods, and a 10-d washout between periods. Treatments were orally dosed daily: 3x10^9 viable spores/d of *B. subtilis* C-3102 (Calpis Co. Ltda, Tokyo, Japan) or placebo. Cows were individually fed a TMR: 50% corn silage, 4.1% Tifton hay, 20.2% soybean meal, 11.2% high moisture corn, and 10.2% citrus pulp. Diet digestibility was evaluated by total collection of feces during d 33 to 35. The NDF digestibility was 52.6% of intake for *B. subtilis* and 55.8 for placebo ($P = 0.28$), OM digestibility was 72.1 and 72.6, respectively ($P = 0.69$). No treatment effect on digesta passage rate and chewing activity were detected ($P > 0.21$). Milk yield was 25.2 kg/d for placebo and 25.4 for *B. subtilis* ($P = 0.66$), DMI was 18.3 ($P = 0.91$). There was no treatment effect on milk solids and MUN ($P > 0.17$). Milk SCC was 97,000 cells/mL for *B. subtilis* and 99,000 for placebo ($P = 0.91$). Proportion of cows with positive *B. subtilis* culture in feces was 22% for placebo and 67% for *B. subtilis*. In trial 2, 30 cows (161 DIM) received the treatments for 16 weeks, in a covariate adjusted randomized block design. Milk samples were obtained weekly. Body weight and condition score were evaluated at 4-week intervals. The TMR contained 42.4% corn silage, 21.8% soybean meal, 15.6% ground corn, and 15.8% citrus pulp. Data was analyzed as repeated measures over time with Mixed of SAS. *B. subtilis* increased the daily secretions of milk (25.3 vs. 23.6 kg, $P = 0.02$) and protein (0.816 vs. 0.763 kg, $P = 0.01$), and had no effect on fat and lactose secretions ($P > 0.35$). The milk and protein yield response was consistent along the entire trial ($P > 0.90$ for the interaction of week and treatment). Milk SCC was 952,000 for *B. subtilis* and 747,000 for placebo ($P = 0.56$). *B. subtilis* tended to decrease MUN from 20.8mg/dL to 19.3 ($P = 0.06$). There was no treatment effect on body weight and condition score ($P > 0.33$). The supplementation of *B. subtilis* spores increased milk and protein yield when the trial was performed with high SCC cows, but the mechanism for the response was not elucidated.

Key Words: *Bacillus subtilis*, direct-fed microbial, probiotic

T282 Milk fatty acids composition of dairy ewes fed increasing levels of an unprotected CLA (UnCLA) supplement.

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This study aimed to evaluate the changes in milk fatty acids (FA) composition in ewes fed increasing doses of UnCLA (29.9% of trans-10, cis-12 CLA as methyl esters). Twenty-three primiparous Lacaune ewes with 40 ± 10 DIM, milk yield of 1.73 ± 0.26 kg/d and 52.1 ± 5.0 kg of BW were fed the following dietary treatments during 14d in an 28-d experimental period: Control (C): 30g of Megalac-E, n = 5; T10: 20g of Megalac-E plus 10g of UnCLA, n = 6; T20: 10g of Megalac-E plus 20g of UnCLA, n = 5 and T30: 30g of UnCLA; n = 7. The fat supplements were mixed into the concentrate (1.0 kg/d) and fed individually in 2 equal meals after a.m. and p.m. milkings. Ewes grazed paddocks of a tropical pasture as the only source of forage. Milk samples were collected on the 14th d of experimental period and analyzed for FA profile. Data were analyzed as a completely randomized design using the REG procedure of SAS. The desaturase indexes and the concentration of ≤C16 FA were linearly decreased, whereas the concentration of >C16, trans-10 C18:1 and the sum of trans-C18:1 FA was linearly increased as the CLA dose increased (Table 1). Moreover, treatments T10, T20 and T30 resulted in 191, 445 and 745% increases in milk trans-10, cis-12 CLA content and 131, 320 and 424% increases in trans-10, cis-12 CLA secretion into milk fat, respectively. The transfer efficiencies of trans-10, cis-12 CLA from diet into milk were 2.16, 1.97 and 1.63% (SE = 0.16; $P = 0.39$) for T10, T20 and T30, respectively. Incremental inclusion of UnCLA changed in a linear manner the milk fatty acid profile to a greater proportion of trans monounsaturated, longer chain fatty acids.

Table 1. Milk fatty acid responses to increasing levels of UnCLA

g/100 g FA	C	T10	T20	T30	SE	P^1
Summary						
<C16	32.0	29.3	26.3	27.9	0.69	0.018
C16 + C16:1	27.4	24.5	24.1	23.2	0.47	0.001
>C16	40.5	46.0	49.5	48.7	1.01	0.001
Desaturase Index						
14:1/14:0+14:1	0.010	0.008	0.008	0.006	0.001	0.001
16:1/16:0+16:1	0.025	0.025	0.022	0.020	0.001	0.017
18:1/18:0+18:1	0.559	0.532	0.501	0.473	0.010	0.001
CLA/18:1 t11+CLA	0.319	0.271	0.258	0.256	0.009	0.010

[1] Significance of linear responses. Quadratic responses were not significant ($P > 0.05$).

Key Words: CLA, dairy ewes, milk fatty acid composition

T283 Effect of monensin and tallow on methane estimation and protozoan and bacterial populations in dairy cows rumen.

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The objective was to evaluate the effect of monensin and/or tallow in the diet of lactating cows on the populations of protozoa and bacteria and the estimation of methane. The ruminants have a significant contribution to the greenhouse gases, due to the production of methane. Recent efforts have been made to explore the effect of different additives (monensin, tallow, etc) on rations and its effect on rumen's microbial populations responsible of methanogenesis. The basal diet was formulated in a ration F:C (Forage:Concentrate) of 40:60. The treatments were: The control diet without additive (T1), control diet plus monensin (3.3g/d, T2), control diet plus tallow (3.0%, T3) and control diet plus monensin and tallow (3.3 g/d, 3.0%, T4). The animals were fed 2 times daily (0800 and 1500 h) and milked twice a day (0400 and 1300 h). An experimental design of 4 × 4 Latin square were used. Samples were collected from 13 to 15 d. Quantification of protozoa, bacteria and VFA′s (to estimate the production of methane with the Wollin equation) were conducted. Data were analyzed using PROC MIXED of SAS; means comparison was made using orthogonal contrasts. Results showed that protozoan population exhibited changes upon the inclusion of different additives to rations ($P \leq 0.06$) among treatment, the combination of monensin and tallow resulted in the lowest protozoan population size ($P \leq 0.0001$) with an average of 5.49 ± 0.07 Log10. Bacteria population size did not change ($P \geq 0.83$) ; however, it was observed a reduce on the population size from 1.3 to 0.68 fluorescence unity (FU). Meanwhile, methane estimate was reduced ($P \leq 0.05$), from 57.3 ± 1.1 mmol/mL in the control diet (T1) to 53.2 ± 1.1, 55.4 ± 1.1 and 54.4 ± 1.1 mmol/mL in T2, T3 and T4, respectively. In conclusion, the most efficient additive to reduce methane production was monensin (3.3%).

Key Words: additives, ionophores, ruminal microorganisms

T284 Hepatic transcriptomics in dairy cows supplemented with SmartamineM or MetaSmart during the peripartal period.

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We used a newly-developed bioinformatics tool (Dynamic Impact Approach, DIA; M. Bionaz, P. Kathiravan, S. Rodriguez-Zas, W. Hurley, and J. Loor, PLoS One; http://dx.doi.org/10.1371/journal.pone.0032455) that allows visualizing the dynamic adaptations of biological pathways to evaluate the impact of Methionine (M) supplementation on liver transcriptome. Twenty 4 multiparous Holstein cows were fed a control diet (ME, n = 8; 1.47 Mcal/kg DM prepartum and 1.67 Mcal/kg DM postpartum), ME plus MetaSmart (MS, n = 8; Adisseo France S.A.S.), or ME plus Smartamine M (SA, n = 8; Adisseo France S.A.S.). All cows received a common diet (1.24 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. Percutaneous liver biopsies for microarrays using a 13,000-gene oligonucleotide microarray were performed at −10, 7, and 21 DIM. Analysis of variance with a false discovery rate (FDR) correction resulted in 2,664 differentially expressed genes (DEG) with a treatment × day (T × D) interaction (FDR <0.10, uncorrected $P = 0.02$). For the DIA analysis the whole data set with Entrez gene IDs, FDR, fold-change, and post-hoc P value between the 3 treatments at each time point were uploaded. A cut-off of FDR = 0.05 and p-value = 0.05 was applied during analysis. The greatest degree of change in terms of up- and downregulated DEG due to T × D occurred with MS vs. ME, e.g., more than half DEG were downregulated by MS at −10 but at 7 DIM ca. 500 DEG were downregulated and > 300 downregulated. The pattern at 21 DIM resembled closely that at −10 DIM. The DIA analysis revealed that MS vs. ME led to an inhibition of cyanoamino acid metabolism at −10, 7, and 21 DIM but it activated taurine/hypotaurine metabolism at 7 DIM. Another novel feature of MS vs. ME was the activation at 7 DIM of riboflavin and nicotinamide metabolism and pantothenate (CoA) biosynthesis. Analysis of DEG due to T × D within treatments revealed that carbohydrate metabolism was among the top-impacted pathways due to ME and SA particularly at 7 vs. −10 DIM when flux of gluconeogenesis and TCA cycle were markedly activated. In contrast to cows fed MS, both ME and SA led to marked activation of glutathione metabolism at 7 vs. −10 DIM. Overall, results from the bioinformatics analysis seem to suggest that the 2 sources of M elicit distinct effects on the liver transcriptome. Such adaptations might be of biological relevance in terms of liver function, dry matter intake, and optimal milk production.

Key Words: systems biology, pathway analysis, genomics

T285 Production response of lactating dairy cows in a confinement operation to a commercial probiotic.

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Thirty-six lactating Holstein cows from the Dairy Research Center at the University of Georgia -Tifton Campus were used in a 10 wk randomized design trial to determine the effects of feeding a commercial probiotic (ProDairy, Donaghys Industries Ltd., Christchurch, New Zealand) on dry matter intake, milk yield and milk composition of lactating Holstein cows. The probiotic is a blend of non-viable lactobacillus species and fermentation extracts including amino acids, vitamins, amylase, and cellulose. During the first 2 wk of the trial all cows were fed the control diet and data collected were uses as a covariate in the statistical analysis. At the end of wk 2, cows were assigned randomly to one of 2 treatments (control (CONT) or supplemental probiotic (PRO) for the following 8 wk. A basal diet was fed to cows once daily behind Calan gates as a TMR in amounts to provide at least 5% refusal. PRO was added to the TMR at a rate of 10 mL/cow/d and mixed for 10 min before feeding. There were no differences in DMI between treatments; 25.3 and 25.4 kg/d for CONT and PRO, respectively. Cows fed PRO have increased yield (kg/d) of milk ($P = 0.001$), protein ($P = 0.05$), and SNF ($P = 0.002$) compared with CONT; 32.7, 0.94 and 2.74 and 30.9, 0.91, and 2.58, respectively. Interactions of treatment and wk were observed for these variables because the difference between CONT and PRO increased throughout the 8 wk experimental period. No differences ($P > 0.10$) were observed among treatments in concentration of milk fat, protein, lactose, or SNF or yield of milk fat and lactose. Concentrations of MUN tended ($P = 0.10$) to be lower for PRO compared with CONT (15.03 and 15.44 mg/dl, respectively). No differences were observed in change of BW or body condition score. Results of this trial indicate that PRO stimulated improvements in nutrient utilization that supported higher yield of milk, protein and SNF.

Key Words: probiotic, milk yield, milk composition

T286 Evaluating in situ procedures for testing lipid encapsulated products — lysine as an example. T. F. Gressley*[1], M. J. de Veth[2], N. K. Diana[1], and E. Mackey[1], [1]*University of Delaware, Newark,* [2]*Balchem Corporation, New Hampton, NY.*

Standardized in situ methods for evaluating lipid encapsulated products have not been described. This study evaluated the effect of bag size and rinsing technique on in situ DM and Lys disappearance from 2 Lys products encapsulated using different technologies. Product A was a matrix type encapsulate (Italian manufacture) and product B was a core-shell encapsulate (US manufacture). Products were tested in 5 × 10 and 10 × 20 cm in situ bags with 50 µm pores (1 g and 5 g product/bag, respectively). Bags were placed without pre-wetting in the rumen of a lactating cow and incubated for 4 or 24 h, removed, and either hand or machine rinsed. Hand rinsed bags were individually rinsed in running tap water at 13°C for 90 s. Machine rinsed bags were rinsed in a front-loading washing machine using the cold water gentle cycle for 8 rinses of 1 min each. Rinsed bags were immediately dried at 50°C for 48 h. Unground subsamples from each bag were analyzed for N by combustion, and Lys content calculated as N × 5.22. Initial samples analyzed 29 and 52% Lys for products A and B, respectively. DM and Lys retention following in situ incubation were calculated as percent of initial sample. All combinations of product, bag size, time in the rumen, and rinsing technique were assessed in quadruplicate. For Lys retention, coefficients of variation (CV) averaged across all quadruplicates were 6.6% for 5 × 10 cm bags, 2.5% for 10 × 20 cm bags, 2.9% for hand rinsing, and 3.9% for machine rinsing. Both DM and Lys retention were affected by product, time, and product × time ($P < 0.001$). Product A retained 92% of DM and 85% of Lys at 4 h and 79% of DM and 50% of Lys at 24 h. Product B retained 95% of DM and 95% of Lys at 4 h and 89% of DM and 84% of Lys at 24 h. Lys retention was not impacted by bag size but was affected by rinsing technique ($P = 0.01$; 80% for hand rinsing vs. 77% for machine rinsing). This small difference may be due to greater microbial N retention in the hand rinsed bags or greater loss of product during machine rinsing. We recommend that in situ testing of rumen protected lipid encapsulated products use 10 × 20 cm bags and machine rinsing.

Key Words: encapsulate, rumen-protected lysine, in situ

T287 Effects of PEG and water on condensed tannin deactivation and nutrient digestibility of sainfoin in Holstein cows. H. Khalilvandi-Behroozyar*[1,2], M. Dehghan-Banadaky[1], K. Rezayazdi[1], and F. Ghaziani[1], [1]*Department of Animal Science, University of Tehran, Karaj, Tehran, Iran,* [2]*Department of Animal Science, University of Urmia, Urmia, West Azerbaijan, Iran.*

Antinutritional factors such as condensed tannins affect nutritive value of forages for ruminants. Antinutritional factors can decrease nutrient availability for ruminants through limitations in microbial digestion or reduced enzymatic activity in post ruminal sections of gastrointestinal tract. Sainfoin is a legume forage with medium to high tannin content. Sainfoin is high quality hay, but little information is available about effects of condensed tannins on nutrient availability of sainfoin. The objective of this study was to examine tannin deactivation effects on nutrient availability from sainfoin. Second cut forage was shade dried and chopped (3 to 5 cm length), and then exposed to nothing (Control) or 5% (wt/vol) solution of polyethylene glycol (PEG 6000 MW) that was sprayed on the forage (vol/wt ratio of 1:1). Water soaking was applied with tap water (vol/wt 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 d for adaptation and 7 d for rectal fecal and forage sample collection. Acid insoluble ash was used as internal marker for determining digestibility of nutrients. 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 MIXED PROC of SAS 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 ether extract, organic matter and acid detergent fiber were not statistically different ($P \leq 0.05$). Differences of means for neutral detergent fiber and CP digestibility among treatments were statistically significant. Tannin deactivation might be responsible for increasing digestibility of crude protein and plant cell wall.

Table 1. Effects of tannin deactivation with PEG and water on nutrient digestibility of sainfoin (g/100 g, CP %)

Treatment	EE	NDF	ADF	CP	OM
Control	72.16	49.25[b]	45.53	63.26[b]	60.41
Water	76.72	58.44[ab]	53.72	73.86[ab]	71.93
PEG	73.81	60.18[a]	51.55	75.42[a]	69.30
SEM	7.273	1.504	4.779	0.619	1.551

[a,b]Means within each column with different superscript letters are statistically different ($P \leq 0.05$).

Key Words: condensed tannin, digestibility, sainfoin

T288 Effect of dietary methionine supplementation in early lactation dairy cows I: dry matter intake, milk yield, milk composition and component yields. A. H. Souza*[1], P. D. Carvalho[1], A. R. Dresch[1], L. M. Vieira[1,2], K. S. Hackbart[1], D. Luchini[3], S. Bertics[1], N. Betzold[4], M. C. Wiltbank[1], and R. D. Shaver[1], [1]*University of Wisconsin-Madison, Madison,* [2]*University of Sao Paulo-VRA, SP 05508, Brazil,* [3]*Adisseo, Alpharetta, GA,* [4]*U.S. Dairy Forage Research Farm, Prairie du Sac, WI.*

Experimental objectives were to measure the effects of supplementing methionine during the postpartum period on lactation performance by dairy cows. Holstein cows (n = 72), were housed in a single pen from day −21 to calving and fed the same basal diet (6.68 Lys % MP, 2.24 Met %MP and 1.23 MCal/kg). From calving to 70 DIM cows were housed in tie-stalls and milked twice daily. Animals were blocked by parity and calving date and randomly assigned to 2 treatments differing in level of dietary methionine supplementation: 1) Methionine (MET); diet composed of (%DM) corn silage (39.7), alfalfa silage (21.8), HMSC (17.2), roasted soybeans (8.6), grass hay (4.6), canola meal (4.0), mineral-vitamin mix (2.7) and ProVAAL Ultra (w/Smartamine, 1.4), formulated to deliver 2875 g MP with 6.8 Lys %MP and 2.43 Met %MP; 2) Control (CON); cows fed the same basal diet but replacing ProVAAl Ultra by ProVAAL Advantage (no added Smartamine), formulated to deliver 2875 g MP with 6.8 Lys %MP and 1.89 Met %MP. Data were analyzed with repeated measures model (proc Mixed, SAS 9.3) including fixed effects of treatment, week and treatment by week interaction, parity as a covariate, and the random effect of cow. The DMI and milk yield measurements were daily and milk samples were collected from both AM/PM milkings twice weekly for determination of milk composition. Methionine supplementation increased ($P < 0.01$) milk protein% (2.92 vs. 2.75) and solids-not-fat (SNF) % (8.73 vs. 8.54). Intake of DM, milk yield, milk fat% and MUN were unaffected ($P > 0.10$). Interestingly, although milk protein yield was not different ($P = 0.11$) between the treatments, an interaction between methionine supplementation and milk production was detected ($P < 0.01$); with ~9% increase in milk protein yield for cows producing below 34 kg/d compared with ~3% increase in cows producing above this level starting at 2nd week of lactation. Dietary methionine supplementation increased milk protein and SNF% in milk in early lactation cows; however, milk protein yield response to methionine supplementation varied by production level. Supported by Adisseo, USDA Grant 2010-85122-20612.

Key Words: dairy cow, methionine, milk production

T289 Effect of dietary antioxidant and increased rumen unsaturated fatty acid load on milk fat yield and fatty acid composition.

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This study examined the impact of increasing rumen unsaturated fatty acid load (RUFAL) in the absence or presence of an antioxidant on feed intake, yield of milk and milk components, and milk fatty acids (FA). Twenty-eight Holstein cows (172 ± 59 DIM) were assigned to treatment in a randomized complete block design. Treatments were a control diet (CON) or an antioxidant (AOX; Agrado Ultra [dry blend of ethoxyquin and propyl gallate], Novus International, Inc.) supplemented diet (6.1 g/d). In period 1 (3 wks) no supplemental corn oil was fed; in periods 2, 3, and 4 (2 wks each) corn oil was supplemented at 0.75, 1.5, and 3.0% of the diet (DM basis) to incrementally increase RUFAL. Total dietary fatty acids were 2.7, 3.3, 3.9, and 5.1% of the diet for the 0.0, 0.75, 1.5, and 3.0% corn oil diets, respectively. The final 3 d of each period were used for sample and data collection. Data were analyzed using date as a repeated measure and preliminary 3.5% fat-corrected milk (FCM) as a covariate. There was no effect of AOX on any of the variables measured; thus data from AOX and CON were combined to assess the effects of dietary corn oil concentration (increasing RUFAL). Increased RUFAL decreased milk yield (44.3, 44.2, 43.0, and 38.4 kg/d, $P < 0.001$), fat concentration (3.38, 3.34, 3.10, and 2.43%, $P < 0.0001$), and fat yield (1.49, 1.46, 1.33, and 0.93 kg/d, $P < 0.001$). DMI decreased (30.2, 29.5, 28.2, and 27.8 kg/d, $P < 0.0001$) and there was a quadratic response for feed efficiency (FCM/DMI, 1.44, 1.46, 1.43, and 1.15, $P < 0.001$) with increased RUFAL. Milk FA concentration of C18:1 *t*10 was 0.84, 1.10, 1.92, and 6.29 g/100 g FA ($P < 0.001$) and for C18:2 *t*10, *c*12 was 0.001, 0.001, 0.007 and 0.030 g/100 g FA ($P < 0.001$) with increased RUFAL. On a FA yield basis, increasing RUFAL decreased < C16 FA (394, 376, 309, and 162 g/d, $P < 0.001$) and C16 FA (533, 477, 400, and 258 g/d, $P < 0.001$). There was a quadratic effect on > C16 FA (560, 609, 616, and 511 g/d, $P < 0.001$). Increasing RUFAL through the addition of corn oil to the diet decreased milk fat production and feed efficiency, and altered the FA composition of milk fat. Supplementation with AOX did not overcome the milk fat depression induced by increased RUFAL.

Key Words: milk fat depression, unsaturated fatty acids, antioxidants

T290 Effects of condensed tannins on ruminal VFA profile in fistulated Holstein cows fed sainfoin (*Onobrychis vicifolia*).

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Condensed tannins as antinutritional factors can limit different microbial actions in ruminants digestive tract. Sainfoin is a tanniferous forage with variable content of phenolic compounds. Our previous experiments using sainfoin showed that sainfoin condensed tannins are very active and limit ruminal protein and cell wall degradability, as shown incremental trend in forages treated for tannin deactivation. In previous experiments, treatment of sainfoin hay with water and polyethylene glycol (PEG) have major effects on deactivation of phenolic compounds and increased significantly ruminal cell wall and protein degradability, compared with alkaline chemicals (data not shown). The objective of this study was to examine effects of sainfoin treatment with water and PEG on ruminal VFA production and profile. Second-cut forage was shade dried and chopped (3 to 5 cm length), and then exposed to nothing (Control) or 5% (wt/vol) solution of polyethylene glycol (PEG 6000 MW) that was sprayed on the forage (vol/wt ratio of 1:1). Water soaking was applied with tap water (vol/wt 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 d for adaptation and 7 d for sample collection. Forages were fed as sole diet (0800 and 1600) along with mineral/vitamins to meet 110% of maintenance requirements of dairy cows. Rumen fluid was obtained in 2 consecutive days (d 15 and 16) from ventral rumen via vacuum pump at before feeding ($t = 0$) and 2, 4 and 8 h after morning meal. Rumen fluid instantly squeezed through 4 layer cheesecloth and preserved with 1 mL of 50% sulfuric acid and frozen at −20°C until analysis for VFA. Volatile fatty acids were determined using a Philips PU4410 apparatus. Peaks of individual fatty acids were determined according to pure standards and quantified. Methyl-4-valeric acid was used as internal standard. MIXED PROC of SAS 9.1 was used for statistical analysis at 0.05 probability level. Treatments were able to decrease condensed tannin up to 90 percent compared with control, but there were no statistical differences among dietary treatments. Total concentration of VFA increased until 4 h after feeding and then slightly decreased. Polyethylene glycol treated sainfoin was resulted in higher molar concentration of total VFA, compared with control and water treated forages in 4 and 8 h after feeding.

Table 1. Effects of sainfoin treatment with water and PEG on rumen VFA (percentage of total; total VFA represented as mM)

	PEG	Water	Control	SEM
Before feeding				
Acetate	81.76	79.80	80.18	0.571
Propionate	11.36	11.24	12.33	0.725
Total	64.93	47.40	54.50	7.499
2 h				
Acetate	77.07	75.64	75.01	2.07
Propionate	15.16	17.60	15.95	1.379
Total	88.90	86.63	102.23	8.711
4 h				
Acetate	78.23	77.20	78.64	1.041
Propionate	13.87	13.67	12.62	0.891
Total	103.83	89.73	91.76	11.885
8 h				
Acetate	79.64	79.37	80.80	0.156
Propionate	12.37	11.99	11.68	0.175
Total	94.60	85.25	80.75	4.888

Key Words: sainfoin, volatile fatty acids, condensed tannin

T291 Influence of ionophore source and a proprietary nutrition supplement on the performance and rumen metabolism of Holstein calves previously fed a high plane of milk replacer.

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Objective was to evaluate the effect of ionophore source with or without a proprietary nutrition package on performance and rumen metabolism in Holstein calves (3 mo old; initial BW = 101 kg) previously fed a high plane of milk replacer. In Exp. 1, 125 calves were randomly assigned to 5 treatments in 25 pens (5 calves/pen). Treatments were administered in a concentrate pellet and included: lasalocid without package (BOV-N), lasalocid with package (BOV-Y), monensin without package (RUM-N), monensin with package (RUM-Y), and High-forage control with monensin without package (HF). The respective pellet was restricted to a DMI of 4.1 kg/calf in BOV-N, BOV-Y, RUM-N, AND RUM-Y and 1.6 kg / calf in HF. Alfalfa hay was offered ad libitum. No differences ($P >$ 0.05) in DMI were reported among diets; however, metabolizable energy intake and ADG were less ($P < 0.05$) for calves fed the HF. Gain:feed was greater ($P < 0.05$) in HF diet compared with BOV-Y, RUM-N, RUM-Y; whereas BOV-N did not differ from all groups. In exp. 2, 10 cannulated calves were used to evaluate rumen metabolism. Calves were fed with same diets used in Exp. 1. Alfalfa DM digestibility (DMD) at 24 and 36 h was greatest ($P < 0.05$) in HF. In addition, alfalfa DMD at 36 h was greater ($P < 0.05$) for RUM-Y vs. BOV-Y and RUM-N, and tended to be greater ($P = 0.11$) than BOV-N. Pellet DMD at 24, 36, and 48 h was greatest ($P < 0.05$) for HF. In addition, pellet DMD at 24, 36, and 48 h for RUM-Y was greater ($P < 0.05$) and tended to be greater (P < 0.07) for BOV-N and BOV-Y, respectively. Ammonia concentration was greater ($P < 0.05$) for BOV-N than BOV-Y, RUM-N, and HF at 6 h. The use of ionophore and a proprietary nutrition package did not improve the performance of growing calves; however, as expected HF calves consumed less metabolizable energy and had lower ADG than calves fed the higher concentrate diets. Calves fed the high-forage diet had improved DMD of both the alfalfa hay and the concentrate pellet. In addition, among calves fed the higher concentrate diets, monensin plus the nutrition package had improved dry matter digestibility of both the alfalfa hay and pellet.

Key Words: ionophore, performance, rumen metabolism

T292 Effect of feeding *Bacillus subtilis* spores on performance of Holstein dairy calves.

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The objective was to determine effects of feeding *Bacillus subtilis* spores on performance of dairy calves in the first 60 d of age. Twenty Holstein female calves were allocated to a sequence of 2 treatments (*Bacillus subtilis* or placebo) in a completely randomized design. Treatments were: 0.3 g/calves/d (3×10^9 viable spores/cow/d) of *Bacillus subtilis* C-3102 (Calpis Co. Ltda, Tokyo, Japan) or placebo. The *Bacillus subtilis* spores were mixed with milk and fed directly to the calves. The animals were housed in individual hutches, with free access to water, starter feed (20% CP), and 8L of liquid diet (milk, 3 times a day) until weaning which occurred abruptly at the ninth week of life. The starter feed intake was recorded daily and body weight measurements were taken on d 0 and 60 of the comparison period. The initial weight was 37.8 kg for control and 35.5 for direct-fed microbial. Weaning weight was 77.55 kg for calves control and 81.6 kg for *Bacillus subtilis*, respectively. There was no treatment effect ($P > 0.05$) on DM of liquid or starter intake between the 2 groups. The average daily gain was 0.664 kg/d for placebo and 0.769 kg for *Bacillus subtilis* ($P = 0.25$), respectively. Feed conversion (ADG/DM intake) was 0.50 for placebo and 0.49 kg for *Bacillus subtilis* ($P =$ 0.99). The supplementation of *Bacillus subtilis* spores did not induce lower performance of dairy calves.

Key Words: *Bacillus subtilis* spores, dairy calves, performance

T293 Interaction between vitamin E and rumen-protected conjugated linoleic acid on milk composition in grazing dairy cows.

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The objective of this study was to evaluate the effect of supplementing protected conjugated linoleic acid (CLA) and vitamin E on the amount of milk fat from lactating grazing dairy cows. Eight milking Holstein cows were used in a rotational grazing system on a mixed pasture of lucerne (*Medicago sativa*) and orchard grass (*Dactylis glomerata*). They got 2 kg of concentrated during each milking (4 kg/d), which contained 5 g of protected CLA. Treatments were: T1) control (basal diet + CLA), T2) 4000 (control + 4000 IU of vitamin E), T3) 8000 (control + 8000 IU of vitamin E), and T4) 12000 (control + 12000 IU). Milk production was measured individually, and determination of milk fat, protein and lactose content were carried out by using an infrared milk analyzer. A crossover experimental design was used and the results were analyzed using the SAS MIXED procedure. There was no difference ($P \geq 0.05$) in milk production or protein and lactose content among treatments, which agrees with those results reported by other authors, who included similar amounts of vitamin E, when adding fat in the diet. Milk fat content was similar ($P \geq 0.05$) among treatments, however, it remained low (2.6%, on average), which, according with different authors, was due to the inclusion of fat on the diet. Thus, it is concluded that even using high doses of vitamin E in the diet of grazing milking cows, these amounts were insufficient to alleviate the milk fat decline when CLA are added to the diet, so it is indeed necessary more research to reverse this effect, because it is important to have milk with higher levels of CLA.

Key Words: CLA, dairy cattle, milk quality

T294 Assessment of lysine released from rumen-protected lysine products exposed to high and low moisture TMR over 24 hours. P. Ji,* C. S. Ballard, R. E. Clark, B. M. Sweeney, and C. Kokko, *William H. Miner Agricultural Research Institute, Chazy, NY.*

A study was conducted to evaluate the stability of 6 rumen-protected lysine products (RPL) when incorporated into TMR diets with different DM contents. Three loads (~350 kg/load) of each of 2 TMR diets only varying in DM content (40.5% as LD vs. 51.8% as HD) were prepared with Super Data Ranger. Duplicate Ziploc bags containing RPL (2 ± 0.03 g) and no RPL (as control samples) were filled and mixed well with 200 ± 1 g TMR from each load. Bags were stored at room temperature (21°C) for 0, 6, 18, and 24 h to simulate RPL exposure to TMR when mixed and delivered once per day. At the end of each time point, bag contents were transferred to strainer bags and soaked in 1 L Milli-Q water containing 500 mg Arg (as internal standard) for ~1 min to solubilize the Lys released in the TMR. Solution was filtered (0.45 μm) and frozen (−80°C) until filtrate was analyzed for Lys using ultra performance liquid chromatography. The Lys content for samples containing RPL were corrected for background Lys measured in control samples and Lys release (LR, %) was calculated. Data were analyzed as split-plot design with PROC MIXED of SAS. Results show that all RPL exhibited increased LR when exposed to TMR over time with differing magnitudes of LR ($P < 0.01$). The DM of TMR did not affect LR of most RPL; however, the overall LR of AminoShure-L was greater in TMR with LD than HD (5.9 and 3.0%, respectively; $P < 0.01$). A significant interaction of TMR DM and exposure time was observed for AminoShure-L and MetaboLys ($P < 0.01$). Our results indicate that less feeding frequency may result in greater Lys loss from RPL due to longer exposure in TMR before consumption by the cow.

Table 1. Lysine release (%) of RPL at 0, 6, 18, and 24 h in TMR

RPL product	0	6	18	24	SEM	*P*-value
AminoShure-L	0.2^{ax}	1.3^{ay}	6.4^{b}	9.8^{c}	0.47	≤ 0.01
LysiPEARL	6.2^{a}	39.7^{b}	47.0^{c}	48.4^{c}	1.66	≤ 0.01
Megamine-L	3.4^{a}	9.8^{b}	16.5^{c}	19.2^{d}	0.76	≤ 0.01
MetaboLys	0.7^{a}	0.8^{a}	2.2^{b}	3.8^{c}	0.25	≤ 0.01
USA Lysine	0.4^{a}	54.2^{b}	51.4^{b}	53.4^{b}	1.72	≤ 0.01
AjiPro-L	0.5^{a}	0.7^{a}	1.3^{b}	1.3^{b}	0.17	≤ 0.01

$^{a\text{–}d}P < 0.05$; $^{x,y}P < 0.10$.

Key Words: rumen-protected Lys, TMR, lysine

T295 Does mechanical mixing of TMR compromise protection efficacy of rumen-protected lysine products? P. Ji,* C. S. Ballard, R. E. Clark, B. M. Sweeney, and C. Kokko, *William H. Miner Agricultural Research Institute, Chazy, NY.*

A study was conducted to determine if mechanical mixing of TMR compromises the ruminal protection efficacy of 6 rumen-protected Lys products (RPL). A Super Data Ranger (SDR) loaded with 350 kg of TMR formulated for high producing cows was used to simulate the routine mixing procedure on a dairy farm. Dacron bags were filled with 1 ± 0.03 g RPL and heat-sealed. Triplicate bags per in situ time point were either mixed with diet for 6 min at full speed in SDR as treatment or indwelled in a bucket of same TMR diet for 6 min as control. Three loads of mixing were performed. After mixing, bags were incubated in the rumen of 3 cannulated cows for 0, 6, 12, and 24 h, one mixing load (control and treatment) per cow. After incubation, bags were gently hand-washed and paper-patted, then air-dried for more than 24 h. Dried RPL residue collected from each bag was acid hydrolyzed with 3 N HCl at 90°C in oven for 60 min and brought to a 100 mL volume with 0.2 mol/L HCl buffer. The solution was filtered and the concentration of Lys was determined by ultra performance liquid chromatography for calculation of ruminal disappearance of Lys (RD, %). Data for each RPL were analyzed separately as a randomized complete block design with MIXED procedure of SAS. The results showed that mechanical mixing increased RD ($P < 0.05$) of LysiPEARL (68.5 vs. 74.7%), MetaboLys (15.0 vs. 17.1%), and USA Lysine (72.2 vs. 75.9%), and tended to increase RD of Megamine-L (51.2 vs. 52.9%; $P = 0.06$), but did not affect that of AminoShure-L (30.6 vs. 33.0%; $P = 0.12$), and AjiPro-L (13.0 vs. 13.1%; $P = 0.92$). Length of ruminal incubation significantly increased RD of all RPL with varying magnitudes ($P < 0.01$). All RPL except AminoShure-L exhibited a significant interaction between mixing treatment and length of ruminal incubation ($P < 0.05$). In conclusion, some RPL are more vulnerable than others to damage caused by mechanically mixing in a TMR that compromises their ruminal protection. However, due to different shape and particle size of RPL, the specific gravity and ruminal passage rate may vary and should be considered when comparing potential ruminal Lys loss of RPL.

Key Words: rumen-protected Lys, mechanical mixing

T296 Ionophore source in a calf starter influences the performance of calves during the immediate post-weaned period. C. J. Cobb*[1], B. S. Obeidat[1], D. L. Hanson[1], M. D. Sellers[1], B. L. Miller[2], J. A. Davidson[2], K. L. Perfield[3], and M. A. Ballou[1], *[1]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [2]Land O' Lakes Purina Feed, Gray Summit, MO, [3]Elanco, Greenfield, IN.*

Objective was to determine if the source of ionophore (monensin vs. lasalocid) in a calf starter influences the performance of calves during the first 3 mo of life. One hundred and 21 Holstein calves (2 ± 1 d old) were randomized to 1 of 2 treatments: Calf starter supplemented with 50 g / ton of monensin (n = 60) or 50 g / ton of lasalocid (n = 58). The ingredient composition of the 2 calf starters were identical and contained 22% crude protein on dry matter (DM) basis. The starter was offered ad libitum after the first week of life. All calves were fed a similar high plane of milk replacer nutrition before weaning. Weaning was initiated during the 7th wk by removing the PM feeding and calves were completely weaned when consuming 800 g DM daily after d 53. Body weights were measured at d 0, 10, 21, 53, 67, and 91. Peripheral blood samples were collected at d 3, 10, 21, 45, 47, 53, and 91 and analyzed for plasma concentrations of glucose, urea nitrogen, and haptoglobin. There was a treatment × time interaction ($P < 0.01$) on starter DM intake; whereas calves fed lasalocid consumed more starter DM during the post-weaning period, from wk 8 to 13 (average of 9.1% increase in starter DM intake among lasalocid). In addition, average daily gains of calves fed lasalocid were greater ($P < 0.05$) during the immediate post-weaned period from d 53 to 67 (0.903 vs. 0.822 ± 0.0259 kg/d). There were no treatment differences in average daily gains ($P > 0.271$) at any other periods. There was no treatment ($P = 0.189$) or treatment × time interaction ($P = 0.617$) on the efficiency of feed utilized for body weight gain. Last, there were no treatment ($P > 0.346$) or treatment × time interactions ($P > 0.339$) on the plasma concentrations of glucose, urea nitrogen, or haptoglobin. Feeding a calf starter with lasalocid increased starter intake over the entire post-weaning period and increased average daily gains, but only during the immediate post-weaning period.

Key Words: calf starter, ionophore, performance

T297 Effects of microbial additives on nutrient metabolism in continuous culture of rumen contents. W. Braman* and L. C. Solórzano, *Chr. Hansen Inc., Milwaukee, WI.*

Reports indicate that microbial additives based on multiple strains of *E. faecium* show positive responses in ruminal fiber and nitrogen metabolism both, in vitro and in vivo. A study was conducted to determine the effects of microbial additives on nutrient metabolism in continuous culture of rumen content when the diet contained 28% starch. Lactation rations were formulated to support 45.5 kg of milk production. The study was comprised of 5 treatments: Control Diet, Control Diet + 3 strains of *E. faecium* + yeast (T1), Control Diet + 2 strains of *E. faecium* + 1 strain of *Lactococcus lactis* (T2), Control Diet + 2 strains of *E. faecium* + yeast (T3); Control Diet + 3 strains of *E. faecium*, + 1 strain of *Lactococcus lactis* + yeast (T4), Control Diet + 2 strains of encapsulated *E. faecium* + Lactococcus lactis (T5) and Control Diet + *Lactobacillus plantarum* (T6). All treatments were added at 2 g/head/day equivalent. Continuous culture fermentations were conducted using conditions simulating rumen parameters of a lactating dairy cow. These conditions were: liquid dilution rate of 13%/h, solids dilution rate of 4.55%/h, solids retention time of 22 h, feed intake 100 g DM/d, a feeding frequency of 25 g DM, 4 times daily at 6 h intervals, a fermentation temperature of 39°C. Culture pH was recorded at 0.5 h intervals. Each diet was fermented in triplicate 9-d fermentations, with effluent samples composited for analysis during the last 3 d. Parameters analyzed included: DM, OM, CP, ADF, NDF, NSC, VFAs, nitrogen partitioning, microbial growth and microbial efficiency. Data were analyzed using the General Linear Model Procedures of SAS. A Duncan's Multiple Range Test at the 5% level of probability was used to detect differences among treatments. There were no differences from the control in the digestibility of OM ($P > 0.33$), CP ($P > 0.35$), NDF ($P > 0.81$), ADF ($P > 0.33$) and NSC ($P > 0.33$) for any of the treatments. There was a numerical ($P < 0.14$) increase in DM digestion compared with the control (67.7%) for treatments T2 (71.9%), T4 (73.8) and T6 (69.8%). Compared with that of the control (0.064), the production of butyrate (moles/d) was suppressed ($P < 0.01$) by treatments T2 (0.054), T3 (0.053), 4T (0.045) and T6 (0.049). This resulted in lower ($P < 0.01$) molar proportions of butyrate in these treatments as well. There were no differences due to the treatments for the partition of N ($P > 0.31$), microbial growth ($P > 0.19$) and microbial efficiency measurements ($P > 0.31$). The microbial parameters results from this experiment are not in agreement with previously published studies. Microbial additives reduced the production and molar proportions of butyrate and numerically increased the digestibility of DM.

Key Words: digestion, microbial additives, rumen culture

T298 Immunometabolic indices in dairy cows supplemented with Smartamine M or MetaSmart during the peripartal period. J. S. Osorio*[1], E. Trevisi[2], P. Ji[1], D. Luchini[3], J. K. Drackley[1], G. Bertoni[2], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Universita Cattolica del Sacro Cuore, Piacenza, Italy, [3]Adisseo, Alpharetta, GA.*

The early postpartal period is characterized by marked changes in hormonal, metabolic, and immune/stress-like conditions all of which may contribute to regulating dry matter intake (DMI) and the supply of nutrients to mammary gland. Peripartal cows are in negative methionine (M) balance due to increased requirements of tissues and cells for methylated compounds and M for milk protein production. Therefore, supplementation of rumen-protected M during the peripartal period may improve yield of milk and protein, and also help coordinate immunometabolic adaptations of the cow. Twenty-four multiparous Holstein cows were fed a control diet (ME, n = 8; 1.47 Mcal/kg DM prepartum and 1.67 Mcal/kg DM postpartum), ME plus MetaSmart (MS, n = 8; Adisseo France S.A.S.), or ME plus Smartamine M (SA, n = 8; Adisseo France S.A.S.). All cows received a common diet (1.24 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 −21, −10, 7, 14, and 21 DIM for profiling of 21 markers of liver function, metabolism, oxidative stress, and inflammation. Concentration of cholesterol (CHOL) and the negative acute-phase protein albumin (ALB) decreased (time $P < 0.05$) around calving but increased by 21 DIM regardless of treatment. Paraoxonase concentration followed a similar pattern (time $P < 0.01$) as CHOL and ALB. Whereas glutamic-oxaloacetic transaminase (GOT) concentration increased (time $P < 0.01$) from −10 through 21 DIM regardless of treatment, bilirubin (BIL) increased between −10 and 7 DIM and then decreased through 21 DIM. However, the increase in BIL tended (treatment × time $P = 0.09$) to be lower in cows fed SA. Those responses were indicative of alterations in liver function particularly after calving. The concentration of haptoglobin, inflammation marker, did not change markedly at 7 vs. −21 or −10 DIM and decreased gradually by 21 DIM regardless of treatment. However, cows fed ME tended ($P = 0.09$) to have greater overall ceruloplasmin concentration due to markedly greater (treatment × time $P = 0.03$) concentration at −10 DIM. That response was suggestive of a more pronounced inflammatory-like status precalving. Despite an increase (time $P < 0.01$) in concentration after calving, reactive-oxygen metabolite concentration did not differ between treatments. Overall, preliminary data provide some evidence that M supplementation during the peripartal period could ameliorate inflammatory-like conditions characteristic of this period. As such, M may play a role in stimulating DMI after calving and promoting normal milk production.

Key Words: methionine, oxidative stress

T299 Ruminal biohydrogenation and abomasal fatty acid flow in dairy cows fed with fatty acids unsaturated sources. J. E. Freitas Jr.*[1], R. V. Barletta[1], K. Havartine[2], S. L. D. A. Robassini[1], M. D. S. Oliveira[3], B. C. Venturelli[1], E. F. Jesus[1], F. G. Vilela[1], G. D. Calomeni[1], J. R. Gandra[1], T. S. Canaes[1], and F. P. Rennó[1], *[1]University of São Paulo, Pirassunumga, SP, Brazil, [2]Penn State University, University Park, [3]State University Julio de Mesquita, Jaboticabal, SP, Brazil.*

The aim of this study was to evaluate ruminal biohydrogenation and abomasal fatty acids flow in dairy cows supplemented with unsaturated fatty acids sources. Eight Holstein cows in the mid lactation (80 ± 20 d in milk; mean ± SD) cannulated in the rumen and abomasum (580 ± 20 kg of weight; mean ± SD) with milk yield of 25 kg/d were assigned randomly into 2 4 × 4 Latin squares and fed the following diets: 1) control (C); 2) refined soybean oil (inclusion of 3% in the total dry matter); (SO); 3) whole soybean raw (WS) (inclusion of 16% in the total dry matter) and; 4) calcium salts of unsaturated fatty acids (CSFA) (inclusion of 3% in the total dry matter). Milk yield and the dry matter intake were measured daily throughout the experimental period. The marker NDFi was used to determine the abomasal dry matter flow. Ruminal contents were evacuated manually through the ruminal cannula at 4.5 h after feeding on d 20, and at 2.5 h before feeding on d 21 of each period. Fractional rates of fatty acids biohydrogenation and passage by the rumen were calculated utilizing the model that accounts for transfer of fatty acids among ruminal pools. Data were analyzed using PROC MIXED of SAS 9.1 according with the orthogonal contrasts (C vs SO + WS + CSFA); (SO vs WS + CSFA) and (WS vs CSFA). The diet with SO increased the biohydrogenation rate to the C18:2 in relation the WS and CSFA diets ($P \leq 0.05$) (93.71 vs 86.35; 82.34% respectively). There was tendency to decrease of the biohydrogenation rate of fatty acid C18:3 by contrast 2 (93.18 vs 86.49; 80.36%; $P \leq 0.06$). The cows fed CSFA showed 29.46% more C18:3 in the abomasal fatty acid flow in relation the cows fed with WS diet (5.60 vs 3.95 g/d). The use of whole soybeans raw and calcium salts of unsaturated fatty acids decrease ruminal biohydrogenation rate in dairy cows in the mid lactation.

Key Words: abomasum, linoleic acid, whole soybeans

T300 Evaluation of models ruminal biohydrogenation in dairy cows fed unsaturated fatty acids sources. J. E. Freitas Jr.*[1], R. V. Barletta[1], K. Harvatine[2], V. P. Bettero[1], M. D. S. Oliveira[3], B. C. Venturelli[1], R. Gardinal[1], J. R. Gandra[1], C. E. Araújo[1], F. G. Vilela[1], V. G. C. Lacuna[1], and F. P. Rennó[1], [1]*University of São Paulo, Pirassununga, SP, Brazil,* [2]*Pennsylvania State University, University Park,* [3]*State University Julio of Mesquita, Jaboticabal, SP, Brazil.*

The aim of this study was to evaluate 2 models ruminal biohydrogenation in dairy cows fed unsaturated fatty acids sources. Eight Holstein cows in the mid lactation (80 ± 20 d in milk; mean ± SD) cannulated in the rumen and abomasums (580 ± 20 kg of weight; mean ± SD) with milk yield of 25 kg/d were assigned randomly into two 4 × 4 Latin squares, fed following diets: 1) control (C) (inclusion of 2.66% of fatty acids); 2) refined soybean oil (inclusion of 5.14% of fatty acids) (SO); 3) whole soybean raw (WS) (inclusion of 5.00% of fatty acids) and; 4) calcium salts of unsaturated fatty acids (CSFA) inclusion of 5.10% of fatty acids). Corn silage was used as roughage in 50% of the total dry matter). Two models were used to calculate the rate biohydrogenation: Model A): calculated by disappearance rate using abomasal fatty acids flow, and fatty acids intake and; Model B): calculated by ruminal turnover, fractional passage rate and fractional biohydrogenation rate and ruminal pool for each fatty acid. The marker NDFi was used to determine the abomasal dry matter flow. Ruminal contents were evacuated manually through the ruminal cannula at 4.5 h after feeding on d 20, and at 2.5 h before feeding on d 21 of each period. Data were analyzed using PROC MIXED of SAS 9.1 according with the orthogonal contrasts (C vs SO+WS+CSFA); (SO vs WS+CSFA) and (WS vs CSFA). The mean biohydrogenation rate (C18:2) to the model A was 88.58% and to model B 81.95% including all diets. The diets with lipids sources showed greater biohydrogenation rate of the linolenic acid in relation to control diet by model A ($P \leq 0.05$) (76.31 vs 80.01%). Model B caused tendency ($P \leq 0.09$) to decrease biohydrogenation rate of linolenic acid when compared with SO and CSFA diets (88.45 vs 77.5%). Diet WS decreased the biohydrogenation of C18:2 in 16.68% and 5.09% in relation to SO diet. Model B results in higher rates of BHB compared with model A. However, lower rates of ruminal biohydrogenation can occur due to methodological errors.

Key Words: mid lactation, passage rate, whole soybeans

Ruminant Nutrition: Feeds

T301 Evaluating the mineral composition of *Vernonia amygdalina* leaf.

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An experiment was conducted to determine the mineral composition of *Vernonia amygdalina* (Va). The atomic absorption spectrophotometer was used to determine any of the minerals (except P) using appropriate lamps. The P was determined with vanadomolybdate using spectrophotometer at 425nm.The principal elements present in Va are Ca, P, K, Na and Mg while the essential trace elements (macro nutrients) are Fe, Mn, Cu and Zn. The Va contained Ca 0.46%, P 0.13%, K 1.21%, Na 0.53%, Mg 0.27%, Fe 468.2mg/g, Cu 26.2mg/g, Zn 580.5mg/g. The high level of minerals found in Va was due to the high ash content recorded. Mineral assayed in this study in order of abundance was K 1.21%, Zn 0.58%, Na 0.53%, Ca 0.46%, Mg 0.27%, P 0.13%, Fe 468.2mg/g, Cu 26.2mg/g. Normally, plant materials are not good sources of Ca and P but the high levels reported in Va would easily satisfy animal needs if they occur in a readily available form. It is often postulated that a mineral supply in excess of dietary requirements is capable of blocking the availability of another. The result of mineral analysis on *Vernonia amygdalina* showed that the leaf contains high levels of micro and macro elements, which is an indication that the productivity of ruminant animals is sustainable.

Key Words: mineral composition, *Vernonia amygdalina* leaf

T302 Determination of the nutritional value of some perennial forage species for ruminants.

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Ruminal OM and CP degradability of cardoon (*Cynara cardunculus* L.; CY), switchgrass (*Panicum virgatum* L.; SW) and immature cereals (IC) were studied with in sacco technique. Two mid-lactating (185 d in milk) and ruminally cannulated Holstein cows were used and fed a TMR (22 kg/d DMI) composed on a DM basis by 63.3% corn silage, 17.4% soybean meal and 19.2% wheat during a 25-d experimental period (21 d of diet adaptation, 4 d of measurements). Ruminal degradation rate of OM and CP was estimated as percent OM (DgOM) and CP degradability (DgCP) from polyester bags incubated in rumen for 2, 4, 8, 16, 24, 48, and 72h. Data were fitted to the nonlinear regression equation: $Dg(t) = a + b(1 - e^{-ct})$ where Dg is percentage disappearance of OM or CP at time t, *a* the soluble fraction and *b* the less rapidly degradable fraction which disappears at the constant fractional rate *c* per time t. Intestinal digestibility of CP was estimated using the in vitro procedure of Calsamiglia and Stern (1995). Switchgrass had numerically greater crude cellulose (41.1% of DM) and lower CP (5% of DM) contents than the other forage sources. Cynara and SW had a low soluble CP fraction (13.9 and 18.6%). The potentially degradable CP fraction was numerically greater and the rate of degradation numerically lower for CY (66.3% and 3.7% h^{-1}) compared with SW and IC (respectively, 21.6% and 5.0% h^{-1}; 33.3% and 5.5% h^{-1}). Effective degradability of CP followed the order IC > CY > SW. Intestinal digestibility of CP was 19% for CY and SW, and 37% for IC. The PDIN and PDIE contents (g/kg DM) were respectively: 23 and 67 for CY, 22 and 45 for SW, and 51 and 70 for IC. Compared with IC and SW, CY exhibited a high estimated energy NE_L value (Mcal/kg DM): 1.77 *vs* 0.90 and 1.03. Immature cereals offer a better nutritional value than CY and SW.

Key Words: nutritional value, perennial forages, ruminal degradability

T303 Dry matter changes in corn silage with rain.

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Dry matter (DM) is the most important nutrient analysis because changes in DM effect total quantity of nutrients supplied in a ration. Since forages have the most variability associated with their DM content, forage DM is measured weekly and new values are entered into feed management software to correct weighing of forages in the ration. The purpose of this research is to determine how much forage (corn silage) DM changes with weather and how it affects ration DM. Corn silage and ration were sampled twice a day at feeding for 5 d and DM was measured according to AOAC methods using a forced-air drying oven at 100°C for 24 h. Corn silage DM was also measured using HarvestLab (near infrared reflectance stationary desktop model, John Deere). Corn silage on average accounted for 55% of the ration on an as fed basis and was correlated with ration DM ($P < 0.05$) with an R2 = 0.52 when ration DM regressed on corn silage DM. Rain (approximately 1 inch) occurred on the afternoon of the second sampling day and resulted in decreases of 3.6% corn silage DM and 6.6% in ration DM (AOAC method) and in a decrease of 2.28% corn silage DM (HarvestLab). By the next feeding, corn silage DM had increased back to pre-rain levels (34.3% vs. 33.9%). Corn silage DM was the primary source of moisture in the ration and rain caused a short-term decrease in ration DM because in a storm of short duration, most exposed silage was fed at the next feeding. Therefore it would be beneficial to adjust corn silage DM in the short-term according to rain events. Currently, feed management software does not allow storage of alternate DM settings that could be used for rain exposure. To determine how much DM should be adjusted for degree and duration of rain and predictability of DM using HarvestLab, more data are needed.

Key Words: dry matter, corn silage

T304 Canola meals from different production plants differ in ruminal protein degradability.

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Lactation trials have shown that production and N-efficiency were improved when dietary soybean meal was replaced with equal CP from canola meal. Three or 4 canola meal samples were collected from each of 12 Canadian production plants (total = 37) and analyzed for differences in chemical composition and in vitro and in situ ruminal protein degradability. In situ incubations were conducted at 0 and 12 h only and estimated rates used to compute rumen-undegraded protein (RUP) assuming first-order degradation and a ruminal passage rate of 0.06/h. The Michaelis-Menten inhibitor in vitro (MMIIV) method was used as described by Colombini et al. (J. Dairy Sci., 94:1967–1977, 2011) to quantify degradation rates and RUP, assuming passage rates of 0.16/h and 0.06 for the soluble and insoluble protein fractions. Differences among plants were assessed using GLM in SAS; LSD-separated means are in the table. Although fraction B3 (NDIN – ADIN) was unaffected, there were differences among plants in CP and NDF contents of canola meals produced. There also were differences among plants in RUP estimated by MMIIV: the only expeller meal had the highest RUP (47.4%),

but meals from 4 other plants had similar RUP values (43.0–46.3%). The RUP estimates from the other 7 meals were lower, including 4 that were different from the 4 meals with the highest RUP values. Estimates of RUP made using in situ methods tended to rank the meals differently from the MMIIV assay. Results indicated that, depending on the plant of origin, canola meal RUP may range from 37 to 47%, a difference greater than 25%.

Table 1.

Plant	Process	CP, % DM	NDF, % DM	B3, % CP	MMIIV RUP, % CP	In situ RUP, % CP
1	S	43.7^{a}	23.8^{de}	8.1	37.0^{c}	50.5^{d}
2	S	41.4^{c}	28.2^{ab}	21.1	40.0^{bc}	65.9^{ab}
3	S	41.5^{c}	24.9^{cd}	18.2	46.3^{ab}	67.7^{a}
4	S	43.8^{a}	23.4^{de}	12.4	39.6^{bc}	55.3^{cd}
5	S	41.8^{c}	25.4^{cd}	8.2	45.0^{ab}	58.9^{bc}
6	S	43.0^{ab}	25.9^{c}	14.6	45.9^{ab}	60.7^{abc}
7	S	39.9^{d}	25.4^{cd}	9.4	36.7^{c}	56.6^{cd}
8	S	42.3^{bc}	26.9^{bc}	16.2	38.1^{c}	61.2^{abc}
9	S	41.2^{c}	29.7^{a}	23.8	43.0^{abc}	59.7^{abc}
10	S	43.7^{a}	22.7^{e}	8.8	36.6^{c}	57.8^{bcd}
11	S	41.4^{c}	25.2^{cd}	9.1	40.7^{bc}	59.4^{abc}
12	E	36.6^{e}	28.7^{ab}	15.3	47.4^{a}	60.2^{abc}
	SEM	0.4	0.7	3.8	2.3	2.9
	P > F	<0.01	<0.01	0.07	<0.01	0.03

$^{a–e}(P < 0.05)$.

S = solvent process; E = expeller process.

Key Words: canola meal, inhibitor in vitro, rumen-undegraded protein

T305 Influence of different levels of exogenous enzymes preparation at two application methods on in vitro ruminal fermentation of some fibrous feeds in sheep.

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The present experiment was aimed at investigating the effect of different levels of exogenous enzymes preparation (ENZ - mixture of cellulase, xylanase, α-amylase and proteases enzymes) on in vitro gas production, some ruminal fermentation parameters (pH, NH3-N and VFA (total and individual acids) and fiber degradability (ADF and NDF) of three fibrous feeds (FF - corn stover, oat straw, sugarcane bagasse) at two methods of application (direct addition or pretreatment for 24h with ENZ) in sheep. The levels of ENZ used were 0, 0.06, 0.12 and 0.24 g/g DM of each FF, and ENZ was dissolved in distilled water to obtain the concentration of each level in 1 mL. Rumen liquor was collected before the morning eating from 4 sheep (40 ± 3.2 kg BW, fed on a total mixed ration of 50% commercial concentrate and 50% alfalfa hay) fitted with permanent rumen cannula. In vitro gas production was recorded at 2, 4, 6, 8, 10, 12, 24, 48 and 72 h of incubation. After 72 h, the incubation was stopped and the inoculant's pH was determined and filtered to determine ADF and NDF degradability, VFA (total and individual acids) and NH_3-N concentrations. In vitro organic matter digestibility and metabolizable energy, were estimated. Data were analyzed as 4 (four doses of ENZ) × 3 (three FF) × 2 (two methods of application) factorial experimental design. Addition of ENZ increased ($P<0.05$) gas production, NH_3-N and VFA concentrations with the FF used. Acetic acid concentration was increased with the addition or pretreatment of FF with ENZ without effect on butyric or propionic acids concentrations. Pretreatment of FF for 24 h with ENZ was increased the ruminal fermentation and fiber degradability (ADF and NDF) of FF. Highest in vitro gas production and ruminal fermentation activities were found in sugarcane bagasse compared with oat straw and corn stover. It is concluded that pretreatment the FF with ENZ for 24 h before the in vitro incubation could improve the ruminal fermentation and fiber degradability in sheep compared to the direct addition in diets. Sugarcane bagasse treated with ENZ could be considered a good roughage for ruminants.

Key Words: exogenous enzymes, fibrous feeds, gas production

T306 Composition of diets fed to different groups of lactating cows on California dairies.

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The objective of this survey was to describe TMR dietary groups and TMR nutrient contents in lactating dairy cows. Forty dairies in Merced County, California, were selected based on the number of cows (mean 787 ± 592 from 210 to 2435 lactating cows/farm) and milk yield per cow (mean 31.8 ± 5.19 from 20.6 to 43.5 kg/d 3.5%FCM). Samples of TMR fed to different groups (n = 118) were taken in duplicate on 2 non-consecutive days and assayed for DM, NDF, ADF, lignin, CP (N*6.25), crude fat, and ash. The grouping systems and nutrient composition of the TMR (means ± SD) are in Table 1. Nine of 40 dairies (22%) fed a single diet to all lactating cows and 31 dairies fed multiple TMR diets to their lactating cow groups. Average milk production per cow for dairies feeding a single diet and multiple diets were 27.5 ± 5.5 and 33.0 ± 4.5 kg/d 3.5% FCM. All dairies with multiple diets had a high and low TMR. Fifty-eight, 32, and 15% of dairies with multiple diets prepared TMR for fresh, first lactation, and mid groups, respectively. Average (Table 1) and ranges of dietary NDF content on dairies with one diet (from 32.9 to 42.2%NDF) were close to the low TMR diets (from 30.6 to 43.5%NDF). Crude Protein contents in multiple diets TMR (fresh, 1st lactation, high, and mid) were similar averaging 17.5%CP. Across farms, CP content for 1st lactation diets were most consistent ranging from 16.7 to 18.0%CP, whereas for the other production groups ranged from 14% to more than 19%. Based on the limited variation in average nutrient concentrations among different diet groups, opportunities may exist to better match cow requirements with TMR composition.

Table 1. TMR dietary groups and nutrient contents

TMR of lactating cows	Dairies (n)	Nutrient content						
		DM%	NDF%	ADF%	Lignin%	CP%	Fat%	Ash%
Multiple diets	31							
Fresh	18	58.0 ± 5.5	34.0 ± 2.3	23.4 ± 1.6	5.4 ± 0.8	17.5 ± 1.3	4.7 ± 1.0	8.3 ± 1.1
1st Lactation	10	59.0 ± 6.3	32.8 ± 2.3	22.6 ± 1.9	5.4 ± 0.9	17.5 ± 0.4	4.7 ± 0.7	8.6 ± 1.5
High	31	58.3 ± 6.1	33.8 ± 1.9	22.8 ± 1.4	5.5 ± 0.8	17.5 ± 1.3	5.0 ± 1.2	8.3 ± 0.9
Mid	15	58.5 ± 7.0	34.6 ± 2.2	23.8 ± 2.1	5.6 ± 1.0	17.5 ± 1.0	4.9 ± 1.2	8.4 ± 1.4
Low	31	54.9 ± 7.3	36.1 ± 3.0	24.5 ± 2.6	6.0 ± 1.3	16.9 ± 1.6	4.0 ± 0.9	8.7 ± 1.3
Single diet	9	56.0 ± 11.4	36.9 ± 3.0	24.3 ± 2.3	5.9 ± 0.6	17.8 ± 1.9	4.1 ± 1.0	8.1 ± 1.0

Key Words: dairy farms, TMR dietary groups, TMR nutrient contents

T307 Ruminal degradability, duodenal flow, and intestinal digestibility of protein from canola meal or corn and wheat distillers grains in growing beef heifers.

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The objective of this study was to evaluate the ruminal degradability, duodenal flows and intestinal digestibility of protein from canola meal or dried corn and wheat distillers grains with solubles (DDGS) in growing beef heifers. Five ruminally and duodenally cannulated Angus heifers (initial BW 386 kg) were assigned to a 5 × 5 Latin square design. The diets consisted of 60% barley silage and 40% barley grain-based concentrate (DM basis) with differing protein supplements: control (CON; no protein supplement), canola meal (CM), wheat DDGS (wDDGS), corn DDGS (cDDGS) or fractional corn DDGS (fDDGS). Contents of CP were 12.5, 14.6, 14.3, 14.1 and 14.2% (% DM), respectively, for CON, CM, wDDGS, cDDGS and fDDGS diets. DMI (kg/d) was lower ($P < 0.05$) for CON (8.9) than for the other diets (average of 10.0) which were not different. Intake (g/d) of N followed the same pattern of DMI with lower N intake ($P < 0.05$) for CON (177) than the other diets (240). There were no differences in mean ruminal pH (6.22 to 6.30) but total VFA concentration (mM) was the greatest ($P < 0.05$) for wDDGS (127) and fDDGS (124), and lowest ($P < 0.05$) for CON (115) and cDDGS (116). Ruminal NH_3 N (mM) was greatest ($P < 0.05$) for CM (7.4) and lowest ($P < 0.05$) for CON (4.9), while the DDGS diets were intermediate (6.2). Ruminal degradability of protein was not different among diets (53 to 57%). Flows (g/d) of NAN and microbial N to the duodenum were lower ($P < 0.05$) for CON (196 and 117) than for other diets (247 and 142). Digestibility (% intake) of N in the intestine (74%) was not different among diets. The results indicate that the 4 sources of feed protein delivered no differences in the amount of protein at the small intestine when the diets were formulated to be isonitrogenous. Corn and wheat DDGS can be used to replace CM to supply the protein requirements of growing cattle fed backgrounding diets based on barley grain.

Key Words: beef heifer, flow and digestibility of N, protein supplement

T308 Tables of nutritive values for farm animals in tropical and Mediterranean regions: an important asset for improving the use of local feed resources.

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The demand for livestock products has been growing steadily in emerging and developing countries and with it the need for information about animal feeds. However, users of these countries often have to resort to feed data that are either obsolete or from temperate countries. The project "Tables of nutritive values for farm animals in tropical and Mediterranean regions" led by INRA, CIRAD and AFZ (and supported by FAO) aims to create an updated and comprehensive set of datasheets for more than 500 fodders and raw materials. Collaborations have begun with research groups in Belgium, Morocco and Spain. A major goal of the project is to better identify and characterize the local feed resources to improve the technical and economic performance of farms. Nutrition modeling, collaborations between research teams and identification of gaps in knowledge are part of the scientific objectives. The datasheets are created by a group of 20 scientists and engineers, who rely on a massive collection of scientific literature and experimental data to write qualitative and quantitative syntheses (via methods such as meta-analysis). A database containing more than 2 million raw data has already been established. Each datasheet provides information such as physical descriptions, pictures, feed availability, forage management, processes and environmental impact, as well as consistent chemical compositions (mean values and variability), feeding recommendations and nutritional values, potential concerns etc. for the main species of farm animals (Ruminant, swine, poultry, rabbit, fish). The publication of the datasheets is due in 2013, first as a FAO website and later in a book form.

Key Words: feed data base, multispecies, nutritive value

T309 Quality evaluation of italian rye grass and whole crop barley with homofermentative and heterofermentative lactic acid bacteria.

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This study was conducted to determine the quality of Italian rye grass (IRG) and whole crop barley (WCB) with addition of monoculture and co-culture of homofermentative and heterofermentative LAB on in situ fermentation. Strains of homofermentative LAB (*Lactobacillus casei* KACC 12416) and heterofermentative LAB (*Lactobacillus reuteri* KCTC 3594) were used in this study. *L. casei* and *L. reuteri* had the highest propionic acid production, thus they were used in fermenting the forage. The forages were fermented using monoculture and co-culture of *L. casei* and *L. reuteri* for 60 days ensiling. Microbial analyses, dry matter, NDF and ADF digestibility were determined and evaluated using SAS (2003). Addition of LAB in IRG inhibits the growth of molds. Dry matter digestibility of IRG was significantly higher on co-culture of *L. casei* and *L. reuteri* at 6and 24 hours of ensiling. On the other hand, dry matter digestibility of WCB was significantly higher in *L. casei* monoculture at 12 hours of incubation and in co-culture at 6 and 12 hours of incubation. ADF digestibility of IRG was significantly higher in L. casei monoculture at 6 hours of ensilage and in co-culture at 6 and 48 hours of ensilage. Furthermore, ADF digestibility of WCB was significantly higher in *L. reuteri* monoculture and in co-culture at 24 hours of ensilage. The result of this experiment suggests the addition of co-culture homofermentative and heterofermentative LAB which improves silage quality as well as inhibits molds.

Key Words: homofermentative and heterofermentative LAB, Italian rye grass, whole crop barley

T310 Sunflower cake in multiple supplements for cattle grazing in the dry season: pH and ruminal ammonia nitrogen.

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The research aimed to evaluate the inclusion levels of sunflower cake as protein source to replace soybean meal in multiple supplements for cattle grazing during dry season on nutritional parameters. Five steers were used, Nellore, uncastrated, with age and average initial weights of 20 months and 354.7 kg, respectively, divided into 5 paddocks of 0.25 ha each, consisting of *Brachiaria brizantha* 'Marandu'. The experiment was divided into a 5 × 5 Latin square design, composed of 5 experimental periods of 15 d each and 5 animals. The strategy adopted was the inclusion of sunflower cake in increasing levels of 0, 270, 406, 540 g / kg supplement as well as an mineral mixture ad libitum (MM). Supplements were formulated to be isonitrogenous (25% CP) and provided the amount of 1.5 kg / animal / day of natural matter. The availability of total dry matter and potentially digestible were 3.120 and 2.379 kg/ha respectively. The different levels of protein replacement of soybean meal by sunflower cake protein did not cause major changes in ruminal pH ($P > 0.10$), it remained around 6.72 at time 0 hours, and 6.57 4 h after supplementation, does not impair the growing rumen microbiota. There was a statistically significant difference ($P < 0.10$), for concentrations of NH_3-N among the animals that received only MM and cattle that received protein supplements in 4 h, that can be explained by the increasing concentration of NH_3-N in the rumen, enhancing the degradation of forage and therefore higher intake. Among the animals that received supplementation, was also observed statistically significant difference ($P < 0.10$), in which the increase in the supply of sunflower cake promoted a decrease in the concentration of NH_3-N in time 4 hours after supplementation, that it can be explained by the higher indigestible portion of sunflower cake compared to soybean meal. It is concluded that the inclusion of sunflower cake in the formulation of supplements did not affect the nutritional parameters, in which it can replace soybean meal in up to 100%, at this level of supplementation evaluated.

Key Words: cattle, co-products, pasture

T311 Prediction of carbohydrate fractions in some tropical grasses.

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Balancing ruminant diets for maximum production requires appropriate levels and types of dietary carbohydrates (CHO). The Cornell Net Carbohydrate and Protein System (CNCPS) has equations based on NDF content that estimate fermentation and passage of feed CHO and protein fractions which can be used to predict ME and protein utilization. In previous versions of the CNCPS, CHO fractions were categorized into 4 fractions: A (sugars, organic acids, and oligosaccharides), B1 (starch and soluble fiber), B2 (available NDF) and C (unavailable NDF). Later, scientists at Cornell University (Lanzas et al., 2007) proposed an expanded CHO scheme. Among some changes, fraction B1 turned out to be only starch, B2 was soluble fiber, B3 was available NDF and C was unavailable NDF. They compared it with the original CNCPS scheme by using a database which involved ingredients commonly used in ruminant rations and mathematical analyses. The present work agrees with the expanded CHO scheme, however, using a different approach: CHO fractions were predicted in 5 tropical forage samples, stalk and leaf tissues, at 3 maturity stages, using the original CNCPS and alternative equations (Queiroz et al., 2008) where NDF was substituted for by another fibrous preparation, crude cell wall (CW) which is obtained after treating the sample with water and organic solvents in a Soxhlet equipment. CW was used because NDF does not provide a complete measure of cell wall components such as pectin, β-glucans and galactans (soluble fiber) that are dissolved by NDF solution. Estimates of CHO fractions were compared by *F* tests from SAS. NDF substitution for CW showed that soluble fiber went to fraction A of CNCPS, the rapidly digestible carbohydrates. Because of its own degradation characteristics it is suggested that the soluble fiber fraction be accommodated in a specific fraction (B2) while the slowly digestible NDF be placed in a new fraction, B3. The fraction B1 would be only starch. Fraction C is still unavailable NDF. The approach used here allowed estimation of soluble fiber by subtracting NDF from CW. Expanded CHO scheme seems to provide better estimation of carbohydrate pools. This work was funded by FAPESP, Brazil.

Key Words: cell wall, CNCPS, NDF

T312 Using the acetyl bromide lignin method to quantify lignin content in forages.

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Lignin is a phenolic polymer that gives structural rigidity to plants; however, it inhibits cell wall digestion by microbial enzymes in herbivores. As a consequence, energy utilization is reduced. To better understand such inhibition it is important the correct quantification of lignin. The spectroscopic method acetyl bromide lignin (ABL) was used to quantify lignin in 21 grass samples (perennial ryegrass, tall fescue, annual ryegrass, sorghum Sudan and Caucasian bluestem) and 18 legume samples (alfalfa, lespedeza and red clover). Estimates of lignin concentrations were compared by *F* tests. SAS was used to draw linear regressions to measure main lignin effects and to correlate lignin content with in vitro forage dry matter digestibility. Grasses showed higher ABL concentrations than did legumes: 62.5 and 43.7 g/kg, respectively. It is pointed out that ABL, as a spectroscopic method, may possess the sensitivity to detect soluble lignin components that would be lost by conventional gravimetric analyses. Grasses, but not legumes, contain substantial levels of ester-linked low molecular weight phenolic acids which could contribute to the UV absorbance. The importance and magnitude these phenolics may be measured together with condensed lignin require more studies. IVDMD was negatively correlated with ABL method ($P < 0.005$) for both grasses and legumes. Grasses showed slightly higher digestibility, although without statistical difference ($P > 0.16$). Regression equations were, grass: $Y = -4.26X + 906.6$ ($R^2 = 0.81$) and legumes: $Y = -4.11X + 811.5$ ($R^2 = 0.61$). Curves had similar slopes ($P > 0.98$). These parallel lines indicate that the degradability of grasses and legumes had similar pattern as lignin concentration increased. In other words, it seems that grass lignin is no more inhibitory to digestion than legume lignin. These results add strength to the hypothesis that lignin's effect on degradability of forage cell walls is primarily related to concentration. In this context, ABL method may be a good alternative to quantify lignin content and to predict forage digestibility. Other lignin methods were studied and their data are being processed. This work was funded by CAPES, Brazil.

Key Words: digestibility, forages, lignin

T313 Estimates of kinetic degradability parameters and passage of materials originated from intercropping between brachiaria grass and plantations of corn and soybeans.

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The study was conducted to determine the kinetic parameters of in situ DM and NDF and the movement of materials from the intercropping of brachiaria grass and crops with corn and soybeans. Three experiments were used, as follows: Experiment 1 – Brachiaria grass and corn consortium at different plant ages. Experiment 2 – Brachiaria grass and corn consortium set in sowing arrangements. Experiment 3 – Brachiaria grass and soybeans consortium. The kinetics of particles transit were determined by the recovery of the indicators in the faces of the animal.

In the degradation test the samples were incubated in the nylon bags at the times of 0, 3, 6, 9, 12, 24, 48, 72, 96, 120 and 144 h. Kinetics data of rumen degradability and particles passage of silages made from material derived from the intercropping of brachiaria grass and crops of corn and soybeans are scarce, which makes comparisons difficult. However, the kinetics of particles passage from corn and brachiaria grass silage (CBS) was 0.030 and Brachiaria grass (BG) was 0.023 had values close to those found in the literature, for soybean and Brachiaria grass silage (SBS) was 0.018 was lower than the data from literature, which were compared with corn and brachiaria grass silage in exclusive culture. The rate of digestion from corn and brachiaria grass silage (CBS) was 0.018 and Brachiaria grass (BG) was 0.0353 had values close to those found in the literature, for soybean and Brachiaria grass silage (SBS) was 0.021. The materials that come from the intercropping caused ruminal repletion. The degradation rates were lower when correlated with data from literature. The values obtained for the parameters of degradation kinetics and passage of materials obtained from the various forms of intercropping of brachiaria grass and crops of corn and soybeans do not compromise the recommendation of the use of forage to increase the profitability of the system.

Key Words: grasses, kinetics of particles transit, degradability

T314 Utilization of infrared thermography image analysis in ruminant feeding experiments.

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Infrared thermography (IRT) is an alternative, noninvasive method, which has been studied as a tool in the identification of several physiological and pathological processes related to changes in body temperature. Heat production in ruminants is increased by high intake of forages. This study aimed to detect through IRT, changes in temperature caused by the ingestion of diets with different amounts of forage. For this purpose an experiment was conducted with 24 Jersey heifers (average body weight of 227 kg), in a replicated Latin square design, with repeated measures in time, with the following treatments: 30, 50 and 70% forage (corn silage) in relation to the diet dry matter (DM). Feeding consisted of a total mixture ration offered (3% of body weight) from 08:00 to 14:00. Each collection period (4 d) was preceded by 7 d of diet adaptation. The thermography images (right and left flank and eyes, feet and forehead), heart rate, respiratory rate and rectal temperature were obtained every 2 h, from 06:00 to 18:00h. Temperature values of the thermography images of the right flank in the 30, 50 and 70% treatments were 29.95, 30.11 and 29.89°C, with a significant difference between the last 2 ($P = 0.0339$). The 50% treatment, which showed the highest temperature of the right flank, also had higher DMI (6.50, 7.24 and 5.95 kg for 30, 50 and 70, $P < 0.0001$); while for NDF intake, there was an interaction ($P = 0.0007$) between treatment and time (1.72, 2.31, 2.86 for 30%; 2.36, 3.03, 3.49 for 50%, and 2.02, 2.78, 3.45 for 70%, at 08:00, 10:00 and 12:00h, respectively). Other variables did not differ between treatments. Although the difference between treatments were of small magnitude, the use of thermographic images enabled detection of a temperature increase associated with higher dietary fiber intake. Financial support FAPESP.

Key Words: dry matter intake, NDF intake, ruminant

T315 Evaluating and refining the CNCPS feed library.

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The Cornell Net Carbohydrate and Protein System (CNCPS) model includes a library of >800 ingredients which is the reference database for describing the chemical composition of a diet. The objective was to evaluate the current feed library against commercial laboratory data, and update the library as required. To conduct the analysis, data sets were provided by 2 commercial laboratories (n > 100,000 analyses; Dairy One, Ithaca, NY and Cumberland Valley Analytical, Hagerstown, MD). The procedure followed 4 sequential steps and bound each feed to the following constraint (Eq 1): (CP + EE + ash + NDF + acetate + propionate + butyrate + lactate + organic acids + sugars + starch + soluble fiber) = 100. In the first step, components used to differentiate farm level characteristics of the same feed were fixed (DM, NDF, CP). Second, linear regression equations were derived from the data provided and used to calculate components from other correlated components within the same feed (R2 > 0.65). Third, factors not predicted using standard linear regression and not in Eq. 1 were calculated using a matrix of regression coefficients derived from data generated using a Monte Carlo (MC) simulation. To complete the analysis, probability density functions of each chemical component of each feed were fit and correlated to each other in @Risk (Palisade, Ithaca, NY). A MC simulation was run for 30,000 iterations, which generated a standardized data set of likely feed compositions. These data were then used to calculate the coefficients for the matrix. Lastly, components that were not assigned values in any of the preceding steps were calculated using a genetic algorithm optimizer (RISKOptimzer, Palisade). Minimum and maximum boundaries for each component within a feed were set using the data sets provided to constrain the optimizer to a likely range of values (mean ± SD). The optimizer was also constrained to satisfy the assumptions of Eq 1. The approach provided an efficient and repeatable way of evaluating and refining the composition of a large number of different feeds against commercially generated data similar to that used by CNCPS users on a daily basis.

Key Words: feed chemistry, optimization, library

Ruminant Nutrition: General II

T316 Investigation on the nutritive value of *Vernonia amygdalina* leaves (bitter leaves) for ruminant animals.

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An experiment was conducted to determine the proximate composition of *Vernonia amygdalina* (Va). Proximate composition of Va was determined according to AOAC (1990). The DM content of Va was high (88.7%) due to the air drying process the leaves were subjected before milling. The crude protein (CP) was 19.7% and this is commensurable when compared with tropical grass species which seldom exceed a CP level of 10%. It compared favorably with that of cassava leaf meal (16.7%), Sunflower leaf meal (16.6%) far exceeds the minimum protein requirement (10–12%), for ruminants. This value is not far from the CP levels of *Leuceana* sp. (22.2%) and *Gliricidia* sp. (22.5%). The crude fiber (CF) level of 15.7% for Va is low compared with that of tropical grass species, which may be as high as 45 – 50% at more matured stages of growth. It is comparable to the CF level of *Chromolaena odorate* leaf meal (16.0%), Cassava leaf meal (15.6%), deep litter manure (16.6%) and guava leaf (16.1%) but lower than the CF leaf of *Tithonia diversifolia* (21.8%). The ether extract content was low (5.6%). This value was lower than the value of 8.1% reported for *Chromolaena odorate* leaf but greater than the value of 2.8% reported for *Tithonia diversifolia* leaf. The total ash content 13.9% was high and this was comparable to the ash content of *Tithonia diversifolia* (14.7%) but greater than the value of 8.3% reported for *Acacia albida* used as a browse plant for sheep in the semi-arid region of Nigeria and greater than the value of 11.0% reported for *Leucaena* sp. to feed Yankassa sheep and 11.5% reported for *Chromolaena odorate* leaf meal but commensurable with the value reported for cassava leaves which has an ash content of 10.1%. The gross energy (GE) value was 2720.0kcal/kg. This is comparable with the GE value of Groundnut cake (2600kcal/kg). The nitrogen free extract level of 33.9% for Va is low compared with that of *Tithonia diversifolia* leaf (44.4%) used to feed West African Dwarf sheep. On average the chemical composition of Va appeared to be suitable as a protein concentrate for ruminants, a suitable replacement for *Gliricidia* and *Leuceana* sp.

Key Words: nutritive value, ruminant animals, *Vernonia amygdalina* leaves

T317 Screening of dairy cows for ketosis by routine analysis of β-hydroxybutyrate in DHI test milk samples.

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Fourier transform infrared analysis (FTIR) was used to determine β-hydroxybutyrate (BHB) concentration in DHI test milk samples, as a fast and inexpensive method to measure herd level subclinical ketosis incidence. Based on a previously published trial comparing blood and milk BHB concentrations, threshold levels were established as follows: cows with milk BHB concentrations ≥0.20 mM were declared ketotic (POS); cows with milk BHB concentrations below 0.15 mM were declared non-ketotic (NEG); and cows with intermediate BHB concentrations were classified as potentially ketotic (SUSPECT). Routine testing of DHI milk samples started in October 2011. Over 235,600 samples were tested, of which 23,577 were from cows between 1 and 35 DIM (7,825 primiparous and 15,752 multiparous cows). Results indicate an average subclinical ketosis incidence (POS and SUSPECT) of 27% over the first 5 weeks of lactation. Distribution of incidence in relation to week after calving was different between primiparous and multiparous cows. Highest incidence for primiparous cows (33.8%) was in the first week postpartum but in the third week for multiparous cows (33.3%). By wk 5 after calving, incidence declined to 19.9% and 22.8% for primiparous and multiparous cows, respectively. Milk yield and composition were affected by the ketotic status of cows (see Table 1). Milk BHB concentration was inversely correlated to the protein:fat ratio ($R = -0.38$; $P = 0.0001$). Routine analysis of milk BHB among DHI test samples provides a fast and inexpensive tool for accurate screening of subclinical ketosis incidence at the herd level.

Table 1. Milk yield and composition according to ketotic status of cows between 1 and 35 DIM

	POS	SUSPECT	NEG	SE	*P*-value
Test-day milk yield (kg)	30.3^{a}	32.4^{c}	31.8^{b}	0.2	0.001
Fat (%)	4.92^{c}	4.48^{b}	4.05^{a}	0.01	0.001
Protein (%)	3.15^{a}	3.18^{b}	3.24^{c}	0.01	0.001
SCC (1000 cells)	365^{b}	349^{b}	243^{a}	14	0.001
Urea (mg N/dL)	8.6^{a}	9.5^{b}	10.0^{c}	0.1	0.001
Protein:Fat ratio	0.66^{a}	0.73^{b}	0.82^{c}	0.003	0.001
TCI[1]	-57^{a}	189^{c}	36b	22	0.001

[1] Transition cow index.

Key Words: ketosis, dairy cow, DHI

T318 Prediction of empty body weight of adult Pelibuey ewes.

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The aim of this work was to assess the relationships between shrunk body weight (SBW), empty BW (EBW), warm carcass weight (WCW) and cold CW (CCW), to develop prediction equations to estimate EBW in non pregnant, non lactating, adult Pelibuey ewes fed fibrous rations. Twenty four ewes with BW of 37.2±4.0 kg were randomly assigned to four groups of six animals each. Six ewes were slaughtered, for baseline measurements of carcass traits. The remaining, were randomly assigned to three groups of six animals each. Ewes were individually housed in metabolic crates, and were fed at levels of metabolizable energy intake (MEI): Low (L), Medium (M) and High (H) for 65 d, to achieve desirable changes in BW. Levels of feeding were established as proportions of ME energy requirement for maintenance (0.426 MJ/kg $BW^{0.75}$/d). Grass was offered in equal portions twice daily, supplying 44 g DM/kg $BW^{0.75}$/d for all treatments, and the concentrate at a rate of 0, 16 and 32 g DM/kg $BW^{0.75}$/d for treatments L, M and H, respectively. Before slaughter, SBW was taken after feed and water were withdrawn for 24 h, gastrointestinal tract (GIT) was weighed before and after emptying. EBW was computed as the difference between SBW and contents of the GIT. Data recorded at slaughter were weight of WCW, and then carcass was chilled at 6°C during 24 h. After refrigeration, the weight of CCW was recorded. Two ewes were removed of the experiment because of illness. Mean (±SD) values (kg) of SBW, WCW, CCW and EBW of adult Pelibuey ewes (n =22) were 35.63±5.02 kg; 14.95±2.40 kg; 14.52±2.50 kg and 27.92±4.19 kg, respectively. Relationships between BW, EBW, WCW and CCW were estimated by regression using PROC REG of SAS. Relationships between SBW, WCW and CCW between EBW, were all significant ($P<0.0001$) and the R^2 ranged between 0.94 and

0.96. The regressions equation were, EBW = −0.945 + 0.809 SBW (R^2 = 0.94; RSD = 1.009); EBW = 2.219 + 1.718 WCW (R^2 = 0.96; RSD = 0.812) and EBW = 4.363 + 1.622 CCW (R^2 = 0.94; RSD = 1.070). Data obtained, indicated that weight of GIT content was approximately 19% of SBW of adult ewes, additionally, WCW and CCW could be employed to predict reliable the EBW of adult Pelibuey ewes.

Key Words: Pelibuey ewes, empty body, carcass

T319 Increased lamb production by implanting melatonin to induce out of season breeding.

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A spring breeding program was evaluated at the Nevada Experiment Station (Reno) in sheep using melatonin or melatonin and progesterone implants. Yearling and mixed aged ewes (n = 120) were randomly allocated to 3 treatments, 40 animals in each group (control, C; melatonin implant, M; and melatonin and progesterone implant, MP). Melatonin implant (one dose contained 18 mg melatonin, released at 0.5 mg/d, Regulin, Schering Pty Ltd., Australia) and progesterone implants (Synchro-Mate-B, USA, gradual release 6 mg/dose) were implanted in accordance to the manufacturer′s specifications. Ewes were managed under natural ambient light and grazed on small pastures for 5 weeks in isolation from rams. Pastures were mixtures of primarily fescue/clover with some winter forbs and native grasses. The M group received one melatonin pellet s.c. at the start of wk 1; the MP group received one pellet at the start of wk 1 and one progesterone implant at the start of wk 4. Ewes were bred with 3 rams randomly for 2 estrus cycles (5 weeks) beginning at wk 6 of the experiment. Data were analyzed by Chi-squared test. Blood melatonin concentration was greater ($P < 0.05$) for M than C group at weekly monitoring during melatonin implantation (Table 1). Number of ewes bred (40, 40 and 30), number of ewes lambed (34, 31 and 13), number of live births (54, 41 and 18), number of weaned lambs (42, 33 and 13), birth weight (4.44, 4.53 and 4.44 kg) and weaning weight (28.57, 29.93 and 28.12 kg) were compared for group C, M and MP, respectively. There was no difference between M and MP for any of measurements, however number of ewes bred, number of ewes lambed, number of live births, and number of weaned lambs were greater ($P < 0.05$) for M and MP compared with C group. This experiment indicated that out of season breeding using melatonin implants can increase sheep reproductive efficiency.

Table 1. Blood melatonin concentration (pg/mL) at weekly intervals

Group	Wk 1	Wk 2	Wk 3	Wk 4
C	12.6	13.1	12.6	14.2
M	83.7	78.7	89.9	109.50

Melatonin concentration was significantly ($P < 0.05$) higher for M group compared with C group at 4 intervals.

Key Words: sheep, breeding, melatonin

T320 Effects of different levels of quebracho tannins and sunflower oil on nutrients digestibility and milk fatty acids composition in dairy ewes.

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In a 3 × 3 factorial setup, the effects of different levels of quebracho tannins (T) and sunflower oil (F) on nutrients digestibility and fatty acids profile in milk fat of dairy ewes have been studied. The levels of both T and F were 0, 2 and 4% of dry matter. Seventy two pregnant ewes were randomly allocated into 9 treatments. The appropriate diet was given to each treatment group from week 2 pre-partum until the end of the trial. In the digestibility trial, the effect of T was negative on the digestibility of organic matter, N, NDF ($P < 0.05$); and ADF ($P < 0.07$). However, digestibility of NDF tended to be reduced by F supplementation ($P < 0.07$). The interaction effect of F×T was negative and tended to reduce digestibility of NDF ($P < 0.06$). Retained N (RN) as a percentage of digested N (DN) enhanced with T supplementation ($P < 0.05$). The highest value of RN/DN detected in treatment group fed F 2% and T 4%. Diets supplemented with either F or T had the highest ratio of unsaturated to saturated fatty acids in milk fat ($P < 0.01$) (Table1). Moreover, the effect of F×T interaction on milk fat content of conjugated linoleic acid (CLA) was significant ($P < 0.05$) (Table1). In conclusion, diet supplementation with F 4% and T 2-4% could be used to increase unsaturated/saturated FA ratio and CLA content of ewes milk fat. The current research was funded by King Abdulaziz City for Science and Technology-Saudi Arabia (No.ARP-28-61).

Table 1. Effects of diet supplementation with quebracho tannins (T; 0, 2, and 4% of DM) and sunflower oil (F; 0, 2 and 4% of DM) on unsaturated (U) to saturated (S) fatty acids ratio and conjugated linoleic acid (CLA) in milk fat

Treatment	U/S FA	CLA (g/100 g FA)
F0-T0	0.52	0.61
F0-T2	0.80	0.69
F0-T4	1.00	0.89
F2-T0	0.72	1.76
F2-T2	0.68	2.46
F2-T4	0.71	2.43
F4-T0	0.90	2.20
F4-T2	1.10	3.15
F4-T4	1.16	2.89
SEM	0.006	0.024
P-values		
(F)	0.001	0.001
(T)	0.001	0.001
(F×T)	0.002	0.050

Key Words: dairy ewes, nutrition, fatty acids profile

T321 Relationships between residual feed intake and performance of Nellore bulls in feedlot.

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The objective of this study was to evaluate performance and efficiency parameters of 114 Nellore bulls classified for residual feed intake (RFI). The animals, with an average of 24 mo of age, were located in individual pens and were weighed at the beginning of the trial and each 21 d, so the average daily gain (ADG) could be determined. The diet was composed by 18.0% corn silage, 5.0% sugar cane bagasse, 24.3% soybean hulls, 3.5% soybean meal, 46.8% sorghum, 0.8% urea and 1.6% mineral mix. Dry matter intake (kg/d) was determined weighing the orts every day. The animals were initially divided into 3 treatments: high RFI, medium RFI and low RFI. RFI was calculated as the difference between observed and predicted feed intake based on $LW^{0.75}$and average daily gain (ADG). Animals were classified as high RFI (>0.66 standard deviation - less efficient, n = 38), medium RFI (±0.66 standard deviation, n = 38), and low RFI (<0.66 standard deviation - more efficient, n = 38). The results were analyzed using the statistical software R (2011). There were differences in initial and final LW, dry matter intake (DMI), NDF intake (NDFI) and crude protein intake (CPI) among RFI levels. The higher DMI observed in the group of low RFI animals may be due to the greater initial BW of these animals. Low RFI animals also were better in feed efficiency (FE) and feed conversion (FC). The average daily gain (ADG) did not differ among treatments. The RFI was positively correlated with FC (−0.25; $P < 0.05$), NDFI (0.50; $P < 0.05$), CPBI (0.59; $P < 0.05$) and negatively correlated with FE (−0.58; $P < 0.05$) and DMI (−0.39; $P < 0.05$). There were no significant correlations with initial and final BW and ADG. Significant correlations between feed conversion and initial LW (0.45; $P < 0.05$) and ADG (−0.65; $P < 0.05$) were detected. The bulls with low RFI can be up to 13.6% more effective than bulls with high RFI.

Key Words: beef cattle, efficiency parameters, selection

T322 Adipose tissue preferences for acetate in finishing steers.

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Increased marbling enhances the quality grade of beef, and as such, high starch diets are often used by feedlots to stimulate this type of fat deposition. In vitro studies suggest that adipocytes from intramuscular fat (IMF) and subcutaneous fat (SCF) may have different preferences for acetate and glucose, and thus may be vulnerable to strategic changes in feeding regimens. We hypothesized, however, that SCF, IMF, and visceral fat (VF) tissue have similar preferences for acetate in vivo. Therefore, the objective of this study was to assess acetate incorporation rates into adipose tissue from SCF, IMF, and VF depots. Four Angus × Simmental steers had been fed corn silage based finishing ration for 120 d. They (513 ± 12 d age and 569 ± 35 kg BW) were infused continuously with [$^2H_3$] acetate (0.2 mol/h) over a 12 h period immediately before harvest. Blood samples were collected from each animal before and after infusion. Blood samples were collected at 1 h intervals from 2 animals during the first 11 h of the infusion, and every 15 min during the last 1 h of infusion. Plasma acetate enrichment levels were determined by GC-MS. Post-harvest tissue samples were collected from SCF, IMF and VF depots. Lipids were extracted from tissues and fatty acid methyl esters were prepared and analyzed in GC-MS for palmitate enrichment. Enrichment of acetate in blood and fat in each depot was used to calculate fractional synthesis rates (FSR, % per h) of palmitate in each depot. DNA concentration, palmitate enrichment in each tissue and FSR were analyzed for the fixed effect of tissue using the GLIMMIX procedure of SAS 9.2. DNA concentration in each tissue was used as a covariate for FSR analysis. A contrast statement was used to compare the VF and the average FSR of IMF and SCF. DNA concentration was different ($P = 0.003$) between IMF and VF, and SCF and VF. Enrichment of palmitate in adipose tissues was not different across depots nor was FSR, though a trend ($P = 0.09$) for a higher FSR was observed in VF as compared with IMF and SCF. These data show that differences in acetate preference by major fat depots do not exist in finishing feedlot steers.

Key Words: acetate, fat depot, fractional synthesis rate

T323 Effects of different amino acid patterns on the expression of four major milk protein genes in primary cultured bovine mammary epithelial cells.

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The objective of this study was to determine whether different amino acid (AA) patterns could affect milk protein gene (αs1-casein, αs2- casein, β-casein, κ-casein) expression in bovine mammary epithelial cells. Mammary tissues were collected from a 3-yr-old lactating Chinese Holstein dairy cow (DIM 100-d), Primary mammary epithelial cells were isolated by modifications of the methods of Miranda et al., (2009). A completely random design was used with 4 AA patterns as treatments (Table 1), each treatment has 3 replicates, and all experiments were repeated 3 times. The expression of genes was determined by RT-QPCR method. Data were analyzed by the ANOVA using the GLM procedure of SAS (9.0). The concentration of total AA in each medium was 534 mg/L. The results showed that different patterns of AA can induce the expression of αs1-casein, β-casein and κ-casein genes differently ($n = 3$; $P < 0.05$), in contrast, the expression of αs2-casein gene was not significantly affected ($n = 3$; $P = 0.26$). The milk pattern, casein pattern and combination pattern of AA increased the expression of αs1-casein and κ-casein genes significantly ($n = 3$; $P < 0.05$) compared with blood AA pattern. The milk pattern, casein pattern and blood pattern of AA upregulate β-casein gene expression significantly ($n = 3$; $P < 0.05$) compared with combination AA pattern. The milk AA pattern might increase major milk protein genes expression, perhaps, an appropriate AA pattern will play a role in milk protein synthesis.

Table 1. Percentage of amino acids in different patterns

AA, %	Blood	Milk	Combination	Casein
Tyr	2.18	5.67	6.30	6.63
Ala	11.66	3.78	2.91	2.77
Gly	29.77	2.27	0.40	0.48
Glu	10.5	29.3	25.0	26.4
Cys	4.15	0.76	1.16	0.48
Phe	2.29	6.05	6.54	6.63
Leu	5.75	10.97	18.52	17.37
lle	3.94	5.30	6.17	6.27
His	1.28	3.78	2.32	2.41
Lys	2.72	10.21	7.46	7.24
Met	0.80	2.27	3.65	3.74
Try	1.65	1.89	1.80	1.57
Thr	6.76	5.67	5.60	5.55
Val	8.25	6.05	6.22	6.39

Key Words: bovine mammary epithelial cells, amino acids pattern, milk protein genes expression

T324 Evaluation of equations to predict body composition in Nellore bulls.

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The equations developed by Hankins and Howe (1946), Valadares Filho et al. (2006), Marcondes et al. (2010) and Marcondes et al. (2011) were evaluate to predict the body composition from the 9-10-11th rib cut in Nellore bulls. These equations estimate the physical and the carcass chemical composition and empty body chemical composition. This experiment used a comparative slaughter technique. Thirty-seven Nellore bulls (14 mo old) with initial shrunk body weight of 259 ± 24.9 kg were used. The bulls were randomly divided into 3 groups: 5 bulls to the reference group, 4 bulls were fed at maintenance level and 28 bulls were fed ad libitum. The bulls fed ad libitum were separated into 4 groups, one of which was slaughtered every 42 d. The reference group was slaughtered at the start of the experiment. All the animals were fed with corn silage and concentrate (55:45). After slaughter, the 9–10–11th rib cut was dissected into muscle, fat and bone fractions. The remaining carcass was similarly dissected. The others parameters evaluated were: empty body weight, dressing percentage, visceral fat percentage and organ and viscera percentage. The regression was evaluated according to the following statistical hypothesis: H0: $\beta 0 = 0$ and $\beta 1 = 1$ and Ha: not H0. The equations obtained by Marcondes predicted correctly ($P > 0.05$) the carcass physical composition. However, the muscle and fat tissues were under- and overestimated ($P < 0.05$), respectively, by Hankins and Howe. The equations obtained by Marcondes predicted correctly ($P > 0.05$) the carcass and empty body chemical composition. The carcass water was underestimated ($P < 0.05$) by Hankins and Howe. The equations by Valadares Filho did not predict ($P < 0.05$) the carcass or empty body chemical composition. The carcass physical and chemical composition and empty body chemical composition can be predicted from the composition of 9-10-11th rib cut by equations obtained by Marcondes while the composition of these components cannot be predicted by Hankins and Howe in Nellore bulls.

Key Words: chemical composition, comparative slaughter, rib cut

T325 Performance of Holstein dairy cows under different feeding strategies in early lactation. M. Fajardo*[1], D. A. Mattiauda[1], A. Meikle[2], M. Carriquiry[1], J. Gil[2], G. Motta[1], G. Guala[1], G. Ortega[1], D. Pelaez[1], P. Sorhouet[1], F. Souza[1], and P. Chilibroste[1], *[1]Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay, [2]Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay.*

The objective of this study was to determine milk yield, body condition score and live weight changes of multiparous Holstein dairy cows (n = 36) subjected to contrasting feeding strategies during the first 10 weeks of lactation. A complete randomized block design was used that included initial BCS and BLW (3.2 ± 0.2 and 731 ± 73.5 kg). Three treatments were compared: TMR: 100% Total mixed ration, G1: 50% TMR + 50% pasture (one grazing session), and G2: 50% TMR + 50% pasture (2 grazing sessions). All the treatments were offered 30kg DM cow/d. TMR cows were always confined. G1 cows grazed from 0700 to 1400 staying confined with access to TMR after pm milking. G2 cows grazed exactly as G1 and had another grazing session from 1600 to 2000, staying thereafter confined with access to TMR. The TMR offered had 151 ± 2.6 g/kg DM of CP, 342 ± 5.0 g/kg DM of NDF and 187 ± 3.5 g/kg DM of ADF. Data were analyzed with a mixed model with repeated measures (GLIMMIX, SAS 9.2). TMR cows produced more milk than G1 and G2 (36.5 ± 0.3 vs. 33.0 ± 0.3 and 33.3 ± 0.4 L/d, $P < 0.05$). G1 cows had higher milk fat content than cows in TMR, but did not differ from G2 cows (3.97 vs. 3.67 and 3.87%, ± 0.08 respectively; $P < 0.05$). Fat production was not significantly different between treatments (1.3 kg/day ± 0.03). Treatments did not differ in milk protein content (3.4 ± 0.06%) but TMR cows had higher milk protein production than G2 and G1 (1.2 vs. 1.1 and 1.1 kg ± 0.03 respectively $P < 0.05$). TMR cows differed from G2 in BCS but not from G1 (2.9, 2.7 and 2.8 ± 0.04 respectively; $P < 0.05$), and G1 tended to be different from G2 ($P < 0.13$). Treatment with one grazing session plus TMR (G1) achieved similar productive results as offering 100% TMR (TMR). On the other hand, treatment with 2 grazing sessions (G2) showed no productive advantages over G1 besides a lower BCS, probably due to the greater energy requirements for walking and/or grazing.

Key Words: autumn calving, nutrition, ruminants

T326 Effect of dietary cation-anion difference (DCAD) on beef tenderness. J. P. Schoonmaker,* K. T. Korn, K. N. Condron, C. N. Shee, M. C. Claeys, T. D. Nennich, and R. P. Lemenager, *Purdue University, West Lafayette, IN.*

The manipulation of acid-base balance has been extensively investigated as a means of altering calcium homeostasis and managing milk fever in dairy cows. A low pre-partum dietary cation anion difference (DCAD) increases urinary Ca, blood-ionized Ca, and responsiveness to Ca-homeostatic hormones. Very little attention, however, has been focused on the possibility of using a low dietary DCAD to increase muscle Ca availability, calpain activity, and meat tenderness of beef cattle. Thus, 90 Angus × Simmental crossbred steers were allotted by weight (590.1 ± 2.4 kg) and breed composition to 3 treatments (6 pens per treatment, 5 steers per pen) to evaluate the effects of DCAD on beef tenderness. Treatments were initiated 2 weeks before slaughter and consisted of 3 DCAD (mEq/100 g) concentrations: +16, 0, and −16. Hydrochloric acid treated soybean meal (PasturChlor, West Central, Ralston, IA) was added to diets to decrease DCAD and sodium bicarbonate was added to diets to increase DCAD. Basal diets (DM basis) were 62 to 64% corn, 6 to 9% soybean meal, and 20% corn silage and were formulated to contain similar concentrations of protein, energy and minerals, with the exception of sodium and chlorine. Performance before initiation of the study did not differ ($P > 0.22$) among treatments. Urine pH did not differ ($P > 0.57$) at the initiation of the study, but did decrease (linear and quadratic, $P < 0.02$) on d 7 (8.13, 7.69, 6.37) and d 14 (8.03, 7.66, 5.68) of the study as DCAD decreased from +16 to 0 to −16, respectively. ADG and feed efficiency responded quadratically ($P < 0.01$) to DCAD, increasing from +16 to 0 DCAD and decreasing from 0 to −16 DCAD. Hot carcass weight, dressing percent, fat thickness, longissimus muscle area, yield grade, marbling score, quality grade distribution, and 48 h muscle pH did not differ ($P > 0.16$) among treatments. In addition, DCAD did not affect ($P > 0.23$) Warner-Bratzler shear force among treatments after 7 and 21 d of aging. Although urine pH was decreased by lowering DCAD, potentially increasing calcium influx into muscle, beef tenderness was not affected.

Key Words: beef, DCAD, tenderness

T327 Performance of early lactation cows fed whole versus chopped sugarcane. J. E. P. de la Ossa*[1,2], R. Lana[1,2], and E. M. Balbino[1], *[1]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]FAPEMIG, Viçosa, MG, Brazil, [3]CNPq, Viçosa, MG, Brazil.*

Eight crossbred Holstein-Gyr cows with 450 ± 30 kg body weight were used to evaluate the effect of whole sugar cane (WSC) compared with chopped sugar cane (CSC) on intake, milk yield and milk composition in early lactation dairy cows fed sugarcane plus 4 levels of supplement (600, 1200, 2400, and 4800 g/cow/day) containing 60% corn meal and 40% soybean meal as nitrogen source. One Latin square with 4 treatments based on level of concentrate comprised rations with WSC, and another Square comprised rations with CSC also differing in concentrates. Periods of 14 d consisted of 7 d of adaptation and 7 d of measurements. Dry matter and neutral detergent fiber (NDF) intakes decreased ($P < 0.05$) in WSC compared with CSC, with values of 25.12 kg/day versus 22.77 kg/day. Milk yield increased ($P < 0.05$) as a function of level of supplement, but not as a function of sugarcane processing. There was no significant difference ($P > 0.05$) for milk composition as a function of treatments. Therefore, sugarcane can be furnished in a whole form for dairy cattle after adaptation of ingestion, reducing production costs such as with machinery and labor, and without processing, the feed decreases losses by fermentation and increases life time of conservation in the feed bunk.

Key Words: chopped sugar cane, whole sugar cane

T328 The relationship of feed efficiency and visceral organ size in growing lambs fed a concentrate or forage-based diet.

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We hypothesized that a portion of individual differences observed for feed efficiency can be attributed to gastrointestinal tract (GIT) size, which would vary based on diet. Growing wethers (n = 77; 51.3 ± 1.2 kg BW) were fed a concentrate (CONC; 12.1% CP, 17.6% NDF, 2.98 Mcal/kg ME) or forage-based pelleted diet (FOR; 16.2% CP, 36.3% NDF, 2.31 Mcal/kg ME) for 49 d. Individual intake was measured with the GrowSafe^{TM} System to determine residual feed intake (RFI). The 20% most (low RFI, n = 8) and 20% least (high RFI, n = 8) efficient lambs from each diet were slaughtered (66.6 ± 2.3 kg BW; n = 32 total), and the viscera was dissected and weighed. Data were analyzed as a 2 × 2 factorial with RFI class (low vs. high RFI), diet type (FOR vs. CONC), and the interaction in the model. Organ mass was not affected ($P > 0.10$) by the RFI class x diet type interaction. Low RFI lambs tended to have greater ($P = 0.09$) pancreas and spleen mass than high RFI, although RFI class did not affect ($P > 0.15$) other organ actual (g) or proportional (g/kg BW) mass. Lambs fed FOR vs. CONC had greater ($P \leq 0.01$) actual and proportional reticulum, omasum, large intestine, and kidney mass and tended to have greater ($P \leq 0.09$) actual and proportional small intestine mass. However, CONC fed lambs had greater ($P \leq 0.05$) rumen, heart, liver, and proportional rumen mass than FOR fed lambs. All other visceral organs were unaffected ($P > 0.11$) by diet type. Proportional abomasum mass tended to be positively correlated ($P = 0.08$) with RFI, whereas pancreas and spleen mass tended to be negatively correlated ($P \leq 0.09$) with RFI. Intake was positively correlated ($P \leq 0.04$) with reticulum, omasum, abomasum, large intestine, kidney, and proportional omasum mass, and tended to be positively correlated ($P \leq 0.10$) with total GIT, small intestine, and proportional large intestine mass. Proportional spleen and heart mass tended to be negatively correlated ($P \leq 0.09$) with intake. Results of this study suggest that visceral organ size in growing lambs is more affected by diet type than individual feed efficiency.

Key Words: feed efficiency, feed intake, gastrointestinal tract

T329 Performance of Nellore young bulls grazing *Brachiaria brizantha* 'Xaraés' supplemented with different lipid sources.

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Dietary supplementation with different lipids source is not a common practice in livestock production in Brazil. However, this alternative may increase the energy balance of the supplementation, and improve the animal performance. So, an experiment was conducted at the forage sector of the São Paulo State University, Jaboticabal – SP, to evaluate the effects of concentrate supplementation with different lipids sources on the intake and animal performance of grazing animal during the period rainy seasons. Ninety Nellore young bulls with average BW of 347 kg were used in completely randomized design with 5 treatment, and 2 replications (paddocks) with 9 animals in each one. Three periods of 28 d were analyzed by repeated measures. The animals were housed in *Brachiaria brizantha* 'Xaraés' pasture in continuous stocking rate grazing system and received one of the following supplements during the experimental period: ad libitum mineral (control) or 0.5 g/kg BW of concentrated supplements formulated with palm oil, linseed oil, soybean grain or Megalac E. All supplements presented the same content of crude protein, and total digestible nutrients (TDN), 260 g/kg DM, and 980 g/kg DM, respectively. The grazing animal behavior measure was taken during daytime (12 h) for 2 consecutive days. Supplements used did not affect the forage chemical composition; it was observed mean values of crude protein, neutral detergent fiber and acid detergent fiber of 89.4, 615.7, and 374.2 g/kg DM, respectively. Grazing time varied due to the supplements and periods ($P < 0.05$). Animals in the control treatment spent more time in grazing 5.7 h following for soybean grain and linseed oil treatment 4.5 h, and the animals in the palm oil treatment spent less time in grazing 3.7 h, and that Megalac E spent 4.1 h in grazing. There was effect of the treatments in the animals weight gain ($P < 0.05$). Animals of control group, and those supplemented with palm oil, soybean grain, linseed oil, and protected fat showed average daily gain of 0.724, 0.697; 0.780, 0.759, 0.864 g/day, respectively. Megalac E supplementation may improve animal performance.

Key Words: *Brachiaria*, lipid, Nellore

T330 Seminiferous tubule traits of lambs fed with cottonseed co-products (*Gossypium* ssp.).

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This study aimed to evaluate the influence of supplementation with cottonseed co-products on testis structure of lambs. Twenty-four Santa Inês lambs (5 mo old and mean live weight 20.6 ± 1.9 kg) were used. The lambs were housed in individual pens and received 4 treatments: 20% of DMI (Dry Matter Intake) whole cottonseed, 20% of DMI cottonseed meal with low oil (MEAL), 20% of DMI cottonseed meal with high oil (CAKE) and a control without use of cottonseed. The concentrate:forage proportion in diet was 60:40. Coast Cross hay (*Cynodon dactylon*) was used as forage, and ground corn was used in the remainder of the concentrate. At the end of experimental period, the animals were slaughtered and samples of testis collected. These samples were fixed in paraffin and contrasted with hematoxylin and eosin for light microscopy analyses. Twenty-five photos of each animal testis were taken. Tubule and lumen diameters of 5 seminiferous tubules were measured in each photo. Seminiferous epithelium thickness was obtained by difference between tubule and lumen diameters. ANOVA was performed with SAS to verify the influence of independent effects (treatment, tubule by photo, animal weight at slaughter and squared animal weight at slaughter) on seminiferous tubule measurements. A factor analysis was used to verify the relation between seminiferous tubule measures, sperm concentration, animal weight at slaughter and gossypol level on diet. Animal weight at slaughter had a significant influence on all seminiferous tubule measures. The animals from the CAKE group had the lowest tubule diameter, lumen diameter and seminiferous epithelium thickness, while the animals that received MEAL had the largest tubule diameter and seminiferous epithelium thickness. The factor analysis showed that heavier animals had larger tubules measurements, as expected. The gossypol level in diet was not related to seminiferous tubule measures. Therefore, feed containing cotton co-products did not have a direct effect on seminiferous tubule measurements. Supported by CNPq and FAPESP.

Key Words: male reproduction, nutrition, testis

T331 Fatty acid profile of meat from lambs fed with cottonseed co-products. T. Paim[1], P. Viana[2], E. Brandão[2], S. Amador[2], T. Barbosa[2], C. Cardoso[2], B. Berenchtein[1], C. McManus[3], A. Abdalla[1], and H. Louvandini*[1], *[1]Center of Nuclear Energy in Agriculture, Piracicaba, SP, Brazil, [2]College of Agronomy and Veterinary, University of Brasília, Brasília, DF, Brazil, [3]Animal Production Department, University of Rio Grande do Sul, Porto Alegre, RS, Brazil.*

The amounts and type of fats in animal products is a topic of frequent public discourse. This study evaluated the changes in fatty acid profile of meat from lambs fed with cotton co-products, as well as, the impact of these diets on carcass traits. Twenty 4 lambs (5 mo old and mean live weight of 20.6 ± 1.9 kg), which received 4 diets: whole cottonseed (40% of concentrate (C)), meal cottonseed (40% of C), high oil meal cottonseed (Cake) (40% of C) and a control group without cottonseed co-products, were used. The concentrate:forage proportion in diet was 60:40. Soybean oil was added to concentrate in control, meal and cake diets, aiming to equalize the ether extract. After 90 d, the lambs were slaughtered and carcass traits were measured. Then, meat samples of Longissumus dorsi muscle at 12th rib were taken for fatty acid profile analyses. Carcass traits and fatty acid profile data were analyzed using GLM and FACTOR procedures in SAS®. The animals that received meal showed a higher hot carcass weight, carcass yield and rib eye area, being significantly greater ($P < 0.05$) than those that received whole cottonseed. This demonstrated that cottonseed meal is a good protein alternative source for lambs. The treatments not differ in fat content and proportion, nor ether extract in 12th rib. The meat from the group that did not received cotton co-products had higher n-3 fatty acid content, higher desirable fatty acids and better n-6 to n-3 ratio compared with others. The meat from animals that received whole cottonseed showed higher saturated fatty acids, related, principally, to higher palmitic acid (C16:0) and stearic acid (C18:0) levels. Animals that received meal and cake had the highest values to vaccenic acid (C18:2 t11) and conjugated linolenic acid (C18:2c9t11), demonstrating that these diets can produce a meat with high levels of CLA, which is good to human health. Therefore, aiming to reduce feed cost by using these cotton products, the recommendation is that the more processed cottonseed co-products (meal and cake) must be preferred for use in ruminant feed rather than whole cottonseed. Supported by CNPq and FAPESP.

Key Words: carcass traits, conjugated linolenic acid, muscle

T332 Inclusion of urea in spineless cactus diets for Girolando steers. R. A. S. Pessoa*[1], R. da Silva Lima[2], W. G. do Nascimento[2], I. Ferraz[3], and P. C. Vasconcelos[2], *[1]Universidade Federal Rural de Pernambuco, Animal Science Department, Recife, Pernambuco, Brazil, [2]Universidade Federal Rural de Pernambuco, Unidade Acadêmica de Garanhuns, Garanhuns, Pernambuco, Brazil, [3]Instituto Agronômico de Pernambuco, Recife, Pernambuco, Brazil.*

The objective of this study was to evaluate the effect of the substitution of cottonseed meal by urea in diets for Girolando steers (5/8 Holstein-Zebu) on the intake, apparent digestibility of nutrients, weight gain, feed conversion and efficiency of microbial protein synthesis. Eighteen animals were used with approximately 320 kg live weight and 24 mo of age, kept in feedlot system and assigned to a randomized block design, established in accordance with the weight of animals, being 3 treatments and 4 blocks. The treatments were 3 urea levels (0.0, 1.5 and 3.0%) in substitution of cottonseed meal (23.0, 11.5 and 0.0%) in diets based on spineless cactus with approximately 12.0% of crude protein and 65.0% of total digestible nutrients. The control diet was composed of 60.0% of spineless cactus, 15.0% of sorghum silage, 0.0% of urea:ammonium sulfate mixture (9:1), 23.0% of cottonseed meal and 2.0% of mineral mixture, in dry matter basis The experimental period lasted 84 d divided into 3 periods of 28 d. The data were submitted to ANOVA using the SAS. The intake and digestibility of dry matter were not influenced ($P > 0.05$) by the inclusion of urea in the diets (average of 7.9 kg/day and 69.0%, respectively). However, there was observed higher ($P < 0.05$) nonfibrous carbohydrate intake and neutral detergent fiber digestibility for control diet (0.0% of urea), being 2.89 kg/day and 48.0%, respectively. The feed conversion and weight gain were higher ($P < 0.05$) for the treatments with 0.0 and 1.5% of urea (average weight gain of 0.92 and 0.86 kg/day, respectively). The efficiency of microbial protein synthesis did not differ ($P > 0.05$) between treatments (average of 115.0g of microbial crude protein/kg of total digestible nutrient). The partial replacement of cottonseed meal by urea did not alter the performance parameters of Girolando steers feed diets based on spineless cactus.

Key Words: nitrogen, *Opuntia ficus indica*, performance

T333 Levels of roughage supplementation with cottonseed hull for cattle grazing during the rainy transition season: Performance. A. J. Neto*[1], J. T. Zervoudakis[1], L. da Silva Cabral[1], L. K. Hatamoto-Zervoudakis[1], R. L. Galati[1], P. V. R. Paulino[2], R. P. da Silva[1], L. C. R. P. Silva[1], J. Q. Soares[1], and A. P. de Souza Borges[1], *[1]Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil, [2]Federal University of Viçosa, Viçosa, Minas Gerais, Brazil.*

The objective was to evaluate levels of roughage supplementation with cotton hulls in the body weight of cattle grazing in the in the dry/rainy transition season on performance. Were used 20 Nelore steers with age and initial body weight average of 22 months and 366 kg, respectively. The experimental area consisted of four paddocks of 1.6 ha with *Brachiaria brizantha* 'Marandu' with forage mass for 1966.87 and potentially digestible dry matter of 1147.32 kg/ha. The experiment was structured in a completely randomized design in the levels of roughage supplementation with cottonseed hull as a function of body weight (BW) cattle, evaluated in relation to total weight gain and average daily gain (ADG) were: 3.6; 4.9 and 6.1 g / kg of the average body weight (BW). The roughage supplementation was given daily at 10 a.m. with the respective amounts: Cap1 - 1.5; Cap2 - 2.0 and Cap3 - 2.5 kg / animal and control animals (MM) were supplemented only with mineralized supplement (ad libitum). The performance was of 0.425 for MM and 0.438; 0.688 and 0.654 kg/animal/day for the respective levels of supplementation: 3.6; 4.9 and 6.1 g/kg of BW. There were differences ($P < 0.10$) between the levels of supplementation and the control group on average daily gain of animals, the level of 4.9 g/kg body weight, which provided better performance.

Key Words: coproducts, pasture, weight gain

T334 Blood cell and metabolic profile of Nellore bulls ranked by residual feed intake. K. K. G. Moreira[1], J. J. de Resende Fernandes*[1,4], T. P. Guimarães[1], E. A. Bento[3,4], E. Arnhold[1], H. F. Oliveira[1], M. D. de Freitas Neto[1,2], V. R. M. Couto[1], É. G. de Moraes[2], and L. F. N. Souza[2], *[1]Universidade Federal de Goiás, Goiânia, Goiás, Brazil, [2]Nelore Qualitas, Goiânia, Goiás, Brazil, [3]Instituto Federal Goiano, Rio Verde, Goiás, Brazil, [4]Conselho Regional de Medicina Veterinaria e Zootecnia, Goiânia, Goiás, Brazil.*

The objective of this study was to evaluate the possible differences in metabolic and blood profile among the classes of RFI (residual feed intake; los, medium and high) in Nellore bulls. Therefore, 30 animals (BW = 407.71 kg ± 34.71), with average of 24 mo of age, were used, and housed in individual pens. The animals were fed the same diet composed of 18.0% corn silage, 5.0% in natura sugarcane bagasse, 24.3% soybean hulls, 3.5% soybean meal, 46.8% sorghum, 0.8% urea and 1.6% mineral mixture. The animals were initially separated from a total of 120 in 3 treatments, high RFI (n = 10), medium RFI (n = 10) and low RFI (n = 10). RFI was calculated as the difference between observed and predicted feed intake based on LW 0.75 and average daily gain (ADG). Animals were classified as high RFI (>0.66 standard deviation - less efficient), medium RFI (±0.66 standard deviation), and low RFI (<0.66 standard deviation – more efficient). The results were analyzed by Pearson correlation using the statistical software R (2011) and mean comparisons were carried out by Tukey test at 5% probability level. No significant correlations ($P > 0.05$) were found among RFI and the variables erythrocytes and platelets; however, there were significant correlations ($P < 0.05$) for hematocrit, hemoglobin and leukocytes (0.38, 0.36 and −0.32, respectively). Regarding the biochemical profile, positive correlation was observed among RFI and total protein (TP) and total cholesterol (0.50 and 0.29, respectively ($P < 0.05$)). The RFI was not correlated ($P > 0.05$) with the other metabolic variables aspartate transaminase (AST), alkaline phosphatase (ALT), urea, creatinine, albumin (Alb) and gamma-GT (GGT). Among the classes of RFI (low, medium and high), the amount TP was lower for the group of animals with low RFI, which suggests an increased synthesis of tissue protein as plasma proteins play a fundamental role in this synthesis; the other variables did not differ among treatments.

Key Words: beef cattle, efficiency parameters, metabolism

T335 Carcass evaluation of subjected to feed restriction. A. R. C. Lima,* M. H. M. da Rocha Fernandes, I. A. M. de Almeida Teixeira, K. T. de Resende, and R. G. Aparecido, *Sao Paulo State University, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Sao Paulo, Brazil.*

Diet significantly affects costs of goat production, then alternatives to minimize the costs have been studied to evaluate if these alternatives can influence animal responses, such as carcass traits. One of the studied alternatives to minimize meat goat production costs is the use of feed restriction, then. The aim of this study was to evaluate the effect of feed restriction on carcass traits of 18 male crossbred (3/4 Boer 1/4 Saanen) goat kids, with initial BW of 20 ± 0.24 kg. The kids were randomly allocated to 3 levels of DMI: ad libitum (0%) and restricted to 30 and 60% of the ad libitum) within 6 groups (blocks). A group was slaughtered when the ad libitum treatment kid reached 35 kg BW. The hot carcass was obtained after separation of the hands and feet in the carpal metacarpal and tarsal metatarsal joint respectively, and the removal of the kidneys, kidney fat and diaphragm. The data were analyzed in complete randomized block Feed restriction had no effect on carcass biological yield percentage and loss by cooling, however hot carcass weight (0% = 17.4 kg, 30% = 14.2 kg, 60% = 10,1 kg), cold carcass weight (0% = 16.95 kg, 30% = 13.82 kg, 60% = 9.8 kg) and ribeye area (0% = 13.56 cm ^{3}, 30% = 12.10 cm ^{3}, 60% = 9.21 cm^3) decreased linearly ($P < 0.0001$) as level of feed restriction increased. Shoulder, neck and loin yields were not influenced by the level of feed restriction, on the other hand ribs yield decreased, while leg yield increased linearly with increasing level of feed restriction. It is concluded that increasing levels of feed restriction resulted in a reduction of hot and cold carcass weight, without affecting dressing percentage and cut yields, which are the main focus of the meat goat industry.

Key Words: Boer, intake level, prime cuts

T336 Carcass traits and meat quality of goats subjected to feed restriction. A. K. Almeida,* L. S. Fonseca, D. C. Soares, S. P. Silva, I. A. M. A. Teixeira, K. T. Resende, and H. Borba, *Universidade Estadual Paulista, UNESP, Jaboticabal, São Paulo, Brazil.*

The objective of this study was to evaluate the effect of feed restriction on carcass characteristics and meat quality of female, intact and castrated male goats. A total of 51 dehorned Saanen goats (18 intact males, 18 castrated males, and 15 females) were used. They were randomized allocated to one of 3 treatments (0, 25 and 50% restriction), the dry matter intake for the 0% restriction treatment animals determined the dry matter intake for the animals in the 25% and 50% restriction treatment. When the animals in the 0% restriction treatment group reached 44.1 ± 1.95 kg BW, the animals in the 25% and 50% restriction treatment groups were also slaughtered. After skinning and evisceration the hot carcass weight (HCW) was determined, the carcasses were placed in a chilled room for 24 h and chilled carcass weight (CCW) recorded. The carcasses were cut longitudinally into 2 halves and the left half was sectioned into retail cuts: neck, shoulder, brisket, 1–5 rib, 6–13 rib, chump and leg. The chump was stored for later analysis, after defrosting, the measures of pH, color (L* a* b*), shear force and cooking losses were performed. The data were analyzed as a completely randomized blocks design in a factorial scheme. Dressing percentage was not affected by feed restriction (mean of 45.9 ± 1.98). Chilling losses (g/kg HCW) were not affected by feed restriction (mean of 34.2 ± 3.14 g/kg HCW). Females showed greater subcutaneous fat deposition (1.3 ± 0.12 mm) then intact (0.7 ± 0.13 mm; $P < 0.001$) and castrated males (0.9 ± 0.11 mm; $P = 0.01$). The retail cuts evaluated (g) were affected by feed restriction and intact males presented heavier 1–5 rib ($P = 0.01$) and neck ($P < 0.001$) than females and castrated males, as result of sexual dimorphism. Color lightness (L*) and pH was influenced by the sex ($P = 0.03$ and $P = 0.04$, respectively). On the other hand meat redness (mean of 17.6 ± 0.38) and yellowness (mean of 6.3 ± 0.22), shear force (2.3 ± 0.08) and cooking losses (32.8 ± 1.69) were not affected by feed restriction neither sex. Despite of the changes caused by the level of restriction on goats BW, the extension of the changes did not affect goat meat quality. FAPESP process number: 2010/02482–4

Key Words: gender, kids, nutrition plan

T337 The relationship between feed efficiency and pancreatic α-amylase and trypsin activity in growing lambs. F. E. Doscher*[1], A. M. Meyer[2], M. J. Ellison[2], K. M. Cammack[2], and K. C. Swanson[1], [1]*North Dakota State University, Fargo,* [2]*University of Wyoming, Laramie.*

The objective of this study was to examine pancreatic protein, as well as α-amylase and trypsin activities in lambs fed concentrate- or forage-based diets with differing feed efficiency as measured by using residual feed intake (RFI). Seventy-seven growing wethers (51.3 ± 1.2 kg BW) predominantly of Rambouillet, Suffolk or Hampshire breeds were fed either an ad libitum concentrate- (CONC; corn-based) or forage-based (FOR; alfalfa- based) pelleted diet for a period of 49 d. Individual feed intake was measured using the GrowSafe Feed Intake system. Residual feed intake was calculated as the actual feed intake – expected feed intake (expected feed intake calculated from regressing metabolic midweight and ADG on actual DMI). The lambs were then ranked based on their RFI and the 20% most efficient (n=8) and 20% least efficient (n=8) lambs from each diet type (forage or concentrate) were slaughtered. The pancreas was removed and weighed, and a tissue sample was taken and immediately flash-frozen on dry ice. The sample was stored at −80°C until further analysis for total protein concentration and trypsin and α-amylase activity. Data were analyzed as a completely randomized design with a 2 × 2 factorial arrangement of treatments with RFI class, diet type, and the interaction in the model. No RFI × diet interactions (P > 0.10) were observed. Pancreatic weight (g) was greater (P = 0.09) in low RFI than high RFI lambs. Pancreatic protein (mg/g, g/pancreas, and mg/kg of BW), pancreatic α-amylase activity (U/g, KU/pancreas, and U/kg of BW), and pancreatic trypsin activity (U/kg of BW, U/pancreas, and U/kg of BW) did not differ (P > 0.10) between low and high RFI lambs. These results suggest that pancreatic weight may be greater in lambs with improved feed efficiency (low RFI), although α-amylase and trypsin activity are not associated with changes in feed efficiency in lambs fed concentrate- or forage-based diets.

Key Words: growing lambs, feed efficiency, pancreatic enzyme

T338 Effect of zinc concentration on performance and carcass characteristics of feedlot steers.

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Three-hundred sixty cross-bred steers (348.1 kg ± 28.9) were utilized to investigate the effects of Zn concentration on performance and carcass characteristics of feedlot steers. Steers were blocked by weight and randomly assigned to 1 of the 5 supplemental Zn treatments (8 pens per treatment; 9 hd per pen). Treatments consisted of: 1) Control (CON; 360 mg Zn/hd/d from $ZnSO_4$); 2) Methionine CON (360 mg Zn/hd/d from $ZnSO_4$ + MHA to equalize 2-hydroxy-4-(methylthio) butanoic acid (HMTBa) across all treatments; MHA contains 84% HMTBa and 12% Ca; 5.4 g/hd/d of HMTBa total); 3) 360 Zn (360 mg Zn/hd/d from Zn-HMTBa + MHA); 4) 720 Zn (720 mg Zn/hd/d from Zn-HMTBa + MHA); and 5) 1080 Zn (1080 mg Zn/hd/d from Zn HMTBa). All steers were fed a typical high concentrate steam-flaked corn based finishing diet twice daily. Steers were individually weighed on d −1, 0, 144, and 145 and pen weighed on d 28, 56, 84, and 111. Ractopamine HCl was fed for the final 29 d of the finishing period to all treatments. On d 145, steers were transported to a commercial abattoir for slaughter. Initial and final body weight, ADG, DMI, and feed efficiency (g/f), were similar across treatments. However, there was a trend ($P < 0.07$) for ADG to be increased when MHA® was added to the control diet when compared with 360 Zn, 720 Zn, and 1080 Zn treatments (4.01, 3.81, 3.79, and 3.93 ± 0.08, respectively). Fat thickness, longissiumus dorsi area, hot carcass weight, KPH, marbling score, and dressing percentage were similar across treatments. Steers receiving 1080 Zn had a greater ($P < 0.01$) yield grade compared with steers receiving 360 Zn (2.99 vs. 2.76 ± 0.08; respectively). There was a trend ($P < 0.07$) for steers receiving MHA® to have a greater yield grade compared with controls (2.82 vs. 2.67 ± 0.08; respectively). These data indicate that under conditions of this trial, increasing Zn concentration in the diet above NRC recommendations has little impact on performance, however, may impact lipid partitioning in steers.

Key Words: feedlot performance, ractopamine HCl, zinc

T339 Effects of feeding corn- or legume/grass silage-based diets on ruminal bacteria and archaea communities.

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Nine lactating cows (DIM = 75 ± 19; BW = 688 ± 66 kg) were used in a triple replicated 3 × 3 Latin square (31-d periods, 14-d adaptation) to examine the effects of replacing legume/grass silage with corn silage in the TMR on bacteria and archaea communities. Cows were fed (ad libitum) TMR (60:40, forage:concentrate ratio) with the forage portion being either legume/grass silage (0% CS), corn silage (100% CS) or a 50:50 mixture (50% CS). Total rumen content was sampled before and 4h after feeding and used for RNA extraction to target the metabolically active microbes. Changes in bacteria and archaea communities were monitored by quantitative and length heterogeneity PCR (qPCR and LHPCR) by targeting the *rrs* (bacteria and archaea) and *mcrA* (archaea) genes. To determine treatments effects, data were analyzed by the MIXED procedure of SAS with Tukey's adjustment. Significance was declared at $P \leq 0.05$. Quantitative PCR revealed that total bacteria, *Prevotella* spp. and archaea densities were greatest for 100% CS compared with 0 and 50% CS diets ($P < 0.05$), whereas the cellulolytic bacteria *F. succinogenes* and *R. albus* as well as the lactate-utilizer bacterium *M. elsdenii* populations remained similar among diets. Similarly archaea population number was greatest for 100% CS compared with 0% CS ($P < 0.05$) and 50% CS ($P < 0.1$), when the *mcrA* gene was targeted. The preliminary fingerprinting (LHPCR) results revealed that the diets changed the microbial structure. In a companion study, feeding 100% CS was associated with a decrease in enteric CH_4 emissions. This is in agreement with the increase in *Prevotella* spp. that favors propionate production which is a concurrent sinks to methanogenesis. On the contrary, the increase in archaea population while CH_4 production was reduced with 100% CS clearly demonstrates that CH_4 production is not directly linked with the number of archaea (*rrs* gene) or their activity (*mcrA* gene). As a conclusion, quantification of both *rrs* and *mcrA* genes is not accurate enough to reflect changes in rumen methanogenesis. Characterization of the community structure could bring more accurate information.

Key Words: archaea, methanogenesis, rumen

T340 Biochemical blood parameters and liver enzymes of Saanen dairy goats fed with diets containing tannin and polyethylene glycol supplement.

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Consumption of feeds containing tannins might lead to lower absorption of nutrients such as glucose and amino acids into the blood. Polyethylene glycol (PEG) reacts preferentially with condensed tannins and prevents the formation of tannin-protein complexes, therefore could be increase absorption of nutrients into the blood. In this study, 9 multiparous dairy goats after the peak of lactation were used in a 3 × 3 Latin square design with 21-d periods, including 14 d of adaptation followed by 7 d of sampling. The individual animals randomly distributed into metabolic cages to evaluate the effect pistachio hull (PH, source of tannin) and PEG (source of tannin binding) on the blood biochemical parameters. Three treatments were formulated: T1) Control, without PH, T2) 30% PH (DM basis) that provided 18.1 g condense tannin per kg DM of diet and T3) 30% PH + 1% PEG (DM basis). In T2 and T3, PH was replaced with alfalfa hay. Blood samples were taken from the jugular vein before and 3 h after morning feeding. Data were analyzed as a repeated measurement design using PROC MIXED of SAS ($P < 0.05$). BUN (Blood Urinary Nitrogen) was significantly decreased at T2 and was compensated by addition of PEG in T3. Plasma concentration of triglycerides in T2 and T3 was higher than control, although significantly in T3. There were no differences between plasma concentrations of glucose, total protein, albumin, and cholesterol. Liver enzymes such as alanine aminotransferase (ALT) and aspartate aminotransferase (AST) were stable. In conclusion, the negative effect of tannins on nitrogen metabolism can be covered by PEG supplementation.

Table 1.

	Experimental diets				
Plasma metabolite	Alfalfa	30% PH	30% PH+PEG	SEM	*P*-value
Glucose (mg/dL)	45.77	47.77	49.00	0.727	0.223
Total protein (g/dL)	8.21	7.97	8.03	0.064	0.312
BUN (%)	16.94^{a}	12.80^{b}	15.31^{ab}	0.491	0.014
Albumin (g/dL)	2.90	2.76	2.80	0.030	0.277
AST (U/L)	86.44	100.44	98.66	2.621	0.167
ALT (U/L)	57.66	62.05	60.50	2.284	0.599
Triglycerides (mg/dL)	1.88^{b}	2.44^{ab}	3.55^{a}	0.224	0.027
Cholesterol (mol/L)	2.83	2.99	3.08	0.103	0.723

[a,b]Means within same row with different superscripts differ ($P < 0.05$).

Key Words: tannin, blood, goat

T341 Levels of concentrate for crossbred Holstein-Zebu cows under grazing. C. P. Ghedini[1], R. P. Lana[1], A. S. Oliveira[2], J. Perottoni[4], D. C. Abreu*[1], R. L. Albino[1], J. E. P. de la Ossa[1], R. M. Paula[1], P. E. P. Barros[3], and F. G. Silva[1], *[1]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]Universidade Federal do Mato Grosso, Sinop, MT, Brazil, [3]Universidade Federal de Lavras, Lavras, MG, Brazil, [4]Universidade Federal de Santa Maria, Santa Maria, RS, Brazil.*

This study investigated the effects of increasing levels of concentrate on milk yield and composition in lactating crossbred dairy cows. Eight crossbred Holstein-Zebu cows (second or third parity; BW = 493 ± 22kg; DIM = 110 ± 82) in pasture were distributed in 2 4x4 Latin squares, in 4 periods of 14 d (samples collected on the last 7 d of each period). All cows were fed on tropical pasture during the rainy season (*Brachiaria decumbens* with 70% of NDF and 8% of CP) as a foraging source (ad libitum) and 4 levels of concentrate (0.6, 1.2, 2.4 and 4.8 kg/day/cow) with 24% of crude protein. The results were analyzed using Minitab. None of the 4 levels of concentrate had any affect on milk production ($P > 0.05$), milk composition ($P > 0.05$), or body weight ($P > 0.05$) (Table 1). This suggests that crossbred Holstein-Zebu under grazing can meet their nutritional demand with only pasture supply and 0.6 kg/day of concentrate with 24% of crude protein in the rainy season, because higher levels of concentrate did not increase milk production, milk composition, or body weight. Supported by Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) and CNPq.

Table 1. Milk yield and milk composition as a function of increased concentrate levels for crossbred Holstein-Zebu in tropical pasture

	Concentrate (kg/d/cow)				Effect (*P*-value)		
Item	0.6	1.2	2.4	4.8	Linear	quadratic	SED[1]
Milk yield, kg/d	12.4	13.1	12.0	12.2	0.07	0.06	0.35
3.5% FCM yield, kg/d	15.3	14.4	13.5	14.4	0.14	0.17	0.63
Fat, %	5.2	4.1	4.6	4.3	0.07	0.07	0.30
Protein, %	3.1	3.2	3.4	3.4	0.36	0.65	0.04
Milk solids %	13.8	12.8	13.4	13.2	0.13	0.12	0.29
BW, kg	499	487	503	481	0.98	0.98	15.0

[1]SED = standard error of the least squares means difference.

Key Words: crossbred milk cow, milk composition, milk yield

T342 The relationship between feed efficiency traits and fertility in young beef bulls. B. J. Awda*[1], S. P. Miller[1], Y. R. Montanholi[1], G. Vander Voort[1], T. Caldwell[1], M. M. Buhr[2], and K. C. Swanson[3], *[1]Department of Animal & Poultry Science, University of Guelph, Guelph, ON, Canada, [2]Department of Animal and Poultry Sciences, College of Agriculture & Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [3]Department of Animal Sciences, North Dakota State University, Fargo.*

The objective of this study was to examine the relationship between feed efficiency traits and bull sperm fertility (sperm motility, viability and scrotal circumference (SC)). From a total of 328 crossbred beef bulls that were subjected to a performance test (112 d), SC was measured and semen collected from 110 bulls (average age ± SE = 417.28 ± 2.55 d). Sperm were extended, cooled, and frozen in liquid nitrogen. Two residual feed intake (RFI) measures were considered with different prediction models for dry matter intake (DMI), RFI_{Koch} included size and growth rate and RFI_{bkft} included the additional adjustment for backfat thickness (BKFT). At the end of the experiment, bulls were slaughtered and a complete carcass separation of a 21-cm rib section conducted. Data were analyzed using the CORR procedure and Tukey-Kramer multiple comparisons to test for trait effect. Body weight (BW) was positively correlated with SC ($P < 0.001$) and DMI was positively correlated ($P \leq 0.05$) with sperm viability, motility, and SC. Feed to gain ratio (F:G) was positively correlated with sperm viability, and progressive motility ($P \leq 0.01$). RFI_{Koch} was positively correlated with sperm viability ($P < 0.05$). RFI_{bkft} was positively correlated with sperm viability and motility ($P \leq 0.05$). The percentage of subcutaneous, intramuscular, and total fat relative to total rib weight were positively correlated with SC ($P < 0.01$). BKFT was positively correlated with sperm viability ($P < 0.01$). Sperm viability, motility and progressive motility of the 10 bulls with the greatest RFI_{Koch} (Hi-RFI_{Koch}) were greater than that of the 10 bulls with the lowest RFI_{Koch} (Lo-RFI_{Koch}; $P < 0.05$, 0.01, and 0.05 respectively). Sperm motility ($P < 0.01$), progressive motility and SC ($P < 0.05$) of the 10 bulls with the greatest RFI_{bkft} (Hi-RFI_{bkft}) were greater than that of the 10 bulls with the lowest RFI_{bkft} (Lo-RFI_{bkft}). F:G for Hi-RFI_{Koch} or Hi-RFI_{bkft} was greater ($P < 0.005$ and 0.05 respectively) than that of Lo-RFI_{Koch} or Lo-RFI_{bkft} groups. In summary, these data indicate that the young beef bulls in this experiment with greater efficiency (low RFI, Koch and bkft) and F:G have decreased sperm motility, viability and SC.

Key Words: beef cattle, fertility, RFI

T343 Influence of tannins extract addition on feedlot-performance of bulls fed sorghum-based diets. R. Barajas*[1], B. J. Cervantes[2], M. A. Espino[1,3], A. Camacho[1], M. Verdugo[1], L. R. Flores[1], S. C. Aréchiga[1], J. J. Lomeli[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, [3]Pronutrient Developers, León, Guanajuato, México.*

Eighty *Bos taurus* × *Bos indicus* bulls 341 kg were used to determine the influence of tannins extract addition on feedlot-performance of bulls fed sorghum-based diets. Next day after arrival to the feedlot, bulls were weighed and blocked by initial weight, and in groups of 5 were placed in 16 ground floor pen (6 × 12 m). In agreement with a complete randomized block design, in each block, bulls were randomly assigned to one of next treatments: 1) Feeding with a finishing diet containing ground sorghum grain 61.83%, corn dry distiller grain 13.66%, peanut meal 1.77%, sugar-cane molasses 8.57%, mineral premix 2.86%, and corn straw 11.31% (Control); or 2) Diet similar to Control, added with

0.3% (dry matter basis) of a tannins extract (TE). Tannins extract was supplied as ByPRO (Pronutrient Developers; Mexico), a premix that contains 72% of a condensed (Quebracho tree) and soluble (chestnut) tannins-blend. In pens assigned to TE treatment, the corresponding amount of tannins extract was dispersed in 1 kg of ground sorghum that used as carrier and top dressed delivery in the feed-bunk. Pens in Control treatment received daily 1 kg of ground sorghum to equilibrate feeding conditions. Diet was offered ad libitum. Bulls were weighed in d 1 and 56. Day 28 blood samples were taken from jugular vein for plasma urea nitrogen (PUN) determination. Mean daily tannins extract intake was 33.6 g by bull, equivalent to 0.28% of the dietary DMI. At end of the experiment TE-fed bulls were 2.13% heavier ($P = 0.06$) than Control (452.13 vs. 461.75 kg). TE supplementation increased ($P = 0.05$) average daily gain 9.17% (1.972 vs. 2.153 kg/d). Tannin extract improved ($P = 0.02$) DMI 6% DMI (11.44 vs. 12.13 kg/d). Feed efficiency was not affected by treatments ($P = 0.30$). TE decreased ($P = 0.04$) the PUN concentration in 18% with mean values of 15.3 and 12.5 mg/dL for TE and Control bulls, respectively. Results suggest, that feeding an extract of condensed and soluble tannins in low dosage proximate to 0.3% of dietary DM, decreases PUN and increases feedlot-performance of bulls even when they are fed sorghum-based diets.

Key Words: bulls, feedlot-performance, tannins

T344 Performance of milking crossbred cows under pasture as a function of levels of concentrate in the diet.

D. C. Abreu*[1], R. P. Lana[1], A. S. Oliveira[2], C. P. Ghedini[1], R. M. Paula[1], R. L. Albino[1], F. G. Silva[1], and E. M. Balbino[1], *[1]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]Universidade Federal do Mato Grosso, Sinop, MT, Brazil.*

The effects of 4 levels of concentrate (1.0, 1.5, 2.0 and 2.5 kg/cow/day) with 24% crude protein on performance of milking cows were evaluated. Four crossbred Holstein-Zebu cows with 453 ± 35 kg were distributed in a 4 × 4 Latin square in 4 14-d periods for evaluation of effects of treatments. The experiment was conducted on brachiaria grass (*Brachiaria decumbens*) pasture in the rainy season and the concentrates consisted of corn meal and soybean meal. The milk production, milk components, and body weight were not affected ($P > 0.05$) by levels of concentrate (Table 1). Cows on pasture during the rainy season and producing 11 kg of milk/day can receive 1.0 kg/day of concentrate. Supported by Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) and CNPq.

Table 1. Milk yield and milk composition as a function of increased concentrate levels in diets of crossbred Holstein-Zebu cows

	Concentrate (kg/d/cow)				Effect (*P*-value)		
Item	1.0	1.5	2.0	2.5	Linear	Quadratic	SEM
Milk yield, kg/d	10.6	11.1	8.7	10.7	0.33	0.31	0.3424
Milk fat 3.5%, kg/d	11.5	12.5	12.2	13.1	0.14	0.16	0.2798
Fat, %	4.04	4.11	4.74	4.45	0.32	0.37	0.1787
Protein, %	3.45	3.25	3.68	3.40	0.85	0.83	0.1453
Milk solids %	12.9	12.9	13.8	13.2	0.50	0.54	0.3615
BW, kg	458	459	446	449	0.76	0.78	2.1880

Key Words: milk composition, pasture, performance

T345 Effect of supplementation of tannin-extract in corn silage based-diets on performance of growing bulls under commercial feedlot conditions.

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Three hundred and 14 *Bos indicus* × *Bos taurus bulls* 253.24 ± SE 10.20 kg were involved in an experiment to determine the effect of tannin-extract supplementation in corn silage based-diets on performance of growing bulls under commercial feedlot conditions. The study was conducted simultaneously in 3 feedlot yards in the State of Sinaloa in the Northwest of Mexico. In feedlot 1, 122 bulls were randomly placed in 2 ground floor pens; in feedlot 2, 120 bull-calves were allotted in 2 ground floor pens; and in feedlot 3, 72 bulls were positioned in 2 ground floor pens, in the 3 feedlots pens size was proximately 25 × 30 m, diets contained 40% of corn-silage, and dry-ground sorghum grain. Each feedlot integrated by 2 pens constituted a block, and the pen was considered as the experimental unit. In a completely randomized block design, inner each block, pens were randomly assigned to receive one of 2 dietary treatments: 1) Regular growing diets of the feedlot yard (Control); or 2) Diet similar to control supplemented with a tannin-extract (TE). Tannin-extract was supplied as ByPRO (Pronutrient Developers; Mexico), a premix that contains 72% of a condensed (Quebracho tree) and soluble (Chesnutt) tannin-blend, and was included in proportion equivalent of 0.3% of dietary DM. The animals were weighed at the beginning (d 1) and at re-implant time, that mean was 57 d (47, 61 and 63 d for feedlot 1, 2 and 3, respectively). Results of ANOVA indicated that final weight was not affected by treatments ($P = 0.14$), period weight gain was 5.4% higher ($P = 0.05$) in Bulls that received tannin with mean values of 93.36 vs. 98.37 kg for Control and TE, respectively. Average daily gain was increased ($P < 0.01$) 4.1% by tannin-extract supplementation, with means of 1.659 vs. 1.727 kg/d for Control and TE, respectively. Dry matter intake and feed efficiency were not altered by treatments ($P > 0.15$). It is concluded that tannin-extract supplementation improves feedlot performance of growing bulls fed corn silage-sorghum grain based-diets, under commercial feedlot conditions.

Key Words: growing cattle, performance, tannin

T346 Effect of pasture type and dietary lipid supplementation on animal performance, carcass composition and fatty acid composition of muscle and adipose tissue in lamb.

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Altering the fatty acid content of meat and other agricultural animal products has potential to benefit human health and create niche marketing opportunities for producers. The objective of this study was to determine the effects of red clover (RC) and tall fescue (TF) pasture types as well as different dietary lipid supplements on animal performance, carcass composition, and fatty acid content of muscle and subcutaneous adipose tissue (subQ) of the market lamb. Thirty-two Suffolk-cross ram lambs were randomly assigned to 1 of 2 pasture types for approximately 12 wk. Lambs were removed from pasture, transitioned to hay and grain and gradually introduced to 1 of 4 lipid supplements [soybean oil (SBO), 50% *c*9*t*11 and *t*10*c*12 conjugated linoleic acid (CLA) isomers + 50% SBO (C+S), enriched fish oil (FO) or control (no supplement)], receiving

50mL/d for 2 wk before slaughter. Lambs assigned to RC had 38.9% ($P \leq 0.01$) greater weight gains on pasture, 8.52% ($P \leq 0.08$) higher carcass weights and 20.7% ($P \leq 0.04$) higher fat depth measurements at the twelfth rib, when compared with lambs on TF. Lipid treatment had significant effects on carcass weight (SBO: 20.8, C+S: 21.6, FO: 19.6 and control: 21.7kg; $P \leq 0.001$). Fat depth at the twelfth rib was significantly affected by pasture type (RC: 11.9, TF: 9.42mm; $P \leq 0.05$) and lipid supplement (SBO: 10.5, C+S: 11.8, FO: 9.5 and control: 10.8mm; $P \leq 0.1$). In comparison to TF, RC tended to increase the fat content of the *longissimus dorsi* muscle from 11.3 to 12.3% ($P \leq 0.1$) while lipid treatment had no effect. There were significant effects of pasture on EPA (eicosapentaenoic acid) content of muscle (RC: 2.14%, TF: 1.61%; $P \leq 0.06$) and EPA and DHA (docosahexaenoic acid) content of subQ (RC: 0.08%, TF: 0.16%; $P \leq 0.03$ and RC: 0.10%, TF: 0.24%; $P \leq 0.05$, respectively), 5 wk post grazing. With no supplemental lipid, the EPA and DHA content of muscle and subQ tended to be greater in lambs that had grazed RC. Lipid supplementation significantly affected the EPA and DHA content of both tissues and the CLA content of subQ.

Key Words: lamb, pasture species, polyunsaturated fatty acids

T347 The effect of diet on feed intake traits and relationships with carcass traits in sheep.

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The objectives of this study were to 1) determine the effects of diet on feed intake traits, and 2) determine the relationship of residual feed intake (RFI) with carcass characteristics in lambs fed either a concentrate or forage-based diet. Growing wethers (initial BW = 51.3 ± 1.2 kg; n = 77) of Rambouillet, Hampshire, and Suffolk breed types were randomly allocated to receive a concentrate (CONC; 50% corn, 31% wheat middlings; 91.6% DM, 12.1% CP, 17.6% NDF, 2.98 Mcal/kg ME; n = 39) or forage-based (FOR; 67.7% alfalfa, 27.5% wheat middlings; 92.3% DM, 16.2% CP, 36.3% NDF, 2.31 Mcal/kg ME; n = 38) pelleted diet. Individual feed intake was measured by the GrowSafe System for 49 d, and BW was recorded weekly. The 20% most (n = 8) and the 20% least (n = 8) efficient wethers from each diet (n = 32 total) were slaughtered, and carcass data were recorded. The MIXED procedure of SAS was used to determine the effect of diet on feed intake, ADG, and G:F using data from all wethers (n = 77), and the effects of diet, RFI class (most or least efficient), and their interaction on carcass traits using data from selected wethers (n = 32); breed and pen were included as random effects. The CORR procedure was used to determine relationships between RFI and carcass characteristics. Overall, feed intake of CONC wethers varied less ($\sigma^2 = 0.08$) than intake of FOR wethers ($\sigma^2 = 0.21$); variation in ADG and RFI did not differ across diets. Feed intake and ADG were greater ($P < 0.001$) in FOR fed compared with CONC fed wethers, although G:F was not affected by diet type ($P = 0.23$). Boneless cut percentage tended ($P = 0.10$) to be greater in FOR versus CONC wethers; there were no other effects ($P > 0.13$) on carcass measures. Residual feed intake and USDA quality grade tended ($P = 0.10$) to be positively correlated, but no other relationships ($P > 0.17$) between RFI and carcass measures were found. These data suggest that feed intake and ADG are affected by diet type, and that greater variation in feed intake is associated with a forage-based pelleted diet. Furthermore, selection for RFI should not unfavorably affect carcass traits in sheep.

Key Words: carcass, residual feed intake, sheep

T348 Effects of roughage level and corn processing method on finishing performance of Nellore bulls.

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The objective of this study was to investigate the optimal level of NDF from forage (NDFf) for finishing *Bos indicus* cattle with high-concentrate, corn-based diets. Nellore bulls (n = 112; 384.1 ± 29.5 kg) were used in a randomized complete block design in a 4 × 2 factorial arrangement. Four NDFf levels from sugarcane silage (3, 8, 13 and 18% of diet DM) were evaluated for 2 corn processing methods (CPrc): high moisture corn (HMC) and finely ground dry corn (FGC). Animals were offered ad libitum access to diets delivered twice daily in individual pens. Sugarcane silage contained 64.0% NDF, corn had 77.2% vitreousness, and corn geometric particle sizes were 1.30 and 5.84 mm for FGC and HMC, respectively. Bulls were adapted to the finishing diet over a 21-d period and fed a total of 81 d. To determine fecal starch (FS) concentration, each animal was sampled by rectal palpation on d 46 and 74 of the feeding period. The first derivative was solved of a 2nd order polynomial to determine optimal NDFf level. There was a quadratic effect of NDFf ($P < 0.01$) on final BW and ADG, with 13% NDFf yielding the highest final BW and greatest ADG ($P < 0.05$). Gain efficiency was 12.2% greater ($P < 0.01$) for animals fed HMC compared with those fed FGC (0.172 vs. 0.151, respectively). An interaction was observed between CPrc and NDFf ($P = 0.05$) for DMI; peak DMI occurred with 11.3 and 13.7% NDFf for FGC and HMC, respectively. An interaction between CPrc and NDFf also was observed for FS ($P < 0.05$). Bulls fed FGC had a linear decrease in FS with increasing levels of roughage, while there was no change in FS for bulls fed HMC with different levels of NDFf. Average FS were 13% and 3% for FGC and HMC, respectively. In conclusion, HMC improved growth efficiency of Nellore cattle by 12.2%, and the level of NDFf required to optimize performance was dependent on method of corn processing.

Key Words: fecal starch, feedlot, zebu

T349 Estimation of carcass and body fat composition using biometric measurements of grazing beef cattle.

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The objective with this study was to develop equations to predict carcass and body fat compositions using biometric measures (BM) and body postmortem measurements and to determine the relationships between BM and carcass fat (CF) and empty body fat (EBF) compositions of 44 animals. Animals were from different crossbred genetic groups (at least 50% Nellore breed) with initial age of 8.4±0.8 mo and shrunk BW (SBW) of 203±35 kg. Animals were grazing under tropical conditions and receiving supplementation. Animals were serially slaughtered in four groups at approximately 84 d (n = 4), 168 d (n = 8), 235 d (n = 8), and 310 d (n = 24) of growth. The day before each slaughter, animals were weighed and BM were taken, including hook bone width (HBW), pin bone width (PBW), abdomen width (AW), body length (BL), rump height (RH), height at withers (HW), pelvic girdle length (PGL), rib depth (RD), girth circumference (GC), rump depth (RuD), body diagonal length (BDL), and thorax width (TW). Other measurements included were subcutaneous fat (SF), internal fat (InF), intermuscular fat (ImF), carcass physical fat (CF), empty body physical fat (EBF), fat thickness in the 12th rib (FT), and 9 – 11th rib section fat (HHF). The stepwise procedure was used to select influential variables. The r^2 and the root mean square error (RMSE) were used to select the equations. Results indicated that BM in association with SBW were precise in accounting for the variability of SF (r^2 = 0.967 and RMSE = 0.94 kg), InF (r^2 = 0.984 and RMSE = 1.26 kg), CF (r^2 = 0.981 and RMSE = 2.98 kg), and EBF (r^2 = 0.985 and RMSE = 3.99). The RD and GC were important in predicting CF and EBF variations. Results also suggested that approximately 70% of body fat was deposited as CF and 30% as InF. Furthermore, the equation with HHF and SBW as predictor of CF and EBF was more adequate than using HHF by itself. We concluded that the prediction of CF and EBF composition of grazing animals can be improved with BM.

Key Words: Adipose tissue, body composition, modeling

T350 Performance of dairy kids submitted to different sources of goat milk replacers.

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The health care and nutrition during suckling are essential for obtaining high productivity. During this period, attention should be given to diseases such as caprine arthritis encephalitis, which can be transmitted by goat milk and promote great morbidity, and decrease production. In addition, goat milk is expensive, and it is also the main source of income for producers. Thus, the objective was to evaluate the performance of kids fed alternative sources to replace goat milk. Forty-eight male kids of Saanen (24) and Alpine Brown (24) were randomly assigned to the treatments, and divided into age groups based on feeding milk for 60 or 90 d. They were offered coast-cross hay, starter ad libitum, and one liter of milk, or replacer, per day. The treatments were goat milk (GM), cow milk (CM), fermented cow colostrum (FC) and lactal - commercial milk replacer (LAC). The statistical analysis was conducted separately for animals fed 60 or 90 d. The data was analyzed as a completely randomized design, and a Tukey test was conducted when a P value less than 0.05 was observed. The average daily gain (ADG), empty body gain (EBG), and carcass weight gain (CWG) were measured after the slaughtering. Animals fed CM up to 90 d had greater ADG, and EBG, when compared with other treatments ($P < 0.05$). No differences were observed in CWG when comparing CM and GM ($P > 0.05$). The ADG, EBG, and CWG were not different for animals fed CM and GM up to 60 d ($P > 0.05$). The ADG in kg/day, for kids fed CM, GM, LAC, and FC up to 90 d, respectively, were 0.178, 0.145, 0.135, and 0.108; the EBG, in kg/day, were 0.143, 0.118, 0.106, 0.083, respectively, and the CWG, in kg/day, were, 0.075, 0.063, 0.055, 0.041, respectively. The ADG in kg/day, for kids fed CM, GM, LAC and FC up to 60 d, respectively, were 0.151, 0.135, 0.110, 0.070; the EBG, in kg/day, were 0.127, 0.113, 0.088, 0.051, respectively, and the CWG, in kg/day, were, 0.067, 0.060, 0.044, 0.023, respectively. In conclusion, kids fed CM have best performance, while feeding FC provide the worst performance. Supported by CNPq/INCT-CA.

Key Words: average daily gain, goat, suckling

T351 Early feeding of low levels of fat supplement suppresses postprandial in vitro rumen metabolism.

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The effects of time of low level fat supplementation on postprandial rumen metabolism were investigated with in vitro rumen fermenters. All fermenters were fed a basal diet of orchard grass hay in unequal portions throughout the day, with the largest meals being fed at 0600h and 1800h. Soybean oil was the fat supplement and was fed to fermenters at 3% of total daily dry matter. Control (C) fermenters did not receive any supplement at any time. Three supplementation times were tested. Supplement was introduced to fermenters at either 0600h (AM), 1800h (PM), or in evenly divided doses at both times (AP). Fermenter effluent samples were collected at eight 3-h intervals over a 21-h period and were analyzed to determine concentration of rumen metabolites (ammonia nitrogen; [NH_3-N], and volatile fatty acid; [VFA]). Fermenter pH was measured each time effluents were collected. Individual VFA concentrations for each sample were summed and reported as total volatile fatty acid concentration [TVFA]. A quadratic postprandial time × treatment interaction ($P < 0.001$) was observed for ruminal pH, [NH_3-N] and [TVFA]. Feeding 3% soybean oil suppressed postprandial [TVFA] between 12 to 18 h (AM and PM) and [NH_3-N] between 15 to 18 h (AM), but did not have similar effects when oil was fed in split doses (AP). The magnitude of suppression in [TVFA] was apparently lower with PM treatment compared with AM treatment. Postprandial ruminal pH fluctuated greatest in AM treatment and least in PM treatment. In AM treatment, postprandial pH increased ($P < 0.01$) by 3h, remained elevated until 9 h, and then declined to lowest ($P < 0.01$) values by 18 to 21 h. In AP treatment, postprandial pH was generally flatlined except for lowest ($P < 0.01$) pH by 15h which was lower ($P = 0.04$) than the pH at 6 h. Control treatment postprandial pH essentially flat lined, but pH at 15 h was greater than at 12 h ($P = 0$ 0.04). Postprandial PM treatment pH was also flat lined. Therefore, feeding low levels of soybean oil (3%) with the first meal fed to in vitro fermenters suppressed postprandial in vitro rumen metabolism.

Key Words: fat supplement, in vitro rumen, metabolism

Ruminant Nutrition: Young Stock

T352 Effects of limiting concentrate during growing period on performance and plasma variables, and gene expression of hepatic gluconeogenic enzymes in Holstein calves. J. D. Lohakare,* N. K. Singh, J. Ghassimi Nejad, K. I. Sung, and S. L. Ingale, *College of Animal Life Sciences, Kangwon National University, Chuncheon, Kangwon Province, South Korea.*

This study elucidated the effects of limited concentrate feeding on growth, plasma profile, and gene expression of gluconeogenic enzymes in the liver of dairy calves. The study utilized 12 Holstein male dairy calves (100 d of age) divided into 2 groups of 6 calves each for 155 d. Control group calves received 1.8 kg/(calf × day) of concentrate, whereas calves in the restricted group only received 1 kg/(calf × day). Good quality forage (Timothy hay) was available for ad libitum consumption to both groups. Body weights (BW) were recorded at start and at fortnightly intervals. Blood samples were collected at start and approximately 50 d interval. On d 100 and 155, liver biopsies were collected from all animals in each group. The BW was not different between the groups at the end of the study, however, at 6,7,8 and 9 fortnights higher ($P < 0.05$) BW were recorded in the control group than the restricted. Total BW gain in the control group was 114 kg as opposed to 98.2 kg in restricted group that led to average BW gain of 736 g/day and 634 g/day in respective groups, and the differences were significant ($P = 0.051$). As planned, the calves in the control group had higher concentrate and lower forage intake than the restricted group. The plasma variables (glucose, total protein, albumin, urea nitrogen, alanine aminotransferase (EC: 2.6.1.2) and amylase (EC: 3.2.1.1)) were within the normal range in both groups, but aspartate aminotransferase (EC: 2.6.1.1) was higher ($P < 0.05$) in control than restricted group and plasma triglycerides tended to be higher ($P = 0.069$) in restricted group than control. The mRNA expressions for the gluconeogenic enzymes, cytosolic phosphoenol pyruvate carboxykinase (EC 4.1.1.32) and pyruvate carboxylase (EC 6.4.1.1) measured by quantitative real-time PCR in liver biopsies showed no differences between groups. Overall, restricting concentrate moderately reduced the growth intensity without affecting the normal plasma indices and gene expression indicating that both concentrate feeding schemes can be successfully applied.

Key Words: calf, concentrate, gluconeogenic enzymes

T353 Plane of nutrition during the pre- and post-weaned periods influences the performance and innate immune activity of Jersey calves. D. L. Hanson*[1], C. J. Cobb[1], M. D. Sellers[1], T. J. Earleywine[2], and M. A. Ballou[1], [1]*Department of Animal and Food Sciences, Texas Tech University, Lubbock,* [2]*Land O'Lakes, Animal Milk Products Co., Shoreview, MN.*

Objective was to determine the influence of plane of nutrition during the pre- and post-weaned periods on the performance and innate immune activity of Jersey calves. Forty six (3 ± 1 d old) calves were randomly assigned to 2 treatments. Treatments were a low (LP; n=23) and high plane of nutrition (HP; n=23). Calves in LP treatment were fed 409 g/d DM of a 20/20 milk replacer; whereas calves in HP treatment were fed 610 and 735 g/d DM of a 28/25 during the 1st wk and wk 2-6, respectively. Weaning was initiated during the 7th wk by removing the PM feeding and calves were completely weaned when they were consuming 800 g of calf starter after d 49. Calves were fed their respective calf starter until the end of the study. Peripheral blood samples were collected on d 0, 7, 21, 28, 42 and 77 for biochemical analyses. Blood samples collected on d 7, 21, 42, and 77 were analyzed for ex vivo innate immune responses. As expected, metabolizable energy intake, crude protein intake, and average daily gain were greater ($P < 0.001$) during the pre-weaning period for HP calves. There were treatment × time interactions ($P < 0.001$) on plasma concentrations of glucose and urea nitrogen. Glucose concentrations were greater ($P < 0.01$) on d 21, 28, 42 and tended to be greater ($P < 0.10$) on d 77 among HP calves. Urea nitrogen concentrations tended to be greater ($P < 0.10$) on d 7 among HP calves, but were less ($P < 0.01$) than LP calves on d 42 and 77. Secretion of tumor necrosis factor-α from diluted whole blood when co-cultured with lipopolysaccharide was greater ($P < 0.05$) among HP calves on d 7. In contrast, neutrophil expression of L-selectin was greater ($P < 0.05$) among LP calves on d 7, 21, and 42. No treatment or treatment × time differences ($P = 0.798$) were observed for neutrophil oxidative burst capacities during the study. Lastly, plasma haptoglobin concentrations were decreased (P 0.05) among HP calves on d 21. These data suggest that HP may prime the pro-inflammatory response of calves on d 7, but that a LP increases the basal expression of L-selectin on circulating neutrophils during the entire preweaned period.

Key Words: calf, immune, plane of nutrition

T354 Influence of tannins-extract supplementation on plasma urea nitrogen concentration of bull-calves grazing Bermuda grass. D. González*[1,2], M. A. Espino[2], and R. Barajas[2], [1]*Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias. Campo Experimental Valle de Culiacán, Culiacán, Sinaloa, México,* [2]*Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México.*

Forty *Bos indicus* × *Bos taurus* bull-calves 176.43 ± SD 17.74 kg were used to determine the influence of tannins-extract supplementation on plasma urea nitrogen concentration of bull-calves grazing Bermudagrass. The experiment was performed from May 6 to June 3 of 2011 in the coast-plains of Sinaloa, localized in the Northwest of Mexico. Bull-calves were individually ear-tagged, weighed and randomly assigned to one of the next treatments: 1) Grazing in Bermuda paddock and receiving 1.5 kg/d of a protein supplement (Control); or 2) Similar to Control plus tannins-extract supplementation (TE). In groups of 20 bull-calves were placed in 2 3-ha paddocks of irrigated prairies of Bermudagrass (*Cynodon dactylon* L.), exclusively fertilized with feedlot cattle-manure. The protein supplement was formulate to contains 21% CP and 1.99 Mcal of NEm by kg of DM, and its composition was as follows: 70.5% Corn dried distillers grains with solubles, 10% ground corn, 2.5% sugar cane molasses, and 17% of sea salt. Protein-supplement was delivery daily in amount equivalent to 1.5 kg/animal. Bull-calves in TE treatment receiving daily 33 g of TMP-Protein Enhancer (Técnica Mineral Pecuaria, México) a premix that contains 56% of condensed and soluble tannins-blend. Tannins extract was incorporated in the protein supplement. In d 1 and 28, blood samples were taken from jugular vein for plasma urea nitrogen (PUN) determination. At the beginning of the experiment in d 1, plasma urea nitrogen concentration was similar ($P = 0.10$) between treatments, with mean values of 16.40 and 17.95 mg/dL for Control and TE treatments, respectively. In d 28, TE-supplementation decreased ($P < 0.01$) 21.6% PUN concentration, with means values of 15.75 and 12.35 mg/dL for Control and TE treatments, respectively. The results suggest that tannins-extract supplementation is able to decreases plasma urea nitrogen concentration of bull-calves grazing tropical grasses as Bermudagrass.

Key Words: tannins, plasma urea nitrogen, bull-calves

T355 The influence of grassland management and housing on voluntary dry matter intake in heifers. O. Latal*[1], J. Pozdisek[2], and J. Bezdicek[1], *[1]Agrovyzkum Rapotin Ltd., Vikyrovice, Czech Republic, [2]Research Institute for Cattle Breeding Ltd., Vikyrovice, Czech Republic.*

The aim of this study was to determine the voluntary dry matter intake (VDMI) of silage from grasslands managed in 3 ways. Fourteen experiments were conducted in 2010 on 2 groups of heifers, 6 per group (Czech Fleckvieh, 300 ± 15 kg LW) and housed in 2 ways: loose-box housing (4 automatic roughage intake control troughs) and tie-stall housing (manual feeding). Each experiment was divided into a habituation period (14 d) and a testing period (10 d). Grasslands were managed as follows: A [Medium Intensive Utilization] - 3 cuts per year, $N_{90}P_{30}K_{60}$ pure nutrients in kg per year and ha; B [Low Intensive Utilization] - 2 cuts per year, $N_{90}P_{30}K_{60}$; and C [Extensive (control) Utilization] - 2 cuts per year, nil-fertilization. The grass silage was made by cutting grass and leaving it to dry naturally in the field. After wilting, (dry matter 38%) the mowed fodder was compressed into round bales. The data were analyzed using GLM with the software R version 2.9.1. The results of the VDMI for each group of heifers was calculated in grams (dry matter) per metabolic body unit ($W^{0.75}$); next displayed as (g/MBU). Value of VDMI ($P < 0.01$) was higher in A (88.41 g/MBU, SE = 0.57) and B (72.14 g/MBU, SE = 0.60) than in C (68.34 g/MBU, SE = 0.63). Value of VDMI ($P < 0.05$) was higher too for the loose-box housing system (80.33 g/MBU, SE = 0.61) than the tie-stall housing system (74.42 g/MBU, SE = 0.65). On average from grasslands managed in 3 ways (from A to C), the NDF content rose from 486.8 to 571.1 g/kg dry matter (DM) and the net energy for lactation (NEL) decreased from 5.4 to 4.9 MJ/kg DM. There was a significant negative correlation between VDMI and the NDF ($r = -0.82$; $P < 0.05$), as well as a positive correlation between the VDMI and NEL ($r = 0.79$; $P < 0.05$). On the basis of the results, we can conclude that the value of the VDMI and nutrient intake was influenced by the grassland management (the higher the intensity of utilization, the higher the VDMI and nutrient intake) and housing system (greater VDMI was found for the loose-box housing).

Key Words: voluntary dry matter intake, grassland

T356 Effect of time of access to temperate forage on intake and digestibility of organic matter and fiber fractions in heifers. A. Félix[1], N. Hernández[1], P. Restuccia[1], S. Ruiz[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 forage (*Lolium multiflorum*, *Trifolium repens*; 19.1% CP, 48.2% NDF, 23.2% ADF DM basis) on OM, NDF and ADF intake (OMI, NDFI and ADFI, respectively) and apparent digestibility of OM, NDF and ADF (D_{OM}, D_{NDF} and D_{ADF} respectively). Pasture was daily cut and offered ad libitum as sole feed during 4, 6, 8 or 24 h from 0800 h (h0), for the treatments T4, T6, T8 and T24, respectively. Daily OMI, NDFI and ADFI were measured for 10 d as the difference between offer and refusal and D_{OM}, D_{NDF} and D_{ADF} were studied for 5 consecutive days determining the daily total amount of food consumed and feces produced. All data were compared between treatments using a mixed linear model. Mean OMI were 40.6, 54.9, 58.8, 70.3 g OM/kg $BW^{0,75}$ (SEM = 3.8), mean NDFI were 21.3, 29.1, 31.1 and 37.3 g NDF/kg $BW^{0,75}$ (SEM = 2.1) and mean ADFI were 10.6, 14.3, 15.3, 18.5 g ADF/kg $BW^{0,75}$ (SEM = 1.0) for treatments T4, T6, T8 and T24, respectively. Organic matter intake, NDFI and ADFI were lower ($P < 0.001$) in the more restricted animals (T4 and T6) than in T24, but no differences were detected between treatments T6 and T8, or T8 and T24. Apparent digestibility of OM, D_{NDF} and D_{ADF} were high for all treatments (mean values: 81.7% (SEM = 1.4), 69.7% (SEM = 3.4) and 55.6% (SEM = 5.5), respectively) with no differences among them ($P > 0.10$), despite the large differences observed in intake. We conclude that restricting time of access to a high quality pasture below 8 h reduced OMI, NDFI and ADFI, but it did not affect its digestibility.

Key Words: feed restriction, pasture

T357 Assessment of bone metabolism in pregnant heifers with high and low residual feed intake. R. Dias[1], J. Kim*[1], S. Lopez[2], Y. Montanholi[1], B. Smith[1], S. Miller[1], and J. France[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Universidad de León, Leon, Leon, Spain.*

It is known that ruminants with lower residual feed intakes (RFI) use nutrients more efficiently than animals with higher RFI. However, the biological reasons and metabolic consequences underlying the variation in RFI between animals are not clear. There is also no information on whether RFI is related to differences in bone metabolism. Within this context 26 pregnant heifers (13 low RFI + 13 high RFI) in their first trimester of gestation were used for a bone metabolism study. Their blood was sampled once in the morning before feeding through jugular catheterization for analysis of osteocalcin and crosslaps in serum. These compounds are biochemical markers of bone formation and resorption respectively considered important clinical tools for assessment and monitoring of bone metabolism. Both markers were determined quantitatively using an immunoassay kit specifically for bovines. The results showed a lack of difference between animals with high and low RFI in the concentration of osteocalcin in serum with average concentration of 27 ± 10.9 ng/mL similar for both groups ($P > 0.05$), indicating that the efficiency of feed utilization by pregnant heifers does not affect their bone formation. Likewise the concentrations of bovine crosslaps were similar between the 2 groups of animals ($P > 0.05$), though the more efficient animals had a mean concentration of 16 ± 10.3 ng/mL and the group of animals with higher RFI gave a mean concentration of 8 ± 7.7 ng/mL. These findings suggest bone resorption is not affected by feed efficiency in pregnant heifers. Thus, this research provides an indication that bone metabolism is similar for pregnant heifers with lower and higher RFI. However more research is needed to provide further information.

Key Words: bone marker, feed efficiency, pregnant heifer

T358 Dried citrus pulp alters feedlot performance of crossbred heifers during the receiving period. J. T. Cribbs*[1], T. R. Young[1], M. A. Jennings[1], N. C. Burdick[2], J. A. Carroll[2], T. R. Callaway[3], T. B. Schmidt[4], B. J. Johnson[1], and R. J. Rathmann[1], *[1]Texas Tech University, Lubbock, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]USDA-ARS, Food and Feed Safety Research Unit, College Station, TX, [4]Mississippi State University, Department of Animal and Dairy Science, Starkville.*

A study was designed to determine the effects of feeding dried citrus pulp pellets (DCP) on feedlot performance of newly received English × Continental heifers. Heifers (n = 180) were sourced in 2 loads (188.7 ± 18.0 kg and 225.2 ± 22.2 kg, respectively) from commercial auction barns and placed on trial at the Texas Tech University Beef Center in New Deal, Texas. A completely randomized block design was used by blocking by

BW nested within arrival load with 3 treatment diets being applied (36 pens; 5 heifers/pen; 12 blocks; 3 pens/block; 12 pens/treatment). Treatment diets were formulated to contain: 1) 0%; 2) 10%; or 3) 20% DCP on a DM basis. Diets containing DCP were formulated to be exchanged with steam flaked corn on a 1:1 basis. Cattle were fed a 63, 73, and 83% concentrate diet from d 0 to 28, d 28 to 42, and d 42 to 56, respectively. From d 0 to 28, there was a linear decrease in DMI ($P < 0.0001$) which resulted in a linear decrease in ADG ($P < 0.0001$) and G:F ($P < 0.01$) as the proportion of DCP in the diet was increased. From d 28 to d 42, DMI decreased linearly ($P = 0.02$) as the proportion of DCP in the diet increased; however, no difference in ADG was observed and G:F increased linearly ($P < 0.01$) in favor of treatments with a higher proportion of DCP. From d 42 to d 56, DMI did not differ across treatments, but ADG ($P = 0.02$) and G:F ($P = 0.04$) decreased linearly as the proportion of DCP in the diet increased. Over the entire 56 d trial period, as the proportion of DCP in the diet increased DMI decreased ($P = 0.02$; 6.70, 6.13, and 5.96 kg, for 0, 10, and 20% DCP, respectively), ADG decreased ($P < 0.0001$; 1.88, 1.27, and 1.00, respectively), and G:F decreased ($P = 0.02$; 0.225, 0.210, 0.91, respectively). Collectively, it appears that regardless of the level of roughage in the diet, the inclusion of DCP pellets at levels of 10% or greater lowers DMI such that feedlot performance suffers. Future studies will need to evaluate inclusion levels of DCP less than 10% or evaluate alternative processing strategies of DCP to offset the negative effects of DCP on intake in diets of newly received calves.

Key Words: newly received cattle, feedlot performance, citrus pulp

T359 Effect of time of access to temperate pasture on nitrogen utilization, digestibility of nitrogen and microbial protein synthesis in heifers.

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The aim of this study was to evaluate if the time of access to forage (*Lolium multiflorum*, *Trifolium repens*; 19% CP, 48% NDF, DM basis) affects the nitrogen (N) utilization, apparent digestibility of N (D_N) and the microbial protein synthesis (MPS) in heifers consuming temperate pastures. Twenty-four 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: T4, T6, T8 and T24 according to the time of access to fresh forage: 4, 6 8 or 24h/d, respectively. Pasture was daily cut and offered ad libitum as sole feed for all the treatments. Daily intake of N was measured for 10 d and D_N was determined for 5 consecutive days. Urine N was studied based on the daily total urine collected during 5 d. The retained N was calculated as: N intake (g/d) - (N removed in feces (g/d) + N eliminated in urine (g/d)). MPS was estimated by the determination of urinary purine derivatives excretion using the HPLC technique. All data were analyzed using a linear mixed model. The D_N was high for all treatments (mean value: 80.9%,SEM = 1.5) with no differences among them ($P > 0.10$), despite the large differences that were observed in intake. Mean N intake were 1.4, 1.9, 2.0 and 2.4 gN/kg $BW^{0.75}$ (SEM = 0.1, $P < 0.001$) for T4, T6, T8 and T24, respectively. The fecal excretion of N was higher for the T24 group than for the T4 group ($P < 0.001$). Similarly, there was a trend for the urinary N removal to increased for animals that were fed all day regarding to T4 group ($P = 0.07$). Animals in T4 had lower N retention than animals in T8 and T24 with mean values of 6.0, 24.3 and 30.1 gN/d (SEM = 3.5, $P < 0.001$). We observed a strong trend toward greater MPS for the unrestricted group (T24) than for the T4 group (46.7 and 20.0 gNM/d respectively; SEM = 7.2, $P = 0.057$). However, there was no difference between treatments ($P > 0.10$) in the efficiency of synthesis expressed as gMN/kgDOMI. We conclude that restricting time of access to forage reduced N intake that could have affect microbial protein synthesis.

Key Words: heifers, microbial protein, nitrogen utilization

T360 Comparison of pH, volatile fatty acids, and microbial quantification on rumen samples from young calves obtained via cannula or stomach tube.

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The objective of this study was to compare rumen samples from young dairy calves obtained via a stomach tube (ST) or a ruminal cannula (RC). Five Holstein male calves (46 ± 4.0 kg of BW and 11 ± 4.9 d of age) were ruminally cannulated at 15 d of age. Calves received 4 L/d of a commercial milk replacer (25% CP and 19.2% fat) at 12.5% DM, and starter and chopped oat hay ad libitum throughout the study (56 d). A total of 29-paired rumen samples, obtained at different ages by each extraction method, were used to determine pH, VFA concentration, and quantify *Fibrobacter succinogenes* by qPCR. A paired *t*-test was used to determine whether the evaluated parameters differed between the rumen samples obtained from the different methods. There was a difference ($P < 0.05$) of 0.30 pH units between ST and RC samples, being greater in ST than in RC samples. Furthermore, the total VFA concentration was greater ($P < 0.001$) in RC than in ST samples. However, when analyzing the proportion of each VFA, the method of sampling only affected ($P < 0.05$) the relative proportion of butyric, isovaleric, and valeric acid. Probably, saliva contamination diluted ST samples lowering the VFA concentrations and causing small changes in VFA profile. On the other hand, the quantification of *Fibrobacter succinogenes* by qPCR was not affected ($P = 0.43$) by the extraction method. In conclusion, when comparing rumen parameters from different studies, it is preferred to use VFA profiles rather than total VFA concentrations, as the latter is more affected by the method of collection. Furthermore, while pH comparisons across studies should be avoided when samples are not obtained by the same sampling method, the comparison of specific rumen bacteria can be acceptable.

Key Words: rumen cannula, rumen samples, stomach tube

T361 Effects of limiting concentrate during growing period on performance and plasma variables, and gene expression of hepatic gluconeogenic enzymes and visfatin in Korean native beef calves.

J. D. Lohakare*[1], S. S. Chang[2], N. K. Singh[1], E. G. Kwon[2], J. Ghassimi Nejad[1], K. I. Sung[1], and S. K. Hong[2], [1]*College of Animal Life Sciences, Kangwon National University, Chuncheon, South Korea,* [2]*Hanwoo Experimental Station, National Institute of Animal Science, RDA, Pyeongchang, South Korea.*

This study elucidated the effects of limited concentrate feeding on growth, plasma profile, and gene expression of gluconeogenic enzymes and visfatin in the liver of Hanwoo beef calves. The study utilized 20 Korean native beef calves (Hanwoo; 60–70 d of age) divided into 2 groups of 10 calves each for 158 d. Control group calves received the amount of concentrate as per the established Korean feeding standards for Hanwoo, whereas calves in the restricted group only received half the amount of concentrate as per standard requirements. Good quality forage (Timothy hay) was available for ad libitum consumption to both groups. Since calves were with their dam until 4 mo of age in breeding pens before weaning, the intake of milk before weaning was not recorded, however, the concentrate and forage intakes were recorded daily. Body weights (BW) were recorded at start and on 10–15 d interval. Blood samples were collected at start and at 50 d interval. On the final day of the experiment, liver biopsies were collected from all animals in each group. The BW was not different between the groups at all times, but tended to be higher ($P = 0.061$) only at final BW in control than restricted group. Total BW gain in the control group was 116.2 kg as opposed to 84.1 kg in restricted group that led to average BW gain of 736 g/day and 0.532 g/day in respective groups, and the differences were significant ($P < 0.01$). As planned, the calves in the control group had higher concentrate and lower forage intake than the restricted group. The plasma variables (glucose, total protein, albumin, urea, triglycerides, aspartate aminotransferase (EC: 2.6.1.1), alanine aminotransferase EC: 2.6.1.2) and amylase (EC: 3.2.1.1)) were within the normal range in both groups, but plasma total protein, and urea were higher ($P < 0.05$) in control than restricted group and aspartate aminotransferase, alanine aminotransferase levels were lower ($P < 0.05$) in control than restricted group showing the effects of diet. The mRNA expressions for the gluconeogenic enzymes such as cytosolic phosphoenol pyruvate carboxykinase (EC 4.1.1.32) and pyruvate carboxylase (EC 6.4.1.1), and visfatin measured by quantitative real-time PCR in liver biopsies showed higher expression ($P < 0.05$) in restricted group than control. Overall, restricting concentrate severely reduced the growth intensity and gene expression in liver and few plasma indices indicating that restricting concentrate in the feeding schemes during early growth for beef calves is not advocated.

Key Words: Hanwoo calves, concentrate, gluconeogenic enzymes

T362 How the provision of forage in pre-weaned calves affects performance and digestibility after weaning. Ll. Castells*[1], A. Bach[1,2], C. Montoro[1], E. M. Rodríguez[1], P. Ureña[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 performance and diet digestibility after weaning in young Holstein calves fed non-forage and forage-supplemented diets during the pre-weaning phase. Sixty female Holstein calves (BW = 39.5 ± 3.76 kg) were randomly assigned to one of the 2 dietary treatments according to age and BW. Calves were individually housed and bedded with wood shavings. Dietary treatments consisted on feeding a pelleted starter (19% CP, 19% NDF) without any forage supplementation during the pre-weaning phase, and oats hay (68% NDF) supplementation post-weaning (CTR) or the same starter and forage fed during the pre and post-weaning phase (OAT). All calves were offered 3 L of milk replacer (MR) at 12% DM fed twice daily until 28 d of age, from 29 to 44 d of age calves received 1.5 L of MR at 12% DM fed twice daily, and from 45 to 51 d of age calves received 1.5 L of MR at 12% DM. Animals were weaned at 52 d of age. Intakes of starter and forage were recorded daily and BW weekly. Two weeks after weaning, total tract apparent digestibility was determined in 6 calves per treatment. Data were analyzed with a mixed-effects model with repeated measures, except for digestibility values that had no repeated measures. Starter intake was greater ($P < 0.05$) in OAT compared with CTR animals (600 vs 503 ± 40.1 g/d, respectively) during the pre-weaning period. As a result, calves in OAT treatment grew faster ($P < 0.01$) than CTR animals (520 vs 419 ± 22.9 g/d, respectively) during the pre-weaning period. After weaning, OAT animals consumed more ($P < 0.01$) forage than CTR animals (146 vs 90 ± 11.7 g/d, respectively), but there were no differences between treatments in ADG and starter intake. Similarly, there were no differences in total tract apparent digestibility between treatments (78.3% DM digestibility, 43.0% NDF digestibility). Offering forage to young calves is necessary, and when offered early in life it allows improvements in growth before weaning.

Key Words: calves, forage, performance

Small Ruminant: Production

T363 The effects of confinement and protein levels on carcass traits of kids raised under mixed-species grazing system. S. Gebrelul,* L. Gray, R. Marshall, and C. Chisley, *Southern University Ag Center, Baton Rouge, LA.*

A long-term mixed-species grazing project was designed to determine the performance of goats and cattle grazing together or separately in continuous or rotational systems. To evaluate the carcass traits and lean yield, 50 kids that were born and weaned under the mixed-specie system were randomly assigned to 4 treatments in a 2 × 2 factorial arrangement. The treatments were housing (confinement vs. semi-confinement) and protein levels in the diet. Kids under confinement system were divided into 2 groups and fed ad lib rations which contained 13% or 16% CP. Kids under semi-confinement were allowed to graze on bermudagrass pastures during the day (for 8h) and supplemented with the same experimental rations during the night. After an adjustment period of 2 wk, live weights (LW) and BCS, (1 = thin, 5 = fat) were taken every 14 d for 8 wk. At the end of the study, 24 male kids (14 from confinement and 10 from semi-confinement groups) were humanely harvested and deboned for carcass study. Hot carcass weight and cold carcass weights (CCW), dressing percentages, cold carcass yield, live grades (LG, Selection 1, 2 or 3), conference grade (CG), fat score, etc. were taken at harvest. Ribs, shoulder, shank, leg, back, and neck were cut from each carcass, weighed and deboned to determine percent of lean meat (PLM) and weight of lean meat yield (WLM). Data were analyzed using SAS MIXED procedure where kids were considered random effects. Stepwise regression was used to determine best live measurement predictors for PLM and WLM. No differences in carcass weights were observed due to housing effect or level of CP in the diet. BCS was the best predictor for PLM ($r^2 = 0.34$) followed by LW and CG. LW was the best indicator for WLM ($r^2 = 0.89$) followed by BCS, CG and LG. WLM yield was significantly ($P < 0.05$) correlated with LW (r = 0.92), HCW (r = 0.96), BCS (r = 0.77), CG (r = −0.52), and LG (r = −0.86). Similar relationships were observed for PLM. Ribs, legs, shoulder, shank, back and neck cuts represented 29.4%, 25.2%, 15.1%, 10.1%, 8.6% and 5.6% of the total carcass weight, respectively. Based on these results, one can feed a lower CP level of 13% without negative effect on carcass traits and lean meat yield.

Key Words: mixed-grazing, carcass, goats

T364 Fatty acids profile in *Longissimus dorsi* of Santa Ines lambs fed with different energy levels. P. C. L. Arruda, E. S. Pereira,* P. G. Pimentel, G. M. B. Moreno, J. N. Rocha Junior, J. G. L. Regadas Filho, and R. M. Fontenele, *Federal University of Ceara, Fortaleza, Ceara, Brazil.*

Nutritional strategies have been used to modify the content and the concentrations of the different fatty acids in animal muscle. The assessment of the nutritional quality of lipids in ruminant carcasses has been performed based on the composition of fatty acids, through the determination of indexes that relate the content of saturated fatty acids (SFA), monounsaturated (MUFA) and polyunsaturated (PUFA) n-6 and n-3. The objective of this study was evaluated the influence of rations with different levels of metabolizable energy on the content of total lipids, cholesterol and fatty acid profile of the *Longissimus dorsi* of Santa Ines lambs. Twenty Santa Ines lambs were used, with age and BW of 50 d and 13.0 ± 0.56 kg, respectively, fed rations with different energy levels: 2.08; 2.28; 2.47 and 2.69 Mcal/kg DM. The animals were weighed weekly to follow the ADG and when the mean BW of the treatments reached 28 kg the animals were slaughtered. The reading of the esters of fatty acids was performed by gas chromatography. The atherogenicity (AI) index AI = [(C12:0 + (4 × C14:0) + C16:0)]/(ΣMUFA + Σn-6 + Σn-3), thrombogenicity (TI = (C14:0 + C16:0 + C18:0)/ [(0.5 × ΣMUFA) + (0.5 × Σn-6 + (3 × Σn-3) + (Σ n-3/Σn-6)]), relation between hypocholesterolemic and hypercholesterolemic fatty acids (h:H = (C18:1cis9 + C18:2n-6 + C20:4n-6 + C18:3n-3 + C20:5n-3 + C22:5n-3 + C22:6n-3)/(C14:0 + C16:0) and the sum of desirable fatty acid = MUFA + PUFA + C18:0 were calculated. The analysis of the lipid profile of the *Longissimus dorsi* muscle presented linear increasing and decreasing effect for the Cis-10 heptadecanoic acid (C17:1) and eicosatrienoic (C20:3), respectively, with the increasing levels of dietary energy. The levels of total cholesterol (mg/100g) decreased with the inclusion of energy in the diets. The relations PUFA:SFA (0.13), PUFA:MUFA (0.12), MUFA:SFA (0.97), desirable fatty acids (66.3), n-6:n-3 (2.19), atherogenicity index (0.63), thrombogenicity index (1.63), relation between hypocholesterolemic and hypercholesterolemic fatty acids (1.98) and the relation (C18:0+C18:1):C16:0 (2.54) were not affected by energy levels ($P > 0.05$). Variation of the energy levels in total mixed rations to lambs influences the lipid profile in *Longissimus dorsi* of Santa Ines lambs.

Key Words: atherogenicity index, lamb meat, unsaturated fatty acids

T365 The effect of induction hypothyroidism on carcass quality and performance in lamb. Y. Baghcheghi,* A. Yousefi, A. Z. Shahneh, M. G. Khanlo, and M. Poorhamdollah, *University of Tehran, Karaj, Tehran, Iran.*

This study was conducted to investigate the effect of induced transient hypothyroidism by propyl-2-thiouracyl (PTU) on the carcass characteristics of Lori-Bakhtiari lambs. In a completely randomized design, 18 Lori-Bakhtiari male lambs (36 ± 4 kg BW, 5 mo old) were divided to 3 groups (n = 6) and subjected to one of 3 treatments: control (C: 0 mg PTU/kg BW), low (L: 10 mg PTU/kg BW), or high (H: 20 mg PTU/kg BW) dose by gavages. Animals were assigned in single pens (2 × 2 m) under ambient conditions for 60 d. Lambs had ad libitum access to fresh water and a fattening diet. Blood samples were collected every week using sterile vacuum tubes before feeding at 8:00 a.m., weekly. Plasma was separated and stored at −20°C before determination of thyroid hormone concentrations. At the end of experimental period, lambs were slaughtered for determination of carcass characteristics. Mean concentrations of T4 and T3 decreased significantly in L and H groups compared with C group (0.72 ± 0.06, 0.90 ± 0.06 and 2.27 ± 0.06, respectively, $P < 0.05$). There were no significant differences among treatment in carcass length, longissimus muscle cross section area, weight of primal cuts, weight of offals, and ADG ($P < 0.05$). Average feed conversion (G: F) ratio in H and L groups improved compared with C group (6.7 ± 0.39, 7.4 ± 0.39 and 8.9 ± 0.39, respectively, $P < 0.05$). Weight percentage of heart decreased in induced hypothyroidism groups (L and H) compared with C group (0.77 ± 0.03, 0.73 ± 0.03 and 0.92 ± 0.03 respectively, $P < 0.05$). Decreased percentages of heart weight and G:F might be a result of decreased basic metabolism in induced hypothyroidism groups.

Key Words: hypothyroidism, meat quality, Lori-Bakhtiari

T366 Effect of transient hypothyroidism on lamb's meat quality. Y. Baghcheghi*[1], A. Z. Shahneh[1], A. Yousefi[1], M. Poorhamdollah[1], and M. Joki[2], *[1]Department of Animal Sciences, University of Tehran, Karaj, Tehran, Iran, [2]Department of food Sciences, University of Tehran, Karaj, Tehran, Iran.*

This study was conducted to investigate the effect of induced transient hypothyroidism by propyl-2-thiouracyl (PTU) on the meat quality of Lori-Bakhtiari lambs. Eighteen Lori-Bakhtiari male lambs (Average BW, 36 ± 4 kg and 5 mo of age) were divided to 3 groups (n = 6) and received one of the 3 treatments as Control (C: 0 mg PTU/kg BW), Low (L: 10 mg PTU/kg BW) and High (H: 20 mg PTU/kg BW) by gavages during 60 d of experimental period. Lambs had free access to fresh water and were fed ad libitum with fattening diet. Blood samples were collected by sterile vacuum tubes before feeding, weekly. At the end of experimental period, lambs were slaughtered and meat quality was determined on *longisimus dorsi* muscle. Data was analyzed by GLM and Mixed procedure of SAS. Mean concentration of T4 and T3 decreased significantly in H and L groups compared with C group (0.72 ± 0.06, 0.90 ± 0.06 and 2.27 ± 0.06, respectively) ($P < 0.05$). There was no significant difference among treatment for pH, chemical composition and shear force value of *longisimus dorsi* muscle ($P < 0.05$). H group had higher ($P < 0.05$) L* (lightness) compare with L and C group (43.0 ± 0.72, 45.2 ± 0.72 and 45.8 ± 0.72, respectively). There were no differences ($P > 0.10$) regarding a* (redness) and b* value among treatments ($P < 0.05$). Hypothyroidism decreased ($P < 0.05$) H and L group cooking loss compared with C group (0.38 ± 0.01, 0.39 ± 0.01 and 0.43 ± 0.01, respectively) ($P < 0.05$). We concluded that, using 10 and 20mL/kg BW of PTU could induce hypothyroidism leading to changes in color and cooking quality of lamb's meat.

Key Words: hypothyroidism, meat quality, Lori-Bakhtiari

T367 Biochemical and hormonal response and chemical composition of milk following ACTH administration in goats fed lemongrass (*Cymbopogon citratus* (DC.) Stapf). T. S. Canaes*[1], S. N. Macedo[1], C. G. Lima[1], V. A. Pimentel[2], and J. A. Negrão[1], *[1]Sao Paulo University, Sao Paulo, Sao Paulo, Brazil, [2]Federal University of Espirito Santo, Sao Mateus, Espirito Santo, Brazil.*

It is evidence that lemongrass can be used as tranquilizer. The aim of this study was to evaluate 4 levels of lemongrass (LG) and their influence on the intravenous ACTH to mimic a stressful response on hormonal (cortisol) and biochemical responses (glucose, urea, creatinine, albumin, cholesterol and HDL cholesterol), milk yield and physico-chemical composition of goat's milk. Forty-four Saanen goats 3 yr of age at 75 d of lactation, BW of 59.2 ± 2.69 kg; BCS of 3.0 and milk yield of 2.58 ± 0.27 kg were used. The animals were kept in 4 feedlot pens (11goats/pen) during 152 d. Four diets were used (roughage:concentrate of 53:47) and provided once a day after milking. The variation was the substitution of corn silage (CS) by lemongrass (LG): T1 control (100% CS), T2 (33.5% LG), T3 (66.5% LG) and T4 (100% LG). They were injected 0.6 IU/kg of BW of ACTH into the jugular vein after 142 d of diet and before the daily feeding. Sterile saline solution was used as the control. Blood samples were collected at 20 min before and 0, 60, 120 and 300 min after application of ACTH. The interval between injection of saline and ACTH was 7 d. The biochemical and hormonal profiles were measured by commercial kits. Milk yield and composition were evaluated for 3 d following application of ACTH. PROC MIXED in SAS 9.1 was used with a repeated week statement to analyze plasma results. Orthogonal contrasts were used to determine the linear and quadratic effects of LG. There was quadratic effect in DMI as the addition of LG was increased. Cortisol concentration was affected ($P < 0.05$) by ACTH and time but not by LG and increased in the plasma of ACTH-treated goat's immediately after application and remained increased throughout 120 min sampling period. The LG in the diet had an influence on concentrations of blood glucose in animals subjected to ACTH application but the interaction of ACTH × LG was observed only in T1. There was no interaction between time groups (saline or ACTH) or diets for the others biochemical variables in plasma. The LG increases the milk yield for T3, but did not change milk composition.

Key Words: cortisol, goat milk, stress

T368 Forage yield and quality changes in mixed cattle and goats grazing practices. Y. Ghebreiyessus,* S. Gebrelul, M. Berhane, and R. Payne, *Southern University Ag Center, Baton Rouge, LA.*

To evaluate the effect of mixed-species grazing on forage yield and quality, 80 Spanish goats and 28 Brangus cows were randomly assigned to continuous or rotational grazing systems, and 3 grazing schemes (goats alone, cattle alone, and goats mixed with cattle) in a 2x3 factorial arrangement of treatments. A forage field of 31 ha of bermudagrass was divided into 6 pastures, 8 ha each for mixed-species grazing, 2 ha each for goats-alone grazing and 5.5 ha each for cattle-alone grazing. The rotational pastures were further divided into 4 paddocks and each paddock was grazed for 7d and allowed to rest for 21d. Animals were stocked at 0.8 ha/AU. Forage samples were collected weekly to determine plant height, forage yield and quality. Forage available for consumption by animals was estimated as the difference of yield of forage from un-grazed (inside a ring) and grazed plots. Forage consumption per animal per day was then determined by multiplying the available forage by the grazing area and dividing the result by the number of animal days. Five goats were assumed to be equivalent to a cow. Data was analyzed using SAS GLM procedure. Plant height ranged from 16 cm in June to 35 cm in April and was significant ($P < 0.05$) in all treatments, including months, years, grazing species, grazing systems, specie x grazing interaction. Available forage yield range was 756 to 2,394 kg/ha in June and April, respectively, while forage available for consumption ranged from 253 to 841 kg/ha for the same period. There was no difference ($P > 0.05$) in available forage between cattle-alone and mixed with goats, indicating presence of goats did not affect negatively the potentially available forage. However, consumption per cow was higher in cattle-alone treatment. Goat consumption of 6.7 kg/hd/d was the lowest ($P < 0.05$) despite the highest available forage. Crude protein content ranged from 8.9 to 11.8%. Acid detergent fiber and NDF values ranged from 31.9% to 39.1% and 47.1 to 62.2% respectively. None of the forage quality measures were affected ($P > 0.05$) due to main effects of months, years, grazing species, grazing systems or interactions. Results demonstrated that goats could graze with cattle without bringing any negative effects to cattle's performances.

Key Words: mixed-grazing, goats, forage quality

T369 Quantitative traits of carcass of Ile de France lambs fed diets containing different percentages of hay mulberry. V. T. Santana, A. G. Silva Sobrinho, L. G. A. Cirne,* V. Endo, N. L. L. Lima, F. A. Almeida, G. M. Manzi, and N. M. B. L. Zeola, *Universidade Estadual Paulista, Jaboticabal, São Paulo, Brazil.*

Alternative protein sources such as mulberry hay can partially or totally replace concentrate feeds commonly used in intensive sheep production system in Brazil. It is essential to study the effect of such rations on quantitative carcass characteristics. This experiment was conducted to evaluate the quantitative carcass traits of Ile de France lambs fed diets containing various percentages of mulberry hay. Twenty-four Ile de France lambs (15.0 kg BW, 3 mo old) were confined in individual stalls and fed one of 3 diets: sugar cane + concentrate with 0.00% mulberry hay; sugar cane + concentrate with 25.0% mulberry hay; or sugar cane + concentrate with 50.0% mulberry hay. The sugar cane was used as forage (variety IAC 86–2480) that gave a total dietary roughage to concentrate ratio of 50:50, with 10.0% surplus allowance. The confinement period comprised of 80 d, and the first 14 d were allowed for adaptation of animals to the diet and the stalls. The data were analyzed using SAS as a completely randomized design, with 3 treatments (n = 8), and the means were compared using the Tukey test. The lambs were slaughtered at 32.0 kg BW and carcasses were weighed to obtain the HCW and kept in cold storage at 6°C for 24 h, to assess the cold carcass weight (CCW). The HCW (14.1 kg) and CCW (13.7 kg) were not affected ($P > 0.05$) by different percentages of mulberry hay in the diet. There was also no difference ($P > 0.05$) in empty BW (25.9 kg) and true yield (54.7%). The results showed that inclusion of mulberry hay in the diet did not alter carcass characteristics, indicating that it can be used in lamb feeding without negative effects on production.

Key Words: confinement, protein sources, sheep

T370 Relationships among internal fat depots and subcutaneous fat in sheep.

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The understanding of the relationships among the different adipose tissue depots as well as accurately predicting their masses is critical for animal growth modeling. Thus, the aims of this study were 1) to evaluate the phenotypic correlations among internal fat masses and subcutaneous fat thickness in sheep and 2) to predict the internal total fat mass using KPH fat weight and subcutaneous fat thickness information. Sheep in this study were either Texel-cross or Santa Ines-cross, 6 to 61-mo old and 27.3 ± 6.5 kg empty BW, composed of ewes (n = 7), ewe lambs (n = 15) and ram lambs (n = 26). Ewes were grazing (*Brachiaria* spp.) whereas ram and ewe lambs were feedlot finished before slaughter. The sum of kidney, pelvic and heart fats (KPH, kg), the mesenteric (MES, kg) and omental (OME, kg) fats were measured at slaughter. The subcutaneous fat thickness was measured 24 h postmortem (0 to 2°C) on the *Longissimus dorsi* muscle, at the 12th-13th rib region. Pearson correlation analyses were carried out. Simple and multiple regressions were employed to generate prediction equations with VISC as the dependent variable and both SFT and KPH as predictors. Linear and quadratic terms were tested. High correlations of KPH with OME, MES and VISC were observed (0.79; 0.70 and 0.92; $P < 0.001$). However, the correlations were only moderate between SFT and OMEN (0.43; $P < 0.01$) and between SFT and VISC (0.43; $P < 0.01$). Correlations between SFT and MES (0.20; $P = 0.12$), and between SFT and KPH (0.53; $P = 0.0001$) were both non-significant and moderate, respectively. The equation generated for predicting VISC as a function of KPH was VISC, kg = 0.31571 + 2.51105*KPH, kg ($R^2 = 0.8418$; RMSE = 0.214 kg). SFT did not entered ($P > 0.05$) in the model with KPH as predictor. The prediction equation using SFT as independent variable was VISC, kg = 0.68429 + 0.2508*SFT, mm ($R^2 = 0.1826$; RMSE = 0.4867 kg). No quadratic terms were significant for both KPH and SFT. The KPH fat weight, unlike SFT, is highly correlated with the fat mass presented on the gastrointestinal tract. Accordingly, the KPH fat but not SFT can be used to predict the total internal fat mass in sheep with relative accuracy.

Key Words: channel fat, visceral fat, *Ovis aries*

T371 Impact of different stocking rates of goats under pine silvopasture systems on understory biomass, crown cover density, and animal productivity.

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Meat goat production has potential to be integrated into the pine silvopasture systems as a means of supplemental income for forest land owners. Objectives were to determine changes in understory plant biomass, crown cover density and animal productivity using different goat stocking rates. A completely randomized design was used on an 11 years old loblolly pine silvopasture systems at the Federation of Southern Cooperatives in Epes, Alabama with 36 Kiko male goat kids ((21.0 ± 1.04 kg initial BW and 4 to 5 mo of age) using low (L; 4 goats/acre), medium (M; 8 goats/acre), and high (H; 12 goats/acre) stocking rates from July through October, 2011. Goat BW, understory plant biomass and plant cover density (CD) were determined before and at the end of grazing. The initial understory plant biomass was similar among treatments ($P > 0.05$) but decreased linearly ($P < 0.05$) with increasing stocking rates at the end of grazing. Goats were similar in BW at the start and at the end but did not grow as expected. Although the initial CD values were similar among treatments ($P > 0.05$), a significant treatment x height interaction was detected for the final CD values. Differences among treatments were detected ($P < 0.05$) at the lower heights (0.5 m and 1.0 m), but no differences among treatments were detected at heights above 1.0 m. Overall fecal DOM and CP ratios were 4.9, 5.1, and 4.8 for L, M, and H stocking rates, respectively and were not different among treatments ($P > 0.05$) indicating that the diet quality selected by goats were similar. Based on these data, goats can be utilized to minimize understory up to 1.0 m in pine silvopasture systems; however, feed supplementation may be required to improve animal performance.

Key Words: meat goats, silvopasture, stocking rate

T372 Influence of trenbolone acetate and estradiol ear-implant level on feedlot-performance of hair lambs.

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Four hundred and 80 hair lambs (21.83 ± SD 2.28 kg) were used to determine the influence of trenbolone acetate and estradiol ear-implant level on feedlot-performance of hair lambs. Lambs were weighed, grouped by initial weight in 4 blocks of 120 lambs, and placed in 4 × 5 m elevated pens fitted with plastic-slot floor (30 lambs per pen). Each block contained 4 pens, and the pen constituted the experimental unit. In a complete randomized block design experiment, inside of each block, pens were randomly assigned to receive one of 4 treatments: 1) Feedlot diet without additional implant (CTRL); 2) Ear-implanted with 20 mg of trenbolone and 4 mg of estradiol (T20); 3) implanted with 40 mg of trenbolone and 8 mg of estradiol (T40); and 4) implanted with 60 mg of trenbolone and 12 mg of estradiol (T60). Trenbolone /estradiol levels were obtained with the application of one, 2 or 3 pellets contained in the regular implant-cartridge of Component TES (Elanco). Lambs were weighed on d 1 and 30. Results were analyzed by ANOVA and the quadratic trend tested by polynomial contrasts. Final weight showed a quadratic response ($P = 0.02$) to implant-level with values of 27.7, 28.3, 28.5 and 28.4 kg for CTRL, T20, T40 and T60 treatments, respectively. A quadratic trend ($P = 0.03$) was observed in ADG, with mean values of 195, 216, 223 and 220 g/day for CTRL, T20, T40 and T60 treatments, respectively. Dry matter intake was not affected by implant level ($P > 0.30$). Gain:feed ratio responded in a quadratic form to implant-level ($P < 0.01$), with mean values of 207, 229, 229, and 222 g of gain/kg of DMI for CTRL, T20, T40 and T60 treatments, respectively. It is concluded that implants containing trenbolone and estradiol improves performance of feedlot lambs, and that dose of 40:8 of trenbolone-estradiol induces the highest biological response.

Key Words: feedlot-performance, lambs, trenbolone

T373 Femur biometry and densitometry of Saanen goats subjected to feed restriction. D. C. Soares,* K. T. Resende, A. K. Almeida, S. P. Silva, M. H. M. R. Fernandes, E. M. Oliveira, S. M. B. Artoni, and I. A. M. A. Teixeira, *UNESP/Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil.*

The aim of this study was to evaluate the effect of sex and feed restriction on biometric aspects and bone mineral density (BMD) of femurs from 51 growing goats (18 non-castrated males, 18 castrated males, and 15 females) with initial BW of 30 ± 0.21kg. The animals were randomly allocated into 17 groups (blocks) of 3 animals of the same gender, subjected to 0, 25 or 50% feed restriction. A group was slaughtered when the animal set in the 0% restriction reached 44.1 ± 1.95 kg BW. After slaughter and evisceration, the carcasses were weighed and cooled at 4°C for 24 h. At the end of this period, the femur of the left leg of each animal was removed for further analysis. The BMD assessment craniocaudal radiographs were taken of femur using a Lunar DPX (DEXA). In the femur, the following measurements were made: weight, length (LE), diameter of the diaphysis (DDIA) and the proximal (DPE) and distal (DDE) epiphysis, length of the latero-lateral (LLD) and craniocaudal (LCCD) diaphysis. The data were analyzed as a randomized block design in a factorial scheme (3 × 3) using SAS. The BMD decreased linearly as feed restriction increased (ranged from 1.02 to 0.83 g/cm^2) and it was greater for female (0.96 g/cm^2) and male (0.93 g/cm^2) than for castrated (0.87 g/cm^2). The biometrics variables were not affected by level of feed restriction, except for femur weight and LE that decreased linearly ($P < 0.001$) as feed restriction increased. All biometric variables were affected by gender ($P < 0.05$), except for LLD (17.74 ± 0.19 cm). The biometric variables DPE, DDE and DDIA were greater ($P < 0.05$) for male (14.1 cm, 17.0 cm and 7.0 cm, respectively) and castrated (14.9 cm, 17.1 cm and 6.9 cm, respectively) than for female (13.1 cm, 15.8 cm and 6.8 cm, respectively). The LCCD was greater for male (19.8 cm) than for castrated (19.1 cm) and female (18.6 cm). In conclusion, BMD is affected by gender and nutritional levels, emphasizing its importance as a tool to investigate bone metabolism in goats (FAPESP project number 2011/04786–3).

Key Words: bone, density, nutrition

T374 Influence of dry period length on blood leukocyte subsets of Sarda dairy ewes and their offspring. P. Bonelli[1], C. Carzedda[2], A. Fenu[2], G. Spanu[2], C. Dimauro*[2], R. Re[1], P. Nicolussi[1], and SPG Rassu[2], [1]*Istituto Zooprofilattico Sperimentale della Sardegna, Sassari, Italy,* [2]*Dipartimento di Agraria, Sezione di Scienze Zootecniche, University of Sassari, Italy.*

The aim of the present work was to evaluate the effects of different dry period lengths on blood leukocyte subpopulations in ewes and lambs during the first month postpartum. Two groups of 8 lactating ewes were dried off 60 d (short dry off—SDO) and 90 d (long dry off—LDO) before lambing. After birth, 6 lambs were included in the same treatment group of their mothers. Ewe and lamb blood samples were collected at 1, 2, 7 and 30 d postpartum and were analyzed for white blood cell differential count (WBC) and lymphocyte subsets. Ovine specific monoclonal antibodies were used to identify T-helper lymphocytes (CD4+), T-cytotoxic lymphocytes (CD8+) and a subset of γδ T lymphocytes (WC1) in flow cytometry. Data were analyzed by a GLM model, using dry off length, sampling time and their interaction as fixed factors. The SDO ewes compared with LDO ewes, had lower WBC (9.9 vs 13.1 cells × 10.000/μL; $P = 0.001$) and eosinophil counts (2.4% vs 4.1%; $P = 0.002$) as well as an increased number of lymphocytes (51.1% vs 47.7%; $P = 0.009$). No significant differences were found between lambs, except for monocytes which were higher in SDO than LDO ewes (3.4% vs 2.1%; $P = 0.006$). Ewe lymphocyte subsets were similar in both groups, while SDO lambs had lower CD4+ (44.6% vs 50.1%; $P = 0.042$) and WC1+ (7.1% vs 9.6%; $P = 0.039$) values compared with LDO lambs. Although differences between groups of ewes and lambs were observed for WBC and for lymphocyte subsets, values were always within the normal reference interval for the ovine species. Our results evidenced that shortening the dry period to 60 d did not significantly affect leukocyte subpopulations of ewes and lambs during the first month postpartum. Further research is required to determine to what extent dry period shortening could influence immune response to possibly, enable lengthening of lactation and milk yield increase without any detrimental effect on animal health. Research funded by OIGA (MiPAAF) and PRIN 2009 (MIUR) Projects.

Key Words: dry period, sheep, leukocytes subsets

T375 Effects of plant extracts and monensin on metabolite status and performance of peripartum ewes. H. Mirzaei Alamouti,* H. Namdarpor, H. Amanlo, M. H. Shahir, and D. Aliyari, *University of Zanjan, Zanjan, Iran.*

Thirty-two estrus-synchronized multiparous Afshari ewes (BW 90 kg and BCS 3, based on 1–5 scale) were used in a completely randomized design and assigned to one of 4 dietary treatments to evaluate the effects of a blend of plant extracts and monensin on metabolite status and performance of ewes in the periparturient period. Afshari is a major fat-tail dual purpose (milk and meat) sheep breed in northwest Iran. Dietary treatments contained 1) no additive (CO), 2) 30 mg/d monensin (M), 3) 2 g/d commercial plant extract containing extracts of peppermint and Plantago major (PE), and 4) a mix of 30 mg monensin and 2 g commercial extract (MPE). Ewes (8/treatment) were individually fed diets with 65:35 forage to concentrate ratio from −21 d relative to expected lambing until 28 d after lambing. Blood was sampled weekly relative to lambing. Data from pre-partum and postpartum was separately analyzed using proc mixed in SAS software. The result showed that ewes fed the M diet had lower DMI pre-partum and ewes fed the MPE diet had greater DMI ($P < 0.05$). Ewes fed the MPE diet had lower ($P < 0.05$) BCS postpartum. There were no differences in DM and organic matter digestibility in the periparturient period. There was no effect of diet on plasma concentration of glucose and albumin in the periparturient period however, the PE diet increased ($P < 0.01$) plasma concentration of cholesterol. The MPE diet increased milk production when compared with others, 1.19 vs 0.87, 0.98, 0.85 kg /d (MPE vs CO, PE, and M, respectively). The PE diet increased milk fat content ($P < 0.05$). Ewes fed the MPE diet produced more milk protein and were more efficient in nitrogen utilization. In conclusion, this study showed some plant extracts have health benefits and a mix of monensin and plant extract peripartum can improve production of fresh ewes.

Key Words: monensin, plant extracts, peripartum ewes

T376 Efficacy of a bovine colostrum replacement product for goat kids.

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For various reasons, adequate doe colostrum is not always available for neonatal goat kids and thus, an alternative source of colostrum is necessary to support health of the neonate. The objective of this study was to determine the efficacy of a commercially available bovine colostrum replacement product (Land O'Lakes Colostrum Replacement, manufactured by The Saskatoon Colostrum Co. Ltd., Saskatoon, Canada) for neonatal goat kids. Alpine goat kids ($n = 29$) were removed from does at birth and a jugular blood sample was taken for analysis of serum IgG. The colostrum replacement containing 100 g IgG/470 g of powder was reconstituted with water using 76 mL of warm water to 40 g of colostrum powder and mixed using a plastic jar with a spring similar to those used to mix protein drinks for athletes. Kids were fed reconstituted colostrum replacement at 10% of BW divided into 3 feedings over a 16-h period. At 6 h after the last feeding, another blood sample was collected for determination of serum IgG. Kids were observed for 10 min after each feeding for any adverse reactions. After the 3 feedings of colostrum, kids were fed a milk replacer twice daily at 470 mL per meal, along with offering a starter diet. Health and BW gain were compared with other kid cohorts fed heat treated goat colostrum up to 3 wk of age. Prefeeding levels of IgG were approximately 0.2 mg/dL and were increased ($P < 0.01$) to 18.9 mg/dL (SE = 0.9) post-feeding. There were no cases of scours or off-feed in test animals or cohorts. Gain of BW was similar for kids fed bovine colostrum replacement or heat treated doe colostrum (138 vs. 121 g/d; $P > 0.10$). In conclusion, the bovine colostrum substitute resulted in satisfactory blood levels of IgG in kids and similar health and BW gain as cohorts consuming heat treated goat colostrum.

Key Words: goats, kids, colostrum

T377 Effect of chromium supplementation on carcass traits and blood parameters of Mahabadi goat kids.

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The objective of this study was to evaluate the possible effects of supplementing chromium-methionine (Cr-Met) on carcass traits and selected blood parameters of goat kids. Thirty-two male kids (BW = 22 ± 2 kg, 4 mo old) were used in a completely randomized design with 4 treatments: 1) control (without Cr),2) 0.5, 3) 1.0 and 4) 1.5 mg Cr as Cr-Met/animal/d. Diets were formulated to meet NRC requirements with forage (alfalfa and corn silage):concentrate ratio of 30:70 in TMR form. Diets were the same except for top-dress addition of Cr-Met fed in 2 equal meals (0800 and 1600 h). Animals were kept in individual pens with self-mangers for 90 d. Kids were weighed after 14 d of adaptation and at 21 d intervals after feed restriction and slaughtered at the end of the trial. Jugular vein blood samples drawn via EDTA vacuum tubes on d 70 of the experiment were analyzed for selected parameters via an autoanalyzer apparatus and commercial kits. Data were analyzed by the GLM procedure of SAS 9.1 and Tukey test ($P \leq 0.05$). Weight at slaughter (WAS), HCW and carcass yield (CY) were not affected ($P > 0.05$) by the Cr supplementation. Addition of different levels of Cr failed to significantly affect red blood cells, neutrophils and monocytes. However, Cr supplementation increased white blood cells count [$P = 0.051$; 8.46, 9.39, 11.8, 12.1 (10^3 μL) for treatment 1, 2, 4, and 3, respectively[. These results indicate that supplementation of goat kid diet with Cr-Met did not influence carcass traits and most blood parameters but increased white blood cells.

Table 1. WAS, HC and CY of kids fed different levels of Cr-Met

	Treatment (mg of Cr)				
Trait	0 (control)	0.5	1.0	1.5	SEM
WAS (kg)	32.2	31.3	32.6	32.9	1.64
HC (kg)	13.1	12.3	13.9	12.7	0.85
CY%	40.8	39.0	42.7	38.8	0.13

Key Words: chromium-methionine, carcass traits, white blood cell

T378 Pasture lambing: An alternative to intensive indoor management at lambing.

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Advantages of pasture lambing include reduced labor and lessened exposure to infectious disease, and the decreased stocking density allows for improved expression of maternal care relative to barn conditions. But, if a flock of sheep has been barn-lambed for decades, is it reasonable to expect those ewes to lamb successfully and raise their offspring on pasture? To test this, 35 Dorset, Finnsheep and Dorset × Finnsheep ewes were lambed on pasture during 30-d June and August lambing seasons. They were compared with random samples of equal numbers of barn-lambing ewes. At the time of ear-tagging and recording, a maternal behavior score (MBS) was recorded. Scores ranged from 1 (ewe flees at approach of the shepherd and does not return to her lamb(s) when ear-tagging is completed) to 5 (ewe makes physical contact with her lamb(s) while they are being ear-tagged). Survival of lambs to weaning (85.7 to 95.5%) did not differ by chi-squared analysis between barn- and pasture-lambing. The statistical model for weight per day of age (WPDA) included main effects of season (June or August), lambing type (pasture or barn), litter size (1 or 2), and all 2- and 3-way interactions. The linear and quadratic effects of ewe age were included as covariates. WPDA was affected ($P < 0.01$) by litter size, ewe age, and the season x lambing type interaction. There were different ($P < 0.003$) quadratic effects of ewe age for lambing type. These effects translated into increasing WPDA with increasing ewe age for barn-lambing ewes, but not for pasture-lambing ewes; suggesting that older ewes on pasture were not able to consume sufficient digestible feed components to maximize milk production. In addition and not surprisingly, for all but the June barn-lambing ewes, WPDA was greater for single than twin lambs ($P = 0.03$). WPDA increased 22.6 ± 9.18 g/d for each increase in MBS for pasture-lambing ewes ($P = 0.021$). Thus, scoring maternal behavior may be a tool to predict a ewe's performance in raising lambs on pasture. These results indicated that moving a barn-lambing flock to pasture lambing should not be a difficult transition, even for a flock that has been barn-lambed for generations.

Key Words: sheep, management, maternal behavior

T379 Evaluation of the impact of dietary sericea lespedeza on rumen microflora and innate immunity in goats.

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Gastrointestinal nematodes have developed resistance to chemical anthelmintics resulting in the need for alternative control strategies such as the use of sericea lespedeza (SL) as a high-quality, low input forage that suppresses gastro-intestinal parasites in goats. However, little is known about its effect on rumen micro flora and innate immunity in goats. A diverse collection of microorganisms is found in the goat rumen. Bifidobacteria are important organisms in the immunity of the gastrointestinal tract and its presence in the goat rumen is not fully studied. The objective of this study was to evaluate the impact of a diet containing SL on goat rumen microflora, especially bifidobacteria and on markers of goat innate immunity. Blood was collected from female goats (n = 16) fed a diet of 75% SL (n = 9) and a control group (n = 7), 0% SL. Serum was extracted and used for evaluation of secretion of pro-inflammatory cytokines (TNFa, IFNr, GCSF, GMCSF, IL-1a, IL-8, IP-10 and RANTES) using a commercial ELISA kit. Rumen contents were collected at slaughter and stored at −20°C. Microbial DNA was isolated from frozen rumen samples using the QIAamp DNA kit (Qiagen) to test for the presence of bifidobacteria. The concentration and purity of DNA were determined using a Nanodrop spectrophotometer. The 16S rDNA targeted genus specific PCR primers for *Bifidobacterium* were used to amplify specific DNA. Amplified samples and DNA markers were separated by electrophoresis on a 2% agarose gel, stained with ethidium bromide and visualized. Data was analyzed by GLM of SAS 9.2. A 580-bp *Bifidobacterium* specific band was observed in samples from goats fed the SL free diet. *Bifidobacterium* DNA was not detected in goats fed a diet containing SL. However, diet affected the secretion of proinflammatory cytokines by increasing ($P < 0.0002$) the serum level of TNFa, IFNr, GCSF, GMCSF, IL-1a, IP-10 and decreasing ($P < 0.0001$) IL-8, and RANTES in goats fed SL in the diet. Dietary tannins may affect the goat′s innate immune response and the composition of rumen micro flora. This approach may be useful in studies to assess the recommended level of SL in the diet and the significance of Bifidobacteria in the immunity of the goat.

Key Words: sericea lespedeza, cytokines, *Bifidobacterium*

T380 Effect of continuous suckling/ewe-rearing and supplementation on growth performance of Katahdin lambs.

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The effects of continuous-suckling and supplementation on growth performance of crossbred Katahdin lambs (Birth weight 4.2 kg ± 0.2 kg) were investigated. Lambs (n = 68; 17.2 kg ± 1.0 kg) were randomly assigned within birth-type to be weaned at approximately 75d or to continuously suckle ewes. All lambs were given ad libitum access to hay, and half of the lambs in each rearing method were randomly assigned to be supplemented (10% CP, 3.5% crude fat lamb pellet) ad libitum (weaned + supplemented, WS (n = 16); suckling + supplemented, SS (n = 17) or received no further treatment (weaned + no supplementation, WNS (n = 18); suckling + no supplementation, SNS (n = 17). All lambs were weighed at birth, at the initiation of the trial and at approximately biweekly intervals for another 3 (3) mo. An ANOVA was used to determine the effect of type of rearing, supplementation and the interaction between the 2 main effects on ADG and final weights of lambs. Average daily gain during the pretrial period (~75 d) did not differ among treatment groups (0.18 kg ± 0.01 kg/d). The ADG during the trial period was greater ($P < 0.001$) in supplemented (WS, 0.22 kg ± 0.01 kg/d; SS, 0.24 kg ± 0.01 kg/d) than in un-supplemented (WNS, 0.06 kg ± 0.01 kg/d; SNS, 0.05 kg ± 0.01 kg/d) lambs. Among supplemented lambs, there was a tendency ($P = 0.1$) for greater growth rates in continuous suckled than in weaned lambs. Average final weights were greater ($P < 0.001$) in supplemented (WS, 36.2 kg ± 1.36 kg; SS, 40.2 kg ± 1.36 kg) compared with un-supplemented groups (WNS, 21.7 kg ± 1.36 kg; SNS, 20.6 kg ± 1.36 kg). Final weights were greater in the SS lambs compared with lambs in all other groups. The results of the current study indicated that supplementation of lambs increased total ADG and end-weight. Furthermore, continuous suckling along with supplementation resulted in the greatest ADG and end weights.

Key Words: continuous suckling, ewe-rearing, weaning

T381 Pre-partum nutritional supplementation strategies in goats managed under grazing conditions: 2. Serum glucose concentration profiles and milk production.

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The aim of this study was to evaluate the effect of nutritional supplementation on d 15 or 35 pre-partum upon both serum glucose levels at kidding and milk yield in goats grazing a semiarid range. Ranging goats (n = 31; 1200 to 1800 h) were divided in 3 experimental groups during the last third of gestation: i) control group (CG; n = 7) without nutritional supplementation, ii) 15-Group (15G; n = 14) which received a 15d pre- to 7d postpartum supplementation of 500 g per animal per day of a mixed ration (20% chicken manure, 37% rolled corn, 37% bran, 4% treacle, 2% salt) during the morning at 0800 h, and iii) 35-Group (35G; n = 10) which received the same mixed ration on 35d pre- to 7d postpartum. Before the onset of the supplementation period and immediately after parturition, blood samples were taken to quantify blood glucose concentration in all animals. In addition, milk yield was measured on d 7 and 15 postpartum; all goats were milked at 2000 h, separated from their off-spring, and milk yield was recorded the next day at 0800 h. Serum glucose concentrations (mg/dL) and milk yield (kg) among groups were compared by ANOVA (SYSTAT 12, 2007, USA). While no differences ($P > 0.05$) for serum glucose concentration were observed among experimental groups on d 35 pre-partum, supplemented groups depicted greater serum glucose concentrations ($P < 0.05$) on d 7 postpartum with respect to control goats. In addition, a greater ($P < 0.05$) milk yield was observed in the supplemented groups either at d 7 or d 15 postpartum with respect to control group (Table 1). Present results demonstrated that a 15-d supplementation period increased both serum glucose levels at parturition and milk production of goats under range-grazing conditions in northern Mexico. Such nutritional scheme represents an important strategy to increase not only the goat’s energy balance but also milk production, while may potentially increase the survival rate of the offspring.

Table 1. Pre-partum serum glucose concentrations (mg/dL) and milk production (kg/day) in goats receiving different nutritional supplementation strategies under grazing conditions in northern Mexico

	Glucose (mg/dL)		Milk production (kg)	
	−35 d	0 d	7 d	15 d
Control	47 ± 4.1^{a}	181 ± 25^{a}	1.1 ± 0.2^{a}	1.0 ± 0.2^{a}
G15	48 ± 3.1^{a}	275 ± 20^{b}	1.6 ± 0.1^{b}	1.5 ± 0.2^{b}
G35	56 ± 4.6^{a}	259 ± 32^{b}	1.6 ± 0.1^{b}	1.6 ± 0.2^{b}

^{a,b}Different letters indicate statistical differences ($P < 0.05$).

Key Words: milk, goats, birth

T382 Comparison of different mathematical models applied to lactation adjustment of F_1 sheep in an organic production system. J. C. Angeles Hernandez,* B. Albarran Portillo, A. V. Gomez Gonzalez, N. Pescador Salas, and M. Gonzalez Ronquillo, *Universidad Autonoma del Estado de Mexico, Facultad de Medicina Veterinaria y Zootecnia, Toluca, Estado de Mexico, Mexico.*

The appropriate adjustment of mathematical models applied to lactation curves, allows the analysis of biological and environmental factors affecting milk yield. The lactation curve models generally come in 2 categories: mechanistic models based on the biology of lactation and empirical models, based on current records on milk production. The aim of the present study was to compare the degree of fit of mathematical lactation curve models, empirical and mechanistics, and to determine the effect of environmental factors affecting lactation curve parameters of F1 sheep under an organic production system. A total of 5,382 weekly records from 150 dairy sheep lactations of F1 (East Friesian × Pelibuey, Suffolk or Blackbelly) were used. Four mathematical models were applied: 2 empirical models, Wood (WD), Wilmink (WL), and 2 mechanistic models, Pollott multiplicative 2 parameters (POL2) and 3 parameters (POL3), to determine the degree of adjustment of each function, using the following criteria: coefficient of determination adjusted to the number of parameters (R2), sum of mean square predicted error (MSPE), and the correlation between the observed and the predicted value (R), plus the comparison of the values of total milk yield (TMY), peak yield (PY), and peak time (PT) estimated from each mathematical model. Factors like number of parity (1,2,3,4), type of lambing (single or twin) and season of lambing (spring, summer, autumn, winter) were analyzed to determine their influence on TMY of each function. The parameters of each model were estimated from a non-linear regression analysis using the NLIN procedure of SAS with Marquardt methodology. There were no differences ($P > 0.05$) for environmental factors, as well as for the adjustment in different mathematical models. The values of R2 and R were higher than 0.90 and 0.95, respectively for all models. Both empirical models (WD and WL) had difficulty to calculate the TMY. Only the WL model presented no difference ($P > 0.05$) between observed and estimated PY, and this parameter was underestimated by the other models. The mathematical models have an adequate lactation curve fitting, whereas empirical models have difficulty estimating PT and PY, due to the shape of sheep's lactation curve in this study showing no PY, resulting in erroneous values of the parameters. Mechanistic models POL2 and POL3 were more flexible at this. According to the evaluation criteria curve fitting, the WL model presented the best adjustment.

Key Words: sheep, mathematical model, curve lactation

T383 Pre-partum nutritional supplementation strategies in goats managed under grazing conditions: 1. Doe and offspring BW dynamics. V. Contreras-Villareal[1], O. Angel-Garcia[1], J. M. Guillen-Muñoz[1], R. Rodriguez-Martinez[1], G. Arellano-Rodriguez[1], C. A. Meza-Herrera[2], M. Mellado[3], and F. G. Véliz*[1], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]URUZA, Universidad Autónoma Chapingo, Gómez Palacio, Durango, México, [3]Universidad Autónoma Agraria Antonio Narro, Saltillo, Coahuila, México.*

The aim of this study was to evaluate the effect of nutritional supplementation on d 15 or 35 pre-partum upon both doe and offspring BW managed under a grazing-semiarid system. Ranging goats (n = 31; 1200 to 1800 h) were divided in 3 experimental groups during the last third of gestation: i) control group (CG; n = 7) without nutritional supplementation, ii) 15-group (15G; n = 14) which received a 15 d pre- to 7 d postpartum supplementation of 500 g per animal per day of a mixed ration (20% chicken manure, 37% rolled corn, 37% bran, 4% treacle, 2% salt) during the morning at 0800 h, and iii) 35-group (35G; n = 10) which received the same mixed ration 35 d pre- to 7 d post-kidding. Before the onset of the supplementation period, (35 d) and at parturition, all goats were weighed; besides, the offspring of the 3 experimental groups were weighted at parturition, and at 7 d and 15 d after birth. Doe and offspring BW of the experimental groups were compared by ANOVA; afterward paired mean comparisons considered X^2 analysis (SYSTAT 12, 2007, USA). While no differences ($P > 0.05$) for doe BW were observed on d35 pre-partum among experimental groups, supplemented does (15G and 35G) depicted greater BW values at kidding ($P < 0.05$) with respect to control goats. Doe BW differences ($P > 0.05$) among groups were observed on 7 d postpartum. Regarding offspring BW, the 35G depicted the largest BW values at birth ($P < 0.05$), without differences among groups on 7 d postpartum. Nonetheless, supplemented groups, either 15G or 35G, depicted the largest offspring weights values ($P < 0.05$) on 15 d post-kidding with respect to the other experimental groups (Table 1). Present results demonstrated that either 15 d or 35 d supplementation period prepartum increased both doe and offspring BW. Such supplementation regimen could be of particular importance because of the well established kid-meat market for milk-fed kids in this region of Mexico with the potential increases in the survival rates of replacement kids.

Table 1. Effect of feed complementation over the mother and kid body weight at parturition in goats from northern Mexico in grazing conditions

	Mother weight (kg)			Kid weight (kg)		
	−35 d	Birth	7 d	Birth	7 d	15 d
CG	54 ± 3.1^{a}	44 ± 2.2^{a}	44 ± 2.2^{a}	3.5 ± 0.2^{a}	4.4 ± 0.2^{a}	5.4 ± 0.3^{a}
G15	54 ± 2.3^{b}	$46 \pm 2.0^{a,b}$	44 ± 1.6^{a}	3.4 ± 0.2^{a}	5.0 ± 0.2^{a}	6.3 ± 0.1^{b}
G35	55 ± 1.3^{b}	49 ± 1.3^{b}	47 ± 1.2^{a}	3.8 ± 0.1^{b}	4.7 ± 0.1^{a}	6.2 ± 0.1^{b}

[a,b]Different letters indicate statistical differences ($P < 0.05$).

Key Words: goats, offspring

T384 Pre-partum nutritional supplementation (energy or protein) strategies in goats managed under grazing conditions: 3. Offspring growth dynamics and doe milk production. V. Contreras-Villarreal[1], O. Angel-Garcia[1], J. M. Guillen-Muñoz[1], R. Rodriguez-Martinez[1], G. Arellano-Rodriguez[1], C. A. Meza-Herrera[2], M. Mellado[3], and F. G. Véliz*[1], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]URUZA, Universidad Autónoma Chapingo, Gómez Palacio, Durango, México, [3]Universidad Autónoma Agraria Antonio Narro, Saltillo, Coahuila, México.*

The effect of 3 nutritional pre-partum regimens in goats under semiarid grazing conditions in northern Mexico upon offspring growth dynamics and doe milk yield were evaluated. Ranging goats (n = 31) were divided in 3 experimental during the last third of gestation: i) Control Group (CG; n = 8) without nutritional supplementation, ii) Protein Group (PG; n = 13) which received a 500 g per animal per day of a mixed protein ration (40% chicken manure, 27% rolled corn, 27% bran, 4% treacle, 2% salt) and iii) Energy Group (EG; n = 11) received 500 g per animal per day of a mixed energy ration (20% chicken manure, 37% rolled corn, 37% bran, 4% treacle, 2% salt). Supplements were offered 25-d pre- to 7-d postpartum during the morning at 0800 h. While kids were weighed at birth, d-7 and d-15 post-kidding, milk production was recorded on d-7 and d-15 postpartum; goats were milked at 2000 h, separated from their offspring, and milk yield was recorded the next day at 0800 h. Offspring BW and milk production of the 3 experimental groups were compared with ANOVA (SYSTAT 12, 2007, USA). While the greatest offspring birth weight ($P < 0.05$) was observed in the EG-group, no differences ($P < 0.05$) among groups occurred on 7-d for offspring BW; however, on d-15, supplemented groups depicted the greater ($P < 0.05$) BW with respect to the CG. The same was true regarding milk production; both supplemented groups, had the greatest ($P < 0.05$) milk production values at either d 7 or d 15 postpartum (Table 1). Present results demonstrate that either energy or protein before and immediately after parturition enhanced both the offspring growth dynamic as well as milk production of goats under range-grazing conditions in northern Mexico, enabling us to recommend a management strategy for goats under marginal production systems.

Table 1. Effect of two diets, one protein and one energetic, given to adult pregnant goats near parturition on their offspring BW and milk production

	Offspring BW			Milk production	
	Parturition	7 d	15 d	7 d	15 d
CG	3.5 ± 0.2	4.5 ± 0.2	5.4 ± 0.2	1.1 ± 0.2	1.0 ± 0.2
PG	3.4 ± 0.2^{a}	4.8 ± 0.2^{a}	6.1 ± 0.2^{b}	1.7 ± 0.1	1.6 ± 0.2
EG	3.6 ± 0.1^{b}	4.8 ± 0.2^{a}	6.4 ± 0.2^{b}	1.5 ± 0.1	1.6 ± 0.1

^{a,b}Different letters indicate statistical differences ($P < 0.05$).

Key Words: offspring, goat, milk

T385 Effects of ground linted cottonseed on growth and carcass characteristics of feedlot lambs fed high-concentrate diets. R. A. Souza, R. S. Gentil, E. M. Ferreira, D. M. Polizel, M. I. C. Alves, L. G. M. Gobato, A. V. Pires, and I. Susin,* *Escola Superior de Agricultura Luiz de Queiroz (ESALQ)/University of São Paulo (USP), Piracicaba, São Paulo, Brazil.*

Linted cottonseed is an ingredient of high interest in ruminant nutrition due to its high content in protein, fiber and energy. The objectives of this experiment were to determine the effects of ground linted cottonseed on growth and carcass characteristics of lambs fed high-concentrate diets. Forty-five Dorper × Santa Inês ram lambs (initial BW 21.3 ± 3.7 kg and 79 ± 6 d old) were assigned to a randomized complete block design defined by BW and age at the beginning of the trial. The experimental diets were isonitrogenous (16% CP) and composed of 90% concentrate and 10% coastcross hay. The levels of ground linted cottonseed (DM basis) were: 0 (CS0), 7 (CS7), 14 (CS14), 21 (CS21) or 28% (CS28). Diets were fed once a day as a TMR and the trial lasted 56 d. At the end of the performance trial, lambs were slaughtered, after a 16-h fast period, and carcass measures (dressing percentage, LM area and back fat thickness) were recorded. There was a linear ($P < 0.01$) decrease in DMI (1.24, 1.12, 1.16, 1.02 and 0.83 kg) as CS increased in the diet. ADG (342, 290, 309, 259 and 182 g), and G:F were 0.29, 0.26, 0.29, 0.25 and 0.22, for CS0, CS7, CS14, CS21 and CS28, respectively. Carcass characteristics followed the linear decrease observed with the performance data. Increasing levels of ground linted cottonseed adversely affected lamb performance and carcass characteristics. However, dietary cottonseed inclusion may be dictated by its cost compared with soybean meal.

Key Words: co-product, feedlot, sheep

T386 Effect of concentrate versus forage diet on feed intake and reproductive traits in crossbred ewes. R. R. Cockrum,* S. L. Lake, R. H. Stobart, and K. M. Cammack, *University of Wyoming, Laramie.*

The aims of this research were to 1) evaluate the effects of ration differences on measures used to determine individual residual feed intake (RFI), 2) establish if individual RFI ranking (most efficient to least efficient) is affected by changes in diet composition, and 3) determine if more or less efficient ewes differ in reproductive parameters. Targhee × Rambouillet (n = 61; 7 mo of age) ewes were evaluated on the GrowSafe System to determine individual RFI values and ranking. Ewes were first tested on a concentrate diet (14.2% CP) for 62 d, and then retested (10 mo of age) with a forage diet (15.2% CP) for 66 d. Differences in RFI, ADG, average feed intake, and metabolic mid-weight (MMWT) from the concentrate and forage diets were analyzed using the GLM procedure in SAS. Residual feed intake rankings from the 2 rations were analyzed for similarity with the CORR procedure using the Spearman method. Ewes (n = 18) were further selected to measure reproductive efficiency based on their forage ration RFI ranking: highly efficient (HE, n = 6), moderately efficient (ME, n = 6) and lowly efficient (LE, n = 6). Age of puberty, date bred, and pregnancy status were determined in RFI selected groups and analyzed using the GLM procedure in SAS. Overall, average intake, ADG, and MMWT were higher ($P < 0.001$) in the forage diet compared with the concentrate diet. There was a high positive correlation ($r = 0.69$; $P < 0.001$) between RFI rankings based on the concentrate and forage rations in both overall and selected ewes. Residual feed intake and average feed intake on the concentrate ration were lower ($P \leq 0.002$) in the HE and ME ewes compared with the LE ewes, but did not differ ($P = 0.161$) between the HE and ME ewes. As expected, RFI and average feed intake differed ($P < 0.001$) between the HE, ME, and LE ewes when on the forage diet. Age of puberty, day bred, and pregnancy status did not differ ($P \geq 0.337$) among selected ewes. Results indicated that the least efficient animals remained in the bottom 15% of RFI ranked ewes regardless of diet (forage versus concentrate). However, re-ranking of RFI is possible in more efficient animals when diet is changed. Additionally, this study and previous literature provide little evidence to support that RFI selection negatively affects reproductive parameters in sheep.

Key Words: diet, reproduction, residual feed intake

T387 Influence of level of zilpaterol hydrochloride supplementation at different live weight on carcass characteristics of feedlot lambs. J. C. Robles-Estrada*[1], H. Dávila-Ramos[1], A. Estrada-Angulo[1], F. G. Ríos[1], K. I. Leyva-Medina[1], and A. Plascencia[2], *[1]Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México, [2]Universidad Autónoma de Baja California, Mexicali, Baja California, México.*

Fifty-four male lambs Pelibuey × Katahdin (41.8 ± 1.64 kg) were used in a 33 d feeding trial (3 pens per treatment in a completely randomized design with a 3 × 3 factorial arrangement) to evaluate the effect of zilpaterol hydrochloride on the carcass characteristics, using the final live weight as covariate. The lambs were fed on cracked corn-based finishing diet (1.40 Mcal/kg of NE_g). Three weight groups (31.6 ± 1.27, 41.8 ± 1.85 and 51.8 ± 1.42 kg) were assigned to receive 0 (Z0), 0.15 (Z15), and 0.30 (Z30) mg/kg of live weight d-1 zilpaterol (as zilpaterol chlorhydrate, Zilmax, Intervet México, México City) during 30 d and withdrawn from zilpaterol for the last 3 d on feed. No interactions ($P > 0.10$) were observed between levels of zilpaterol and weight groups. The HCW was greater ($P < 0.01$) for Z30 compared with Z15, but both were greater with respect to Z0 (24.2, 25.1 y 26.0 kg for Z0, Z15 and Z30, respectively). The dressing percent (52.2, 54.7, and 55.7% for Z0, Z15 and Z30, respectively) and LM (5.81, 6.29 and 6.60 cm^2 for Z0, Z15 and Z30, respectively) were higher ($P < 0.01$) for Z30 and Z15 compared with Z0. The zilpaterol supplementation did not affect ($P > 0.10$) the KPH fat (2.18%) and fat thickness (2.46 mm). We concluded that the zilpaterol response was not affected by the weight group; however, the zilpaterol improved the HCW, dressing percent and LM area without affecting the deposited fat.

Key Words: β-agonist, lambs, zilpaterol

T388 Fatty acids in milk of goats fed sunflower seeds at different crude protein levels in the diet and thrombogenicity and atherogenicity indexes.

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Fatty acids are part of the human diet and are involved in important functions. In the 70s, a concern began to reduce saturated fats in the human diet. One approach focuses on its intake, an important factor in determining the fat content and composition of the milk. The amount and type of fatty acid supplement is the result of fat in the animal feed, particularly those products from extraction of oils. The objective was to identify the profile of fatty acids in milk from goats fed on pasture and supplemented with 2 levels of protein (12 vs 14% CP). Milk was obtained from 8 dairy goats (60 ± 2 kg BW) fed on pasture (35%), corn silage (20%), supplemented with a concentrate of 12% or 14% CP, based on sunflower seed, corn grain, soybean meal and minerals. Chemical analysis were performed using the infrared Ecomilk Milk Analyzer (Milkana Kam 98–2 meetings, Hillerød, Denmark). The fatty acid profile was performed by detergent solution with 50 g of sodium hexametaphosphate (SHMP) and 24 mL of Triton X-100 dissolved in distilled water. Samples were processed in water bath (90°C) until fat separation from the milk. Samples were injected into the gas chromatograph (Perkin Elmer Autosystem 9000). The percentage of each fatty acid was calculated by dividing the area under the curve of each peak by the sum of the integrals of the fatty acids identified. To calculate the index of atherogenicity (IA) and thrombogenicity (IT) the formulas proposed by Ulbricht and Southgate (1991) was used. Animals were distributed in a 2 × 2 Latin square design, repeated 4 times. Experimental periods consisted of 15 d for adaptation and 5 d for sample collection. There were no differences ($P > 0.05$) between treatments with 12% and 14% CP in milk content and fatty acids profile (Table 1). Also there were no differences ($P > 0.05$) in terms of atherogenicity and thrombogenicity indexes. Levels of IA and IT for the treatment of 12% CP were 1.23 and 0.78, respectively. This content is low and is not indicative of promoting increased serum cholesterol levels in humans. There are similar characteristics of the 2 treatments, suggesting that a diet containing 12 or 14% protein did not change fatty acid profile of milk.

Table 1. Effect of the crude protein supplemented to dairy goats on the fatty acids (FA) profile (g/100g) of milk

Item	C8:0	C10:0	C12:0	C14:0	C16:0	C18:0	C18:1	C18:2	C18:3
14% CP	3.98	13.01	5.33	9.81	23.1	10.1	25.4	3.34	0.80
12% CP	3.92	13.0	5.34	10.03	24.6	10.5	25.1	3.09	0.76
SEM	1.35	0.88	1.33	1.02	1.08	0.79	1.31	1.3	0.88
P-value	0.69	0.26	0.28	0.26	0.16	0.06	0.64	0.19	0.20

Key Words: atherogenicity, fatty acids, thrombogenicity

Swine Species II

T389 Genistein decreases LPS-stimulated production of TNF-α in porcine peripheral blood mononuclear cells. L. Seefeldt* and J. Clapper, *South Dakota State University, Brookings.*

Endotoxemia is often manifested by an overproduction of circulating pro-inflammatory cytokines, such as tumor necrosis factor-α (TNF) in response to lipopolysaccharide (LPS). Genistein, a non-steroidal tyrosine kinase inhibitor, has been shown to decrease the release of TNF from circulating peripheral blood mononuclear cells (PBMC) in response to LPS in several species. To further examine if genistein could be used to reduce LPS stimulated TNF release in the pig the following experiment was performed. Blood (20 mL) was collected by jugular venipuncture from 5 mo old barrows and the isolated leukocyte rich plasma was layered over Histopaque 1077 and centrifuged to obtain an enriched PBMC population. PBMC were washed twice in sterile DPBS, counted, diluted and added to 24-well culture plates (5×10^5 cells/well) and incubated at 37°C in 5% CO_2 for 2 h to allow cells to adhere. Non-adherent cells were decanted and adherent cells covered with RPMI 1640 plus 1% FBS and 0, 10 μM, 20 μM and 40 μM genistein with and without 10 ng/mL LPS (*E. coli* O111:B4). Cells were incubated for 10 h at 37°C in 5% CO_2 after which the media was collected and frozen at −80°C until assayed for TNF by ELISA. Triplicate wells were prepared for each genistein-LPS combination. Optimal cell number and LPS concentration were determined by a previous dose response experiment. Differences in media concentrations of TNF were determined by ANOVA. LPS treatment increased media concentrations of TNF 7 fold over controls ($P < 0.01$). Genistein dose dependently decreased ($P < 0.01$) media concentrations of TNF. The 40 μM dose of genistein decreased ($P < 0.01$) media concentrations of TNF to a greater extent than 10 and 20 μM, however, all doses of genistein decreased ($P < 0.01$) media concentrations of TNF compared with LPS stimulated controls. Additionally, 20 and 40μM genistein decreased ($P < 0.01$) media concentrations of TNF in non-LPS-stimulated cells but no difference ($P > 0.05$) was detected between the 2 doses. These preliminary data suggest genistein may be useful in ameliorating LPS stimulated TNF production in the pig.

Key Words: pig, LPS, genistein

T390 Effort on an oral endotoxin challenge in pigs. S. Schaumberger* and G. Schatzmayr, *Biomin Research Center, Tulln, Austria.*

The effect of endotoxin (lipopolysaccharide - LPS) of *E. coli* O55:B5 was tested in vivo in weaners. The aim of the study was, to develop an oral endotoxin challenge model to better understand the mechanism of endodoxic shock. In the first trial, 3 groups with 3 pigs in each were conducted: group I received 200 μg LPS per kg body weight intravenously. Pigs in group II were administered 20 mg LPS per kg body weight orally. Group III served as a negative control which was orally given 40 mL physiological saline. The trial lasted for 14 h where blood samples were drawn hourly. At the end, all pigs were euthanized and necropsy was performed. Blood samples were analyzed for LPS, tumor-necrosis-factor-α (TNF- α) and interleukin-6 (IL-6). Pigs of group I showed severe clinical signs (hyperventilate, cyanosis, vomiting) starting 15 to 20 min after administration and one pig had to be euthanized within the first hour due to muscle spasms. Five hours after administration, a second pig died. The third pig recovered. The 3 pigs of group II did not show severe clinical signs. They laid down most of the time as did the animals in the negative control. An increase of LPS values as well as IL-6- and TNF- α-values were observed within blood samples in group I, compared with the other groups. As this trial did not reveal a positive oral endotoxin challenge in another attempt, 9 piglets were weaned at 3 weeks of age and were fed a diet with a higher protein source for one week, to trigger permeability of the intestinal wall and to ensure that, orally administered LPS can enter the circulation. Pigs were divided into 3 groups: group I orally received 20 mg of LPS per kg body weight. Pigs in group II were orally administered 20 mg LPS diluted in sun flower oil per kg body weight, as fatty acids should promote the resorption of LPS from the intestine. Group III served as negative control group which was orally given physiological saline. This trial was elongated to 22 h and again hourly blood sampling and necropsy were performed. After this challenge, no clinical signs were observed during the whole 22 h. No severe macroscopic or histological lesions were observed in the intestine. Blood samples of all 9 animals were inconspicuous. Further approaches have to be investigated for the development of an oral endotoxin challenge model.

Key Words: pigs, endotoxin, challenge

T391 Effect of Actigen supplementation in gestation and lactation on sow and piglet performance, colostrum Ig level and milk composition. R. S. Samuel* and K. M. Brennan, *Alltech Center for Animal Nutrigenomics and Applied Animal Nutrition, Nicholasville, KY.*

Actigen (Alltech Inc.) is a second-generation yeast-cell-wall (YCW) product containing mannanoligosaccharides that have been shown to increase sow body weight gain and reduce piglet mortality. Our aim was to assess whether inclusion of YCW sow diets changes milk composition and improves sow and piglet performance. Sows were fed non-medicated gestation (n = 657) and lactation (n = 633; parity 1–8) diets without or with YCW (900 ppm). Feed from d 3–100 of gestation was provided as per body condition. Additional feed (909 g/d) was fed after d 100. Sows were offered lactation feed ad libitum after d4 post-farrowing. Piglets (including stillborns) were weighed after farrowing. Cross-fostering within treatment was completed within 24 h post-farrowing and post-foster litter weights recorded. Sow BW was recorded pre- and post-farrowing. Milk samples (120 per treatment) were analyzed for immunoglobulin and nutritional content. Conception rate tended to be greater ($P \leq 0.09$) among sows fed YCW compared with controls. Sows fed YCW had lower ($P \leq 0.05$) post-farrow net BW and lost less BW ($P \leq 0.001$) during lactation (3.2 vs. 11.3 kg; SEM 2.6) than controls. Litter birth weight; piglets born alive and dead per sow; adjusted litter gain; sow ADFI; post-weaning BW; pre- and post-farrowing backfat thickness; and milk fat, lactose, milk energy, somatic cell count, milk urea N, and total solids did not differ between treatments. Protein (%; $P \leq 0.01$) and total solids less fat (%; $P \leq 0.03$) were greater in milk from YCW-fed sows compared with controls. Milk IgG concentrations from parities 1, 3 and 6 were greater ($P \leq 0.05$) with YCW. Number of piglets weaned per sow was greater ($P \leq 0.02$) for parity 4 sows fed YCW. Feeding YCW to sows during gestation and lactation significantly reduced lactating sow BW loss without affecting weaning weight or the number of piglets weaned per sow.

Key Words: mannan oligosaccharides, piglet, sow

T392 Effect of maternal Actigen supplementation during gestation and lactation on piglet gut development and gene expression.

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Our aim was to determine the effect of adding a yeast-cell-wall-based product (Actigen, Alltech Inc., Nicholasville, KY) to maternal gestation and lactation diets on piglet intestinal gene expression and morphology. Sows (parity 1–8) were housed in farrowing crates at a commercial production research facility and randomly assigned to 1 of 2 treatments: commercial gestation and lactation diets without (control, CON) or with 0.90 kg/t of Actigen (ACT). On d 10 post-farrowing, 1 piglet per sow (n = 15 per treatment) was randomly selected and euthanized. Jejunum samples were flash-frozen for microarray analysis and fixed in buffered formalin for histologic analysis. Intestinal morphology was evaluated using H-E staining of the jejunum (n = 6 per treatment). No differences in goblet cell count, goblet cell area or villus height were observed. Intestinal gene expression was evaluated using the Affymetrix Porcine Genome Array. Of the 15,000 transcripts, 659 genes were affected (262 upregulated, 397 downregulated) by maternal ACT ($P \leq 0.05$, FC $\geq$1.2). Genes significantly affected by ACT were classified by biologic function: growth and proliferation, metabolic process, immune system process, response to stimulus, cell cycle, cell communication, or organ development. Different functions showed evidence of positive regulation due to ACT (z-score $\geq$1.5) including cellular growth and proliferation, cell signaling and post-translational modification. Negative regulation was observed (z-score $\leq$ 1.5) in cellular movement and organismal injury and abnormalities. Multiple pathways were activated in piglets from ACT sows including cholecytokinin/gastrin-mediated signaling, ephrin receptor signaling and gonadotropin signaling. Gastrin is a potent cell-growth factor that has been implicated in a variety of biologic processes including maintenance of the gastric mucosa, proliferation of enterochromaffin-like cells, and neoplastic transformation. Ephrin is fundamental for the cell to cell signaling in different pathways related to cell migration and angiogenesis. Gonadotropins are known to play different roles in growth and reproduction. Although performance and intestinal morphology did not differ between treatments, transcriptional changes d10 post-farrowing implies long-term ACT gut health, growth and development benefits.

Key Words: mannan oligosaccharide, gene expression, piglet

T393 Effect of social ranks on oxidative stress status, reproductive performance, and immune status of sows housed in groups during gestation.

Y. Zhao,* W. L. Flowers, and S. W. Kim, *North Carolina State University, Raleigh.*

This study was to determine if social ranks of gestating sows housed in group would affect their oxidative stress status, reproductive performance, and immune status. On d 35 of gestation, 72 multiparous sows were checked for pregnancy and randomly assigned to 24 gestational pens with 3 sows per pen. The social rank of sows within a pen was determined by observing their aggressive behavior for a 4-d period after allotment and classified into high-, middle-, and low-ranking groups (HR, MR, and LR) according to their percentage of winning interactions. On d 109 of gestation, sows were moved to individual farrowing crates. Litter size and piglet weight were recorded during lactation and blood samples from sows were taken during gestation and lactation. Plasma malondialdehyde, protein carbonyl, and 8-hydroxy-deoxyguanosine (8-OHdG) were analyzed. Immunoglobulin G and IgM in sow plasma and colostrum were measured. Sows in HR showed higher ($P < 0.05$) BW than sows in MR and LR. Sows in HR had greater ($P < 0.05$) number of born dead (2.6) than sows in MR (1.2) and LR (1.4). On d 18 of lactation, litter size was greater ($P < 0.05$) in LR (9.6) than in HR (7.2) and MR (8.2). Sows from LR tended to have greater ($P = 0.067$) litter weight (51.8 kg) than sows from HR (43.1 kg). Piglet from LR tended to have smaller ($P = 0.094$) ADG (207 g) compared with HR (233 g). Plasma 8-OHdG in LR (0.61 ng/mL) was greater ($P < 0.05$) than HR (0.36 ng/mL) and MR (0.43 ng/mL). The concentration of protein carbonyl was shown to be negatively correlated ($P < 0.05$) with litter performance in MR and LR. Plasma 8-OHdG was shown to be negatively correlated ($P < 0.05$) with reproductive performance of sows in HR and LR. Sows in HR tended to have greater ($P = 0.068$) IgG (163.8 mg/mL) in colostrums compared with sows in MR (127.5 mg/mL). In conclusion, for all ranks, it was shown that the reproductive performance was related to oxidative stress status of sows. Sows in HR had similar litter size, litter weight, and piglet ADG at wean compared with sows in MR. The farrowing rate of sows in LR was lower compared with HR and MR, which could be caused by higher DNA damage during late gestation and lactation.

Key Words: oxidative stress, social rank, sow

T394 Novel strategies to stimulate GLP-2 secretion and intestinal adaptation in weanling piglets.

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Weaning-induced intestinal atrophy is partly related to reduced secretion of glucagon-like peptide 2 (GLP-2). Recent studies showed that stimulating GLP-2 secretion in total-parentally-fed piglets promotes gut growth. We conducted 2 infusion trials (IT) and 1 feeding trial (FT) to investigate the hypothesis that stimulating GLP-2 secretion immediately after weaning may improve intestinal integrity in piglets. In each trial, 36 piglets weaned on average at 21 d of age and 6.1 kg of BW were individually housed and fed ad libitum. In the IT (n = 12), treatment solutions were chenodeoxycholic acid [60 mg/kg BW, (CDC)] and β-sitoesterol [100 mg/kg BW, (BSE)] in IT1; and CDC (120 mg/kg BW) and zein protein hydrolyzate (1.4 g/kg BW) in IT2. Until d 6 postweaning, all piglets were intragastrically infused once daily with 50 mL of either water (control) or treatment solutions; on d 5, serial plasma samples were obtained from 6 pigs/treatment. In the FT (n = 18), a prestarter diet without (control) or with CDC (60 mg/ kg BW) was fed from 0 to 14 d postweaning; afterward, pigs were fed a starter diet until d 35. In all studies, 6 pigs/treatment were sacrificed and their intestines were collected for later analyses. Data were analyzed as a mixed-effect model with pig treated as random variable. Compared with control, infusing CDC at 60 mg/kg BW increased ($P < 0.05$) mean plasma GLP-2 by 77%, small intestine length, intraepithelial lymphocytes and cleaved caspase in the ileum; tended to increase ileum weight and length ($P < 0.08$) and mean plasma GLP-1 ($P < 0.13$) without affecting intake and final BW. At 120 mg/kg BW, infusing CDC also increased ($P < 0.05$) GLP-1 and GLP-2, but reduced intake, BW, and ileal crypt depth. Other treatments did not affect measured parameters, except that BSE tended to depress GLP-1 (27%) and GLP-2 (42%) compared with control. In the FT, CDC did not affect intestinal weight and piglet performance compared with control. In conclusion, oral CDC treatment potently enhanced GLP-2 secretion in weanling piglets, but the mitigation of weaning-induced intestinal atrophy was apparently counterbalanced by increased inflammation and reduced feed intake.

Key Words: GLP-2, bile acids, pigs

Teaching/Undergraduate and Graduate Education

T395 Student perceptions and moral conflict of animal use in society. M. Amstutz, K. Bennett-Wimbush,* and D. Willoughby, *Ohio State ATI, Wooster.*

Animal production practices have increasingly come under attack from emotion-driven animal rights groups. Therefore, it is imperative that animal science students be able to distinguish animal rights from animal welfare. To determine if students, particularly those majoring in animal sciences, could make this distinction, incoming freshman (n = 136) completed a 20-question survey (Likert scale 1–5; range 20–100, summed and reported as a composite score) regarding perceptions of animal use, rights and welfare. Survey format, scoring and some content was modified from Davey, 2006. Composite scores (CS) ranged from 54.8 to 81. Lower scores were consistent with animal rights positions and higher scores corresponded with animal use values. Composite scores were examined for correlation to varied student demographics. Major ($P < 0.001$); career objective ($P < 0.01$) and history of animal ownership ($P < 0.001$) significantly altered CS. Livestock science majors (70.1 + 1.1) scored higher than either equine (57.7 + 1.3) or horticulture majors (57.9 + 1.4). Students with livestock production career objectives scored higher (69.5 + 1.6) than students interested in either equine production (61.5 + 2.5) or veterinary medicine (61.2 + 1.6). Animal ownership (commercial livestock, show livestock, equine, pets and all possible combinations) were analyzed. Commercial livestock ownership, reported by 39.9% of students, dramatically increased ($P < 0.001$) CS compared with students reporting equine, pet or no animal ownership. Additionally, students from NE Ohio had lower CS than students from SE Ohio, likely due to the increased urban population of the region. As part of the survey, students were asked if they perceived a difference between animal rights and welfare. Sex ($P < 0.05$), age ($P < 0.05$), and home residence ($P < 0.01$) all significantly influenced responses. Males, non-traditional students (age >21), and urban dwellers were less likely to differentiate between animal rights and welfare than females, 17–20 year olds, and students from non-urban backgrounds (farm, rural, suburban), respectively. This study indicates most students CS are consistent with supporting animal welfare and use.

Key Words: animal rights, welfare, undergraduate

T396 Developing horsemanship skills through the understanding of equine behavior. M. Nicodemus* and S. Lindsey, *Mississippi State University, Mississippi State.*

As prey animals, horses are instinctively unique from their human handlers, and thus, these handlers need to understand the innate behaviors that dictate how the horse responds during the training process, and thus, University horsemanship programs are meeting this need with the introduction of behavioral sciences in their equine curriculum. Mississippi State University has offered a behavioral science course, ADS 2102 Equine Behavior & Training, for a decade, but only recently has introduced a lecture component to the laboratory where students study behavioral sciences principles and current research in equine behavioral sciences, and then, supplement their studies with the laboratories focused on these principles and research. Therefore, the study objectives were to determine how effective an equine behavioral science course was in building students' confidence in their potential horsemanship skills. A survey was given to students (n = 28) at the start and conclusion of the course with a 18 question survey focused on students′ evaluation of their horsemanship skills using a 5-point scale with a higher score indicating a stronger confidence in performing a skill. Scores were analyzed by a one-way ANOVA to determine the effectiveness of this course ($P < 0.05$). While 9 questions showed significant improvement in scores by the end of the semester ($P < 0.05$), only 2 questions showed 100% of the respondents scoring 5 by the final survey and these questions focused on the basic ground handling of horses, both trained (initial score = 3.6) and untrained horses (initial score = 3). Of those questions only 4 was focused on riding activities, and that may be due to the lack of riding activities during the laboratories. Only 1 question showed no change in the score, 2.6, and that was focused on riding a green broke horse. Greatest improvement associated with confidence in riding abilities was seen in students' abilities to ride a horse with behavioral problems (initial score = 2.6, final score = 4.2). While the course was not focused on horsemanship, results suggest students understanding of equine behavior strengthened their confidence in their horsemanship skills.

Key Words: equine behavior, horsemanship

T397 A web-based computer simulator to teach dairy farm management. S. Calsamiglia,* L. Castillejos, A. Ferret, G. Vera, and G. Espinosa, *Universidad Autonoma de Barcelona, Barcelona, Spain.*

A web-based software was developed to describe the life cycle of a dairy cow and used to simulate a dairy farm. This e-learning tool has 3 levels of control: the administrator that coordinates the system; the instructor that controls all events in his class, and the student that controls all actions in his farm. Within a class, each student has its own farm defined at random within limits determined by the instructor. Events and variables are defined by default but can be modified within each class by the instructor (i.e., heat detection rate, fertility, incidence of diseases, costs, dietary ingredients). Actions taken by students include: heat detection/synchronization, insemination, dry off, diet specifications, assignment of and transfer of animals between groups, diet formulation, colostrum and milk feeding, weaning, treatment of diseases, milk withdrawal if antibiotics are used, buying and culling of cows or calves, and so on. Modeled events are based on physiologic functions and work at random around a predefined average and ranges. The daily output provides information on milk production and composition, economic performance and counters for errors incurred by the student as a feedback for students and evaluation purposes. Instructors can evaluate student semi-automatically based on performance and error indicators, and may also develop exercises based on their own farm (i.e., calculate required space for cows, land for forages or manure spreading). This e-learning tool has been used by students of first and third year in the Veterinary School with excellent evaluations of the learning process by student's surveys. In a non-planned exam conducted 2 weeks before the final exam, students were 5 times more likely to respond correctly to the same type of questions about dairy cows than other species taught in the same semester. The e-learning program is written in Catalan, Spanish, and English. For information, connect to www.dairyfarm.com.

Key Words: e-learning program, dairy farm management, web-based simulator

T398 Relationships between course schedule and student academic performance and attendance in undergraduate animal science courses.

K. Stutts, M. Beverly,* S. Kelley, M. McMillan, A. Bullion, and L. McMillan, *Sam Houston State University, Huntsville, TX.*

The objective of this study was to evaluate the effect of course schedule (meeting time and day of the week) on academic performance and attendance in undergraduate animal science courses. Data were collected on 2,313 students enrolled during the 16-week fall and spring semesters of 2007 through 2011. Data collected included number of absences and final course grade for each student, and the time of day and day of the week that each course met. Least squares means for final course grades and number of absences were calculated using the mixed procedure of SAS. Significant differences existed for time of day and day of week for final course grades and attendance. Mean final course grade was lowest ($P < 0.01$) for courses that met early in the morning (before 10am; 76.94) compared with courses that met late morning (10am-12pm; 82.05), early (12–3pm; 82.27) afternoon, or late (after 3pm; 82.71) afternoon. Mean number of absences was also greatest ($P < 0.05$) for early morning (4.55) classes. Mean final course grade was greatest ($P < 0.01$) for courses that met once per week on Thursday-only for 3 h (86.21) and lowest for courses that met 3 times per week on Monday, Wednesday, and Friday (76.01). Mean number of absences was lowest ($P < 0.05$) for courses that met only once per week (<1.95), intermediate for courses that met twice per week (<3.75), and greatest for courses that met 3 times per week (6.29). These results indicate that a relationship exists between course schedules and student academic performance and attendance. In this study, student performance and attendance were lowest in courses that met early in the morning and in courses that met 3 times per week. If possible, courses should be scheduled to meet later in the morning or in the afternoon, and should meet no more than twice per week to encourage attendance and increase academic performance of students.

Key Words: undergraduate, course schedules, academic performance

T399 The effects of note-taking method on academic performance in undergraduate animal science courses.

K. Stutts,* M. Beverly, S. Kelley, M. McMillan, A. Bullion, and L. McMillan, *Sam Houston State University, Huntsville, TX.*

Many books and articles on how to succeed in college emphasize the importance of taking good lecture notes. The objective of this study was to evaluate the effect of note-taking method on academic performance and attendance in undergraduate animal science courses. During the first year of the study, students were provided with an outline of material presented in lecture. In the second year, students were provided with a detailed set of notes. Final course grade and attendance data were collected on 814 students enrolled in the fall semesters of 2010 and 2011. Note-taking method data were collected on a subsample of 159 students. Least squares means for final course grades and number of absences were calculated using the mixed procedure of SAS. There was no difference in mean final course grade or mean number of absences for the general population of students between the 2 years. The authors hypothesized that there would be a greater number of absences for the students that were provided with a detailed set of notes since those students were given a complete copy of the material that was covered in class; however, there was no difference ($P = 0.68$) in mean number of absences between the 2 note-taking methods. A significant difference in mean final course grade did exist between the 2 note-taking methods. Students that were provided with only an outline of the material had a higher ($P < 0.05$) mean final course grade (83.70) than students that were provided a detailed set of notes (80.45). These results indicate that students provided with only an outline of course material, and presumably took a more active role in learning by taking additional notes, performed at a higher level than students that were provided with a detailed set of notes.

Key Words: undergraduate, note taking, academic performance

Tuesday, July 17, 2012

SYMPOSIA AND ORAL SESSIONS

ADSA Multidisciplinary and International Leadership Keynote (MILK) Symposium: How Dairy Exporters Can Provide Food Security

301 Making safe, affordable, abundant food a global reality. T. A. Armstrong,* *Elanco Animal Health, Greenfield, IN.*

A growing wave of food insecurity threatens more than 1 billion people globally. Food costs are near record highs. The number of hungry is increasing and could grow staggeringly as the population reaches 9 billion by 2050. Will we allow this to continue, or will we tackle it with solutions that exist today? Technology solutions can help meet food needs, but consumers do not want technology used in food production. Right? To better understand consumer opinions on technology, Elanco commissioned a research review of 28 studies accounting for more than 97,000 consumers in 26 countries. It found that 1) 95% are food buyers. They are either neutral or supportive of using modern technology to grow food. In general, they make purchases based on taste, cost, and nutrition and 2) 4% are lifestyle buyers. They are looking for gourmet, organic, locally grown, or other types of products. Price is not a factor. Food buyers and lifestyle buyers are not mutually exclusive. That leaves a small fringe group with a loud voice that wants to impose their opinions on others. They want to protect consumers from modern food production threats. It is time to stop being swayed by the fringe and shift the dialog toward a more important question: how can we sustainably feed a growing world? The 2 most important ingredients to safe, affordable, abundant food are technology and choice. Technology enables three basic rights: 1) Food, a basic human right. Every child has the right to be fed. Technology affords a more abundant, more affordable food supply; 2) Choice, a consumer right. Whether it is the Chinese consumer who wants to add animal protein to the diet, or the American consumer who wants locally grown, consumers have the right to a broad variety of food choices. Technology helps allow these choices; and 3) Sustainability, which is environmentally right. We will not be able to feed future generations if we neglect our resources. Technology allows more efficient production, which has made it possible for farmers to feed more people while consuming fewer resources and generating less animal waste. With food supplies tight and prices increasing, we have a unique window of opportunity to act. Together, we can make a difference.

Key Words: technology, food

302 How dairy foods aid in food security. V. Lagrange,* *US Dairy Export Council.*

In the past, the WHO-recommended management of severe acute malnutrition required the administration of highly specialized milk-based liquids (F-100) in a hospital environment. Over the past decade, ready-to-use therapeutic foods (RUTF) have been developed as an alternative to treat severe acute malnutrition. These lipid-based products, that can be used as part of community-based treatments, have revolutionized the effectiveness and coverage of programs addressing malnutrition. Recent clinical trials demonstrate the effectiveness of RUTFs on health outcomes for other vulnerable groups, such as HIV AID patients treated with anti-retro viral therapy. RUTF are typically made with skim or whole milk powder, and the intense use of milk can represent up to 50% of the cost of the rations. Alternative formulations containing whey proteins are being tested for the formulation of ready-to-eat supplementary foods (RUSF). In such a trial, the research team developed a recipe meeting the WHO specifications for RUTF in which milk powder is totally replaced by whey protein concentrate 34% as main source of protein. Based on organoleptic and tolerance acceptability, as well as weight gain (primary outcome), the whey-containing RUSF products were found as effective as traditional RUTF formula. Animal studies are under way to measure the effectiveness of whey permeate in formula used during re-nutrition, and document the application of both lactose and phosphorus found in this ingredient. Other studies pilot the use of RUSF to increase food security for other vulnerable groups such as pregnant and lactating women. Current state of knowledge indicates that cow's milk products have a central role in the treatment of both severe and moderate acute malnutrition. There is growing evidence that their benefit extends to the prevention of malnutrition, and delivery of other desirable health outcomes for vulnerable groups in developing countries.

Key Words: whey protein, milk powder, malnutrition

303 Development of local dairy production: The Indian experience. G. Sohani,* *BAIF Development Research Foundation, Pune, Maharashtra, India.*

Starting from humble levels, India today has the highest aggregate milk production in the world. Production levels have increased from 17 M tons in 1950–51 to over 110 M tons today, with 2022 targets at 180 M tons. In spite of growing population, the per capita milk consumption has also grown from 130 g per day to 263 g per day. Hidden behind the high aggregate production levels there is a skewness - both geographically and among various producer segments. This is a challenge as well as an opportunity. The growth has been through productivity enhancement and creation of processing capacity. Productivity enhancement has been the outcome of not just new technology, but also comprehensive approach covering breeding, feeding and health care, as well the mindset change required for assimilation of new technology. The growth is also unique, through 2 types of bovines: cattle as well as buffalo. The combination has important lessons for dairy development in tropical/sub-tropical parts of the developing world. BAIF, a professional non-profit PVO, has the pride and privilege of having contributed to dairy development in India. BAIF applied cutting-edge technologies for animal production through appropriate adaptations and by creating a novel delivery system to reach the dairy farmers in the remotest locations. This approach is now adopted and emulated across the country. BAIF's program has reached over 4 M farmers directly, and there is regular programmatic contact with close to 3 M farmers in over 50,000 villages of rural India. The value of annual milk production by this group is of the order of US$3 billion. Moreover, this represents income accrual to small farmers, contributes to their food and income security, and to the nutrition security of an even larger number of households. Future challenges will require expanded breeding programs, fodder/nutrition security, health care, and application of newer technologies such as sexed semen, QTL and ET. The paper covers the Indian journey of four decades, the contexts and achievements, their relevance to the developing world, and emerging needs and directions.

Key Words: dairy development, Indian dairy production, milk production and productivity enhancement

Animal Health III

304 Effect of vaccination technique and antibody level on primary and secondary response in beef calves after vaccination against bovine viral diarrhea virus. M. R. Rey*[1], J. C. Rodriguez-Lecompte[1], T. Joseph[3], J. Morrison[2], A. Yitbarek[1], K. M. Wittenberg[1], M. Undi[1], and K. H. Ominski[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [2]Department of Biosystems Engineering, University of Manitoba, Winnipeg, MB, Canada, [3]Veterinary Diagnostic Services, Manitoba Agriculture, Food and Rural Initiatives, Winnipeg, MB, Canada.*

In this study, antibody response was measured in calves following vaccination against bovine viral diarrhea virus (BVDV) using either needle-free (Pulse 250) or needle-syringe (NS) vaccination techniques. The Pulse 250 needle-free (NF) injection device utilizes compressed carbon dioxide to power vaccine injections. At 2 mo of age (d 0), calves were vaccinated either via a needle-syringe injection (n = 39) or a needle-free injection (n = 47) technique, while 10 calves were left unvaccinated (Control). The vaccine administered was a 5-way modified-live respiratory virus containing BVDV types 1 and 2. On d 119 post vaccination, calves received a second immunization using the same product. Body weight was recorded and blood samples were taken on d 0, 21, 42, 119, and 140. Antibody levels in serum, as measured by S/P ratio, were analyzed by a semiquantitative BVDV enzyme-linked immunoassay (ELISA). To understand the effect of antibody level on primary and secondary antibody response in terms of population, calves in each treatment group were ranked by antibody level. Throughout the study, antibody levels against BVDV were not significantly different ($P > 0.05$) between vaccination techniques. Higher ($P < 0.05$) antibody levels in vaccinated relative to unvaccinated calves on d 42, 119 and 140 of the study, demonstrated that animal exposure to BVDV did not occur during the study. The population distribution shows that both vaccination techniques provide homogeneous BVDV antibody production and that anabolic and catabolic trends are dependent on the level of circulating antibodies present before vaccination. The data suggests that the antibody response acquired after vaccinating against BVDV is the same using a needle-syringe or needle-free vaccination technique. However, the level of circulating antibodies (either maternal or vaccination-induced) to BVDV before vaccination seems to have a critical effect on primary and secondary antibody response.

Key Words: needle-free injection, bovine viral diarrhea virus, antibody response

305 Bacteria counts in on-farm pasteurized milk for dairy calves versus season and time post-pasteurization. D. J. Wilson*[1], K. A. Rood[1], and G. M. Goodell[2], *[1]Utah State University, Logan, [2]The Dairy Authority, Greeley, CO.*

On-farm pasteurized milk to be fed to dairy calves was studied for SPC changes over time on 3 commercial farms during 4 seasons. Aseptic milk samples (n = 276) were collected before pasteurization at 63°C for 30 min, then following pasteurization as soon as milk cooled to 49°C, and 1, 2, 3, 4, 5, 6, 7, 8, 10, 12 and 24 h post-pasteurization. All milks had 2 aliquots, one incubated indoors at 4°C (winter/W), 22°C (fall/F, spring/SP) or 37°C (summer/SU), the other outdoors at seasonal temperatures. Outdoor temperature means were W 8°C, F 8°C, SP 10°C, SU 30°C. Only SU had higher outdoor temperature than the other seasons ($P < 0.0001$, ANOVA, Tukey's). Bacterial SPC (cfu/mL) were measured from 6 milk dilutions on Petrifilm. Mean pre-pasteurized SPC was 14,634,257, post-pasteurized was 2,633. A general linear model ($R^2 = 0.70$, $P < 0.0001$) found factors associated with Log SPC: time post-pasteurization, season, farm, time x season, season x farm. Summer had distinctly higher SPC sooner after pasteurization than other seasons; despite the interactions this significant effect was seen on all farms. Fall and SP indoor incubated samples' SPC were not >10,000 for 8 or 12 h respectively, reaching a median of 206,364 and 8,900,000, respectively by 24 h. None of the W samples or F and SP outdoor samples were >1,435 for 24 h. In contrast, SU indoor samples′ SPC were >10,000 by 2 h, 186,800 by 4 h, median 14,500,000 by 24 h. Summer outdoor samples′ SPC were >10,000 by 1 h, 104,733 by 6 h, median 44,000,000 by 24 h. Despite speculation regarding a safe threshold of bacteria count for milk fed to calves, no consensus exists, and there is no definitive health based standard. These data suggest that a reasonable goal would be to feed pasteurized milk to calves if SPC <10,000 cfu/mL. During fall and spring (unless unseasonably warm days occurred) milk could have been safely fed for at least 8 h, in winter for at least 24 h, but in summer for only 2 h post-pasteurization.

Key Words: pasteurization, milk, calves

306 *Salmonella* carriage rates in neonatal dairy calves. E. M. Chavez*[1], R. B. Harvey[2], K. Andrews[2], T. S. Edrington[2], C. M. Scanlan[3], and G. R. Hagevoort[1], *[1]Agricultural Science Center at Clovis, New Mexico State University, Clovis, [2]Food and Feed Safety Research Unit, Agricultural Research Service, USDA, College Station, TX, [3]Department of Veterinary Pathobiology, Texas A&M University, College Station.*

In recent years, it appears that the incidence and carriage rates of *Salmonella* in dairy calves, heifers, and cows have increased. *Salmonella* colonization has induced clinical disease in cattle, but more importantly, has potential implications for foodborne disease. Because the authors have noted *Salmonella* colonization in dairy calves of 6 mo and younger, the present study was conducted to determine the prevalence of *Salmonella* in neonatal dairy calves from calf ranches in the southwestern United States. In 2 studies (February and September, 2011), rectal fecal samples were collected twice weekly from calves 24 h to 4 weeks old and quantitative and qualitative cultivation techniques were used to determine *Salmonella* colonization rates. In the first study, we detected *Salmonella* in 34 of 54 samples (63%) by spiral plating with concentrations of 10^2 to 10^6 cfu/g beginning in calves as early as 24 h old. With an enrichment technique, 100% of calves were positive for *Salmonella* at least one time during sampling and 16.7% were positive at every sample time. In the second study, 9 of 30 calves were positive by spiral plating with fecal concentrations of 10^2 to 10^4 cfu/g at 24 h of age. Upon enrichment, 100% of calves were positive for at least one sampling, and 24 of 30 (80%) were positive at every sampling. *Salmonella* serotypes were not clonal as there were 7 serogroups (C_1, C_2, B, E_1, K, I, and Poly A-I) represented by isolates from both studies. Previous research in our laboratory has reported a high *Salmonella* prevalence in dairy calves from a few days old to a week of age, but this is the first time we examined calves within 24 h of parturition. To the authors' knowledge, this is the first report of dairy calves colonized with *Salmonella* within 24 h of birth. We do not have a ready explanation for this, nor do we understand the biological significance of such high GI tract concentrations of *Salmonella* in neonates. Follow-up studies are being conducted.

Key Words: *Salmonella*, neonatal, dairy calves

307 The association between colostrum bacteria counts and immunoglobulin absorption, calf growth and mortality.

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The objective of this analysis was to evaluate the association between both total bacteria count (TBC) and coliform count (CC) in colostrum and the apparent efficiency of absorption (AEA) of immunoglobulin G (IgG), average daily gain (ADG) and mortality before weaning. Records from 172 heifer calves from 8 New England and California dairy farms were used in this analysis. Calves received 3.5 to 3.8 L of colostrum 137 ± 107 min after birth. TBC and CC in colostrum samples collected before feeding averaged $10^{5.31}$ and $10^{2.45}$ cfu/mL, respectively. Colostrum and serum IgG concentrations in serum samples collected from calves between 1 and 7 d of age were measured by radial immunodiffusion and averaged 74 ± 28 and 21 ± 9 mg/ml, respectively. Birth and weaning body weights were only available at the California site; therefore, AEA and ADG were calculated from a subpopulation of 90 calves that were tube fed 3.5 L of colostrum and were bled between 24 and 48 h of age. Multivariable General Mixed models were used for the analysis of AEA and ADG and Cox regression for the mortality outcome. Significant difference was established at $P < 0.05$. AEA was numerically lower when CC were above any of the cutpoints defined in Table 1; however, the difference only was significant when CC $\geq 10^4$ cfu/ml. ADG was not different between the bacteria counts cutpoints. Interestingly, there was a higher mortality in calves receiving colostrum with TBC above 10^6 or CC above any of the cutpoints. Serum IgG was also a significant mortality predictor. However, when including both serum IgG and colostrum TBC or CC in the mortality model, colostrum TBC or CC were still the largest predictors of death.

Table 1. Apparent efficiency of absorption (AEA) and mortality for calves fed colostrum with different total bacteria (TBC) and coliform count (CC) cutpoints

	AEA % (no.)	Mortality % (no.)
TBC $<10^6$ cfu/mL	31^a (70)	8^a (144)
TBC $\geq 10^6$ cfu/mL	29^a (20)	14^b (28)
TBC $<10^5$ cfu/mL	28^a (23)	8^a (110)
TBC $\geq 10^5$ cfu/mL	31^a (67)	10^a (62)
CC $<10^4$ cfu/mL	31^a (83)	7^a (161)
CC $\geq 10^4$ cfu/mL	23^b (7)	36^b (11)
CC $<10^3$ cfu/mL	31^a (64)	7^a (125)
CC $\geq 10^3$ cfu/mL	29^a (26)	15^b (47)

[a, b]Superscripts indicate significance at $P < 0.05$.

Key Words: calves, colostrum, bacteria

308 Adding an anti-inflammatory lactic acid bacteria to a *Bacillus*-based direct-fed microbial improves calf immune development.

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A *Bacillus*-based direct-fed microbial selected for reducing bacterial pathogens increased expression of inflammatory cytokines in vitro and activated immune development in scouring calves. *Enterococcus faecium* ID7 reduced expression of inflammatory cytokines caused by *Bacillus* spores *in vitro*. The objective of this experiment was to determine the effect of adding anti-inflammatory lactic acid bacteria to a *Bacillus*-based DFM on immune development in calves. Calves (72) were randomly assigned to 3 treatments, control, *Bacillus* DFM (2×10^9 cfu/head/day) or *Bacillus* DFM plus ID7 (2×10^9 *Bacillus*, 1×10^9 ID7 cfu/head/day), administered in non-medicated 20:20 calf milk replacer until weaning at 6 weeks. Blood samples were collected at d 7 and 35. Serum was isolated for analysis of α_1-acid glycoprotein (AGP). Leukocytes were isolated for flow cytometric analysis of macrophage phagocytosis activity and immunophenotyping. The *Bacillus* DFM plus ID7 increased ($P = 0.03$) average daily gain and feed efficiency over 8 weeks compared with control calves. At d 35, AGP levels were higher ($P < 0.05$) in *Bacillus* fed calves than control and *Bacillus* plus ID7 fed calves. At d 7, macrophages from *Bacillus* plus ID7 fed calves phagocytosed more ($P = 0.03$) *E. coli* per cell than *Bacillus* fed calves and had a higher ($P = 0.02$) density of CD172a on macrophages than control calves. Calves fed *Bacillus* had a greater ($P = 0.03$) proportion of activated B cells ($AM8^+$) than control calves. Calves fed *Bacillus* plus ID7 had a greater ($P = 0.02$) proportion of activated cytotoxic T cells ($CD26^+$) than calves fed *Bacillus*. *Bacillus* plus ID7 resulted in a greater proportion of $\gamma\delta$ T cells compared with *Bacillus* fed calves ($P = 0.04$) and $CD4^+CD8^+$ cells within the $\gamma\delta$ T cell population compared with control ($P = 0.04$). These results indicate that adding *E. faecium* ID7 alters immune development in calves divergent from the administration of *Bacillus* alone.

Key Words: direct-fed microbial, calf, immunity

309 An evaluation of the efficacy of Metacam NSAID therapy for improving calf vigor, general health and overall performance in newborn Ontario dairy calves.

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The objective of this research was to evaluate a newborn calf vigor assessment tool. In addition, the usefulness of pain management therapy for excessive trauma and enhancement of newborn calf vigor using meloxicam injectable solution was studied. A total of 842 heifer and bull calves from 10 commercial dairy herds were enrolled in this randomized double blind clinical field trial. At birth, calves were assessed for vigor using a scoring system and given either a 1-mL subcutaneous injection of 20mg/mL Metacam or placebo solution by the producer. A birth record was also completed including information on the calving event, colostrum administration and other details. It was hypothesized that NSAID treatment of calves born from a hard pull would reduce the risk of long-term health problems. At 1, 2, 3 and 6 weeks of age, each calf was assessed for growth and given a standardized clinical score for general health. It was found that calves born from a hard pull had less vigor than individuals from unassisted calvings ($P < 0.001$). However, newborn calf vigor score was not significantly associated with health outcomes. Calves treated with Metacam had better health until 6 weeks of age than placebo treated calves ($P < 0.01$). Better total health score was also significantly associated with increased weight gain ($P < 0.05$). Other factors associated with better total health score were feeding colostrum within 2 h compared with 7–12 h after birth ($P < 0.01$), and for calves born in the fall compared with the winter ($P < 0.001$) or spring ($P < 0.05$). Total weight gain over the 6 week period was significantly lower for calves born in winter ($P < 0.001$) or spring ($P < 0.05$), calves having less responsiveness at birth ($P < 0.001$), having a higher 6 week body temperature ($P < 0.05$) and attitude score ($P < 0.01$) and having been fed frozen/thawed colostrum compared with fresh ($P < 0.05$). Overall, some calf vigor factors and neonatal management practices may be important in long-term calf health. Metacam therapy may be appropriate to decrease long-term health effects in some calves.

Key Words: vigor, newborn calf, health

310 Innate immunological or metabolic status prior to an oral *Salmonella typhimurium* challenge is not predictive of a heightened acute phase response in weaned Jersey calves.

M. A. Ballou,* M. D. Sellers, D. L. Hanson, A. R. Pepper-Yowell, C. J. Cobb, and B. S. Obeidat, *Department of Animal and Food Sciences, Texas Tech University, Lubbock*

Objective was to determine if baseline metabolic and innate immunological variables are indicative of a heightened acute phase response to an oral *Salmonella typhimurium* (ATCC14028) challenge in weaned Jersey calves. Twenty Jersey bull calves (77 ± 1 d old) were classified into 2 groups (positive responders or negative responders) based on their plasma haptoglobin (Hp) response (>2 fold increase) after they were challenged orally with *Salmonella typhimurium*. All calves survived the 10 d observation period. Seven calves were categorized as Hp positive responders, of which 4 showed clinical signs of disease (anorexia, decreased response to stimuli, and distended head) at some point during the observation period; whereas none of the negative Hp calves displayed any clinical signs of disease. Neither the percent of neutrophils positive ($P = 0.501$) for producing an oxidative burst when cocultured with an *Escherichia coli* nor the geometric mean fluorescence intensity of the positive neutrophil population ($P = 0.516$) were different between Hp groups before the challenge. Similarly, baseline neutrophil expression of L-selectin ($P = 0.825$), whole blood secretion of tumor necrosis factor-α when cocultured with lipopolysaccharide ($P = 0.273$), and plasma concentrations of Hp ($P = 0.678$) were not different between the Hp groups. Calves that had a positive Hp response following the *Salmonella typhimurium* challenge had greater rectal temperatures before the challenge (39.12 vs. 38.89 ± 0.062; $P < 0.05$). Following the challenge, Hp positive calves had greater rectal temperatures ($P < 0.01$) over the entire observation period and the neutrophils had increased oxidative burst intensities ($P < 0.05$) beginning 72 h after the challenge, which persisted through the end of the study. No other differences were observed between the Hp groups after the challenge. Rectal temperature before the *Salmonella typhimurium* challenge was the only variable that was predictive of whether calves were at an increased relative risk for a heightened acute phase response following the challenge.

Key Words: calf, health, immune

311 Outdoor group-housed calves have improved performance and heightened innate immune responses during the neonatal and weaning periods compared to outdoor single-housed calves.

C. J. Cobb,* D. L. Hanson, M. D. Sellers, A. R. Pepper-Yowell, B. S. Obeidat, and M. A. Ballou, *Texas Tech University, Lubbock.*

Objective was to determine if outdoor group housing of calves influences metabolic and innate immunological responses compared with individually housed calves. Forty-nine Holstein calves (2 ± 1 d old) were randomly assigned to 2 treatments: individually housed (G1, n = 22) or 3 calves/pen (G3, n = 27). The space allowances per calf were 4.75 and 7.0 m^2 for G1 and G3, respectively. All calves received an identical high plane of milk replacer nutrition. Weaning was initiated during the 7th wk by removing the PM feeding and calves were completely weaned when they consumed 800 g dry matter (DM) daily after d 53. At d 91, calves were randomly commingled into groups of 5 outdoors. Peripheral blood was collected during the neonatal (3, 10, 21 d), weaning (45, 47, 53 d), and commingling periods (91, 94, 99 d) and was analyzed for neutrophil oxidative burst (OB) capacity when cocultured with an *Escherichia coli*, neutrophil L-selectin expression, whole blood secretion of tumor necrosis factor-α (TNF) when cocultured with lipopolysaccharide. Total DM intake was greater ($P < 0.05$) for G3 during the post-weaning period, wk 8 to 12. Average daily gain of G3 tended ($P < 0.10$) to be higher from d 21 to 52 and were higher ($P < 0.05$) from d 53 to 67. During the neonatal period, G3 calves had more activated innate immune responses as evidenced by increased ($P < 0.05$) neutrophil L-selectin expression and tendency for increased ($P < 0.10$) percentage of neutrophils producing an OB. During weaning, G3 calves continued to have more activate innate immune responses with increased ($P < 0.05$) L-selectin expression on d 45 and 47 and a greater OB intensity throughout the period. Immediately before commingling, G1 calves tended to have lower ($P < 0.10$) L-selectin expression with all immune variables being equal ($P > 0.362$) to G3 calves at d 94 and 99. Outdoor group housed calves had improved performance and heightened innate immune responses when compared with individually housed calves, which may be due to increased immunogenic stimulation.

Key Words: calf, housing, immune

312 Immune, health, and growth responses of beef calves administered modified-live virus respiratory vaccine during the presence of maternal antibody versus a traditional vaccination regimen.

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Crossbred beef calves (n = 253) from 3 breeding herds were used to determine the health, performance, and immune response to different pentavalent [bovine herpesvirus-1, bovine viral diarrhea virus (BVDV) types 1 and 2, parainfluenza-3 virus, and bovine respiratory syncytial virus] modified-live virus (MLV) vaccine regimens administered initially at either 62 or 188 d of age. Calves were stratified by date of birth, gender, BW, and dam age then assigned randomly to 1 of 2 vaccine regimens. Calves in the early vaccination (EV) treatment group received a pentavalent MLV respiratory vaccine containing *M. haemolytica* bacterin-leukotoxoid [Pyramid 5 + Presponse SQ, Boehringer Ingelheim Vetmedica, Inc., St. Joseph, MO] and a multivalent clostridial bacterin-toxoid on d 0 (calf age = 62 ± 17 d, mean ± SD), or calves in the traditional vaccination (TV) treatment group received the same respiratory vaccine and a multivalent clostridial bacterin-toxoid on d 126 (avg. calf age = 188 d). Calves in both treatment groups were revaccinated with the MLV respiratory and clostridial vaccines on d 147 (weaning). No calves required treatment for bovine respiratory disease during the study that ended after an 84-d post-weaning period. Interim and overall gain performances were similar ($P \geq 0.84$) between treatments. Antibody titers to BVDV type 1a were present but similar ($P = 0.50$) among treatments on d 0; yet BVDV antibody titers were greater for EV on d 21, 126, and 147. The EV calves had a greater (treatment × day, $P = 0.05$) CD25 expression index of CD8+ cells than TV calves on d 126. Differences in BVDV type 1a titers and CD25 expression indices suggest calves develop humoral and cell-mediated immunity when vaccinated at 62 d of age. Furthermore, growth performance or health were not affected by vaccine regimen, supporting early vaccination as a cost-effective alternative to traditional calfhood vaccine regimens.

Key Words: beef calves, bovine viral diarrhea virus, maternal antibody interference

313 Dietary adjuvanting prior to vaccine administration increases maternal antibody transfer to calves. A. D. Rowson, T. H. Schell, Y. Wang, N. E. Forsberg, and S. B. Puntenney,* *OmniGen Research LLC, Corvallis, OR.*

Several factors have been documented to increase the efficiency of maternal antibody transfer in neonatal calves, including colostrum quantity ingested, timing of colostrum delivery, and concentration of colostral antibodies. Perinatal vaccination protocols targeting increased IgG1 titers have been used successfully to reduce morbidity and mortality to calfhood enteric pathogens. Previous studies with OmniGen-AF pre-fed in bovine diets before vaccination have shown increased serum titer response to IBR, BRSV, and BVD-1. We hypothesized that the pre-fed additive would elicit increased colostral antibody expression to a commercial scours prevention vaccine administered to preparturient cows, potentially increasing passive transfer of maternal antibodies to calves. Multiparous Angus cows were randomly assigned by parity to a control diet or the same diet with 50g of OmniGen-AF pre-fed for 28 d before a booster vaccination with Pfizer's Scourguard 4KC. Blood samples were taken from dams 60 d post-vaccination and at calving, and from calves pre-suckle and at 7 d. A pre-suckle colostrum sample was taken following parturition. Samples were assayed by serum neutralization (SN) and indirect immuflourescence assay (IFA) for rotavirus and coronavirus. Results showed a strong effect of parity between second calf heifers versus 3rd plus parity cows ($P < 0.001$). Aged cows had significantly higher IFA serum titers at calving than non-treated controls for Rotavirus ($P < 0.007$) and higher IFA serum titers at 60 d post vaccination by 1.85× ($P < 0.02$), in colostrum by 1.7× ($P < 0.05$), with calves having 2 fold higher IFA serum titers ($P < 0.01$) for Corona virus. There were no significant differences in serum titers or colostrum antibody concentrations for 2nd calf parity cows. SN assays yielded similar results to IFA assays for all parameters. Serum and colostrum antibody titers for 2nd parity cows were approximately double that of 3rd plus parity cows. This data suggests that the feed additive may have benefit in the restoration of the ability of older animals to initiate antibody production.

Key Words: antibody, vaccination, OmniGen-AF

314 Correlation between circulating white blood cell counts and level of protective immune response against bovine viral diarrhea virus elicited by a modified live vaccine. S. M. Falkenberg*[1], J. Ridpath[1], J. R. Tait[2], B. Vander Lay[1,2], and J. M. Reecy[2], [1]*USDA-ARS-National Animal Disease Center, Ames, IA,* [2]*Iowa State University, Ames.*

Two trials (T1 and T2) were conducted to examine the range of responses elicited against bovine viral diarrhea virus (BVDV) by vaccination with modified live vaccine (MLV) and to determine the level of response required for prevention of clinical disease. For T1, BVDV neutralizing (BVDV VN) titers were determined on 216 spring born beef calves (177.03 ± 30.05 kg BW) 20 d after the booster vaccination (49 d from initial vaccination) with a MLV. The presence of titers against BVDV was also measured using a commercial ELISA to determine if this method gave comparable results to VN titers. Trial 2 utilized 120 fall born beef calves (141.06 ± 29.43 kg BW) that followed the same vaccination protocol in T1, but an extra sample was obtained to determine circulating white blood cell counts (WBC) when blood samples were obtained for determination of antibody response. For T2, titers against BVDV were initially determined using the commercial ELISA. In both trials all calves were stratified into low, medium and high response groups based on standard deviations from the mean. Twelve calves, for each trial, were selected to represent 3 low, medium and high response groups. After selection, serum from selected calves was collected and evaluated for BVDV response by VN. VN values for the 3 groups (n = 4; low (titer <1/4), mid range (titer 1/4 to 1/16) and high (titer >1/16). Calves were moved to BL2 containment and challenged with a high virulence BVDV strain 101 d after the initial vaccination. Blood samples were collected on d −2, 2, 4, 6, 9, 11 and 13 post challenge to determine levels of circulating white blood cells, viral shed and levels of BVDV VN titers. While, overt respiratory or enteric disease was not observed in any of the calves, challenge did result in a decrease in circulating WBC in some animals. Calves in the high response T1 group (titers greater than 1/16) did not have significant decreases in WBC, but calves in the mid and low titer groups had a decrease in circulating WBC and lymphocytes on d 4 ($P < 0.05$). Because a correlation between WBC on day −2 and a protective response elicited by vaccination for the 12 calves in T1 was observed, WBC was determined for all 120 calves at booster vaccination in T2. Similar to the 12 calves in T1, a positive correlation was observed between WBC and level of BVDV antibodies as determined by ELISA for calves in T2. Results from these 2 trials provide evidence that there is a relationship between WBC and the response to vaccination. Further investigation before vaccination is warranted to discern if vaccination changes WBC or if WBC alter response to vaccination.

Key Words: cattle, titer, vaccine

315 Omnigen-AF restores GR-1, L-selectin, and RANTES expression by immunosuppressed murine PMN challenged with lipopolysaccharide in a MyD88-dependent manner. R. J. Ortiz-Marty[1], N. E. Forsberg[2], J. D. Chapman[3], and I. K. Mullarky*[1], [1]*Virginia Polytechnic Institute and State University, Blacksburg,* [2]*OmniGen Research LLC, Corvallis, OR,* [3]*Prince Agri Products Inc., Quincy, IL.*

Bovine mastitis costs the dairy industry billions of dollars every year and presents a health challenge in dairy operations. Immunosuppressive effects of the periparturient period result in an increased risk for mastitis. During this time, cattle experience an increase in circulating cortisol, which reduces neutrophil (PMN) function and ability to clear infection. OmniGen-AF is a feed additive that restores PMN function during periods of immunosuppression in cattle. Signaling pathways involved in restoring PMN function are undetermined. We hypothesized that OmniGen-AF restores PMN function through cross-regulation of TLR signaling. To test our hypothesis, wildtype or MyD88 knockout (KO) mice were unsupplemented or supplemented with OmniGen-AF in the diet, challenged with LPS, immunosuppressed with dexamethasone, or immunosuppressed with dexamethasone and challenged with LPS. PMN were isolated through intraperitoneal lavages and analyzed for gene expression profiles. Results indicate that LPS significantly ($P < 0.05$) upregulated GR-1, L-selectin, and RANTES (genes) in PMN isolated from wildtype mice as compared with immunosuppressed mice. Interestingly, LPS did not upregulate genes in PMN from supplemented wildtype mice as compared with supplemented wildtype immunosuppressed mice. LPS differentially induced genes in PMN from MyD88 KO mice as compared with PMN from supplemented MyD88 KO mice. These results suggest that OmniGen-AF supplementation restores the response of immunosuppressed PMN to LPS challenge and that the restorative role may be MyD88-dependent. Future research needs to determine the specific TLR, transcription factors, and biochemical properties of OmniGen-AF that restore gene expression in immunosuppressed PMN.

Key Words: immunity, neutrophil, OmniGen-AF

ARPAS Symposium: Feed Efficiency: Opportunities for improvement, economics, and integration with environmental sustainability

316 Feed efficiency: Basic principles and opportunities for improvement. M. VandeHaar*[1], L. Armentano[2], D. M. Spurlock[3], J. Patience[3], and J. Taylor[4], *[1]Michigan State University, East Lansing, [2]University of Wisconsin, Madison, [3]Iowa State University, Ames, [4]University of Missouri, Columbia.*

The efficiency of converting feed to meat and milk in the US has increased in over the past century largely as the indirect result of increased productivity (faster lean accretion or more milk per cow) and the resulting dilution of maintenance requirements. Further increases in productivity have a diminishing impact on feed efficiency, and, in fact, if digestibility is depressed at higher intakes, increased productivity has the possibility of decreasing efficiency. Therefore, we must find new ways to improve lifetime feed efficiency through enhanced efficiency of digestion, metabolism, and product formation without impairing health or fertility. Ideally, feed efficiency should incorporate all inputs and outputs of energy, protein, and other nutrients as well as land, fuel, and human-edible foods during an animal's lifetime. However, the traits that are routinely measured in individual animals are outputs such as growth rate or milk yield and not feed inputs; thus the feed efficiency phenotype for most animals is not known. In 2011, USDA-NIFA funded 3 large projects to improve the efficiency with which the beef, dairy, and swine industries use feed. All target genetic improvement using genomic selection. Genomic selection makes use of a reference population of animals with both phenotypic and genotypic data to develop models of predicting genetic merit from genotype, thus enabling genetic selection without phenotypic data. Because the heritability of feed efficiency is likely in the range of 20 to 40%, the reference population must include thousands of animals to produce estimates of breeding value with reasonable accuracy. Our research aims are to develop these reference populations, better characterize the genetic and biological basis of feed efficiency and its interactions with diet, and develop marker-assisted and genomic selection tools for feed efficiency. We will use residual feed intake as our measure of the feed efficiency phenotype and medium/high-density whole genome SNP panels for genotypes. Decision tools and on-farm demonstrations are being developed to enhance adoption of best management practices, and teaching programs are underway to nurture scientists who will lead future improvements in the feed efficiency of animal agriculture.

Key Words: feed efficiency, genomic selection, genetics

317 Impact of milk yield, herd size, and feed efficiency on economic change between and within California dairies from 2006 through 2010. L. Rodriguez*[1], G. Bethard[2], D. Tomlinson[1], and M. McGilliard[3], *[1]Zinpro Corporation, Elk Grove, CA, [2]G & R Consulting, Blacksburg, VA, [3]Virginia Tech, Blacksburg.*

Milk and feed prices have been volatile in the California (CA) dairy industry in the last 5 years, bringing stress and difficult strategic decisions to managers. Our objective was to find financial and production trends that improved profitability of CA dairies. The CA Department of Agriculture milk production cost farm database from 2006 to 2010 (705 herd-years) included milk yield, herd size, feed efficiency (FE), housing type and milking frequency, as well as measures of milk income and various expenses. Variables of expense per 45.5 kg, FE and profit per 45.5 kg were analyzed with a model that included year, breed, linear and quadratic effects of either yield, size, or FE, and all interactions with breed. A second analysis was limited to 97 Holstein (H) herds present in all 5 years to estimate intra-herd linear relationships. Grouped into categories, H herds producing less than 31.8 kg/d differed from those greater than 36.4 kg/d of solids-corrected milk (SCM) in total cost/45.5 kg (TC) of $14.97 and $13.49, respectively. Jersey herds producing less than 25.0 kg/d differed from those greater than 29.5 kg/d of SCM with TC of $17.67 and $15.58. Holstein herds with FE (SCM/DMI) exceeding 1.45 compared with less than 1.33 were $1.29 lower in TC. Milk net income (MNI) per 45.5 kg SCM was -$0.29 versus $1.12 in H herds with less than 31.8 kg/d and more than 36.4 kg/d SCM. Jersey herds producing less than 25.0 kg/d and more than 29.5 kg/d of SCM differed in MNI, -$1.36 and $0.72. The TC decreased linearly and quadratically for larger herds, with H herds of more than 2,000 cows having $1.31 smaller TC compared with herds with fewer than 1,000 cows. Jersey herds of more than 2,000 cows were $2.09 less in TC compared with herds of fewer than 500 cows. From 2006 to 2010, TC increased $0.40/yr in H herds. In H herds increasing SCM by 0.91 kg/yr TC increased only $0.26/yr. In H herds decreasing SCM by 0.91 kg/yr TC increased $0.73/yr. Change in FE/yr and change in MNI/yr increased linearly as SCM change per year increased. Efficient herds had higher profitability in the CA dairy industry.

Key Words: dairy profitability, feed efficiency, herd economics

318 Integrating productivity and whole-farm efficiency to achieve environmental sustainability. J. L. Capper*[1] and D. E. Bauman[2], *[1]Washington State University, Pullman, [2]Cornell University, Ithaca, NY.*

Environmental sustainability (ES) is a crucial consideration for livestock producers as consumers, retailers and policy-makers become more aware of resource use and greenhouse gas (GHG) emissions associated with animal agriculture. Optimal environmental sustainability can only be achieved by improving efficiency throughout the food production system; yet on-farm productivity (resource use per unit of output) and production processes make the greatest contribution to environmental impact and thus offer the greatest opportunity for mitigation. Popular perceptions of ES are often associated with extensive livestock systems, with the concept of "efficiency" being regarded as undesirable. Nonetheless, deterministic models of ruminant production have revealed that improved productivity in modern intensive systems confers considerable reductions in resource use and GHG emissions per unit of food product from dairy or beef. Environmental gains through this "dilution of maintenance" effect result from a combination of improved productivity in the productive (growing or lactating) sector of the population diluting resource requirements over greater output; and reducing resource requirements within the non-productive sector of the supporting population by requiring a smaller number of animals to maintain total output. A significant contribution may also be made via "reduction of maintenance" - reducing the total bodyweight of animals within the supporting population through the use of smaller breeds, while maintaining total animal protein output. Whole-farm analysis may be used within dairy production, yet is an inadequate measure of ES in a fragmented industry such as beef production, where interactions between the cow-calf, stocker and feedlot operation can have long-lasting consequences. For example, despite the perception that feedlot operations are major contributors to GHG emissions, whole-system analysis demonstrates that the cow-calf operation accounts for 72% of carbon output. Ultimately however, the considerable interaction between dairy and beef production systems necessitates a combined dual-system analysis to define the practices that contribute to true sustainability.

Key Words: productive efficiency, carbon footprint, dilution of maintenance

Bioethics Symposium: Bioethical Challenges in Education: New challenges and opportunities

319 Challenges and opportunities in teaching agricultural animal bioethics. C. C. Croney*[1], W. R. Stricklin[2], and D. Scott[3], *[1]Purdue University, [2]University of Maryland, College Park, [3]University of Montana.*

Decisions about acceptable agricultural systems and use and treatment of animals are ultimately based on personal and societal ethics. Thus, it can be argued that there is a growing need to create curricula that address the ethical foundations of animal agriculture. Yet, many people in animal agriculture either do not fully understand or appreciate this need, and contend that "science alone" should dictate standards of animal care and welfare. Certainly, science is necessary to make informed decisions. However, the field of ethics, rather than science has traditionally been viewed as the appropriate domain to address questions pertaining to "what should be." Despite the significant and increasing role of ethics in formulating public opinion about animals, students and professional animal scientists typically receive little or no formal ethics education. Additionally, most animal science curricula either lack an emphasis on animal welfare or include it only as a current issues topic with minimal or no specific emphasis on ethics. Faculty from 5 universities have been funded by a USDA NIFA Challenge Grant to address bioethics education in animal agriculture. The major objectives of the grant include: 1) developing teaching modules and pedagogical strategies that will facilitate fruitful student discussions instead of debate, and 2) extending the educational material and information to other animal science educators. Student participation is a necessity when including ethics in animal welfare courses. Ideally, animal science students learn even more when interacting with students from other majors who may hold differing opinions and values. Thus, it is critical that the instructor create a classroom environment in which students feel safe and free to express their opinions. Well-planned discussion questions and case studies combined with rules regarding respect for the views of all persons are as critical as a properly prepared and informed instructor. We will explore these elements as well as additional pedagogical experiences and strategies for developing agricultural animal bioethics course content that addresses farm animal welfare, policy, agricultural environmental ethics, and rural societal issues.

Key Words: agriculture, animal welfare, bioethics

320 Assessing the merits of animal welfare assessment tools: A philosophical framework from virtue ethics and narrative ethics. R. Anthony,* *University of Alaska, Anchorage.*

This presentation will cover factors conscientious animal scientists and veterinarians struggling to evaluate animal welfare and to facilitate responsible discussions on the topic should consider when welfare priorities collide. The Ethical Matrix (Mepham, 2000), Ethics Assessment Process (Campbell and Hare, 1997) and the Four-Box Method (Jonsen et al., 1992) will be described and discussed in light of an ethic of outcomes and an ethic of responsibility. Limitations and strengths of each will be exposed, and a philosophical basis that is steeped in virtue and narrative ethics will be proposed to guide the ethical assessment process. The philosophical basis of animal welfare assessment that will be articulated is motivated by the context of moral evaluation that recognizes that animal welfare is typically understood as 'feeling well, functioning well, and having the ability to perform species characteristic behaviors.' Decision-making should be integrated into habits that promote the human-animal bond and with an eye toward being a steward for the environment. Humane slaughter and euthanasia of animals will be discussed as examples of the animal welfare philosophy and how to incorporate them into animal production.

Key Words: animal welfare, animal welfare assessment, bio-ethics

321 Challenges and opportunities for bioethicial education in extension/outreach activities. H. M. Zaleski*[1] and D. Newman[2], *[1]University of Hawaii at Manoa, Honolulu, [2]North Dakota State University, Fargo.*

This presentation will address challenges and opportunities for bioethical education in extension/outreach activities in animal agriculture. Extension's challenge is to engage both the general public and those involved in animal production on issues and ethics in animal agriculture. Effective extension personnel need to be prepared to identify issues, provide science-based knowledge, use facilitation, and discuss ethical dimensions related to production agriculture. Extension educators can teach management practices affecting animal bioethics through producer programs, such as Pork Quality Assurance Plus and Beef Quality Assurance, and present standards such as pork's We Care ethical principles. Programs are also needed to educate the public who are not involved in agriculture on animal production methods, the underlying science, and the world's food supply. Nontraditional programs that create new ways of thinking and learning provide an opportunity for extension to address critical issues in bioethics. Since 2010 Hawaii Cooperative Extension has used a case-study approach (adapted from undergraduate classes) that has been effective in helping 4-H youth understand ethical principles. The discussion is controlled by the youth with the leader in the role of facilitator, and there is no pre-determined "right" answer. Although the principles developed may lack sophistication, they have power in that the youth "own" them. Since 2008 North Dakota State University has delivered the "NDSU BBQ BOOT CAMP" program to over 3200 consumers and producers. This extension program goes out into communities and provides face-to-face education about animal agriculture; provides consumers and producers with information about the importance of agriculture and the role of society in providing a safe food supply, including topics on animal welfare; and explains the roles and activities of the extension service. Participants gave the BBQ Boot Camp program an average score of 4.6 on a 5-point scale (5 = highest). Consumers indicate that they prefer this type of programming over social media, television, and radio and that they are more likely to believe facts that are explained by experts in the field of animal agriculture. Extension personnel can play a significant role in educating society on the ethical issues surrounding animal agriculture.

Key Words: extension, bioethics, communication

Breeding and Genetics: Dairy Cattle Breeding II–Applied molecular biology and genomics

322 Effects of genomic inbreeding on production, reproduction, and udder health in Holstein dairy cows. D. W. Bjelland*[1], K. A. Weigel[1], D. J. Nkrumah[2], and N. Vukasinovic[2], *[1]Uinversity of Wisconsin-Madison, Madison, [2]Pfizer Animal Genetics, Kalamazoo, MI.*

The objective of the present study was to assess the effects of genomic inbreeding on production, reproduction, and udder health in Holstein dairy cows. First and second lactation data were collected from 1,061 Holstein dairy cows, which were born between 2006 and 2008, from 5 commercial herds across the United States. All cows were genotyped for 54,609 single nucleotide polymorphism (SNP) markers. SNPs were edited based on call rate and allele frequency. The remaining SNPs were separated into SNPs that were or were not in Hardy-Weinberg (HW) equilibrium. The SNPs that were not in HW equilibrium were assumed to be under selection and were removed from the analysis of genomic inbreeding. Homozygosity of the remaining 43,398 SNPs that were in HW equilibrium was calculated and utilized as the measure of genomic inbreeding in this study. Average homozygosity was 66.7 ± 1.6%, with a minimum and maximum of 60.4 and 75.3% respectively, and cows with a greater percentage homozygous loci were assumed to be more highly inbred. Total lactation milk, fat, and protein yield decreased by 15.8, 1.4, and 0.6 kg, respectively, per 1% increase in homozygosity. Furthermore, days open increased by an average of 1.96 d per 1% increase in homozygosity, but somatic cell score did not change with an increase in homozygosity. The results presented herein suggest a possible relationship between increasing homozygosity and decreasing lactation performance and reproductive ability.

Key Words: genomics, inbreeding

323 Maternal grandsire confirmation and discovery in dairy cattle. G. R. Wiggans[1], T. A. Cooper*[1], P. M. VanRaden[1], J. R. O'Connell[2], and L. R. Bacheller[1], *[1]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [2]University of Maryland School of Medicine, Baltimore.*

Accurate pedigree information is essential for selecting dairy animals to improve economically important traits. Two methods of maternal grandsire (MGS) discovery were compared. The first compared one single nucleotide polymorphism (SNP) at a time using a genotype from one or both parents (SNP method). The second compared haplotypes of a potential MGS to the animal′s maternal haplotype, which included linkage information across all loci (HAP method). Modified pedigrees with 5% of true MGS replaced by a random genotyped bull from the same birth year and 5% set to missing were created to test the HAP method. To test the SNP method, the same group of animals (including multiple genotypes for some animals and excluding imputed dams) was used. Both methods ranked the most likely MGS. The SNP method can be performed as soon as a genotype is received because no imputation is required. The HAP method was expected to have greater accuracy because it includes low-density genotypes imputed to the 45,187 SNP used for genomic evaluation as well as additional imputed animals. Accuracy of predicting true MGS was evaluated using genotypes for 4,620 Holsteins, 659 Jerseys, and 160 Brown Swiss with confirmed genotyped sires for the SNP method and modified pedigrees for 4,134 Holsteins, 552 Jerseys, and 142 Brown Swiss for the HAP method. Accuracy of true MGS prediction for Holsteins, Jerseys, and Browns Swiss was 95, 91, and 94%, respectively, with the SNP method and 97, 95, and 97% with the HAP method. Lack of imputed SNP decreased accuracy of the SNP method for low-density genotyped animals (78%) compared with BovineSNP50 genotyped animals (97%). Predicted MGS accuracy with the HAP method was 98% for BovineSNP50 genotypes, 94% for Bovine3K genotypes, and 92% for imputed genotypes. When the HAP method was extended to great grandsires, accuracy of maternal great-grandsire confirmation and discovery was 92% for 652 Holsteins, 95% for 33 Jerseys, and 85% for 20 Brown Swiss. Because most dairy bulls have been genotyped, parentage and MGS analysis can accurately confirm, correct, or discover parents and more distant ancestors for most animals.

Key Words: haplotype, maternal grandsire, SNP

324 Sequence analysis and methylation patterns of the bovine IWS1 gene localized to a region of BTA2 involved in postnatal growth. I. G. Imumorin*[1], M. De Donato[1,2], S. O. Peters[1,3], A. M. Corn[1], Y. Bing[1], H. E. Rudolfo[2,4], M. Al-Abri[1,4], and T. Hussain[1,5], *[1]Cornell University, Ithaca, NY, [2]Universidad de Oriente, Cumana, Venezuela, [3]Federal University of Agriculture, Abeokuta, Nigeria, [4]Sultan Qaboos University, Muscat, Oman, [5]University of Veterinary and Animal Sciences, Lahore, Pakistan.*

Our previous genome scan identified the proximal end of bovine chromosome 2 as containing a putative parent-of-origin effect quantitative trait locus (POE-QTL) affecting postnatal growth in cattle. We embarked on bioinformatics and experimental search for possible positional candidate genes in this region. A search of human and mouse genomes of known and putative imprinted genes identified the homolog of *Saccharomyces cerevisiae* serine protease inhibitor 1 (SPN1 also known as IWS1) in this region. This gene is part of a transcription factor complex that regulates transcription. We previously showed that this gene is expressed ubiquitously in 18 bovine tissues and has 99.9% homology with the predicted mRNA sequence in cattle. A comparison of this sequence with the predicted mRNA sequence in sheep and pig shows 97.9 and 92.9% homology, respectively. A phylogenetic analysis of the protein sequence predicted from these mRNAs and those of dog, panda, horse, human, marmoset, mouse, rat, elephant, opossum and platypus, using the lizard protein as an out group, shows high conservation among all the eutherian mammals but not as much with marsupials and monotremes. In this study we screened the coding region for mutations in 19 cattle breeds and found several SNPs. In addition, we carried out DNA methylation analysis in multiple bovine tissues and showed that this gene is differentially methylated. These further show that this gene may be of significance for the traits of interest mapped to bovine chromosome 2.

Key Words: SNP, cattle, IWS1 gene

325 Characterization of sequence diversity of IFNAA and INFB1 in Pakistani breeds of cattle. T. Hussain*[1,2], M. E. Babar[1], A. Nadeem[1], A. Ali[1], A. Wajid[1], M. Al Abri[2], M. De Donato[2,3], S. O. Peters[2], and I. G. Imumorin[2], *[1]Institute of Biochemistry and Biotechnology, University of Veterinary and Animal Sciences, Lahore, Pakistan, [2]Department of Animal Science, Cornell University, Ithaca, NY, [3]IIBCA, Universidad de Oriente, Cumana, Venezuela.*

Interferons (IFN) are glycoproteins made and released by host cells in response to the presence of pathogens to trigger the protective defenses of the immune system. Among the type I IFNs, IFNA and INFB1 are very important to activate the initial immune response. The objective of this study was to characterize sequence polymorphisms in IFNA and INFB1 genes. We studied 46 samples from Pakistan: 4 Achai, 4 Bhagnari, 6 Cholistani, 4 Dhani, 4 Dajal, 4 Lohani, 4 Nari Master, 6 Red Sindhi, 6 Sahiwal and 4 Tharparker and compared them to sequences from 3 Hereford, 3 Angus and 8 Holstein cattle from the US and 4 Muturu, 11 White Fulani and 4 Sokoto Gudali from Nigeria. Sequences were analyzed by MEGA5 software and Panther to determine the phylogenetic and functional implications of the different variants found. We found 8 polymorphic sites in the amino acid sequence of IFNAA and 20 polymorphic sites in IFNB1. The phylogenetic analysis indicated significant amount of sequence variation and the divergence of Pakistani cattle breeds of these genes from other breeds of taurine cattle. Most of the amino acid changes were non-synonymous and produced changes in the protein structure. The phylogenetic analysis indicated significant divergence of Pakistani cattle breeds from other taurine breeds of cattle, and comparison were made with *Bubalus bubalis*, *Capra hircus* and *Ovis aries*. The functional analysis of the variants show amino acid changes that can affect the structure of the proteins potentially producing changes in the interaction between the other proteins involved in the immune response. This is the preliminary report on Interferon genes in Pakistani cattle breeds. This information is valuable for the association with the resistance or tolerance to infectious agents in cattle in this region.

Key Words: cattle, immune genes, SNP

326 Effect of GHR *Alu*I polymorphism on reproductive performance of Holstein cows.

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The recovery of the growth hormone (GH)/insulin-like growth factor (IGF-I) axis is implicated in an early return to ovulatory cycles and a shorter calving to conception interval in postpartum dairy cows. Based on this, the aim of this work was to determine effects on the reproductive performance of Holstein cows of a GH receptor (GHR) AluI polymorphism, a point mutation upstream from its mRNA start codon. Holstein cows (n = 80) were on the study until 210 days in milk (DIM). Blood samples were collected at 7 and 21 DIM for serum IGF-I determination. For GHR genotyping, DNA was extracted from blood and the presence of the alleles determined after digestion of the corresponding GHR gene region with the *Alu*I enzyme. Milk samples were collected 2 times/week for progesterone analysis. Progesterone higher than 1 ng/mL in 2 consecutive samples was considered indicative of ovulation. Cows were submitted to an OvSynch-TAI protocol at 55 DIM and repeated for cows diagnosed as not pregnant 30 and 60 days after AI. Data was analyzed with SAS for polynomial effects of the presence of the two GHR *Alu*I alleles. Among the cows, 40% had the *Alu*I(+/+) genotype, 50% had *Alu*I(–/+) and 10% were *Alu*I(–/–). Interval from calving to first ovulation was not different among these three genotypes ($P > 0.05$), but reduced for all cows carrying at least one *Alu*I(–) compared to *Alu*I(+/+) cows: 27 ± 3 vs. 33 ± 3 days, respectively ($P = 0.07$). There was a linear effect of the *Alu*I(–) allele on the calving to conception interval, being 80 ± 13, 94 ± 6 and 115 ± 8 days for the GHR *Alu*I(–/–), *Alu*I(–/+) and *Alu*I(+/+) cows, respectively ($P = 0.02$). For serum IGF-I concentration there was a quadratic effect of the *Alu*I(–) allele ($P = 0$ .04): 101 ± 10, 60 ± 5 and 63 ± 5 ng/mL for GHR *Alu*I(–/–), *Alu*I(–/+) and *Alu*I(+/+) cows, respectively. In summary, the presence of the GHR *Alu*I(–) allele in Holstein cows was associated with increased serum IGF-I concentrations and fewer days to first postpartum ovulation that contributed to a shorter calving to conception interval.

Key Words: fertility, GHR, SNP

327 Genomic evaluation of rectal temperature in Holstein cattle.

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Heat stress negatively affects the production, fertility, and health of dairy cattle. Rectal temperature (RT) has unfavorable genetic correlations with production, longevity, economic merit, and somatic cell score in Holstein cows. The objectives of the current study were to perform a genome-wide association study (GWAS) for rectal temperature in dairy cows under heat stress conditions, and to determine with what genes single nucleotide polymorphisms (SNP) of large effect are associated. Rectal temperature was measured between 1500 and 1700 h in 5,590 lactating Holstein cows sired by 3,322 bulls during the summer in north central Florida. Rectal temperature averaged 38.8°C ± 0.57°C, and ranged from 37.0°C to 41.6°C. The model included fixed effects of parity; random effects of herd-year, animal, and permanent environment; and regressions on temperature-humidity index and test-day milk yield. The pedigree file included 886 sires with Illumina BovineSNP50 BeadChip (Illumina, Inc., San Diego, CA) genotypes. After edits for call rates <0.90, minor allele frequencies <0.05, and Mendelian conflicts, 30,0018 markers remained. Genotypes for 9 animals were dropped due to low call rates. (Co)variance components and breeding values were calculated using the AIREMLF90 and BLUPF90 software packages from the University of Georgia (Athens). The GWAS was performed with a one-step procedure as implemented in the POSTGSF90 software. The heritability and repeatability of RT were 0.06 and 0.22, which is lower than recent estimates, possibly because most sires had only a few daughters with records and pedigree ties were limited. The 20 SNP with the largest solutions were examined to determine if they were located in or near genes that could account for heat stress effects. Five SNP were located in introns: *C1H21orf59* on *Bos taurus* autosome (BTA) 1, *INADL* on BTA3, *ZNF335* on BT13, *VPS13* on BTA16, and *FTO* on BTA18. The third-ranked SNP was located in an exon of *CCT6B* on BTA12. These results will help identify genes involved in physiological responses to heat stress. Additional phenotypes are needed to improve estimates SNP effects.

Key Words: rectal temperature, genomic selection, genetic evaluation

328 Feasibility of genomic prediction of fatty acids composition in milk of dairy cattle from Luxembourg using single-step procedure.

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Milk composition in fatty acids (FA) portrays a class of novel traits of interest for both human health and animal robustness. With the exception of Wallonia, Luxembourg is currently the only place in the world where, using mid-infrared spectrometry, milk composition in 29 FA is routinely recorded for dairy cows. Since 2007, spectral data has been recorded so far on 87,368 cows from 690 different herds, by 2 main control methods (T-method: one sample of only one milking, morning or evening, and S-method: proportionate sample of all daily milkings).

Additionally, milk, fat and protein yields are available since 1990. The availability of FA allows many options for management use and animal breeding but requires advanced modeling (e.g., adapted to the testing methods). In the context of animal breeding, genomic selection has been widely developed in dairy cattle, where single-step approach (ssGBLUP) is particularly well suited for small-sized populations, as the dairy cattle population of Luxembourg (365,892 animals currently in pedigree) and is completely integrated into mixed modeling of phenotypic data. The objectives of this study were: (1) to assess the potential benefits of a single-step genomic evaluation on milk FA composition in a small-sized population and in particular (2) to quantify the impact of genomic information on reliability (REL) of estimated breeding values (EBV) of FA in Luxembourg. In a preliminary study for a single FA, oleic acid (C18:1 *cis* 9) genetic evaluations were performed on 47,613 milk records; collected by S-method, from 8,000 cows in first parity with a random regression test-day model using second order Legendre polynomials. For this sample, molecular data was simulated for 422 AI sires, ancestors of recorded cows. Prediction error variances (PEV) were used to compute REL and effective daughter contributions (EDC). First results showed a low increase in REL and EDC. Extension of this research to all sampling methods and research on the optimum structure of the reference population (bulls, cows) will be done to fit the Luxembourg-specific situation.

Key Words: genomic selection, fatty acids, small population

329 Microsatellite markers based genetic evaluation of Pakistani cattle breeds.

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Animal Genetic Resource of Pakistan is very diverse. There are 15 distinct breeds of cattle in Pakistan all belonging to zebu (humped type) cattle (*Bos indicus*) for which very little information on genetic architecture is available. Microsatellite markers are being widely used for breed characterization in animals. In the present study 345 individuals of 11 breeds (10 Pakistani cattle breeds and exotic Holstein Friesian breed) were genotyped using 22 labeled microsatellite markers to assess genetic variation and relationships among them. All markers were polymorphic and observed number of alleles ranged from 8 (TGLA122) to 18 (ILSTS029, BM6526) with mean value 13.54 ± 2.80 per locus. Average values of observed and expected heterozygosity were calculated as 0.462 ± 0.155 and 0.823 ± 0.06. Mean values of Fis, Fit, Fst and gene flow were 0.328, 0.432, 0.155 and 1.362 respectively. The average PIC value was 0.81 showing suitability of these markers for forensic analyses. Nei's genetic distance estimates indicated relatively close genetic identity between Tharparker and Red-Sindhi breeds of Sindh Province of Pakistan while Tharparker and Dajal breeds were found most distinct. The UPGMA-based phylogenetic tree constructed from the genetic distances also indicated that the cattle breeds of Pakistan can be classified into distinct genetic groups based on these markers. This is the first comprehensive report on molecular characterization of Pakistani cattle breeds using microsatellite markers. This study can be helpful for making breed conservation strategies of cattle in Pakistan in future.

Key Words: microsatellite markers, heterozygosity, Pakistani cattle breeds

330 Effects of β-casein, κ-casein and β-lactoglobulin gene allelic variants on milk production and protein composition traits of Brown Swiss cows.

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Milk protein composition influences many aspects of the dairy industry as well as the nutritional value and the technological properties of milk. The aim of this study was to investigate the effect of β-casein (*CSN2*), κ-casein (*CSN3*) and β-lactoglobulin (*BLG*) gene allelic variants on milk production and the relative concentration of the major milk proteins: α-lactalbumin (α-LA), β-lactoglobulin (β-LG), α_{S1}-casein (α_{S1}-CN), α_{S2}-casein (α_{S2}-CN), β-casein (β-CN) and κ-casein (κ-CN) of individual milk of Brown Swiss cows. A total of 1,271 cows distributed in 85 herds were milk sampled once from January 2010 to February 2011. Individual samples were collected during the evening milking and detailed milk protein composition was analyzed using reversed-phase high performance liquid chromatography (RP-HPLC). Genotypes of cows for *CSN2*, *CSN3* and *BLG*, were also derived by RP-HPLC. The allele frequencies for *CSN3* (A: 0.232, B: 0.768) and *BLG* (A: 0.331, B: 0.669) were unbalanced in favor of the B variant. All genes were in Hardy-Weinberg equilibrium. An association study for*CSN2*, *CSN3* and *BLG* allelic variants was performed using a linear model. The model included effects of days in milk, parity, *CSN2*, *CSN3*and *BLG* genotypes, and the random effect of the sire of the cow. Effects of genotypes on milk yield were weak. The *CSN2* genotype influenced the percentage of α_{S1}-CN, α_{S2}-CN and β-CN, calculated on total casein, the CN number, calculated on total protein κ-CN percentage, and total protein content. The *CSN3* genotypes affected the percentage of α_{S1}-CN, α_{S2}-CN, and β-LG, the latter calculated on total whey protein, percentage of β-CN, CN number, κ-CN percentage, and total protein content. The BLG influenced the percentage of β-LG, protein content, total whey protein, CN number, and percentage of β-LG. All these associations were statistically significant ($P < 0.05$). Our findings could be used to identify animals that produce milk with desired composition or desired processing and manufacturing properties.

Key Words: milk protein composition, protein variant, dairy cow

331 Associations between single nucleotide polymorphisms in multiple candidate genes on milk yield, composition, coagulation properties and individual cheese yield in Brown Swiss cows.

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The fraction of milk used for cheese making is growing worldwide. Although genetic variation for traits related to cheese-making exists, their inclusion as breeding goals in conventional selection programs is hampered by phenotyping costs. A possible solution can be found in the identification of candidate genes that affect milk quality, composition and technological traits and that can be integrated in gene-assisted selection programs. The aim of this study was to investigate the association between 46 single nucleotide polymorphisms (SNP), in 33 candidate genes, and the aforementioned traits in individual milk samples from Italian Brown Swiss cows. A total of 1,271 cows were sampled once in 85 herds. Milk and blood samples were collected during the evening milking concurrently with the monthly test-day milk recording. Individual milks were used for measuring: milk quality traits (i.e., protein, casein and fat percentage), milk coagulation properties and individual cheese yield. Genotyping was performed by using a custom VeraCode

GoldenGate approach. A mixed linear model, considering effects of herd, days in milk, parity, SNP genotype and the random effect of the sire of the cow, was used for the association analysis. Each SNP was analyzed separately. Results showed that 16 out of the 46 SNPs were significantly associated with at least one of the traits. Within these SNPs, the ATP-binding cassette sub-family G member 2 (*ABCG2*) and α_{S1}-casein (*CSN1S1*) genes were found to be associated with technological traits considered. Although further research is needed to validate the SNPs in other populations and breeds, the association between these markers and milk technological traits could be exploited in gene-assisted selection programs for genetic improvement purposes.

Key Words: milk coagulation property, individual cheese yield, candidate gene

332 Sire and vaccine treatment effects on immune response to BVDV 1b challenge.

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Yearling Angus-Nelore F_2 and F_3 steers born in spring of 2009 and 2010 (n = 182) were evaluated for immune response to vaccination and viral challenge. Calves were stratified by composition (F_2 or F_3) and sire across 3 vaccination treatment groups of non-vaccinated (NON, n = 61), 2-injection killed vaccine (n = 60), or single-injection modified live vaccine (MLV, n = 61). All calves were determined to be free of bovine viral diarrhea virus (BVDV) persistent infection and challenged with BVDV 1b (d 0); serum was collected on day of vaccination(s) and d 0, 14, 28, and 42 evaluated for neutralizing antibodies against IBR, and BVDV types 1a, 1b, and 2. Titers (reciprocal base 2 log of the highest neutralizing dilution) were analyzed as repeated measures with mixed models; fixed effects included vaccine treatment, day, vaccine treatment by day interaction, year, and sire nested within composition. No differences existed between F_2 and F_3 steers. Large ranges in animistic titer values among steers were observed, particularly for BVDV1b on d 14 among killed (0 to 12) and MLV (0 to 10) and d 28 for NON steers (3 to 9). Sire nested within composition affected ($P = 0.003$) IBR and approached significance ($P = 0.09$) for BVDV1b. LS means for IBR titers ranged from 0 to 2.2 for F_2 sires and 0.12 to 2.2 for F_3 sires. There was vaccine treatment by day interaction ($P < 0.001$) for IBR, and BVDV types 1a, 1b, and 2. Calves vaccinated with killed vaccine had higher ($P < 0.05$) titers at all post-challenge times compared with MLV or NON calves. NON calves had the lowest animistic titers from d 14 to 42 and appeared to reach peak titer at d 42 for all BVDV types (3.9, 7.5, and 2.9 for 1a, 1b and 2, respectively). MLV steers also had peak BVDV titers at d 42 (4.9, 7.4, and 3.0 for types 1a, 1b and 2, respectively). The killed treatment appeared to have peak BVDV titers on d 14 (9.2, 11.2, and 9.2 for types 1a, 1b and 2, respectively). These data indicate that variation among families in antibody response to vaccination and viral challenge can exist and that response across pathogens may not be uniform across families.

Key Words: *Bos indicus* crosses, BVDV challenge, vaccine response

333 Genome-wide DNA methylation fluctuation in mastitis mice infected by *Staph. aureus*.

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Introduction and objectives: *Staph. aureus* is one of the most crucial causes of mastitis in dairy cattle worldwide. It can survive and reproduce in keratin and phagocyte that normally reject the growth of bacteria. What′s more serious is that *Staph. aureus* can generate β-lactamase which can inactivate antibiotics, resulting in great trouble on clinical therapy. Considering mastitis was corporately affected by bacteria, genetic and epigenetics, in addition, DNA methylation is a key epigenetic marker, which play an important role in the regulation of gene expression in eukaryotes, this study mainly aimed to exploring the DNA methylation changes in mastitis mice infected by *Staph. aureus*. Materials and methods: The *Staph. aureus* mastitis model of dairy cow was established with CD-1 mice by our lab (Fan et al. 2012). A total of 6 *Staph. aureus* mastitis mice and 6 control mice (CD-1) were randomly selected at 12~13 weeks old. We detected the cytosine methylation pattern of the mice genome of breast tissue at 24h post infection. The technique of fluorescent methylation-sensitive amplified polymorphism (F-MSAP) was used, which is a modification of the amplified fragment length polymorphism (AFLP) method to detect DNA methylation on genome-wide (Xu et al. 2005). A total of 7 primer pairs were designed for F-MSAP analysis. Results: The fragments range from 50 to 600bp were count to analyze the DNA methylation levels qualitatively between the 2 groups. Our results showed that a total of 147 bands were detected, and *Staph. aureus* infected group (51%) had decreased incidence of DNA methylation than the controls (55%) although the chi-squared test revealed no significant differences between the 2 groups. DNA methylation fluctuation on specific genes were significantly different between the 2 groups, which depends on the variances of 32 bands. Conclusions: DNA methylation modification is varied after *Staph. aureus* infection in the mastitis mice model. The demethylated and upmethylated region/gene and the role of DNA methylation regulation induced by *Staph. aureus* in dairy cows are warranted to study in further work.

Key Words: DNA methylation, *Staph. aureus* mastitis, F-MSAP

CSAS Symposium: Are We Experiencing a Paradigm Shift in How We Feed Livestock As Industrial Agriculture Evolves in the 21st Century?

334 Are we experiencing a paradigm shift in how we feed livestock as industrial agriculture evolves in the 21st century? J. Newman,* *American Feed Industry Association, Arlington, VA.*

Myriad factors are imposing change in costs, sustainability, utilization and other factors on the animal food industry′s ability to use grains and resources for feedstuffs. An in-depth report commissioned by the feed industry will be presented that will examine the pressure to use feed ingredients for human consumption, the changing dynamics of grain production, the usage of grain for fuel production, environmental issues of using natural resources and the effect of climate change, among other issues. An economic forecast will be presented that will detail the state of the feed industry and future of it and its economic relationship to animal agriculture.

Key Words: future feedstuff availability, economics of livestock feeding, competition

335 Rethinking and expanding the role of co-products and crop residues as livestock feeds. S. S. Donkin*[1] and M. J. Cecava[2], *[1]Purdue University, West Lafayette, IN, [2]Archer Daniels Midland Company, Decatur, IL.*

Food and energy security are critical issues facing the world and it′s population. Population growth coupled with increasing wealth will expand demands for animal source foods. At the same time, the biofuels industry will continue expanding and altering processes resulting in new coproduct feeds having characteristics different than those of existing feed coproducts. Quality, quantity and affordability of energy containing feeds for food animal production will be a keen focus, as will efficiency of protein conversion. Record high corn, cereal and oilseed prices have intensified the adoption of alternative feeds and feed processing technologies for livestock production including increasing use of biofuel coproducts such as distillers grains, glycerol, condensed distillers solubles and most recently, crop residues such as straw and stover. Many of the former are geographically restricted and marketed through commodity channels whereas the latter are mainly disaggregated and geographically dispersed. Crop residues comprise approximately half of the dry weight of plants and therefore a high proportion of energy captured by plant growth is available for recovery once soil sustainability metrics are met. Corn stover and straw represent 2 of the most widely available feedstocks which may be collected and processed on-farm or in centralized depots to improve the metabolizable energy content of the residue. Pre-processing includes shearing-fragmentation followed by chemical and/or enzymatic treatments to partially depolymerize recalcitrant fiber. Historically, because of poor digestibility, stover and straw have been used in low amounts in dairy cattle diets mainly to provide fiber for rumen health. However, pre-processing technologies can improve digestibility of residues thereby increasing their value and use and in particular, feeding in combination with biofuel coproducts may enable substantial grain substitution in cattle rations. Resource assessments and animal performance data point to the potential for improved integration of both crop and livestock production to optimize food and biofuel production per unit of land mass.

Key Words: biofuels crop residues, corn replacement, food security

336 Feeding low starch diets to swine. A. D. Beaulieu*[1] and R. T. Zijlstra[2], *[1]Prairie Swine Centre Inc., Saskatoon, SK, Canada, [2]University of Alberta, Edmonton, AB, Canada.*

The increased cost of feed grains is forcing North American swine producers to consider greater usage of alternative ingredients, including co-products. Distillers dried grains with solubles (DDGS), a co-product from the ethanol industry is widely available, often at competitive prices. Ethanol is produced from fermentation of starch in grains, thus relative to the original grain, DDGS have reduced starch content. A typical corn-soybean diet for finishing pigs contains 50% starch and starch contributes 60% of the NE. High incorporation of DDGS or other co-products such as canola meal and wheat millrun, will reduce starch content by at least 45% and will increase fiber and protein content. Formulating these diets to be isoenergetic requires added fat and/or glycerol. Glucose, fatty acids and amino acids are oxidized within pigs for energy. Adequate amounts of either starch or lipid will spare protein, which is an inefficient fuel source. A starch requirement for pigs has not been defined; however, this requires re-examination with the current and potential further reduction in the starch content of swine diets. When growing pigs (25 to 40 kg BW) were fed semi-purified, isoenergetic diets, the efficiency of CP deposited (g CP/kcal DE intake) increased as starch content increased from 2 to 20% at the expense of crude fiber and fat. Further work is required using low starch diets that represent those encountered in commercial practice. The increased fiber and protein content typical of low starch diets can cause concerns for feed intake and growth performance. While the feed intake response has been variable, lean growth, measured as carcass lean, tends to be reduced when pigs have been fed diets high in low starch co-products. Knowledge of the effects of feeding low starch diets on performance and protein deposition is required to fully exploit low starch co-products for commercial swine production.

Key Words: swine, starch, DDGS

337 Alternatives to starch-based feeding programs for growing and finishing cattle. J. J. McKinnon*[1] and T. A. McAllister[2], *[1]University of Saskatchewan, Saskatoon, Saskatchewan, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.*

In the last decade, there has been a shift to value-added processing of products from the grain and oilseed sectors. For example, the corn-based ethanol industry now ferments as much corn as the livestock sector uses for feed. While supply has kept pace with demand, corn prices have risen. In western Canada, canola production and processing is at record levels. The increase in seeded canola acreage has come at the expense of wheat, barley and oat. This trend is disturbing to the livestock sector which relies on feed barley and wheat as energy sources. To offset high prices and reduced supply, cattle feeders have turned to by-product feeds as alternatives to starch-based feeds. The nutritional profile of by-product feeds varies with the original grain or oilseed and the nature of processing employed. Consider dried distillers grains with solubles (DDGS), a by-product of ethanol production. Our results indicate that depending on the cereal grain fermented (i.e., corn, triticale or wheat), CP content will range from 30 to 40%, NDF from 33 to 44% and ether extract from 4 to 14%. Originally, fed as a protein supplement, DDGS is now fed as an energy source typically replacing 20% or more of the concentrate (DM basis) in finishing rations. Canola meal, a by-product of the canola crushing industry is also high in CP (36 to 40%) and NDF (20 to 28%). As with DDGS, it has been fed as a protein supplement. Research in our laboratory has shown that it can replace barley grain at levels up to 30% of the diet DM in backgrounding diets, however in finishing diets feed efficiency is comprised when fed at this level. We have also shown that wheat bran, a by-product from pre-processing of wheat for ethanol can replace 50 to 100% of barely grain (DM basis) in backgrounding diets with no effects on daily gain; however, feed:gain is increased by 10 to15%. These are just a few examples of by-product feeds that can be fed to growing/finishing cattle. The key to successful utilization is knowledge of their contribution to metabolizable energy and protein supply, their effect on the site and extent of digestion and pricing relative to cereal grain sources.

Key Words: cattle, cereal grains, by-product feeds

338 Ethanol co-products for dairy cows: There goes our starch... now what? H. Paz and P. J. Kononoff,* *University of Nebraska-Lincoln, Lincoln.*

The rise of the corn-ethanol industry has resulted in a dramatic increase in the availability of distillers grains and solubles (DDGS) which can be used for animal feed. Although the dairy industry utilized approximately 25% of the yearly production of DDGS, research investigating the use of this feed in lactating dairy cow diets has only begun. The cost of ingredients that have traditionally been used for energy continues to grow, thus there is a need to understand the nutritional value of corn milling co-products and their potential impact on milk yield and composition. Two concerns with feeding DDGS are the potential to negatively affect milk fat and protein. Indeed publications note that these situations may occur but usually when diets are poorly balanced. Through a series of studies, we have developed feeding recommendations for DDGS and these will be reviewed. Additionally, using the NRC (2001) and data from a total of 27 published studies and 73 observations, we used a meta-analytical procedure to evaluate the impact of feeding corn milling co-products on lactating dairy cows. Data were analyzed using SAS and a random coefficient model to account for the random effects of experiment as well as the fixed effect for co-product (CoP) inclusion. For each experiment Metabolizable Protein (MP) and Net Energy of Lactation (NEL) were computed using NRC (2001) equations. All studies contained treatment serving as a zero control as well as diet treatments that contained CoP which averaged 17.6% of the ration DM. Based on our model, the inclusion of CoP did not affect DMI ($P = 0.31$) or 3.5% FCM ($P = 0.24$) which averaged 23.4 +/− 0.44 and 34.2 +/− 0.90 kg/d respectively. Additionally, the percent milk fat and protein in the milk was not affected ($P = 0.83$ and 0.51) and averaged 3.09 +/− 0.07 and 3.57 +/− 0.06% respectively. We also retrospectively evaluated the predicted flow of Lys and Met for these studies. As expected the modeled flow of Lys was significantly ($P < 0.01$) reduced from 6.45 +/− 0.06 to 5.81 +/− 0.05% of MP when CoP were included. Conversely the flow of Met was not affected ($P = 0.19$) and averaged 1.90 +/− 0.03% of MP. We tested the effect of CoP on the error associated with MP and NEL allowable milk calculations of the NRC model. The error associated with NEL allowable milk averaged 5.28 +/− 1.18 kg and was not affected by CoP ($P = 0.57$). Conversely error associated with MP was significantly ($P = 0.04$) higher for cows consuming CoP by 1.88 kg/d. These results reinforce the concepts that CoP can be used as a effective feed for lactating dairy cows.

Key Words: dairy, DDGS, nutrition

Extension Education I

339 The Missouri Show-Me-Select Replacement Heifer Program: A retrospective on marketing and sales. J. M. Nash,* N. T. Martin, J. M. Thomas, B. D. Mayhan, M. F. Smith, S. E. Poock, and D. J. Patterson, *University of Missouri, Columbia.*

The Missouri Show-Me-Select Replacement Heifer Program has improved reproductive efficiency and increased individual farm income for program participants. The objectives of the program include: 1) implementation of a total quality management plan to enhance health and management of replacement beef heifers; 2) improved marketing opportunities for participating producers and added value to Missouri-raised heifers; and 3) creation of reliable sources of quality commercial and purebred replacement beef heifers based on management, reproduction, and genetics. Over the past 15 yr, 719 farms enrolled 99,805 heifers in the program. Heifers undergo a prebreeding evaluation administered by a veterinarian before the breeding season, and are required to meet minimum management requirements, including herd health and vaccination schedules. Heifers meeting the minimum requirements for enrollment are classified as Tier 1 replacements. Heifers are distinguished as Tier 2 replacements based on the sire of a heifer meeting minimum accuracy requirements for specified traits at the time of sale, including: calving ease direct, calving ease maternal, weaning weight, carcass weight, and marbling. Data for sales from fall 2010 through fall 2011 were compared. Tier 2 heifers carrying AI sired pregnancies ($1,751) sold on average for $259 more per heifer than Tier 1 heifers carrying natural service sired pregnancies ($1,492). Similarly, Tier 1 heifers carrying AI sired pregnancies ($1,654) sold for $162 more per heifer than Tier 1 heifers carrying natural service sired pregnancies. To date, the Show-Me-Select Replacement Heifer Program facilitated the sale of 23,936 heifers in 113 sales from 1997 through December 2011. The aforementioned sales generated interest from 8,063 registered buyers and resulted in $27,348,050 in gross sales revenue. Show-Me-Select Replacement heifers have sold into 18 states, including AR, AZ, CO, FL, GA, IA, IL, IN, KY, KS, LA, MO, NE, OK, SC, SD, TN, and TX. The Show-Me-Select Replacement Heifer Program is estimated to have had a $60 million impact on Missouri′s economy since the program′s inception in 1997.

Key Words: heifer development, reproductive management, beef cattle

340 The Missouri Show-Me-Select Replacement Heifer Program: Prebreeding reproductive evaluation of heifers and subsequent pregnancy outcome after fixed-time AI. J. M. Thomas,* J. M. Nash, N. T. Martin, B. D. Mayhan, M. F. Smith, S. E. Poock, and D. J. Patterson, *University of Missouri, Columbia.*

The Missouri Show-Me-Select Replacement Heifer Program has resulted in improved reproductive efficiency and has increased individual farm income for program participants. The objectives of the program include: 1) implementation of a total quality management plan to enhance health and management of replacement beef heifers; 2) improvement of marketing opportunities for beef producers while adding value to Missouri-raised heifers; and 3) creation of reliable sources of quality commercial and purebred replacement heifers based on management, reproduction, and genetics. Over the past 15 yr, 719 farms enrolled 99,805 heifers in the program. Twenty-five regional extension livestock specialists coordinate the program, and work closely with the 212 veterinarians involved with the program statewide. Enrolled heifers must meet minimum management standards and follow approved animal health regimens. Prebreeding exams [reproductive tract scores (RTS)] are performed by licensed veterinarians before the breeding season. Additionally, initial pregnancy diagnoses must be performed within 90 d of the start of breeding and reconfirmed after the end of the breeding season. In recent years, program participants have increased use of fixed-time AI (FTAI) programs in their herds. Data collected from 2010 to 2011 were used to evaluate relationships between RTS and pregnancy outcome after FTAI. The reproductive tract scoring system ranges from 1 to 5: 1 = infantile; 2 and 3 = noncycling/prepubertal; 4 and 5 = cycling/pubertal. A summary of RTS and FTAI pregnancy rate (PR) for heifers evaluated from 2010 to 2011 is provided: RTS 5 (n = 1,816; FTAI-PR = 59.4%); RTS 4 (n = 1,535; FTAI-PR = 52.1%); RTS 3 (n = 1,571; FTAI-PR48%); RTS 2 (n = 189; FTAI-PR = 36.0%); and RTS 1 (n = 15; FTAI-PR = 0.0%). These data support the practice of establishing prebreeding criteria (e.g., minimum RTS = 3 before the breeding season) for identification of heifers that are good candidates for a FTAI program.

Key Words: heifer development, reproductive management, beef cattle

341 The Missouri Beef Project: An industry partnership designed to link economic incentives with technology adoption. D. J. Patterson,* D. S. Brown, S. E. Poock, and M. F. Smith, *University of Missouri.*

The beef industry in Missouri is a leading segment of the state′s economy and efforts to increase the value of Missouri′s cattle have widespread effects throughout the state. The Show-Me-Select Replacement Heifer Program changed production practices related to management of beef heifers in Missouri. Effects of these changes are realized by producers, veterinary practices, feed dealers, the pharmaceutical and AI industries, and related local economies. The addition of Tier Two to the Show-Me-Select Program arose from funding of 2 integrated project proposals funded by NIFA-AFRI in program areas that include Animal Reproduction and Prosperity for Small and Medium-sized Farms. These integrated project awards supported research and development of protocols to successfully inseminate beef cows and heifers at predetermined fixed times. Additionally, funding from these grants supported the initial transfer of fixed-time AI (FTAI) technology to the field coupled with use of genetically superior high-accuracy AI sires. Adoption of these technologies is resulting in 2 significant outcomes: Increased numbers of genetically superior females, and a similar increase in numbers of genetically superior steer mates. Increased domestic and global demand for high-quality proteins including beef, coincident with the decline in the US beef cow inventory, offers the potential to increase premiums for high-quality beef products. Stacking technologies (FTAI and high accuracy AI sires) sets the stage for a new programming effort focused on The Missouri Beef Project. This project streamlines production and marketing of cattle with a focus on high-quality endpoints. The project involves a partnership including the University of Missouri, Irsik and Doll Feed Yard (Garden City, KS), Pratt Feeders (Pratt, KS), Accelerated Genetics, Genex Cooperative, Select Sires Mid-America, and Certified Angus Beef. The project objectives are to: 1) assist beef producers in gaining access to markets for high-quality cattle, and 2) educate Missouri producers to understand and capture the greater economic returns available for high-quality cattle.

Key Words: High-quality beef, artificial insemination, high-accuracy sires

342 Impact of management practices on the value of heifers sold in Texas auction barns.

K. Stutts,* M. Beverly, S. Kelley, and B. Freel, *Sam Houston State University, Huntsville, TX.*

The objective of this study was to evaluate the impact of management practices on the selling price of heifers in Texas livestock markets. Data were collected at 9 weekly Texas livestock auctions on 6,855 lots of heifers consisting of 42,376 head. The data were collected by trained livestock market reporters and included horn status, body condition, fill, health status, lot size, and selling price. An ANOVA was performed. Heifer characteristics were analyzed individually in a model that included BW and location as covariates. 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. Mean selling price of polled ($127.46) heifers was greater ($P < 0.01$) than that of horned ($113.65) heifers and mixed (polled and horned; $125.50) lots. Differences in mean selling price existed among body condition categories as well. Heifers that were classified as very thin ($131.35) and thin ($129.33) had a greater ($P < 0.01$) mean selling price than heifers classified as average ($126.00), fleshy ($125.23) or fat ($125.23) condition. Differences ($P < 0.01$) in mean selling price existed among all fill categories with gaunt, average, and full heifers selling for $131.50, $125.70, and $127.28, respectively. Heifers that were pre-conditioned ($131.00) had a greater ($P < 0.001$) mean selling price than heifers that were classified as healthy ($125.97) or heifers that appeared sick ($83.62). Lot size also influenced mean selling price. Heifers sold in lot sizes of 10 or more ($132.51) had a greater ($P < 0.01$) mean selling price than heifers sold in smaller ($123.56) lot sizes. Lots that were uniform ($127.19) had a greater ($P < 0.01$) mean selling price than lots that lacked uniformity ($125.67). These date indicate that producers can greatly influence the selling price of their heifers through modification of their management practices such as dehorning, monitoring body condition, and selling heifers in larger, more uniform lots.

Key Words: heifers, livestock auction, selling price

343 Phenotypic characteristics that affect the value of heifers sold in Texas auction barns.

M. Beverly, S. Kelley,* K. Stutts, and B. Freel, *Sam Houston State University, Huntsville, TX.*

This study was conducted to evaluate the effect of phenotypic characteristics on selling price of heifers in Texas livestock markets. Data were collected at 9 weekly Texas livestock auctions on 6,855 lots of heifers consisting of 42,376 head. The data were collected by trained livestock market reporters and included subjective identification of age, breed, color, USDA frame and muscle scores, and selling price. An ANOVA was performed. Heifer characteristics were analyzed individually in a model that included BW and location as covariates. 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. The mean selling price of yearling heifers ($128.15) was greater ($P < 0.01$) than the mean selling price of heifer calves ($125.26). Breed type had a significant influence on mean selling price of heifers. Five breed types were analyzed resulting in British ($128.64) breed types having the highest ($P < 0.01$) mean selling price and Continental ($126.38) breed types having the second highest selling prices. American or Brahman-influenced ($118.68) heifers had the lowest ($P < 0.01$) mean selling price. Eleven color categories were analyzed. Gray ($129.39) and black ($129.15) heifers garnered the greatest mean selling prices and were not significantly different from each other. Spotted ($94.57) heifers had the lowest ($P < 0.01$) mean selling price of all color categories. Differences ($P < 0.05$) existed between all frame size categories. Mean selling price for large-, medium-, and small-framed heifers were $130.91, $125.47, $107.18, respectively. Mean selling price also differed ($P < 0.01$) among all muscle scores. Mean selling price for muscle scores 1, 2, 3, and 4 were $132.07, $118.03, $125.36, and $122.99, respectively. These data indicate that producers can influence the selling price of their heifers through proper age, breed selection, and genetic selection within breeds to meet market demand.

Key Words: heifers, livestock auction, selling price

344 Beef Excellence Education for You: A program to teach youth about the beef industry.

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Since 2008, over 300 youth from Alabama and Florida have participated in a hands-on, interactive Beef Excellence Education for You (B.E.E.F. U) program. At the program's inception, the goal was to teach youth how their feeder or show cattle fit the US Beef Industry. While the goal remains the same, B.E.E.F. U continues to evolve each year to further enhance participants' knowledge of the US Beef Industry. Targeted youth audiences attending the day-long program include 4-H and FFA members and home-school groups, but any interested youth (ages 8 to 18) is welcome. Participants rotate through multiple sessions focusing on live animals, carcasses and further processing. Sessions include live cattle terminology, beef conformation, feeder calf basics, and fed cattle evaluation as well as beef carcass terminology and carcass evaluation. Further processing stations teach participants how to make kielbasa, steak nuggets and main beef meals. Participants learn which ingredients to use when making the product, where meat cuts are fabricated from the carcass, and how to prepare the product. Other modules have included feeds cattle eat, properly giving injections and taste and texture of variety meats. Modules are taught by Animal Sciences faculty, students and staff and Alabama Cooperative Extension System (ACES) specialists and agents. Participants evaluate B.E.E.F. U using a likert scale at the end of the program. When asked if they would attend another B.E.E.F. U program, 78% said yes, 5% said no and 17% said they were unsure. To date, 60% of participants have attended more than one program. When asked how well they understood the material at each rotation, 74% said they understood the material well or very well, 16% said they understood the material some, while 11% said they did not understand the material or in limited amounts. The majority of participants found the materials interesting or very interesting (82.3%), 11.5% found it somewhat interesting and 6.3% found the material boring or somewhat boring. The majority of the youth stated time spent at each rotation was just right (60%), while 21% indicated the time was too long and 17% stated the time was too short.

Key Words: beef industry, youth education

345 A survey of the presence, structure, and effectiveness of Beef Quality Assurance (BQA) or BQA-type programs across the United States.

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In an effort to improve the effectiveness and impact of Beef Quality Assurance (BQA) Programs in the US, a nationwide survey of state and regional BQA Program coordinators was conducted. In early 2011, coordinators were asked to complete a 37-question on-line survey about the BQA Program that they oversee. Survey questions were intended to summarize basic information about each program, identify unique and successful approaches to educating and(or) certifying producers, and estimate the effect of BQA efforts nationwide. Representatives from 45 of the 50 states completed the survey on behalf of their BQA Program or cattle industry, if no program existed. In 62.2% of states, university extension personnel coordinated the BQA Program. State beef councils provided funding for BQA Programs in 60.0% of states, followed by university extension (53.3%), pilot project grants from the National BQA Program (35.6%), and state cattlemen′s associations (31.1%). User fees were used in 22.2% of states. Formal BQA Certification was offered by 91.0% of states, and 71.1% of states required at least 2 h of face-to-face training in order for an attendee to become certified. Only 13.3% of states offered multiple levels of BQA Certification, and just 11.1% included an on-farm assessment or audit associated with BQA Certification. In terms of additional BQA-related components offered, relatively few states offered dairy BQA Certification (20.8%) or feedyard BQA Certification (35.4%). Youth BQA Certification was available in 43.8% of states, but only 27.1% required youth to be BQA Certified to show and sell an animal at the county fair level. On average, there were 28 trainers per state BQA Program. However, most programs (57.1%) had 1 to 9 trainers, while 22.8% had 10 to 49 trainers. At least 50 trainers were present in 20.0% of programs. Overall, 709 trainers were available to BQA Certify producers across the US In summary, these data suggest that the BQA Program includes a large infrastructure of personnel across the US; however, many states offer little beyond basic BQA Certification. Further, the large amount of variation among programs may make development of a uniform nationwide program challenging.

Key Words: Beef Quality Assurance, cattle, survey

346 National Animal Identification System versus National Livestock Identification System.

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On December 19, 2003, a major event happened in the animal agriculture industry. At Vern's Moses Lake Meat Co., a dairy cow infected with bovine spongiform encephalitis (mad cow disease) was slaughtered in the US. Inspired by this event, the USDA secretary Ann Venemen announced a need for a national animal identification system (Roberts, Pittman). Nine years later, in 2012, the US still does not have a national animal identification system in place. However, in other countries such as Canada, New Zealand, the European Union and Australia there are similar programs in place for their livestock production. Dairy farmers around the world are taking advantage of all the benefits that an electronic identification program can provide. Benefits such as accurate identification, automatic sorting, disease traceability, accurate record keeping for animal events such as heat, treatments, sire selection etc (Semple). This benefit of electronic identification has improved the dairy industry both on and off the farm in other countries. The American dairy industry can easily apply those same benefits, which would lead to an overall support of a similar animal identification program here in the United States.

Key Words: national identification, international benefits, on-farm benefits

347 Development of the pioneer organic beef supply chain in the Mexican tropics—Promotion of sustainable beef production through integration of extension, education and research.

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In 2001, a strategic alliance was formed in Veracruz between academia, a lead producer and an organic certification agency, collaborating in extension, education and research to integrate the pioneer organic beef supply chain (OBSC) in the Mexican tropics. Twenty producers received guided conversion to organic beef production. Training included 2 theoretical-practical courses, then symposia and workshops including students. Teaching originated with a graduate course on sustainable livestock systems that introduced students to the project. Four generations then visited the lead producer and 2 did their course extension project analyzing his supply chain. Applied research evolved from a case study of the newly integrated OBSC to a detailed financial and energy analysis used to evaluate its feasibility and sustainability during a decade. Continuing education, extension visits and exchange of experiences with other states followed. The lead producer converted his traditional beef cattle production system (TBCPS) to an OBSC certified by Bioagricert, IFOAM in 2003. In 2010, 693 crossbred Zebu cattle grazed 736 ha in agroforestry systems and beef from 150 to 200 head/year were sold to organic markets/stores in 7 states with a 35% value added. The return on investment was 16.6% in the TBCPS and 31.2% in the OBSC and marginal gain was USD 43,912 and 93,339, respectively. Energy efficiency was 49.6% for the OBSC and18.3% for the TBCPS and the OBSC remained profitable in 6 future scenarios. Volume of beef produced is increasing without deterioration of natural resources and energy efficiency and economic stability continue to improve, demonstrating the sustainability of the OBSC. More than 500 producers and faculty and students at 14 universities in Mexico have been trained and projects initiated in 8 states. Education material is disseminated nationally and research results also internationally. Integration of extension, education and research has led to the project's success and expansion.

Key Words: organic beef, sustainability, integrated approach

Forages and Pastures I

348 Sustainable goat farming: Pasture enhancement and identification of suitable forages for goats.

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Meat-goat farming is becoming popular to many small-scale farmers in Alabama. However, making this business sustainable is a challenge, especially with the existing poor pastures and grazing practice. Not much information is available on suitable forages for improving goat pastures and managing them sustainably. The objectives of this study were 1) to improve the existing goat pasture by incorporating selected cool-season forages, and 2) to determine goats' preference for the selected forages. The study was conducted in Selma and Phenix City, Alabama as a completely randomized design with 3 replications in each site. Five treatments: combination of annual ryegrass (*Lolium multiflorum*) and one of the selected cool-season legumes (arrowleaf clover, *Trifolium vesiculosum*; berseem clover, *Trifolium alexandrinum*; crimson clover, *Trifolium incarnatum*; hairy vetch, *Vicia villosa*; and winter peas, *Pisum sativum*) and a control of sole annual ryegrass plantings were tested. Pastures were managed by rotational grazing. Forage biomass before grazing, and forage height both before and after grazing were measured. The average forage-biomass production in Selma (1.0 ± 0.28 t ha-1) and Phenix City (1.4 ± 0.21 t ha-1) remained similar among the treatments. Average height reduction after grazing was much lower for peas (8.0 ± 1.51 cm) compared with other forages (18.0 ± 2.06 cm). Preliminary results show that all selected forage species, except winter peas, were readily grazed by goats. Findings of this research will be very useful to goat producers and Extension personnel for improving and managing goat pastures, and eventually promoting the sustainability of goat farming.

Key Words: cool-season legumes, grazing management, sustainable goat farming

349 Effects of co-grazing on herbivory patterns and performance by cattle and goats grazing native tallgrass rangeland infested by sericea lespedeza (*Lespedeza cuneata*).

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Sericea lespedeza (SL) is classified as a noxious weed in the Great Plains and infests over 0.6 million acres of rangeland in Kansas. Beef cattle avoid grazing SL, presumably due to its high tannin content; however, goats readily graze this plant. Lactating crossbred cows with calves (n = 145; initial BW = 579 ± 91 kg) and non-pregnant, nonlactating Boer × nannies (n = 200; initial BW = 42 ± 1.9 kg) were used to evaluate the effects of co-grazing on herbivory patterns and animal performance while grazing native pastures infested heavily by SL (average SL biomass in October = 2,061 kg/ha; 56% of total forage biomass). Nine pastures were assigned randomly to 1 of 2 season-long grazing systems: 5 pastures (65 ha) were grazed by cows + calves only (single species; 0.8 ha/AUM) and 4 pastures (32 ha) were grazed by cows + calves (0.8 ha/AUM) and goats (multispecies; 0.8 ha/AUE/month). Cows + calves and goats were assigned randomly to pastures. Animal BW was measured at 28-d intervals from June 1 to October 1; BCS were assigned to cows also at those times. Two permanent 100-m transects were marked at the outset of the study (June 15) within each pasture to estimate botanical composition and SL herbivory. Season-long cow BW change, season-long calf ADG, and cow pregnancy rates were not different ($P \geq 0.40$) between multispecies and single-species pastures. Conversely, season-long cow BCS change was greater ($P < 0.01$) on multispecies pastures than on single-species pastures (0.04 vs. −0.38, respectively). Biomass of SL was not different ($P = 0.97$) between pastures at the outset of the study. The percentage of individual SL plants that had been grazed at the end of the trial was greater ($P < 0.01$) on multispecies pastures than on single-species pastures (94.2 vs. 77.5%, respectively). Final SL biomass in multispecies pastures averaged 1,692 kg/ha, whereas final SL biomass in single-species pastures averaged 2,230 kg/ha (SE = 739.4 kg/ha; $P = 0.37$). Residual forage biomass at the end of the study was not different ($P = 0.54$) between treatments and averaged 3,622 kg/ha, indicating that forage availability did not limit forage intake during our trial. Our results were interpreted to suggest that grazing cows + calves and goats in combination increased grazing pressure on SL without negatively affecting beef cow or beef calf performance or residual forage biomass.

Key Words: *Lespedeza cuneata*, multispecies grazing, condensed tannins

350 Effect of different regrowth ages of *Andropogon gayanus* grass silages on intake, digestive efficiency and methane emissions in sheep.

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Andropogon gayanus is an important grass due to its high biomass production and its adaptability to withstand a long dry season, and low fertility acidic soils. Currently, there is little research assessing the nutritional quality of *A. gayanus* grass silage at increasing days of regrowth. Thus, the objectives of this study were to determine the effects of different regrowth ages of *A. gayanus* grass silage on dry matter intake (DMI), dry matter digestibility (DMD), net energy, energy balance and CH_4 production in sheep. *A. gayanus* grass silage was made using 56, 84, or 112 d of regrowth in 200 L metallic barrels and fed to sheep (n = 18) for a period of 21 d after which DMI and DMD were measured for 5 consecutive days. Net energy, energy balance and methane emissions were determined with an open circuit respirometry chamber. The animals stayed inside the chamber for 24 h during feeding and fasting. The experimental design was completely randomized with 3 treatments (silage age) and 6 repetitions (sheep). The data were subjected to ANOVA and linear regression. The DMI were similar among treatments ($P > 0.05$) averaging 54.36 g/$BW^{0.75}$; however, DMD reduced linearly ($P < 0.01$) with increasing regrowth age, averaging 52.60, 43.64 and 37.99% for 56, 84 and 112 d of regrowth, respectively. Silage net energy was also reduced linearly ($P < 0.05$) with increasing regrowth age. Furthermore, the energy balance of the animals reduced linearly ($P < 0.01$) with increasing regrowth age and was below zero in the higher regrowth age. Methane emissions (g/kg) of DMD showed a tendency ($P < 0.10$) to increase as regrowth age increased. When methane emissions were expressed in g/kg of digestible cellulose it increased linearly ($P < 0.05$) with increasing regrowth age. Therefore results from this study show that increasing regrowth age of *A. gayanus* grass silage reduced digestive efficiency and increased methane emissions in sheep, which indicates that this forage should be ensiled at younger regrowth age.

Key Words: energy efficiency, grass maturity, methane

351 Effects of feeding perennial peanut hay on growth, development, attainment of puberty, and fertility in beef replacement heifers. K. M. Bischoff*[1], T. E. Black[1], V. R. G. Mercadante[1], G. H. L. Marquezini[1], R. O. Myer[1], A. T. Adesogan[2], N. DiLorenzo[1], and G. C. Lamb[1], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]Department of Animal Sciences, University of Florida, Gainesville.*

We determined the influence of supplemental feeding of perennial peanut hay (*Arachis glabrata*) on growth performance, attainment of puberty, and fertility in replacement heifers. Over 2 yr, 120 heifers (60 heifers/yr) were allocated into pens (5 heifers/pen) and assigned to receive one of 3 supplement treatments during a 140 d development phase (DP) before initiation of the breeding season: 1) 1.23 kg DM/d of a mix of 80% cracked corn and 20% soybean meal, DM basis (CSBM); 2) 2.74 kg DM/d of perennial peanut hay (PPH); and, 3) no supplement (CON). Pen was the experimental unit. During the DP all heifers received ad libitum access to bermudagrass hay (*Cynodon dactylon*). After the DP, heifers were comingled for a 77-d breeding season. During the DP ADG was influenced ($P = 0.002$) by 28-d period. In addition, ADG of CSBM (0.48 ± 0.109 kg/hd/d) and PPH (0.46 ± 0.109 kg/hd/d) treatments tended ($P = 0.07$) to be greater than the CON (0.18 ± 0.109 kg/hd/d) treatment. There was a treatment × period interaction ($P = 0.06$) for mean BW with heifers in the CSBM and PPH treatments having a greater ($P < 0.05$) BW than the CON heifers during the periods from d 84 to 112 and d 112 to 140. Total DMI during the 140 d DP was greater ($P < 0.01$) for PPH (5.3 ± 0.25 kg/hd/d) than for CSBM (4.3 ± 0.25 kg/hd/d), which were greater ($P < 0.01$) than CON (3.4 ± 0.25 kg/hd/d). Treatment did not alter age ($P = 0.38$), BW ($P = 0.16$), or BCS ($P = 0.27$) at attainment of puberty or d on treatment before attainment of puberty. No differences existed in fetal age 30 d following the end of the breeding season ($P = 0.34$), however overall pregnancy rates differed ($P = 0.05$) by treatment with PPH (88 ± 6.7%) having greater pregnancy rates than CON (64 ± 6.7%), whereas CSBM (78 ± 6.7%) were intermediate. We conclude that attainment of puberty was not altered by treatment, although differences in DMI intake existed. However, pregnancy rates of heifers receiving PPH were greater than CON, indicating that PPH may be a suitable alternative for development of replacement beef heifers.

Key Words: perennial peanut, replacement heifer, heifer development

352 Effects of different sources of rumen-degradable protein supplementation on performance of cows and calves grazing limpograss stockpiled pastures in Florida. A. D. Aguiar*[1], J. M. B. Vendramini[1], J. D. Arthington[1], and L. E. Sollenberger[2], *[1]Range Cattle Research Education Center, Ona, FL, [2]University of Florida, Gainesville.*

Limpograss (*Hemarthria altissima* [Poir.] Stapf & C.E. Hubb.) is a warm-season grass used as a stockpiled forage during the winter for cow-calf production in South Florida, however, the usual decreased CP and RDP concentrations may affect animal performance. The objective of this study is to investigate the effect of supplements with different sources of RDP on performance of cow-calf pairs (*Bos* sp.) grazing stockpiled limpograss pastures. The experiment was conducted in Ona, FL from January to March 2011. Treatments were: 1) Cows receiving 1.3 kg/d of cottonseed meal (CSM) and 2) Cows receiving 0.13, 0.33, and 0.9 kg/d of urea, feather meal and corn meal respectively. Treatments were isonitrogenous (48% CP) with similar concentrations of RDP (62 kg RDP/kg CP). All treatments received additional 2.3 kg/d of sugarcane (*Saccharum officinarum* L.) molasses. Treatments were distributed in randomized complete block design with 4 replicates. Twenty 4 cow-calf pairs (420 ± 59 and 78 ± 12 kg, respectively) were randomly distributed in 8 limpograss pastures (experimental units; 1.0 ha/pasture; 3 cow-calf pairs/pasture). Cows BCS and cows and calves weights were recorded every 28 d to calculate ADG. Herbage mass (HM) and nutritive value was measured every 14 d. The data were analyzed using PROC GLMMIX with treatment and months as fixed effects, and replicates as random effects. There was no difference in HM ($P = 0.13$; mean = 5392 kg/ha; SE = 134), CP concentration ($P = 0.21$; mean = 14.9%; SE = 0.7), IVOMD ($P = 0.38$; mean = 46.7%; SE = 1.9) between treatments. There was no effect of the treatments on cow ADG ($P = 0.34$; mean = 0.0 kg/d; SE = 0.1), milk production ($P = 0.37$; mean = 6.5 kg/d; SE = 1.2), and blood urea nitrogen concentrations ($P = 0.83$, mean = 12.25 mg/dL; SE = 0.77), and calf ADG ($P = 0.78$; mean = 0.85 kg/d; SE = 0.04). However, there was an effect on final BCS for cows consuming CSM supplement compared with urea (5.2 vs. 4.7, $P = 0.039$), respectively. There was an increase in BCS of cows consuming CSM supplement, however performance of cows and calves were not improved.

Key Words: cow-calf pairs, limpograss, protein supplementation

353 Effects of three levels of rumen-undegradable protein supplementation on performance of early weaned calves receiving stargrass. J. M. B. Vendramini*[1], J. D. Arthington[1], and L. E. Sollenberger[2], *[1]University of Florida/IFAS Range Cattle Research and Education Center, Ona, [2]University of Florida, Department of Agronomy, Gainesville.*

Warm-season grasses have reduced concentrations of CP fractions A and B and microbial protein alone may be insufficient to meet the metabolizable protein requirements of young growing cattle. The objectives of this study was to evaluate the effects of increasing levels of rumen-undegradable protein supplementation on performance, forage intake, and total DM intake of early weaned calves receiving stargrass (*Cynodon nlemfuensis*). The experiments were conducted in Ona, FL from May to August 2007 and 2008. The treatments were 3 levels of rumen-undegradable protein supplementation, soybean meal (SBM, 35% RUP 65% RDP), a 50:50 mixture of SBM-Soyplus (modified expeller soybean meal with 60% RUP 40% RDP), or Soyplus, supplemented at 0.15% BW, and distributed in a randomized complete block design. The calves (*Bos* sp.) received additional 0.85% BW of soybean hulls daily. In experiment 1, 4 calves (initial BW = 217 ± 30 kg) were assigned to 8 experimental units (0.51-ha pastures, each divided into 2 paddocks for rotational stocking (14-d grazing and 14-d rest period). Calves were weighed every 28-d and average daily gain calculated. There was no difference ($P \geq 0.10$) in forage CP (11%), IVDOM (64%), herbage mass (2600 kg/ha), and herbage allowance (1.4 kg DM/kg BW) among treatments. Calves average daily gain and liveweight gain per ha did not differ among treatments ($P \geq 0.10$; 0.56 kg/d and 238 kg/ha, respectively). In experiment 2, 3 early weaned steers (160 ± 18 kg BW) were distributed in a 3 × 3 Latin square, 3 treatments (same treatments described for experiment 1) and 3 periods (10 d adaptation, and 7 d data collection). Ground stargrass hay (11% CP, 51% IVDOM) was offered daily and adjusted to allow 10% refusals. Daily offered forage and refusals were weighed, and subsampled for DM determination. Total feces production was collected. There was no difference ($P \geq 0.10$) in forage DM and total DM intake among treatments (2.0 and 2.9% BW, respectively). However, there was a linear increase in the diet apparent digestibility with increasing levels of Soyplus ($P = 0.08$; from 60 to 64%). Increasing levels of RUP did not improve performance of early-weaned calves grazing stargrass pastures.

Key Words: supplementation, RDP, stargrass

354 Ruminal availability of iron in forages.

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Iron (Fe) is an essential trace element that is required for several important biological processes. However, excessive Fe can lead to the production of free radicals and expose sensitive tissues to oxidative stress. Many feedstuffs fed to ruminants are frequently high in Fe. Little is known regarding bioavailability of Fe naturally found in feedstuffs. A study was conducted to examine water solubility and ruminal availability of Fe from 4 forages (white clover, KY 31 tall fescue, Max-Q tall fescue, and orchardgrass) at 3 growth stages. Clipped forage samples were collected at 14-d intervals beginning in early April (vegetative stage) and continuing through early May (mid bloom stage). The Fe content of forages ranged from 24.4 to 315.4 mg/kg DM. The percentage of water-soluble Fe in forages varied considerably. Orchardgrass had the highest ($P < 0.05$) Fe water solubility at 50.9% ± 13.3%; compared with white clover (13.6% ± 0.4%), KY 31 tall fescue (12.2% ± 6.4%), and Max-Q tall fescue (18.2% ± 6.7%) which were similar. Release of Fe from forages in the rumen was measured using the Dacron bag technique. Dacron bags (10 × 20 cm with 4.0 g sample) were incubated in duplicate for 3, 12, or 24 h in 2 fistulated steers. Despite the greater percentage of water soluble Fe in orchardgrass, percent disappearance of Fe from Dacron bags was less ($P < 0.05$) for orchardgrass compared with the other forages after 3, 12, and 24 h of ruminal fermentation. Iron disappearance after 24 h of incubation was 83.8 ± 1.8, 73.1 ± 9.5, 71.6 ± 5.2, and 45.3 ± 14.2% for white clover, KY 31 tall fescue, Max-Q tall fescue, and orchardgrass, respectively. Disappearance of Fe was greater ($P < 0.05$) for white clover than the tall fescue varieties after 12 and 24 h. Increasing stage of maturity was associated with reduced ($P < 0.05$) Fe disappearance during ruminal fermentation for the grasses studied, but not for white clover. This study indicates that a large portion of the total Fe in most forages is released in a soluble form in the rumen within 24 h of ruminal digestion.

Key Words: iron availability, forage, ruminants

355 Nutritional profile of native warm season grass grown as a mono- or multi-species pasture.

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The objective of this study was to evaluate the nutritional profile of mono- or multi-species pastures of native warm season grasses (NWSG). Twelve pastures were randomly assigned to one of 4 treatments: 1) Bermudagrass (BG; *Cynodon dactylon*); 2) Indiangrass (IG; *Sorghastrum nutans*); 3) MIX G (Indiangrass, little bluestem (*Schizachyrium scoparium*), big bluestem (*Andropogon gerardii*)) established at 9.0 kg/ha seeding rate; and 4) MIX NG the same as MIX G but established at 4.5 kg/ha seeding rate. The fourth treatment (MIX NG) was not intended to have cattle grazing to facilitate a congruent wildlife research project. One month before grazing was initiated (mid April) P, K, and lime was added per individual pasture recommendation. For IG, MIX G and MIX NG, N was applied at 38 kg/ha while BG was 67 kg/ha. Growing steers (n = 225, BW = 237 ± 1.5 kg, 2.7 steers/ha) were randomly assigned to one of 9 pastures. Animals were weighed on 2 consecutive days at initiation and termination of the experiment and once every 28 d during the experiment. Grass samples were taken from all pastures every 28 d during 4-mo period and were analyzed for DM, NDF, ADF, OM, EE, and IVDMD. Dry matter was greater ($P < 0.05$) for all NWSG (33.6, 30.7, and 29.5% for MIX G, IG, and MIX NG, respectively) compared with BG (27.5%). However, OM was similar ($P > 0.05$) for all treatments (between 91.2 and 92.61%). Neutral Detergent Fiber, ADF and hemicellulose were greater ($P < 0.05$) for all NWSG (66.9, 67.8, and 66.6% NDF, 34.6, 35, and 33.5% ADF, 32, 32.8, and 33.1% hemicellulose for IG, MIX G, and MIX NG, respectively) compared with BG (63.6% NDF, 32.9% ADF, and 30.6% hemicellulose). Fat was similar ($P > 0.05$) for all treatments (between 10.8 and 11.1%). Crude protein was less ($P < 0.05$) for NWSG (8.6, 8.2, and 8.6% for IG, MIX G, and MIX NG respectively) compared with BG (10.7%). Crude protein decreased ($P < 0.05$) with increased maturity (12.7% May to 6.6% September) while NDF, ADF, and hemicellulose increased ($P < 0.05$; NDF = 58.3% May to 70.2% Sept.; ADF = 30.4% May to 36.3% Sept.; hemicellulose = 27.8% May to 33.8% Sept.). More forage ($P < 0.05$) was available and consumed by steers on all NWSG pastures compared with BG. It appears that NWSG may offer a viable alternative to BG for grazing cattle during the summer.

Key Words: native grass, pasture, beef cattle

356 Using switchgrass to produce stocker cattle gain and bioenergy feedstock I: Production potential.

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Switchgrass (*Panicum virgatum* L.) has been identified as a potential feedstock for cellulosic bioenergy production. To mitigate the risk of establishing this crop for bio-fuel feedstock production only, producers are looking to incorporate switchgrass into early spring grazing systems. The objective of this study was to determine the effect of stocking density on measures of animal performance and end-of-season residual feedstock yield in an early spring stocker grazing system. Twelve, 0.81-ha paddocks were established in southern Oklahoma in 2007 and evaluated over 3 grazing seasons (2008 – 2010). Four stocking densities; control (0 steers ha^{-1}), low (2.5 steers ha^{-1}), med (4.9 steers ha^{-1}) and high (7.4 steers ha^{-1}) were utilized. Animal weights were collected following 16h shrink at start and end of grazing period. All residual feedstock was harvested following plant senescence. Animal performance and forage yield data were analyzed using random effects mixed ANOVA models. Average daily gain was 1.05, 1.04, and 0.83 kg hd^{-1} d^{-1} for the high, med and low stocking densities, respectively with no significant effect detected ($P = 0.12$). Stocking density also has no significant effect on total gain with 199, 215 and 167 kg ha^{-1} for the high, medium and low stocking densities, respectively ($P = 0.07$). Grazing days were significantly affected by stocking density with the low, med and high densities grazed for 81, 43, and 28d, respectively ($P < 0.01$). Non-grazed controls produced significantly more biomass than any grazed treatments ($P < 0.01$). On average, the control produced 15320 kg ha^{-1} of biomass, whereas the low, medium and high stocking densities produced 10539, 8110 and 7771 kg ha^{-1} of residual feedstock, respectively. Within stocking density, the low density produced significantly more biomass as compared with medium and high stocking densities ($P < 0.05$). Results from this study indicate that switchgrass has the production potential to be used for stocker cattle gain and the production of bioenergy feedstock; however, further analysis would be important to determine the economic potential of the dual-use crop.

Key Words: stocker cattle grazing, switchgrass, bioenergy

357 Using switchgrass to produce stocker cattle gain and bioenergy feedstock II: Economic potential.

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Switchgrass (*Panicum virgatum* L.) has been identified as a leading source of biomass feedstock for conversion into bioenergy products in the southern Great Plains. Currently, no large-scale refineries exist in the region; however, in anticipation of the development of a large-scale industry, producers are curious about the economic potential of integrating switchgrass into their present livestock production systems. The objectives of the study were to determine the effects that stocking density treatments have on feedstock yield, ADG and total gain, and to determine the most economical gain/feedstock production system. Data for steer performance and residual feedstock yield were collected from a 3-year (2008–2010) CRD grazing study in south-central Oklahoma. Stocking density treatments [0 (an un-grazed control), 2.5, 4.9, and 7.4 hd ha^{-1}] were randomly assigned to a total of 12, 0.81-ha, switchgrass pastures. Enterprise budgeting was used to compute expected values of economic net returns for 5 systems: graze only, no forage (G/NF); no graze, feedstock only (NG/F); lightly grazed plus feedstock (LG/F); moderately grazed plus feedstock (MG/F); and heavily grazed plus feedstock (HG/F). Net return for each system was calculated for feedstock prices ranging from \$0 to \$165 Mg^{-1}. The effects of system on yield, gain, and net return were analyzed using random-effects mixed ANOVA models. F-tests were used to determine differences in means between systems and LSD tests were used to rank the profitability of systems. At \$0 Mg^{-1}, the most profitable system was the MG/F system, which realized \$45 ha-1. At \$55 and \$83 Mg^{-1} net return was \$232 and \$524 ha^{-1}, respectively, when grazing lightly and by marketing 10.54 Mg ha^{-1} of residual feedstock. At prices greater than \$110 Mg^{-1}, producers would not graze switchgrass, they would only produce and market feedstock. Early adopters could generate breakeven profitability by grazing switchgrass while waiting on biorefinery development. Moreover, switchgrass will likely not be economically competitive with conventional grazing systems commonly used by producers in the region if the biorefinery's purchase price for feedstock is less than \$110 Mg^{-1}.

Key Words: bioenergy economics, stocker cattle grazing, switchgrass feedstock

358 Investigating the nutritive value of *Panicum maximum* leaves for ruminant animals.

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The *Panicum maximum* leaf (Pml) is a perennial grass readily available to grazing livestock in south western Nigeria. The objective was to determine the proximate composition of Pml. The samples of Pml were collected from the teaching and research farm, university of Ibadan during the onset of the wet season and analyzed for dry matter (DM), crude protein (CP), crude fiber (CF), ether extract (EE), ash and gross energy (GE) using standard procedures. Ten samples of Pml were slashed at 6cm above ground from a grazing paddock and bulked together and a representative sample was collected for proximate analysis. The samples were at vegetative stage and replicated thrice. Average total height of the forage at harvest is 1m. The Pml (g/100gDM) Contained CP 7.95; CF 31.0; EE 4.0, ash 8.90; and GE 3.2 kcal/g. The CP content was 7.95% and this was compared with tropical grass species, which seldom exceed a CP level of 10% and whose protein content is satisfactory for animal production for only about 4 mo of the year. It is far lower than that of cassava leaf meal (16.67%), and far below the minimum protein requirement (10–12%) for ruminants. The CF level of 31.00% for Pml is low compared with that of tropical grass species which may be as high as 45 – 50% at more matured stages of growth. It is higher than the CF level of *Amaranthus* spp. (17.01%), Siam leaf meal (16.0%), Cassava leaf meal (15.63%), deep litter manure (16.60%) and guava leaf (16.10%). %). The ether extract content was low (4.00%). This value was lower than the values of 5.61% reported for *Vernonia amygdalina* leaf and far lower than the value of 8.14% reported for Siam weed but higher than the EE reported for *Tithonia diversifolia* (2.81%). The total ash content of 8.90% was low and this was far lower than the ash content reported for *Vernonia amygdalina* leaf (13.86%) and *Tithonia diversifolia* leaf (14.68%) but higher than the value of 8.28% reported for *Acacia albida* used as a browse plant for sheep in the semi-arid region of Nigeria and lower than the value of 11.00% reported for *Leucaena spp* to feed Yankassa sheep and 11.54% reported for Siam weed leaf meal. The Gross Energy (GE) value was 3200kcal/kg. This is comparable with the GE value of Groundnut cake (2600kcal/kg) and *Vernonia amygdalina* leaf (2720kcal/kg) but far higher than the GE of *Tithonia diversifolia* leaf (1900kcal/kg). The Nitrogen Free Extract level of 48.15% for Pml was comparable to that of Siam leaf meal (44.40%) and *Tithonia diversifolia* leaf (44.38%) both used to feed West African Dwarf Sheep but lower than the value of 33.85% reported for *Vernonia amygdalina* leaf. On the whole, gross chemical analysis indicates that Pml contained appreciable level of nutrients that could be utilized in the diets of ruminants.

Key Words: nutritive value, *Panicum maximum* leaves, ruminant animals

359 Evaluating the mineral composition of *Panicum maximum* leaves.

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The *Panicum maximum* is a perennial grass readily available to grazing livestock in south western Nigeria. The objective was to determine the mineral content of *P. maximum*. Ten samples of *P. maximum* were slashed at 6cm above ground from a grazing paddock and bulked together and a representative sample was collected for mineral analysis. The samples were at vegetative stage and replicated thrice. Average total height of the forage at harvest is 1m. The atomic absorption spectrophotometer was used to determine any of the minerals (except P) using appropriate lamps. The P was determined with vanadomolybdate using spectrophotometer at 425nm. The principal elements present in *P. maximum* are Ca, P, K, Na and Mg while the essential trace elements (macro nutrients) are, Mn, Cu and Zn. The *P. maximum* contained Ca 0.42%, P 0.31%, K 1.03%, Na 0.49%, Mg 0.32%, S 0.24%, Cu 10.00ppm, Zn 50.00ppm and Mn 20.00ppm. Normally, plant materials are not good sources of Ca and P but the levels reported in *P. maximum* would easily satisfy animal needs if they occur in a readily available form. It is often postulated that a mineral supply in excess of dietary requirements is capable of blocking the availability of another. The result of mineral analysis on *P. maximum* leaf showed that the leaf contains high level of micro and macro elements, which is an indication that the leaf can sustain the nutritional and physiological status of the animal.

Key Words: mineral composition, *Panicum maximum* leaf

Horse Species I

360 Influence of maternal plane of nutrition and arginine supplementation on mares and their foals: Determination of voluntary dry matter intake of mares during late pregnancy. K. N. Winsco*[1], J. A. Coverdale[1], T. A. Wickersham[1], C. J. Hammer[2,3], and J. L. Lucia[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.*

Thirty-two mares (468–668 kg BW; 3–19 yr) were blocked by expected foaling date and randomly assigned within block to treatments. Treatments were arranged as a 2 × 2 factorial with 2 planes of nutrition (Nutr), moderate (Mod; 0.5% BW AF grain/d) or high (High; 1% BW AF grain/d) and 2 levels of L-arginine supplementation, 0.21 g/kg/d (Arg) or no supplemental Arg (Con; L-alanine to maintain isonitrogenous diets). The objective was to evaluate the impact of altered plane of nutrition on voluntary forage dry matter intake (FDMI) and determine the ability of Arg to mitigate these effects. Treatments began 110 d before expected foaling date and terminated at parturition. Mares were housed by block and allowed ad libitum access to coastal bermudagrass (*C. dactylon*) hay, and fed commercial grain 2 × /d in individual stalls. To evaluate FDMI, a dual marker system was used at 9, 10, and 11 mo gestation. Titanium dioxide (TiO_2) was dosed at 10 g/d for 14 d by top dressing onto the grain meal. Fecal grab samples were obtained the last 4 d of TiO_2 supplementation 2 × /d via rectal palpation at 12 h intervals with times advancing 3 h each d to account for diurnal variation. Fecal samples were analyzed for TiO_2 using a colorimetric procedure (Titgmeyer et al., 2001). Fecal, grain, and hay samples were analyzed for ADIA using the ANKOM fiber system. Data were analyzed using the PROC MIXED procedure of SAS. There was no effect of Arg on FDMI ($P \geq 0.60$). Nutrition tended to influence FDMI ($P \leq 0.10$) with Mod mares consuming a greater percentage of their BW compared with High. Regardless of dietary treatment, month of gestation influenced FDMI ($P \leq 0.01$) with all mares consuming less during the 11th mo ($P \leq 0.05$). Upon calculation, grain contained 3.60 Mcal/kg DE and hay contained 1.98 Mcal/kg. Based on calculated FDMI, Mod mares consumed an average of 28.21 Mcal DE/d while High mares consumed 34.60 Mcal DE/d which exceed NRC (2007) requirements for late gestation. In summary, maternal plane of nutrition had a tendency to alter FDMI and FDMI was influenced by gestation.

Key Words: intake, arginine, broodmares

361 The effect of hay steaming on forage quality and intake by horses. J. E. Earing,* M. R. Hathaway, C. C. Shaeffer, J. C. Paulson, S. L. Privatsky, and K. L. Martinson, *University of Minnesota, St. Paul.*

Heaves is a common equine disease. Current management strategies include soaking or wetting hay before feeding. Hay steaming is gaining popularity in the US, however, little is known about its impact on forage quality or palatability. Therefore, the objectives were to determine the effect of steaming on forage quality and intake. Two alfalfa-orchardgrass hays were tested: a moderately moldy hay (MM) and a lower mold hay (LM). While nutrient composition was similar, the mold content differed (MM: 373,000 cfu/g; LM: 120,500 cfu/g; $P = 0.0003$). Six mature horses were used in a 10 d crossover design. Three horses were assigned to each hay type; treatments were switched on d 6. Each day, one bale of each hay was steamed for 90 min using a commercial hay steamer. Two flakes of steamed and 2 flakes of unsteamed hay (MM or LM) were weighed and offered simultaneously to each horse in individual hay nets. Hay nets were located on opposite walls of the stall; location of the steamed and unsteamed hay was switched daily. The amount of hay offered was in excess of ad libitum intake. Horses were allowed access to hay for 2 h starting at 15:00 h, then orts were collected and DMI calculated. For each hay, paired *t*-tests were used to compare steamed and unsteamed hay nutrient content and DMI. Prior to steaming, the DM of both hays was similar (90%); steaming significantly reduced DM to 81 and 77% for MM and LM, respectively. In both MM and LM, steaming reduced P content ($P < 0.007$). Steaming reduced WSC by 13% ($P = 0.001$) and ESC by 27% ($P = 0.003$) for MM, but had no effect on LM ($P > 0.05$). Similarly, steaming reduced mold levels in MM by 85% ($P = 0.009$), but did not affect levels in LM ($P > 0.05$). No other forage quality components were affected by steaming. DMI of MM was not affected by steaming ($P > 0.05$); intake averaged 1.34 kg of unsteamed and 1.21 kg of steamed hay. Intake of LM was affected by steaming; horses ingested 0.64 kg of unsteamed and 2.02 kg of steamed hay ($P < 0.0001$). In moderately moldy hay, steaming reduced mold levels, but did not improve intake. However, for hay with low mold levels, steaming appeared to increase the palatability of the hay, while exerting no effects on forage quality.

Key Words: DMI, equine, mold

362 High non-structural carbohydrate diet in ponies alters location and absorptive capacity of glucose, phosphorus and glutamine across the gastrointestinal tract. B. E. Aldridge*[1], A. D. Woodward[2], J. S. Radcliffe[1], R. J. Geor[3], L. J. McCutcheon[3], and N. L. Trottier[2], *[1]Purdue University, West Lafayette, IN, [2]Michigan State University, Department of Animal Science, East Lansing, [3]Michigan State University, Department of Large Animal Clinical Science, East Lansing.*

Sixteen ponies were used to test the hypothesis that exposure to a rich non-structural carbohydrate (NSC) containing diet decreases small intestinal (SI) glucose transport capacity, and affects large intestinal (LI) absorptive nutrient profile compared with a strict forage-based diet. Ponies (n = 16) of mature age (BW 270 ± 74.4 kg) were equally assigned and fed one of 2 diets (n = 8) containing 12% CP: a control diet (CON) composed of grass hay (2.3% BW) and balancer pellet (0.2% BW), and a high NSC diet (CHO) containing 42% NSC, and composed of sweet feed and oligofructose (1.5% BW), grass hay (0.95% BW) and balancer pellet (0.05% BW). Ponies were subjected to a 4-wk adaptation period to the CON diet, followed by individual feeding of test diets for 7 d and euthanasia by single injection of pentobarbital. Segments of jejunum (J), ileum (I), left ventral (LVC) and left dorsal colon (LDC) were immediately mounted in Ussing Chambers to measure capacity for active glucose, phosphorus (P), and glutamine (Gln) absorption, based on change in short circuit current (Isc, $\mu A/cm^2$). Feeding CHO decreased active glucose transport ($P < 0.001$) across J and I compared with CON. Glucose transport across LVC and LDC did not differ between diets. In ponies fed CON, glucose transport capacity increased ($P = 0.008$) across J and I compared with that of the LVC and LDC, but in ponies fed CHO, glucose transport capacity between small and large intestinal segments did not differ. Feeding CHO did not affect active transport capacity of Gln or P across J and I, and increased ($P = 0.048$) active transport capacity of Gln by 239 and 60% and of P by 52.7 and 30.7% across LVC and LDC, respectively. Carbachol-induced Cl ion secretion was 30% lower ($P = 0.048$) across intestinal sections in CHO-fed ponies. In conclusion, abrupt exposure to NSC decreased SI glucose active transport capacity, increased LI active transport capacity of P and Gln, and reduced Cl ion secretion. Results indicate that abrupt dietary intake of NSC reduces the absorption of glucose by the SI of equids.

Key Words: equine, carbohydrate, intestine

363 Exercise-induced suppression of lymphocyte function is unaffected by a higher level of dietary selenium.

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The effect of dietary selenium (Se) concentration on lymphocyte function and viability following prolonged exercise was evaluated in 12 unconditioned Thoroughbred horses (mean ± SE, 11 ± 1 y, 565 ± 11 kg). Horses were randomly assigned to receive either 0.1 mg Se/kg DM (NRC-Se; n = 6) or 0.3 mg Se/kg DM (HIGH-Se; n = 6) for 36 d. Horses were individually fed 1.6% BW/d of coastal bermudagrass hay (0.02 mg Se/kg), 0.4% BW/d of whole oats (0.24 mg Se/kg) and a mineral/vitamin premix containing no Se. Sodium selenite was added to achieve either 0.1 or 0.3 mg Se/kg DM in the total diet. On d 35, horses underwent 2-h (26 km) of submaximal exercise in a free-stall exerciser (heart rate 135 ± 39 bpm). Blood samples were obtained on d 0 and 34 for determination of serum Se, and before exercise and at 6 and 24 h post-exercise for identification of leukocyte populations and isolation of peripheral blood mononuclear cells. Data were analyzed using the MIXED procedure of SAS (v. 9.2) with repeated measures. Serum Se remained unchanged in NRC-Se horses, but increased ($P < 0.01$) in HIGH-Se horses after 34 d of supplementation. Exercise resulted in an increase in circulating neutrophils ($P < 0.001$) and decreases in lymphocytes ($P < 0.001$) and eosinophils ($P < 0.001$), which persisted through 24 h post-exercise. Suppressed lymphoproliferative responses to concanavalin A ($P < 0.001$), phytohemagglutinin ($P < 0.01$) and pokeweed ($P < 0.01$) mitogens were noted at 6 h and 24 h post-exercise. Lymphocyte cell viability following in vitro hydrogen peroxide exposure was decreased ($P < 0.05$) at 24 h post-exercise. Level of dietary Se had no effect on leukocyte populations or lymphocyte proliferation or viability following exercise. These data indicate lymphocytes may be more vulnerable to oxidative damage and may not function properly during recovery from exercise, which could put horses at risk for infection. Feeding Se at 3 × the current NRC recommendation failed to mitigate exercise-induced suppression of lymphocyte viability and function.

Key Words: sodium selenite, prolonged exercise, immune function

364 Feeding graded amounts of lysine to yearling Thoroughbred colts does not activate the mTOR signaling pathway.

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Lysine (Lys) is known to be the first limiting amino acid (AA) in typical equine diets and therefore it is of prime interest when considering the nutrition of growing horses. AAs, as a group, have been shown to stimulate the mammalian target of rapamycin (mTOR) pathway and the activation of this pathway has been used as an indicator of protein synthesis at the tissue level, particularly in muscle. However, it is unknown whether Lys intake specifically can affect the activation of mTOR signaling factors. The objective of this study was to determine how feeding graded amounts of Lys affects mTOR signaling activation in growing horses. Six Thoroughbred colts (401 ± 5 d) were studied while receiving each of 6 levels of Lys intake: 80, 95, 110, 125, 135, and 145 mg/kg/d in a 6 × 6 Latin square. Diets consisted of a concentrate portion, which varied in Lys, and timothy hay cubes. Diets were isocaloric, isonitrogenous, and met or exceeded NRC recommendations for all nutrients except lysine. Each horse was fed each diet in random order for a period of 6 d. On d 6 a venipuncture sample and gluteal medius muscle biopsy were collected approximately 100 min post feeding of the morning meal. The ratio of phosphorylated to total protein was determined via Western blots quantified using ImageJ. Although plasma Lys concentrations increased in a dose-dependent manner with increasing dietary Lys intake ($P < 0.0001$), Lys intake did not affect eukaryotic initiation factor 4E binding protein 1 (4EBP1), ribosomal protein S6 (rps6), or protein kinase B (Akt) ($P > 0.1$) activation. Despite differences in Lys intake, the diets did provide the same amount of nitrogen and therefore these results suggest that Lys is not an independent activator of mTOR signaling. Alternatively, it is also possible that mTOR signaling was already maximized by the lowest intake of Lys provided and that subsequent increases in Lys intake did not result in any further increases in mTOR signaling. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2010–65206–20638 from the USDA National Institute of Food and Agriculture.

Key Words: lysine, horse, mTOR signaling

365 Influence of oral glucosamine supplementation on young horses in training: Pharmacokinetics.

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Twenty-one yearling Quarter horses (442 to 565 d of age and 351 to 470 kg) were utilized in a pilot trial to determine pharmacokinetic parameters of oral glucosamine derived from a non-GMO fungal biomass fermentation product. Horses were arranged in a randomized complete block design, and assigned 1 of 3 treatments via nasogastric intubation: control (CON; no glucosamine, 1000 mL saline), glucosamine HCl 15 mg/kg BW (GLU15; Activesure liquid; Cargill, Eddyville, IA), and glucosamine HCl 30 mg/kg BW (GLU30; Regenasure powder; Cargill). Horses were fasted for 12 h before nasogastric intubation. The GLU15 and GLU30 treatments were diluted in saline to reach a volume of 500 mL. Horses receiving GLU15 and GLU30 were given a saline flush of 500 mL post administration to ensure treatment was received in its entirety and reach a final volume of 1000 mL. Blood samples were obtained via jugular venipuncture at 0, 1.5, 3, and 12 h after treatments were administered. Plasma was harvested and stored at −20°C, before glucosamine analysis via HPLC. Data were analyzed using PROC MIX procedure of SAS. Plasma glucosamine concentrations increased as dosage of oral glucosamine increased ($P \leq 0.01$). Following intubation, plasma glucosamine values for GLU15 and GLU30 peaked at 3.0 h ($P \leq 0.05$) and 1.5 h ($P \leq 0.01$), respectively, and returned to baseline by 12 h. Additionally, there was a treatment by time interaction with GLU30 horses experiencing a sharp rise in plasma glucosamine concentration by 1.5 h post administration, resulting in a 6-fold increase compared with horses receiving GLU15 ($P \leq 0.01$). Both glucosamine products resulted in increased plasma glucosamine concentrations and the response was dose dependent. Further research will be conducted to determine the influence of oral glucosamine supplementation over time, including plasma and synovial fluid incorporation.

Key Words: equine, glucosamine, pharmacokinetics

366 Effects of prolonged exercise and citrulline supplementation on metabolic status in equine blood and skeletal muscle.

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Metabolic gene expression in skeletal muscle, as well as indicators of oxidative stress, in response to prolonged exercise and citrulline supplementation were evaluated in 12 untrained Thoroughbred and Quarter Horse mares (mean ± SE 11 ± 0.7 y, 552 ± 9 kg). Horses were randomly assigned to one of 2 isonitrogenous supplements for 15 d: 86 mg citrulline malate/kg BW (CIT; n = 6) or 25 mg urea/kg BW (n = 6). Additionally, horses were individually fed a fortified commercial feed and Coastal bermudagrass hay. On d 15, horses underwent 2 h (27.5 km) submaximal exercise in a free-stall exerciser (mean heart rate 142 ± 2 bpm). Blood samples were obtained before exercise and 1 h post-exercise for analysis of serum creatine kinase (CK) activity and total plasma lipid hydroperoxides (LPO). Biopsies of the middle gluteal muscle were obtained before exercise and 1 h post-exercise and gene expression was determined by quantitative RT-PCR using 18S as a reference gene. Data were analyzed using the MIXED procedure of SAS (v. 9.2) with repeated measures. Muscle expression of *MT1B* increased ($P = 0.04$) nearly 2.5-fold from pre- to 1 h post-exercise, indicating the exercise was sufficient to elicit oxidative stress. Muscle expression of *PDK4* increased ($P = 0.002$) over 64-fold from pre- to 1 h post-exercise, whereas expression of *iNOS*, *GLUT4*, *PGC1α*, and *SLC7A* remained unchanged through 1 h post-exercise. Serum CK activity ($P = 0.009$) and plasma LPO ($P = 0.04$) increased from pre- to 1 h post-exercise. However, CIT supplementation had no effect on expression of *MT1B*, *PDK4*, *iNOS*, *GLUT4*, *PGC1α*, or *SLC7A* in muscle or on serum CK activity or plasma LPO following exercise. Prolonged exercise in untrained horses upregulates aerobic metabolism (via expression of *PDK4*) and also appears to result in measurable tissue damage and lipid peroxidation. However, short-term CIT supplementation at rates sufficient to decrease production of reactive oxygen species in human athletes had no effect on markers of oxidative stress in exercised horses.

Key Words: horse, skeletal muscle oxidative damage, skeletal muscle metabolism

367 Selenium supplementation and immune function.

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Some studies indicate an effect of Se status on immune function. This study investigated the effect of Se supplementation on Se status and immune response in mature horses. Twenty-eight horses, blocked by age and sex, were randomly allocated to one of 4 groups: LS, AS, SP and SS. For 35 wk LS, SP and SS received a low Se diet (0.07 ppm Se) and AS received an adequate Se diet (0.14 ppm Se). For the next 29 wks LS and AS were maintained on the same diet while SP received a high organic Se diet (0.3 ppm; Sel-Plex, Alltech, Nicholasville, KY) and SS received a high inorganic Se diet (0.3 ppm; sodium selenite). The basal diet consisted of low Se pasture, hay, cracked corn and a balancer pellet either low (LS, SP, SS) or adequate (AS) in Se. The SP and SS supplements were top dressed on the balancer pellet. Whole blood Se and glutathione peroxidase activity (GPx) were monitored monthly. Horses were vaccinated with 10 mg ovalbumin (OVA) at wk 22 and 25. Blood samples were taken for 7 wk following vaccination for serum separation and at pre-, 3 and 5 wk post initial vaccination for peripheral blood mononuclear cell (PBMC) isolation, and whole blood cytokine mRNA evaluation. Data were analyzed as ANOVA with repeated measures (SAS 9.2). An effect of treatment, time and treatment x time ($P < 0.05$) existed for both Se and GPx. At the start of the 29 wk period Se was lower for LS, SP, and SS compared with AS. At 22 wk Se was higher for SP and SS than AS ($P < 0.05$). Whole blood GPx had a similar but delayed response. At 27 wk GPx was higher for SP and SS than AS, suggesting that maximum GPx activity is not maintained by dietary Se intakes of 0.1 ppm. The response to OVA vaccination, evaluated as OVA specific IgG production, cytokine mRNA expression of PBMC stimulated with OVA in vitro, and lymphocyte proliferation was unaffected by Se status. However, PBMC stimulated with phorbol 12-myristate 13-acetate indicated lower mRNA expression of some cytokines for LS ($P < 0.05$). Whole blood mRNA expression of IL-10 was higher for SS compared with LS, AS and SP ($P < 0.05$). Although the OVA vaccination response was unaffected by Se status, other measures of immune function suggest that low Se status affects cell-mediated immunity.

Key Words: horse, glutathione peroxidase, ovalbumin

368 Effect of strenuous exercise on stallion sperm quality.

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Performance ability of an equine athlete is one of the major considerations when selecting a stallion for breeding, and thermal stress associated with training exercise may affect sperm quality and the future reproductive capability of the stallion. Previous investigators reported that a prolonged increase in testicular temperature (3–3.5°C) decreased percentages of progressive motility and morphologically normal sperm. A subsequent study found contrasting results with no effect on semen quality when stallions were subjected to moderate exercise (0.8°C increase in internal scrotal temperature). It remains unclear what level of exercise imparts a negative effect on sperm quality. The objectives of this study were to compare sperm quality of strenuously exercised (EX) and non-exercised (CN) stallions. Strenuous exercise was determined by maintaining a heart rate between 145 and 155 bpm during work bouts. Miniature stallions (n = 7) implanted with subdermal thermosensory devices in the subcutaneous neck and scrotal tissue were matched by age and sperm quality and assigned to treatment group. Stallions (EX; n = 3) were exercised 4 d/wk for 90 min for 12 wk. Semen was collected from stallions for 5 consecutive d every 4 wks to evaluate semen quality (raw, 24 h and 48 h cooled). Internal scrotal (ST), rectal (RT) and neck (NT) temperatures were recorded along with heart rate of the stallions. Spermatozoa data were normally distributed; therefore, they were subjected to parametric analysis by repeated measures (wk) using the PROC MIXED procedure (SAS v 9.1; SAS Inst. Inc., Cary, NC). Model included treatment (CN or EX), time (wk 0, 4, 8, or 12), and stallion as the subject of the repeated measures. Compared with the CN group, EX stallions had elevated body temperature (avg RT 39.0 vs 37.2°C, NT 40.9 vs 38.5°C, and ST 34.9 vs 33.4°C) but parameters of spermatozoa quality remained unaffected by treatment ($P > 0.05$). While previous studies have illustrated that prolonged insulation of the testes reduces semen quality, strenuously exercising stallions for up to 90 min under hot and humid ambient conditions may not be harmful to spermatogenesis.

Key Words: heat stress, sperm, stallion

Lactation Biology II

369 Milk fat synthesis in thyroid hormone responsive spot 14 null mice is acutely responsive to *trans*-10, *cis*-12 conjugated linoleic acid (CLA). K. J. Harvatine*[1], M. Tanino[2], Y. R. Boisclair[2], and D. E. Bauman[2], [1]*Penn State University, University Park,* [2]*Cornell University, Ithaca, NY.*

Trans-10, *cis*-12 conjugated linoleic acid (CLA) reduces milk fat concentration and markedly reduces mammary de novo lipogenesis in both cows and mice. Thyroid hormone responsive spot 14 (S14) is decreased in mammary tissue of both the cow and mouse during CLA treatment. We have previously reported a functional role of S14 in CLA-induced inhibition of fat synthesis using the S14 null mouse. Mammary de novo lipogenesis of S14 null dams is hyper-responsive to CLA treatment. After 5 d of CLA treatment milk fatty acids (FA) less than 16 carbons are reduced about 2-fold more in S14 null mice compared with wild-type (WT) mice. Three experiments were conducted to further characterize the response to CLA in S14 null mice. Dams were bred to males of the opposite genotype and fed a low fat chow diet (Teklad 8640). First, recovery after termination of CLA treatment was tested in S14 null mice in a randomized block design. Starting at 8 to 9 d of lactation S14 null received oral doses of water (control) or 18 mg/d of CLA for 3 d. Two pups were euthanized for collection of stomach milk clots and the remaining pups were euthanized 5 d after termination of CLA treatment. CLA decreased pup growth and milk FA less than 16 carbons by approximately 60%, but both responses recovered by 5 d after termination of CLA (CLA × Day interaction $P < 0.01$). Second, the short-term response to CLA was investigated using WT and S14 null mice in a randomized block design with a 2 × 2 factorial arrangement of treatments (genotype × CLA). Starting on 10–12 d of lactation, S14 null and WT dams received water (control) or 20 mg/d of CLA for 24 h. The effect of genotype, CLA, and genotype by CLA interaction was tested. CLA reduced pup weight gain and there was no genotype x CLA interaction. However, there was genotype x CLA interaction for milk FA less than 16 carbons ($P < 0.001$; WT −17% vs S14 null −67%). Lastly, the sensitivity to CLA was tested using a similar randomized block design with WT and S14 null dams. Starting on 6 to 8 d of lactation, S14 null and WT dams received water (control) or 3.5 mg/d of CLA for 5 d. Dose selected was half the lowest dose previously used in a WT dose titration experiment that partially reduced milk fat. There was a genotype x CLA interaction for milk concentration of FA less than 16 carbons with an 8.9% decrease in WT and a 28.7% decrease S14 null. Overall, results demonstrate that the absence of S14 increases the responsiveness of mammary de novo lipogenesis to CLA without affecting sensitivity.

Key Words: CLA, spot 14 (S14), lipogenesis

370 Increased milk production by Holstein cows consuming endophyte-infected fescue seed during the dry period. R. L. Baldwin VI*[1], A. V. Capuco[1], C. M. Evock-Clover[1], P. Grossi[2], R. K. Choudhary[3], T. H. Elsasser[1], G. Bertoni[2], E. Trevisi[2], D. L. Harmon[4], and K. R. McLeod[4], [1]*Bovine Functional Genomics Lab, USDA-ARS, Beltsville, MD,* [2]*Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy,* [3]*Department of Animal and Avian Sciences, University of Maryland, College Park,* [4]*Department of Animal Sciences, University of Kentucky, Lexington.*

Ergot alkaloids in endophyte-infected grasses inhibit prolactin (PRL) secretion and may reduce milk production of cows consuming endophyte-infected grasses. We hypothesized that consumption of endophyte-infected fescue during the dry period inhibits mammary differentiation and subsequent milk production. Twenty-five multiparous Holstein cows were randomly assigned to 3 treatment groups. Starting at 90-d prepartum, cows were fed endophyte-free fescue seed (control, CON; n = 9), endophyte-free fescue seed and 3x/wk subcutaneous injections of bromocryptine (0.11 mg/kg BW; positive control, BROMO; n = 8), or endophyte-infected fescue seed as 10% of the as-fed diet (INF; n = 8). Although milk yield of groups did not differ at −90 d prepartum, at dry-off (−60 d) INF and BROMO cows produced less milk ($P < 0.05$) than CON (averaging 20, 11 and 14 kg/d for CON, INF and BROMO cows). Throughout the treatment period, concentrations of PRL in the circulation were lower in INF and BROMO cows than CON cows ($P < 0.05$). Basal concentrations of PRL in venous plasma averaged 25.3, 2.8 and 3.7 ng/ml for CON, INF and BROMO cows, respectively. Prepartum release of PRL was also reduced by ergot alkaloids, averaging 19.5, 9.2 and 1.1 µg PRL/ml*h (area under curve) for CON, INF and BROMO cows, respectively. At 10 d of lactation, when treatments were terminated, basal concentrations of PRL in plasma averaged 22.5, 1.6 and 1.4 ng/ml for CON, INF and BROMO cows, respectively. Three wk after the end of treatment, circulating concentrations of PRL were equivalent across groups ($P > 0.05$). Gestation length did not differ between groups. Although treatment 4 wk before dry-off reduced milk yield in INF and BROMO cows, milk production in the ensuing lactation was increased 8% and 9% in INF and BROMO cows relative to CON ($P < 0.05$). We reject our initial hypothesis, as data show that consumption of ergot alkaloids during the dry period increases milk production in the ensuing lactation. We propose that this effect is due to a reduction in PRL during the dry period, analogous to the production effect realized by exposing cows to reduced photoperiod (low PRL) during the dry period.

Key Words: endophyte-infected fescue, prolactin, milk production

371 Association between plasma insulin and progesterone concentrations and the composition of milk fatty acids and lipids. N. Argov-Argaman,* H. Malka, and R. Mesilati-Stahy, *Animal Science Department, Hebrew University, Rehovot, Israel.*

This study examined the association between plasma insulin and/or progesterone concentration and milk fatty acid and lipid composition. Holstein dairy cows, 60 DIM, were synchronized (estrus = d 0) and held as controls (n = 20) or drenched for 14 d (d −5 to d 11) with 500 mL/d liquid propylene glycol to increase plasma insulin level (treatment, n = 20). Milk and blood samples were collected on d −5, 1 and 8 of the cycle. Insulin and progesterone concentrations were determined in the plasma, and fatty acid, polar and neutral lipid compositions were determined in the milk. While not significant, plasma insulin concentration was higher in the treated vs. control group on d 1 (6.09 and 3.8 ng/mL, respectively) and on d 8 (6.2 and 4.5 ng/mL, respectively). In both groups, plasma progesterone concentration increased ($P < 0.001$) through the estrous cycle with an average concentration of 0.18 and 3.7 ng/mL on d 1 and 8, respectively. However, on d 8, peak progesterone level was higher ($P < 0.04$) in the treatment group than in the controls (4.33 vs. 3.09 ng/mL, respectively). Milk fat concentration tended ($P < 0.08$) to negatively interact with plasma insulin and positively interact ($P < 0.07$) with plasma progesterone concentrations. Milk fatty acid composition was associated primarily with the day of the cycle. For instance, saturated fatty acid concentration decreased from 65.8% on d 1 to 63.5% on d 8 ($P < 0.04$). Treatment was the major factor associated with long-chain saturated fatty acid content in the milk, with higher concentrations in the control vs. treatment groups on both d 1 ($P < 0.05$; 9.3 and 8.0%, respectively) and d 8 ($P < 0.009$; 10.3 and 8.4%, respectively). Treatment was also associated with stearoyl CoA desaturase activity, as reflected by a 15% increase on d 1 ($P < 0.03$) and 10% increase on d 8 ($P < 0.08$). The results suggest that milk fatty acid composition changes during the estrous cycle in association with plasma progesterone concentrations. Propylene glycol administration increased progesterone concentration and to some extent that of insulin, which in turn might affect fatty acid composition.

Key Words: lipids, estrous, propylene glycol

372 Ontogeny of nuclear and cytoplasmic myoepithelial cell markers in pre-weaning Holstein heifers. S. Safayi[1], N. Korn[1], A. DiMascio[2], R. M. Akers[3], A. V. Capuco[4], and S. Ellis*[1], [1]*Clemson University, Clemson, SC,* [2]*University of Georgia, Athens,* [3]*Virginia Polytechnic Institute and State University, Blacksburg,* [4]*USDA-ARS, Beltsville Agricultural Research Center, Beltsville, MD.*

Myoepithelial cells (MC) have roles in cell proliferation and differentiation and hence may affect mammary parenchymal morphogenesis. Because MC can limit parenchymal growth in other species, it is important to understand MC-related mechanisms involved in early bovine mammary development. We previously saw changes in expression of the nuclear marker transformation-related protein 63 (P63) and the cytoplasmic marker common acute lymphoblastic leukemia antigen (CD10), corresponding with changes in the pattern of MC development in prepubertal heifers between 40 and 160d of age. In this study, we investigated the ontogeny of MC development during the pre-weaning period by tracking P63 and CD10 expression with immunofluorescent staining. Holstein heifers (n = 4/age) were sacrificed and sampled at 0 (<12 h of birth), 7, 14, 21, 28, 35, and 42 d of age. The basal epithelium was traced and MC marker expression within the outlined region was quantified using multispectral imaging of stained paraffin sections from each parenchymal sample. Fluorescent intensity (FI) of the markers in traced regions on each slide was normalized against a reference sample and then evaluated statistically using Mixed procedures in SAS. Samples were also used for subjective histologic assessment of MC marker distribution. Our analysis showed increased FI of CD10 and P63 at d 42, relative to d 0 ($P \leq 0.02$). The ratio of CD10 to P63 remained constant ($P = 0.94$) from d 0 to d 42. The increased intensity but consistent ratio values could be explained by our observation that P63+ nuclei were more closely spaced in the older calves. These results highlight a need to analyze expression within individual nuclei rather than quantifying expression within the entire basal layer. Double positive (P63+/CD10+) and double negative (P63-/CD10-) cells and single positive cells expressing either marker (P63-/CD10+ or P63+/CD10-) were present in both basal and supra-basal layers. As a result, our data does not yet define a sequential progression of bovine mammary MC differentiation. Further studies with additional MC markers are therefore required to define the sequence of bovine MC ontogeny.

Key Words: myoepithelial, mammary development, heifer

373 Ultrasonographic monitoring of mammary parenchyma growth in preweaned Holstein heifers. K. M. Esselburn*[1], T. M. Hill[2], K. M. O'Diam[1], V. A. Swank[1], H. G. Bateman II[2], R. L. Schlotterbeck[2], and K. M. Daniels[1], [1]*Department of Animal Sciences, The Ohio State University, Ohio Agricultural Research and Development Center, Wooster,* [2]*Nurture Research Center, Provimi North America, Brookville, OH.*

Mammary parenchyma (PAR) is present at birth in negligible quantities and undergoes extensive postnatal growth. Researchers have long been interested in nutritional effects on the mammary gland. However, monitoring in vivo growth of PAR has historically been difficult, necessitating slaughter studies to measure PAR quantity. Advances in ultrasound (US) technology warrant revisiting its use as a non-invasive tool to monitor PAR growth in vivo. Holstein heifers (n = 24; 41 ± 1kg initial BW) from a single farm were randomly assigned to 1 of 3 milk replacers (MR) at 2–3 d of age. Heifers were fed MR at 660 g/d until weaning at 42 d. MR contained 27% CP and was formulated with 3 fat and fatty acid compositions. MR treatments were A) only lard, 17% fat, B) animal fat supplemented with 1.25% NeoTect4 (MR, Provimi North America, Brookville, OH), 17% fat, and C) milk fat, 33% fat. Starter (20%CP) and water were fed ad lib for 56d. A real time B-mode US with a 7.5-MHz convex probe was used to examine 2-dimensional (2D) PAR area in all 4 glands of heifers once weekly from 2 to 3 d of age to 52 d. Individual digital images of each gland were saved for further analysis. At 52 d of age, heifers were slaughtered to validate final US measurements. At slaughter, the left half of the mammary gland was removed and examined by US 24 h later. Also at that time, left front and left rear glands were bisected to produce a sagittal plane view of PAR for comparison to US images. In all cases 2D areas of PAR were determined using ImageJ software (NIH). Data were analyzed using mixed procedure of SAS. Additionally, 8wk paired data were analyzed using the correlation procedure. There were no differences in PAR area due to diet. Regardless of dietary treatment, PAR grew over time (0.049cm^2 initially; 0.420cm^2 at 52 d ante-mortem; SEM = 0.020), as expected. Positive correlations existed between all paired variables analyzed (PAR area of bisected sagittal plane view; PAR area ante-mortem from US; PAR area postmortem from US; all r >0.60). Methodology used here demonstrates that US is an effective tool for measuring weekly changes in PAR area in vivo.

Key Words: ultrasound, mammary, dairy calf

374 Proteomic analysis of the nuclear phosphorylated proteins in dairy cow mammary epithelial cells treated with prolactin. J.-G. Huang, X.-J. Gao,* Q.-Z. Li, L. Zhang, F. Zhao, N. Zhang, Y. Lin, and Z. Sun, *Key Lab of Dairy Science, Ministry of Education, Northeast Agriculture University, Harbin, Heilongjiang, China.*

Prolactin (PRL) is a versatile signaling molecule and regulates a variety of physiological processes, including mammary gland growth and differentiation and the synthesis of milk proteins. While PRL is known to be necessary for high levels of milk protein expression, the mechanism by which the synthesis of milk proteins is stimulated at the transcript level is less known. A major modification important in the transcript level is protein phosphorylation. To gain additional insights into the molecular mechanisms at the transcript level underlying PRL action on the dairy cow mammary epithelial cells (DCMECs), nuclear phosphoproteins whose expression distinguishes proliferating regulated by PRL in DCMECs were identified. A phosphoprotein-enriched fraction from nuclear proteins was obtained by affinity chromatography, and a 2-dimensional gel electrophoresis (2-DE) and matrix assisted laser desorption/ionization time of matrix-assisted laser desorption/ionization/time of flight mass spectrometry (MALDI-TOF MS) were used to identify the changes of nuclear phosphoproteins in DCMECs treated with prolactin. Results: Seven proteins displaying ≥ 2-fold difference in abundance upon PRL treatment in DCMECs were identified by MALDI-TOF MS. The protein–GARS (GlyRS), which belongs to the class-II aminoacyl-tRNA synthetase family, plays a global role in the milk protein synthesis. SERPINH1 (Heat shock protein 47), which is the first heat shock protein found to be a member of the serpin superfamily, regulates physiologic functions such as complement activation, programmed cell death, and inflammatory processes. PRDX3, which belongs to a family of antioxidant enzymes, plays an important role in scavenging intracellular reactive oxygen species (ROS). ACTR1A, belongs to the actin family, which is associated with transport of p53 to the nucleus. Annexin A2, a Ca^{2+}-dependent phospholipid-binding protein, maintains the viability and cell cycle regulation of DCMECs. PSMB2, PSMD10, which belong to ubiquitin-proteasome system, are involved in several cellular processes, including cell cycle control, cellular stress responses, intracellular signaling. This screening reveals that prolactin influences the levels of nuclear phospho-proteins in DCMECs. This result opens new avenues for the study of the molecular mechanisms linked to the synthesis of milk proteins.

Key Words: nuclear phosphorylated protein, prolactin, 2-DE

375 Analysis of differentially expressed miRNA in dairy cow mammary gland identifies HK2-regulating miRNAs.

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MicroRNAs (miRNAs) are non-coding RNAs of about 22 nucleotides in length. Functional studies have demonstrated that miRNAs play critical roles in a wide series of biological processes including development and disease pathogenesis. To investigate the functional roles that miRNA play in the mammary gland (MG) of lactating cows, the bovine MG miRNA transcriptomes were profiled using microarray. A custom-designed microarray assay was performed to analyze miRNA expression patterns in the MG of lactating and nonlactating dairy cows. Compared with non-lactation MG, a total of 226 miRNAs in the lactating MG showed significant differences in expression ($P < 0.01$). There were 120 miRNAs including bta-miR-199b and bta-miR-125b downregulated, whereas 106 miRNAs such as bta-miR-133a and bta-miR-500 were upregulated. Meanwhile other 73 new miRNAs in bovine MG were detected. Target prediction and network construction speculated that 5 differentially expressed miRNAs (bta-miR-125b, bta-miR-199b, bta-miR-181a, bta-miR-484 and bta-miR-500) could contribute to the lactation by targeting the hexokinase 2 (HK2) gene, the key enzymes in glucose metabolism. The potential target sites for all these 5 miRNAs were identified in predicted bovine HK2 3′UTR. These miRNA mimics were introduced into MAC-T cells to evaluate their effects on the HK2 at the translation level. Of these miRNAs, bta-miR-484 and bta-miR-500 showed the most inhibitory effect on production of HK2 protein, while this was not the case for other 3 miRNAs. These results indicated that miR-484 and miR-500 may exert their effect on lactation function via targeting HK2. The present study provides a systematic transcriptome profiling differentially expressed between lactating and nonlactating bovine MG.

Key Words: bovine mammary gland, hexokinase 2, microRNAs

Meat Science and Muscle Biology Symposium: In Utero Factors that Influence Postnatal Muscle Growth, Carcass Composition, and Meat Quality

376 Fetal programming of skeletal muscle mitochondrial function and insulin sensitivity: Perspectives from non-human primates and mouse models. J. A. Houck[1], K. L. Grove[2], and C. E. McCurdy*[1], [1]*Department of Pediatrics, University of Colorado,* [2]*National Primate Research Center, Oregon Health and Sciences University.*

Maternal obesity is associated with an increased and earlier risk for the offspring to develop early onset-obesity. In skeletal muscle from either obese adults or lean adult offspring of mothers with type 2 diabetes, reduced mitochondrial density, increased muscle triglyceride accumulation and impaired oxidative function have all been observed and the traits have been linked to skeletal muscle insulin resistance. Accordingly, it has been suggested that the fetal environment may have a profound effect on programming of skeletal muscle metabolism and subsequently have a substantial effect on life-long muscle growth, muscle self-renewal/repair and substrate partitioning. This talk will focus on the influence of maternal diet and obesity on offspring mitochondrial function, fiber typing and insulin sensitivity from both mouse models and a non-human primate model of maternal obesity. Female Japanese Macaques were fed either a control (10% fat) or a high fat/calorie diet (35% fat; HFD) for 2–4 years. Skeletal muscles were collected from fetuses (F-CON or F-HFD) terminated early-3rd trimester. Mitochondrial biogenesis, electron transport activity, and gene expression were analyzed in whole muscle homogenates and isolated mitochondria. Insulin-stimulated 2-deoxyglucose uptake (2DG) was measured in isolated muscle strips from F-CON and F-HFD at sub-maximal [0.3 nM] and maximal [12 nM] doses. Similar studies were performed in mouse models of maternal obesity to investigate post-weaning skeletal muscle mitochondrial development, persistence of insulin resistance and muscle progenitor cell populations. Mitochondrial copy number and citrate synthase activity were significantly reduced in male, but not female, fetal skeletal muscle from F-HFD vs. F-CON. Additionally, key transcriptional regulators of mitochondrial biogenesis, PGC1α, PGC1β, tFAM and Mitofusin-2, were also significantly downregulated in F-HFD. Analysis of maximal mitochondrial complex activity showed significant increase in mitochondrial complex activities and increased ROS damage with maternal obesity. Ex vivo insulin-stimulated 2DG uptake at submaximal and maximal insulin doses was significantly reduced in both male and female rectus femoris and soleus of F-HFD, demonstrating impaired insulin sensitivity and responsiveness that persists at 1 year of age. Additionally in mouse models, we find that maternal obesity leads to a significant shift in the offspring skeletal muscle progenitor cell population favoring adipogenic/fibrogenic precursor cells. Our results demonstrate that the intrauterine environment has profound effects on mitochondrial function and insulin sensitivity in fetal skeletal muscle. Impairments in these 2 key skeletal muscle metabolic functions would undoubtedly predispose the offspring to metabolic complications and poor or impaired muscle growth. It will be essential to determine the extent to which these effects persist in postnatal life. This work was supported by NIH grant K12 HD057022 (CEM) and DK090964 (CEM, KLG).

377 Manipulating mesenchymal progenitor cell differentiation to optimize performance and carcass value of beef cattle. M. Du,* *Department of Animal Sciences, Washington State University, Pullman.*

Beef cattle are raised for their lean, and excessive fat accumulation accounts for large amounts of waste. On the other hand, intramuscular fat or marbling is essential for the palatability of beef. In addition, tender beef is demanded by consumers, and connective tissue contributes to its background toughness. Recent studies show that myocytes, adipocytes and fibroblasts are all derived from a common pool of progenitor cells during the embryonic stage. It appears that during the early developmental stage, multipotent mesenchymal stem cells (MSCs) first diverge into either myogenic or adipogenic/fibrogenic lineage; myogenic progenitor cells further develop into muscle fibers and satellite cells, while adipogenic/fibrogenic lineage cells develop into the stromal-vascular fraction of skeletal muscle, which contains adipocytes, fibroblasts and resident fibro/adipogenic progenitor cells. Strengthening myogenesis (formation of muscle cells) enhances lean growth, promoting intramuscular adipogenesis (formation of fat cells) elevates marbling, and reducing intramuscular fibrogenesis (formation of fibroblasts and synthesis of connective tissue) improves overall tenderness of beef. Nutritional, environmental and genetic factors affect MSC differentiation; however, up to now, our knowledge regarding mechanisms governing MSC differentiation remains rudimentary. Altering MSC differentiation through nutritional management of cows, or fetal programming, is a promising method to improve cattle performance and carcass value.

Key Words: stem cell, myogenesis, adipogenesis

378 In utero nutrition related to fetal development, postnatal growth, and pork quality. N. Oksbjerg,* *Aarhus University-Foulum, Dept. of Food Science, Tjele, Denmark.*

Sub-optimal in utero nutrition gives rise to small birth weights (IUGR) and may cause long lasting effects on postnatal performance and economical loss in meat production. The objectives are to summarize the most important results of our research in this area. Our results show that increased (ad lib) global maternal feed intake in various windows had no main effects on performance and meat quality of the offspring. However, muscle growth rate was reduced in small pigs when the sow was feed ad lib from d 25 to 50 of gestation. On the other hand, when sows were fed a diet containing 30% less protein, the daily gain of the offspring tended to decrease. The meat quality traits, pH_{45} and shear force as well as calpastatin level, were increased and decreased, respectively, in entire male pigs, but not in female pigs following a maternal low protein diet. Comparing small and heavy pigs selected at slaughter at the same age or at birth (IUGR) showed that the small pigs had lower daily gain, fewer muscle fibers, and mean fiber area and increased kg feed/kg gain. Estimated content of DNA/fiber was lowest in the small pigs. Also shear force and calpastatin were increased in pigs born small. When blood was drawn at d 110 of gestation from the umbilicus cord and subjected to NMR metabolomics analyses, it was shown that the smaller fetuses had a lower concentration of glucose and a higher concentration of inositols compared with the heaviest littermates. Proteomic analyses of muscle samples identified 5 proteins which were differentially expressed depending on sex. In conclusion, our results suggest that pigs which were born small had lower performance due to a lower muscle fiber number and satellite cell proliferation which were at least partly due to reduced nutrition. Dietary manipulation of the pregnant sows also programmed the meat quality of the offspring dependent on the sex.

Key Words: maternal nutrition, offspring performance, muscle fiber traits

379 Maternal nutrition on pasture mediates long-term consequences for offspring primarily through effects on growth early in life of beef cattle. P. L. Greenwood,* L. M. Cafe, and D. L. Robinson, *Australian Cooperative Research Centre for Beef Genetic Technologies, and NSW Department of Primary Industries, UNE, Armidale NSW, Australia.*

Long-term consequences for offspring due to dam nutrition, beyond those due to variation in early-life growth were studied. Hereford cows were mated in consecutive years to Piedmontese or Wagyu sires. When confirmed pregnant, cows (n = 513) entered low or high pasture quality and availability treatments until parturition and (or) weaning. At weaning (7 mo), offspring (n = 240) within steer and heifer cohorts were selected for further study into 4 early-life growth groups (Low-Low, Low-High, High-Low and High-High), resulting in multi-model distributions based on maternal nutrition and offspring growth to birth and to weaning. A stepwise regression procedure specified covariates including birth (B) and weaning (W) weight, age at measurement (A), and effects of nutrition during pregnancy (P) and lactation (L), calf sex (S), year (Y), sire breed (G), and first order interactions of factors and with covariates. B was affected by P, and W by L and by P over and above differences due to B. For feedlot entry (26 mo) and exit (30 mo) weights and for carcass weight (C), there were significant linear effects of B and W, and effects of G, S and Y, but no effects of P or L beyond those due to differences in B and W. Average differences of 6 kg in B of calves due to P and 55 kg in W due to L both translated into differences of ~20 kg in C, 11–12 kg in retail yield and 6 kg of fat trim, but did not affect beef tenderness. When adjusted to a constant C, heavier W cattle had more fat trim and less retail yield. There were few interactions however at the same C there was a significant G x W interaction for rib eye area: Piedmontese-sired, Low 95.7 vs. High 88.4 cm^2; Wagyu-sired, both groups 85.7 cm^2. Feedlot feed intake (n = 142) was affected by B and W but not when corrected for weight at start of intake test. FCR was affected by W and L, and whether dams were lactating in early pregnancy. Maternal nutrition did not affect RFI. Overall, there were few long-term influences of maternal nutrition on offspring beyond those related to early-life growth within our pasture-based system. Optimal maternal nutrition to maximize capacity to re-breed has greater economic impact than longer-term consequences for offspring.

Key Words: birth weight, fetal programming, nutrition

Nonruminant Nutrition: Management/Metabolism

380 Diet form and by-product level affect growth performance and carcass characteristics of grow-finish pigs. R. S. Fry,* W. Hu, S. B. Williams, N. D. Paton, and D. R. Cook, *Provimi North America, Akey Nutrition and Research Center.*

Two experiments were conducted to determine the effect of diet form and by-product (BP) level on growth performance and carcass characteristics of grow-finish pigs. In experiment 1, 384 pigs (22.2 ± 0.27 kg BW; 12 pigs/pen) were randomly assigned to one of the following treatments in a 2 × 2 arrangement: 1) low BP (LBP) meal [30% dried distiller grains with solubles (DDGS) and 15% wheat middlings (WM)] or 2) high BP (HBP) meal (50% DDGS and 15% WM) with diets fed either in meal or pellet form. In experiment 2, 1008 pigs (23.7 ± 0.27 kg BW; 21 pigs/pen) were randomly assigned to one of the following treatments in a 2 × 3 arrangement: 1) corn-soybean meal (CSBM), 2) LBP meal (25% DDGS and 7.5% WM), or 3) HBP meal (50% DDGS and 15% WM) with diets fed either in meal or pellet form. In both experiments, complete blocks of pigs were marketed when each block reached approximately 130 kg BW. In experiment 1, ADG was greater ($P < 0.01$) for pigs fed pelleted vs. meal diets. Increasing by-products in meal diets reduced ADFI, but not in pelleted diets ($P < 0.05$; diet form × BP level). Increasing by-products in meal diets improved G:F, but this did not occur when pelleted diets were fed ($P < 0.05$; diet form × BP level). In experiment 2, G:F was improved ($P < 0.01$) when diets were fed as a pellet vs. meal. Increasing by-product level decreased ($P < 0.01$) G:F. As BP level increased in meal diets ADG decreased, while increasing BP level in pelleted diets decreased ADG to a lesser extent ($P < 0.05$; diet form × BP level). As BP level increased, ADFI tended to decrease when meal diets were fed but not when pelleted diets were fed ($P < 0.10$; diet form × BP level). Increasing BP level decreased ($P < 0.05$) carcass yield and backfat. Pelleting tended ($P < 0.10$) to increase carcass yield. These data suggest that pelleting high by-product diets improves performance, and pelleting lessens the negative effects of by-product level on pig performance.

Key Words: pigs, by-products, pellet

381 Influence of ingredient complexity, feed form, and length of feeding of the phase I diets on nutrient digestibility and productive performance of Iberian pigs. J. D. Berrocoso, B. Saldaña, L. Cámara, M. P. Serrano, M. A. Ibáñez, and G. G. Mateos,* *Universidad Politécnica de Madrid, Madrid, Spain.*

In total, 216 Iberian piglets weaned at 28 d of age were used in a 35 d trial to evaluate the influence of ingredient complexity, feed form, and the length of feeding of the phase I diets on growth performance and total tract apparent digestibility (TTAD) of nutrients. There were 12 treatments with 2 type of diets that differed in CP content (20.5 vs. 18.5%) and in the percentage of inclusion of high quality ingredients (heat processed corn, protein concentrate, fish meal, and dried whey; HQ: high quality and LQ: low quality), 2 feed forms (mash vs. pellets), and 3 lengths of feeding the phase I diets (7, 14, and 21 d). From 7, 14 or 21 d to 35 d on trial, all pigs were fed a common phase II mash diet based on wheat and soybean meal. Cumulatively (0 to 35 d on trial), pigs fed the LQ phase I diets had higher ADFI ($P < 0.01$) and ADG ($P < 0.05$) than pigs fed the HQ diets. Pelleting improved ($P < 0.01$) G:F but not ADFI or ADG. Feeding the phase I diets for 21 d reduced ADFI and ADG but improved G:F as compared with 7 or 14 d feeding ($P < 0.01$). The incidence of diarrhea (DI) was higher in pigs fed the phase I diets for 21 or 14 d than in pigs fed these diets for 7 d ($P < 0.01$). Pigs fed pellets had higher ($P < 0.01$) DI than pigs fed mash. From 0 to 21 d of trial, pigs fed the HQ diets had lower ($P < 0.05$) ADFI than piglets fed the LQ diets and pelleting improved ($P < 0.01$) G:F. Increasing the length of feeding of the phase I diets improved G:F ($P < 0.01$). Also, DI was higher ($P < 0.01$) in pigs fed pellets than pigs fed mash and higher in pigs fed the phase I diets for 21 or 14 d than in pigs fed these diets for 7 d ($P < 0.01$). TTAD of nutrients was higher for pigs fed pellets ($P < 0.01$) or the HQ phase I diets ($P < 0.05$) than in pigs fed mash or the LQ phase I diets. From 21 to 35 d on trial, pigs previously fed the LQ diet had higher ($P < 0.01$) ADG and ADFI than pigs fed the HQ diet. Based on these results the use of LQ feeds in pellet form for only 7 d after weaning is recommended in Iberian pigs.

Key Words: diet complexity and feed form, growth performance, total-tract apparent digestibility

382 Hepatic gene expression analysis of nursery pigs fed simple and complex starter diets. M. Rudar,* L. D. Skinner, and C. F. M. de Lange, *University of Guelph, Guelph, ON, Canada.*

Reduced use of complex animal proteins in pig diets can reduce both feed costs and growth performance during the starter phase. The long-term consequences of this practice are unclear, as it may induce compensatory growth and alter disease resistance during the grower-finisher phase. The objective of this study was to explore potential indicators of health status, immune function, and nutrient partitioning that predict the effect of diet stressors on subsequent growth performance. Starter pigs were fed either simple (plant protein, non-medicated, n = 12 pens) or complex (milk and plasma proteins, medicated, n = 12 pens) diets formulated to be otherwise equivalent for 6 weeks. Liver tissue was collected from 4 pigs per treatment at 2 weeks post-weaning when the growth rate of pigs fed simple diets was reduced (397 vs 459 g/d, $P < 0.05$). Total RNA was isolated from liver and aminoallyl-modified cRNA was hybridized to Agilent Porcine Gene Expression Microarray in a reference design. The gene expression data were normalized, filtered, and analyzed using a simple linear (ANOVA) model. A total of 182 genes were detected to be differently expressed between the diets ($P < 0.10$, Benjamini-Hochberg false discovery rate adjustment). Pigs fed simple diets had increased hepatic gene expression of urea cycle enzymes (arginase-1, $P < 0.06$; and carbamoyl phosphate synthase-1, $P < 0.06$) and antioxidant enzymes (glutathione peroxidase-1, $P < 0.06$; and glutathione peroxidase-3, $P < 0.06$). Pigs fed complex diets had increased hepatic expression of genes involved in endogenous antigen processing and presentation (swine leukocyte antigen [SLA]-2, $P < 0.10$; SLA-8, $P < 0.08$; antigen peptide transporter-1, $P < 0.06$; and antigen peptide transporter-2, $P < 0.07$), and in exogenous antigen processing and presentation (SLA-DMA, $P < 0.08$; SLA-DMB, $P < 0.06$; SLA-DQA, $P < 0.06$; SLA-DQB1, $P < 0.03$; SLA-DRA, $P < 0.08$; SLA-DRB1, $P < 0.06$; CD74 invariant chain, $P < 0.09$; and cathepsin S, $P < 0.06$). These results indicate increased disease resistance of starter pigs fed complex diets in the nursery that may persist as they grow.

Key Words: immunity, microarray, pigs

383 Development and evaluation of a model estimating nitrogen partitioning in lactating sows.

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The impact of nitrogen excretion from swine operations on the environment is of growing concern. There are very few models that predict nutrient excretion from sows, therefore, our objective was to develop and evaluate a whole animal model that predicts the nitrogen partitioning by lactating sows and nutrient excretion. A factorial approach was taken to estimate requirements for maintenance, milk production and body deposition. It was assumed that the priority for nutrient partitioning was in the order of maintenance, milk production and body deposition with body tissue losses constrained within biological limits. The model inputs were dietary composition, potential litter size (LS), litter gain (LG), and BW of the sow. Nitrogen input (NI) was predicted and the other outputs from the model were nitrogen excretion in milk (NL), urine (NU) and feces (NF). The model also predicts the loss of body fat (dL) and protein (dP) during lactation. The model was evaluated using existing nitrogen balance data from the literature. The information on potential LS, LG, sow BW, dietary composition and feed intake from the literature was used as input to the model and the predicted values for the nitrogen balance was compared with the values given in the publications. The root mean squared prediction error (RMSPE) and concordance correlation coefficients (CCC) were used in the evaluation. The mean values for observed and predicted NI, NU, NF, and NL were 95.4, 34.6, 10.9, and 65.6 g/d and 94.8, 38.5, 10.9, and 64.5 g/d, respectively. The RMSPE for NI, NU, NF, and NL were 9.9, 9.8, 1.4 and 5.6 g/d, respectively. The CCC for NI, NU, NF, and NL were 0.97, 0.93, 0.95 and 0.80, respectively. The prediction of dL and dP was evaluated using publications with relevant information. The RMSPE was 5.2 and 1.9 kg for dL and dP, respectively. The CCC was 0.74 and 0.70 for dL and dP, respectively. In conclusion, the evaluation shows that the model can predict nitrogen partitioning, dL and dP in lactating sows, and it is a potential tool for assessing intervention methods such as dietary manipulation on nutrient loading in the environment.

Key Words: nitrogen, lactation, sow

384 Dynamics of nitrogen retention in entire male pigs immunized with Improvest.

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Immunization against gonadotropin-releasing hormone (GnRH) reduces the occurrence of boar taint compounds in male pigs, and is likely to alter growth performance and whole body protein deposition (Pd). The latter is an important determinant of dietary amino acid requirements. Thirty-six male PIC pigs were used to determine the effects of immunization against GnRH with Improvest (Pfizer Animal Health) on plasma levels of androstenone and skatole and Pd (N-retention × 6.25). Four treatments were used: [1] conventional, early castrates (EC), [2] entire males (EM), [3] entire male pigs immunized with Improvest (IM), and [4] entire male pigs surgically castrated at 25–40 kg body weight (late castrates; LC). Improvest was injected at 30 kg and 70 kg BW. Within each of 9 litters, 4 males were randomly assigned to one treatment. Pigs were fed corn and soybean meal based diets that were not limiting in essential nutrients for high Pd. Five consecutive N-balances were conducted on days: −9 to −4, 1 to 7, 9 to 16, 20 to 26 and 30 to 36, relative to the second injection at d 0; blood was sampled on days: −4, −1, 2, 5, 8, 11, 14, 19, 28 and 37. Plasma androstenone became not different from zero in IM ($P > 0.10$) and equal to EC and LC ($P > 0.10$) by d 8. Treatment had no effect on plasma skatole levels (overall mean: 0.32 ± 0.10 ng/g; $P > 0.10$). There was an interactive effect of treatment and time on Pd ($P < 0.001$). Across periods, Pd for EC and LC were similar (204.4 vs 207.5 g/d, $P > 0.10$), and lower than EM (244.8 g/d, $P < 0.001$). Pd in EM and IM was similar up to d 7 (239.5 vs 242.1 g/d, $P > 0.10$), tended to be higher for EM than IM during d 9 to 16 (239.7 vs 216.7 g/d, $P = 0.07$) and was higher for EM than IM after d 20 (252.7 vs 202.6 g/d, $P < 0.05$). Between d 9 and 36 IM Pd was similar to EC and LC ($P > 0.10$). Immunization with IMPROVEST was effective at reducing plasma androstenone. Between d 7 and 16 after the second injection, Pd in IM changed gradually from EM levels to EC and LC levels, which should be considered when developing feeding programs for IM.

Key Words: entire males, Improvest, nitrogen retention

385 Effects of dietary protein and lipid levels on growth and stress tolerance of juvenile tilapia (*Oreochromis niloticus*).

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The objectives of this study were to determine optimal dietary protein and lipid levels in diets on rate and efficiency of growth and stress response of juvenile tilapia cultured in a high-intensity recirculating-water system. A 3 × 3 factorial arrangement of diets formulated to contain 3 levels of dietary protein (28, 32 and 36%) and 3 levels of dietary lipid (3, 6, and 9%) was employed. Juvenile tilapia (34.5 ± 0.4g) were randomly assigned to each of the tanks (30 fish/tank), with 3 replicate tanks for each treatment except for the 3% lipid level (2 replicates). Fish were fed 3 times per d to apparent satiation, 6 d per wk for 12wks. Fish were weighed every 3 wks and feed efficiency (G:F) was calculated. All data were subjected to a 2-way ANOVA to determine the effects of dietary protein and lipid and their interactions on fish growth, performance and body composition and blood chemistry following a simulated hauling trial. There was no protein by lipid interactions for either rate or efficiency of gain. Fish fed 36% CP had higher ($P < 0.05$) weight gains and lower ($P < 0.05$) G:F when compared with either 28% or 32% CP diets. Fish fed 3% crude lipid had higher ($P < 0.05$) G:F (1.56) when compared with diets containing 6% and 9% crude lipid (1.41 and 1.40 respectively). Tissue composition was significantly ($P < 0.05$) affected by diet, but fish fed 36% CP retained more ($P < 0.05$) whole body protein but less whole body lipid than fish fed diets with 32% or 28% CP. Feeding fish diets with 9% lipid increased ($P < 0.05$) whole body lipid concentrations as well as whole body gross energy. Following the completion of the growth trial, tilapia were subjected to a 24-h simulated live haul. Glucose, lactate, and cortisol measurements were determined at 0, 24, and 72 h. There were significant effects ($P < 0.01$) of protein level on initial blood lactate. Fish fed 32% CP had higher lactate levels than fish fed 36% CP. After 24 h fish fed 36% CP had higher lactate levels than fish fed 32% CP suggesting that fish fed higher protein levels were more stressed during the live haul. An interaction was measured for cortisol at 24 h ($P < 0.05$), with fish fed 28% CP and 6% crude lipid having higher levels than other dietary treatment. Diets containing, 36% protein and 3% lipid supported faster growth compared with diets with higher levels of protein and lipid.

Key Words: tilapia, protein by energy, stress

386 Comparison of the in vitro fermentation activity of fecal inocula from piglets and dogs.

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It is expected that gut microbiota from dogs and piglets are different in terms of number and species. This would be reflected in differences in the fermentative activity. So, the aim of this study was to compare the microbiota potential of dogs and piglets to ferment different feedstuffs. Nine substrates (0.5 g of either ryegrass, citrus pulp, apple pomace, piglet and dog food, soy hulls, corn, barley and inulin) were incubated in vitro with 10 mL of diluted feces (1:5 w/v with 9 g/L NaCl solution) from 3 piglets and 3 adult dogs fed a soybean-corn based diet and a commercial dog food respectively (3 flask/inoculum, plus 3 blanks, n = 60). Gas volume was recorded at 2, 4, 6, 8, 10, 12, 18, 24, 48 and 67 h after inoculation. Asymptotic gas production (a, mL/g OM), rate of gas production (K_d, h^{-1}) and lag time (L, h) were determined. Data were analyzed by PROC MIXED considering the substrate and inoculum effects and its interaction. If interaction substrate*inoculum was significant simple main effect of inoculum was analyzed by the SLICE option. Interactions between inoculum and substrate were observed for a ($P < 0.001$), kd ($P = 0.011$) and L ($P = 0.002$). Inoculum from piglets produced more gas for all substrates incubated, except for corn, where gas production was similar among inoculum sources. Despite the fermentation rate was similar between inoculum sources, inulin fermentation rate was higher for piglets than for dogs (0.155 vs 0.099, $P < 0.001$). Lag times recorded were lower for ryegrass, citrus pulp, apple pomace, soy hulls and inulin when inoculum from dogs was used. In conclusion, inocula behaved different and it seems that piglets presented a microbiota more active to ferment substrates than that from dogs.

Key Words: hindgut fermentation, canine, swine

387 Prediction of voluntary feed intake in weaner pigs using physicochemical properties of bulky diets.

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Prediction of voluntary feed intake of growing pigs is crucial in the management and welfare of growing pigs; it facilitates the accurate formulation of feeds. The objective of the study was to predict maximum feed intake in weaner pigs using the physicochemical properties of bulky feeds. A total of 124 six-week-old pigs weighing 18.1 (SD 1.37) kg BW were given, ad libitum, diets containing 0, 80, 160, 240, 320 and 400 g/kg of either lucerne hay, maize cob, maize stover, saw dust, sunflower husks or grass hay. The basal feed contained 13.7 MJ digestible energy and 180 g of CP/kg DM. Each of the 31 diets was given to each of the 4 pigs, in individual cages, for 4 weeks. Properties of bulkiness measured were water holding capacity (WHC; g water/ g DM), bulk density (g DM/mL), neutral detergent fiber (NDF) and acid detergent fiber (ADF). Average daily feed intake was expressed per unit BW to determine scaled feed intake (SFI; g/kg/day) for each pig. Stepwise regression was used to identify significant physicochemical properties that affect SFI. Response surface regression was used to determine the relationship between SFI and each of the physicochemical properties of the bulky feeds. Water holding capacity, bulk density, NDF and ADF affected ($R^2 = 0.65$; $P < 0.01$) SFI. The SFI was quadratically related to WHC using the function $SFI = 19.1 (\pm 3.49) + 10.0 (\pm 1.61) WHC - 1.1 (\pm 0.17) WHC^2$ ($P < 0.01$). The SFI was also related ($P < 0.01$) to NDF and ADF by quadratic functions $SFI = 24.3 (\pm 3.55) + 0.1(\pm 0.23)NDF - 0.0001 (\pm 0.000036)NDF^2$ and $SFI = 30.2 (\pm 1.95) + 0.1 (\pm 0.02)ADF - 0.0003(\pm 0.000061)ADF^2$, respectively. Using differentiation, the gut capacity was attained when WHC = 4.76 g water/g DM, NDF = 367.12 g/kg DM and ADF = 138.50 g/kg DM, respectively. In conclusion, WHC, NDF and ADF contents are appropriate measures of bulkiness responsible for constraining intake of bulky feeds.

Key Words: bulky feeds, gut capacity, water holding capacity

Physiology and Endocrinology Symposium: The Current Status of Heat Shock in Early Embryonic Survival and Reproductive Efficiency

388 Influence of sire breed on heat stress tolerance of in vitro-produced bovine embryos. C. M. Barros* and R. A. Satrapa, *Department of Pharmacology, Institute of Biosciences, University of Sao Paulo State, Botucatu, Sao Paulo, Brazil.*

In bovine, hyperthermia reduces both quality and quantity of sperm in males and decreases fertility in females. The detrimental effects of heat stress on embryo development are critical during the first cleavage divisions, when most of the embryonic genome is inactive. However, as pregnancy advances the deleterious effects of heat stress on embryonic survival decrease. Several in vitro studies indicate that *Bos indicus* embryos are better able to survive heat stress at early stages of development and are more capable of originating pregnancies following heat stress than *Bos taurus* embryos. The evidence that embryonic genotype determines resistance to heat shock leads to the question as to whether embryos sired by *Bos indicus* breeds exhibit superior resistance to heat stress than those sired by *Bos taurus*. Contrary to previous reports, in one of our in vitro studies we found that Holstein oocytes fertilized with *Bos indicus* semen (Nelore breed) were more resistant to heat stress than those fertilized with *Bos taurus* (Angus) semen, suggesting that the sire breed influences embryo tolerance to heat stress. However, in this particular experiment, only 2 sires from each breed were used. Therefore, we suspected that the sire effect may have overshadowed the breed effect; that is, the better tolerance to heat shock was due to the bull itself and not to the breed of the bull. To minimize the bull effect, we repeated the same experiment using 6 sires from each breed. It was observed that sire breed did not influence embryo tolerance to heat stress. Overall these results indicate that the oocyte plays a more crucial role in the ability of the embryo to resist the effects of heat stress than the spermatozoa. Supported by FAPESP (Sao Paulo, Brazil).

Key Words: embryo, heat stress, IVF

389 Associations between heat shock protein 70 genetic polymorphisms and calving traits in crossbred Brahman cows. C. Rosenkrans Jr.*[1], M. Brown[2], H. Brown Jr.[1], and M. Looper[1], [1]*University of Arkansas, Fayetteville,* [2]*USDA-ARS, El Reno, OK.*

Stressors such as heat, cold, toxins, and oxygen deprivation are known to induce heat shock proteins. Genetic polymorphisms associated with heat shock protein genes have been associated with decreased male and female fertility. Our objectives were to 1) confirm single nucleotide polymorphisms (SNP) located in the promoter region of the bovine heat shock protein 70 (*Hsp*70) gene and 2) evaluate associations among *Hsp*70 SNP, breed, forage system, and lifetime calving rates of multiparous cows (n = 88). Angus (n = 22), Brahman (n = 30), and reciprocal crosses (n = 36) cows were assigned to and remained on their respective forage system for the duration of the experiment (8 years). Forage systems were endophyte-infected toxic tall fescue (E+) or common bermudagrass (CB). Genomic DNA was extracted from buffy coats of EDTA-treated whole blood. Primers HSP-Pro749F (GCCAGGAAACCAGAGACAGA) and HSP-Pro1268R (CCTACGCAGGAGTAGGTGGT) were used for PCR amplification of a 539-base segment of the bovine *Hsp*70 promoter (GenBank accession number M98823). Ten SNP were detected: 7 transitions (G1013A, n = 4; G1045A, n = 7; C1069T, n = 8; A1096G, n = 3; G1117A, n = 36; T1134C, n = 6; and T1204C, n = 65), 2 transversions (A1125C, n = 62; and G1128T, n = 34), and one insertion/deletion at base position 895 (C895D; n = 12). Minor alleles numerically were associated with Brahman cattle; however, G1117A was the only site associated ($P < 0.05$) with breed with minor allele frequencies of 11, 25, and 43% respectively for Angus, reciprocal crosses, and Brahman. Interaction ($P < 0.05$) between forage system and C895D genotype affected lifetime calving percentage (87, 86, 80, 85, and 20 for CC-CB, CD-CB, DD-CB, CC-E+, and DD-E+; respectively). A similar interaction ($P < 0.05$) was observed for G1117A and forage system. Homozygous guanine cows grazing E+ had lower ($P < 0.05$) lifetime calving rates when compared with GG cows grazing CB (76 vs. 90%). Our results demonstrate that Hsp70 promoter SNP will be useful in marker assisted management programs.

Key Words: cattle, *Hsp*70, tall fescue

390 Expression of heat shock protein genes and their splice variants in in vivo and in vitro bovine preimplantation embryos. H. Khatib,* *University of Wisconsin, Madison.*

Heat shock proteins (HSP) are among the first proteins produced during embryonic development and are essential to cell function. Their activities include folding, unfolding, transport, and localization of proteins and differentiation and regulation of the embryonic cell cycle. Although HSPs have been extensively studied in human and mouse, there is limited information on the roles of these genes in bovine embryos. As such, the objectives of this study were to profile the expression of HSP and their splice variants in bovine embryos (degenerates vs. blastocysts) and to carry out association analysis with fertility traits. Quantitative real time PCR analysis revealed significant differences in expression in degenerate embryos compared with blastocysts. Interestingly, all members of the HSP40 family were found to be upregulated in degenerates. Analysis of current bovine Ensembl data showed that 13 HSP genes have one transcript each, 2 genes have 2 transcripts each, and 2 have 3 transcripts each. The results indicate that some splice variants show differential expression between degenerates and blastocysts while others were not expressed at all in embryos, which implies different functions of these transcripts in embryonic development. In addition, the expression profiles of HSPs were compared between in vitro produced embryos and in vivo embryos. The most significant differentially-expressed genes were further investigated for association with fertility traits. Single nucleotide polymorphisms some HSP genes were found to be associated with blastocyst rate and fertilization rate. Collectively, results of the present study point to the important roles of HSPs in fertilization and early development of cattle embryos.

Key Words: heat shock protein, expression, alternative splicing

391 Consequences of heat shock on development of the preimplantation bovine embryo: Role of free radicals, antioxidants, apoptosis, and heat shock proteins. P. J. Hansen*[1] and M. Sakatani[2], [1]*University of Florida, Gainesville,* [2]*Kyushu-Okinawa Agricultural Research Center, National Agriculture and Food Research Organization, Kumamoto, Japan.*

The preimplantation embryo is one of the most sensitive of mammalian cells to hyperthermia. Exposure to temperatures as low as 40°C can reduce competence of the bovine embryo to continue development. Temperature sensitivity in at least some species (cow, sheep, pig) is

transient, however, and the embryo acquires resistance to elevated temperature (i.e., heat shock) as it advances through development. For the bovine embryo, there is little effect of heat shock on development after the 8-cell stage. Developmental acquisition of thermotolerance can be exploited to improve fertility in heat-stressed females through transfer of embryos at advanced stages of development. Experiments with the bovine indicate that developmental changes in embryonic sensitivity to heat shock are due to changes in several molecules and processes important for thermotolerance. Perhaps most important is the change in redox balance of the embryo. Heat shock can increase free radical production and the level of at least one antioxidant, glutathione, is lowest at early cleavage stages. Moreover, some antioxidants have been reported to increase embryonic resistance to heat shock in vitro. Apoptosis, if limited in extent, can be beneficial to embryonic survival after heat shock. Inhibition of apoptosis in embryos at d 4 or 5 of development increased the magnitude of heat shock effects on development. In this regard, it is instructive that the embryo does not gain the ability to undergo apoptosis in response to heat shock until about the 8–16 cell stage. The embryonic genome is also not fully activated until the 8–16 cell stage. The lack of transcription in early embryos may contribute to their thermal sensitivity because of the inability to produce proteins that stabilize cellular function. However, heat shock protein 70 (HSP70) is not likely to be a limiting protein in determining thermosensitivity. Levels of HSP70, as determined by immunofluorescence, are similar between 2-cell embryos and d 5 embryos. Heat shock can induce changes in HSP70 synthesis as early as the 2-cell stage. Moreover, steady-state mRNA for *HSP70* is higher for 1-cell and 2-cell embryos than for d 5 embryos. To date, a suitable treatment for increasing embryonic resistance to heat shock in the pregnant cow has not been identified but experiments with mice suggest that provision of a suitable antioxidant might enhance fertility of heat-stressed females.

Key Words: heat shock, embryo, bovine

Production, Management and the Environment: Beef Production

392 GPS/GIS technology in range cattle management. D. M. Anderson,* *USDA-ARS, Jornada Experimental Range, Las Cruces, NM.*

Animal-dominated landscapes are dynamic and not fully understood. Electronics were first employed in the mid-1970s to monitor free-ranging cattle behavior and its effect on forage utilization. By the mid-90s, satellite positioning systems were being used to monitor wildlife and had all but removed human observation from animal tracking. However, not until the end of the 90s did animal-borne satellite receivers catapult range cattle management into the world of microchip technology. This advent eliminated some challenges associated with terrestrial-based systems but added others, not the least of which has been how best to provide sustained power to animal-borne electronics. This question caused a conundrum for researchers deciding how to balance data collection rates with battery power drain because satellite-based systems have the potential to collect data in fractions of a second. To assist in interpreting the vast reservoirs of time-stamped positional data available, researchers began looking to biotic and abiotic information in the vicinity of the animal's geographical location to help explain the animal's behavior. Enter the Geographic Information System (GIS) with its origins in the late 50s and 60s. It provides hardware and software capable of capturing, storing, retrieving, manipulating, analyzing, and displaying geographically referenced data. By combining GIS and Global Positioning System (GPS) satellite data, researchers were given a robust way to accurately associate possible cause and effect relationships. Because of the complexity associated with electronically obtained data, it is mandatory that multifaceted teams be established from the onset not only to keep electronics operational but also to optimize the design, gathering, summarization, analyses, interpretation and application of data. Though electronics have replaced the drudgery and incompleteness of manual data gathering, electronics should never be used in an attempt to replace the art of human observation and discernment that ultimately provides the interpretation and application of field-based management.

Key Words: foraging, range animal ecology, animal tracking

393 Detection of pregnancy in Arizona range cattle using near infrared spectroscopy of feces. D. R. Tolleson* and D. W. Schafer, *University of Arizona, V Bar V Ranch, Rimrock.*

Near infrared spectroscopy (NIRS) of feces has been used to determine pregnancy in cattle but not in the southwestern US. Fecal constituents affected by pregnancy in amounts sufficient to affect near infrared spectra are yet to be identified. Crossbred beef cows (n ~375) were used to evaluate the ability of fecal NIRS to determine pregnancy under commercial ranch conditions in Arizona. All cows were synchronized using the 5-d CO-Synch+CIDR protocol in mid-June of 2011 and then turned out with bulls for 75 d. Fresh fecal samples from individually identified cows were collected off the ground in the pasture on the day of AI, 2 weeks later, and ~monthly thereafter until mid-October. Samples (n = 78) were frozen and later analyzed by NIRS. Pregnancy was determined by rectal palpation in mid-September and used to estimate day of pregnancy for each cow on the date feces were collected. Fecal spectra (1100 to 2500nm) were paired with the corresponding pregnancy values to create a discriminant calibration data set. Validation was accomplished with ~25% of the samples (n = 17) randomly selected and removed from the original 78. Previous research has identified 30 d of gestation as the minimum threshold for detection of pregnancy via fecal NIRS. Successful identification of cows greater than 30 d gestation was 4/5 (80%) and for cows not-pregnant, or pregnant less than 30 d was 8/12 (67%). Discrimination was also attempted for arbitrary groupings (A versus B) of the calibration set. This exercise yielded a validation success rate of 1/5 (20%) for group A and 7/12 (58%) for group B, respectively. The proportion of successful individual identifications for the biological (71%) versus arbitrary (47%) group validation was numerically greater ($X^2 = 1.94$, $P = 0.16$). A comparison between the observed and fecal NIRS predicted percent of the herd pregnant in late June, mid-July, mid-August, and mid-September was 0 versus 2, 34 versus 16, 63 versus 50, and 72 versus 79, respectively ($r^2 = 0.88$, $P = 0.06$). Herd pregnancy status of range beef cows was predicted well enough to inform forward planning for reproductive management.

Key Words: fecal, near infrared spectroscopy, pregnancy

394 Effect of beef heifer development system on ADG, reproduction, and feed efficiency during first pregnancy. A. F. Summers,* T. L. Meyer, S. P. Weber, and R. N. Funston, *University of Nebraska, West Central Research and Extension Center, North Platte.*

A 3-yr study was conducted to determine the effects of heifer development system on ADG, reproductive performance, and subsequent feed efficiency as a pregnant heifer. Crossbred Angus heifers (n = 299) were assigned by initial BW to graze corn residue (CR) or developed in a dry lot (DL). Corn residue heifers grazed native pasture 33 d before grazing CR 74 d. Corn residue heifers were then placed on dormant forage pastures 66 d and then with DL heifers for approximately 40 d for synchronization and AI. Heifers assigned to DL grazed dormant forage for 98 d and then placed in a DL for 112 d. The following winter a subset of pregnant CR and DL heifers (n = 114) were stratified by BW and development treatment, and placed in a Calan Broadbent individual feeding system for 84 d during late gestation. The remaining pregnant heifers were placed on CR. Prebreeding BW was greater ($P = 0.01$) for DL heifers compared with CR heifers (349 vs. 314 ± 9 kg). At pregnancy diagnosis BW remained greater ($P = 0.06$) for DL compared with CR heifers (422 vs. 403 ± 10 kg). Dry lot heifers had greater ($P = 0.01$) overall ADG during development compared with CR heifers. There was no difference ($P \geq 0.41$) in percent cycling (43 vs. 53 ± 15%), AI pregnancy (71 vs. 64 ± 6%), or final pregnancy rates (93 vs. 91 ± 3%) for CR and DL, respectively. However, CR heifers had greater ($P = 0.09$) ADG (0.77 vs. 0.64 ± 0.05 kg/d) from AI to pregnancy diagnosis compared with DL heifers. At the beginning of the second winter, DL heifers had greater ($P = 0.09$) BW compared with CR; however, pre-calving BW was similar ($P = 0.37$). Gestation length, calving date, and calf birth BW were similar ($P \geq 0.28$) between development treatments. During the individual feeding period, DL heifers had greater final BW compared with CR heifers (516 vs. 506 ± 9 kg). Dry matter intake and RFI were similar ($P \geq 0.39$) between treatments. Dry lot heifers had greater ($P \leq 0.05$) ADG (0.80 vs. 0.69 ± 0.14 kg/d) and G:F compared with CR. Heifers developed on CR had reduced BW through early pregnancy; however, reproductive performance was similar to DL developed heifers.

Key Words: beef cattle, feed efficiency, heifer development

395 Use of MTB-100, provided through a mineral mix, in a strategic supplementation plan to alleviate the effects of fescue toxicity when lactating beef cows graze endophyte-infected tall fescue.

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Sixty-three, 3 to 5 yr-old, Angus crossbred cows and their calves were used in a 3-yr study to evaluate response to strategic supplementation with a nutritional supplement produced from a carbohydrate-based toxin adsorbent (MTB-100, Alltech, Inc., Nicholasville, KY). MTB-100 was mixed with a complete mineral so daily intake was projected to be 0 or 20 g/cow. The experimental period extended from May 5 to Oct 2 and was divided into 3 strategic periods: P1 = May 5 to Jul 5; P2 = Jul 5 to Aug 18; P3 = Aug 18 to Oct 2. Treatments were either 0 or 20 $g\cdot hd^{-1}\cdot d^{-1}$ MTB-100 within a period (Trt 1 = 0, 0, 0; Trt 2 = 20, 0, 20; Trt 3 = 0, 20, 0; Trt 4 = 20, 20, 0; and Trt 5 = 20, 20, 20). In P1, 10 to 14 cow/calf pairs were managed in each of 9, endophyte-infected (>90%) KY 31 tall fescue pastures (re-randomized annually). On Jul 5 each year, pre-designated pairs were allotted to 21 individual, 1.6-ha plots of equivalent pasture and supplemented with either 0 or 20 $g\cdot hd^{-1}\cdot d^{-1}$ MTB-100, depending on treatment, until Oct 4. There was no significant effect of treatment on total cow weight changes from May 5 to Oct 4 (34, 38, 30, 35 and 35 kg for Trt 1, 2, 3, 4 and 5, respectively). Corresponding BCS changes were not significant. Overall, differences ($P < 0.10$) were found for rectal temperature changes. Calf gains for Trt 1 and 5 were 54 and 60 in P1 ($P < 0.10$), 47 and 56 in P2 ($P < 0.05$), and 24 and 22 kg ($P < 0.05$) in P3. Overall, calves receiving no MTB-100 (Trt 1) gained less (125 vs. 138 kg; $P < 0.10$) than calves receiving continual supplementation (Trt 5). Gains of calves receiving strategic supplementation during the 150 d (Trt 2, 3 and 4) were intermediate to gains of calves in Trt 1 and 5. These results show strategically invoked MTB-100^{TM} consumption, through a mineral mix available ad libitum, can increase performance of cows and calves grazing endophyte-infected tall fescue forage.

Key Words: fescue, cow/calf pairs, MTB-100

396 Effects of anti-phospholipase A2 antibody (aPLA2) supplementation on DMI, feed efficiency and blood differentials of steers fed forage and grain-based diets.

V. R. G. Mercadante*[1], K. M. Bischoff[1], G. H. L. Marquezini[1], J. D. Arthington[2], N. DiLorenzo[1], and G. C. Lamb[1], [1]*North Florida Research and Education Center, University of Florida, Marianna,* [2]*Range Cattle Research and Education Center, University of Florida, Ona.*

We determined whether supplementation of anti-phospholipase A2 antibody (aPLA2; BIG BEEF, Aova Technologies, Madison, WI) would alter voluntary DMI, feed efficiency (FE) and blood differentials (BD) due to a change in diet from a forage-based to a grain-based diet. Individual daily DMI was measured on 80 cross-bred steers during a 141 d period using a GrowSafe system (GrowSafe Systems Ltd., Alberta, Canada) at the University of Florida NFREC Feed Efficiency Facility. On d 0, steers were blocked by BW and assigned to receive a basal diet (0.97 Mcal NEg/kg of DM and 16% CP) comprised of 69% concentrate, 31% bermudagrass hay, and a vitamin and mineral supplement containing the following treatments: 1) no additive (CON; n = 20); 2) 30 mg of monensin and 8.8 mg of tylosin per kg of diet DM (MT; n = 20); 3) same as CON, but including aPLA2 at 0.4% of the diet DM (BB0.4%; n = 20); 4) same as CON, but including aPLA2 at 0.2% of the diet DM (BB0.2%; n = 20). On d 60 all steers were transitioned into a 90% concentrate diet (74% cracked corn; 1.32 Mcal NEg/kg of DM, 11.4% CP) over a 21-d "step-up" period while continuing to receive their supplement treatments. On d 0, d 60, d 81 and d 141 BW was recorded. Blood samples were collected on d 60, 63, 65, 67, 70, 72, 74, 77, 79, 81 and 84, and BD was assessed using a hematology cell counter (IDEXX ProCyte Dx Hematology Analyzer, Westbrook, ME). No differences existed for BW on d 0 (212 ± 34 kg), BW on d 141 (388 ± 46 kg), overall ADG (1.24 ± 0.16 kg/d), DMI (8.00 ± 0.94 kg/d), and residual feed intake (RFI). However, steers receiving the CON (0.34 ± 0.15 kg/d) treatment had greater ($P < 0.05$) RFI than the BB0.2% (−0.13 ± 0.15) and BB0.4% (−0.25 ± 0.15 kg/d) treatments, whereas the MT (0.06 ± 0.15 kg/d) treatment was intermediate. During the grain-based diet period, the BB0.2% (−0.12 ± 0.21 kg/d), BB0.4% (0.38 ± 0.21 kg/d), and MT (0.09 ± 0.21) steers tended ($P = 0.07$) to have greater RFI than the CON (−0.39 ± 0.21 kg/d) steers. During the step-up period the CON (7.09 ± 0.23 k/μL) and BB0.2% (7.62 ± 0.23 k/μL) treatments had greater ($P < 0.05$) concentrations of lymphocytes than the MT (6.73 ± 0.23 k/μL) and BB0.4% (6.73 ± 0.23 k/μL) treatments, and tended ($P = 0.06$) to have greater white blood cell counts (12.87 ± 0.42; 13.61 ± 0.42; 12.16 ± 0.42; 12.37 ± 0.42 k/μL for CON, BB0.2%, BB0.4% and MT, respectively;). We conclude that aPLA2 supplementation improved FE of steers fed forage-based diets and tended to reduce blood leukocyte concentrations when exposed to a transition into grain-based diets.

Key Words: feed efficiency, blood differentials, residual feed intake

397 Effects of acclimation to human handling on temperament, physiological responses, and performance of beef steers during feedlot receiving.

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The objective was to compare temperament, plasma concentrations of cortisol and acute-phase proteins, and performance during feedlot receiving of Angus × Hereford steers acclimated or not to human handling. Sixty steers were initially evaluated, within 30 d after weaning, for BW and temperament score (average chute score and exit velocity score; d −30). On d −28, steers were ranked BW and temperament score, and randomly assigned to receive or not (control) the acclimation treatment. During the acclimation phase (d −28 to 0), steers were maintained in 2 pastures according to treatment, and acclimated steers were exposed to a handling process twice weekly (Tuesdays and Thursdays). The acclimation treatment was applied individually to steers by processing them through a handling facility, whereas control steers remained undisturbed on pasture. On d 0, all steers were loaded into a commercial livestock trailer, transported for 24 h, and returned to the research facility (d 1). Upon arrival, steers were ranked by BW within treatment, and randomly assigned to 20 feedlot pens. Total DMI was evaluated daily from d 1 to d 28, and shrunk BW was collected on d −31, 1, and 29 for ADG calculation. Blood samples were collected on d −29, 0 (before loading), 1 (immediately upon arrival), 4, 7, 10, 14, 21, and 28 for determination of cortisol, ceruloplasmin, and haptoglobin. Steer temperament was assessed again on d 0 and 28. During the acclimation phase (d −28 to 0), no treatment effects were detected ($P = 0.14$) on steer ADG. Acclimated steers had reduced chute score compared with control on d 0 and 28 ($P \leq 0.01$). During feedlot receiving (d 1 to 28), acclimated steers had reduced ADG ($P < 0.01$), DMI ($P = 0.07$), and G:F ($P = 0.03$) compared with control. Acclimated steers had greater plasma cortisol on d 1 ($P = 0.06$), greater haptoglobin on d 4 ($P = 0.04$), and greater ceruloplasmin from d 0 to 10 ($P \leq 0.04$) compared with control. In conclusion, steers exposed to the acclimation process had greater stress-induced cortisol and acute-phase protein responses, resulting in decreased performance during feedlot receiving.

Key Words: steers, handling, feedlot

398 Effects of 24-h transport or 24-h nutrient restriction on acute-phase and performance responses of feeder cattle. R. S. Marques*[1], R. F. Cooke[1], C. L. Francisco[1,2], T. Leiva[1], F. Sanches[1], A. Bouck[1], F. N. T. Cooke[1], and D. W. Bohnert[1], [1]*Oregon State University, EOARC, Burns,* [2]*Universidade Estadual Paulista - FMVZ/DPA, Botucatu, SP, Brazil.*

The objective was to compare acute-phase and performance responses of weaned beef calves exposed to transport or nutrient restriction. Angus × Hereford steer (n = 30) and heifer (n = 15) calves were balanced by sex and BW, and randomly assigned to 15 pens on d −12 of the experiment. On d 0, pens were randomly assigned to 1 of 3 treatments: 1) transport for 24 h in a livestock trailer (TRANS); 2) no transport, but feed and water deprivation for 24 h (REST); or 3) no transport and full access to feed and water (CON). Treatments were concurrently applied from d 0 to 1. Total DMI was evaluated daily from d 1 to d 28. Full BW was recorded before treatment application and at the end of experiment. Blood samples were collected on d 0, 1, 4, 7, 10, 14, 21, and 28. Mean ADG was greater ($P < 0.01$) in CON vs. TRANS and REST calves, but similar ($P = 0.46$) between TRANS and REST calves. No treatment effects were detected on DMI, but CON had greater G:F vs. TRANS ($P < 0.01$) and REST calves ($P = 0.08$), whereas G:F was similar ($P = 0.21$) between TRANS and REST calves. Plasma cortisol concentrations were greater ($P \leq 0.05$) in REST vs. CON and TRANS calves on d 1, 4, 7, 14, 21, and 28, and tended to be greater ($P = 0.10$) in TRANS vs. CON calves on d 1. Serum NEFA was greater ($P < 0.01$) in REST and TRANS vs. CON calves on d 1, but also greater ($P < 0.01$) in REST vs. TRANS calves on d 1. Plasma ceruloplasmin peaked on d 4 for TRANS and REST calves (day effects; $P < 0.01$) but did not change ($P = 0.58$) for CON calves. Hence, CON calves had reduced mean plasma ceruloplasmin concentration vs. TRANS ($P = 0.07$) and REST ($P = 0.01$) calves. Plasma haptoglobin peaked on d 1 for TRANS and increased from d 1 to 14 in REST calves (day effects; $P < 0.01$) but did not change ($P = 0.65$) for CON calves. Hence, TRANS calves had greater plasma haptoglobin vs. CON and REST calves on d 1 ($P < 0.01$), whereas REST calves had greater ($P \leq 0.05$) plasma haptoglobin vs. TRANS and CON calves on d 7. In conclusion, 24-h transport and 24-h nutrient restriction elicited acute-phase protein reactions, and similarly reduced performance of feeder cattle.

Key Words: cattle, nutrient restriction, transport

Ruminant Nutrition: Beef Production II

399 Precision processing barley grain improves the feeding value of barley grain in beef cattle. W. Z. Yang*[1], M. Oba[2], and T. A. McAllister[1], *[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.*

The objectives of this study were to determine the effects of barley grain quality and precision processing (processing based on kernel size and volume weight) on DMI, ruminal pH and fermentation, and apparent total tract digestibility in steers. Eight ruminally cannulated steers were used in a replicated 4 × 4 Latin square design with 21-d periods. The 4 treatments were: 1) light barley (LB); 2) heavy barley (HB), LB and HB processed optimally with processing index ranging 75 to 80%; 3) LB and HB precision processed and mixed in equal proportions (PP); and 4) LB and HB mixed in equal proportions then processed at a single roller setting (industry standard; CON). All diets consisted of 10% barley silage, 67% barley grain, 20% corn DDGS and 3% supplement (DM basis). DMI was greater ($P < 0.04$) for steers fed LB than for HB (13.2 vs. 12.2 kg/d) with greater ($P < 0.01$) NDF intake (4.0 vs. 2.8 kg/d) but less ($P < 0.01$) starch intake (4.7 vs. 5.8 kg/d). Intakes of DM, NDF and starch were greater ($P < 0.04$) for PP (13.0, 3.6 and 5.4 kg/d, respectively) than for CON (12.0, 3.3 and 5.0 kg/d, respectively). There were no differences in mean ruminal pH (5.82 to 5.89) or in the duration of pH < 5.8 (9.9 to 11.5 h) and pH < 5.5 (5.0 to 6.6 h) between LB and HB, or PP and CON. Ruminal NH3-N (9.5 to 10.3 mM) and total VFA concentrations (122 to 133 mM), and VFA profile were not affected by treatment. Digestibility of DM was lower ($P < 0.05$) for LB than HB (68 vs. 72%), whereas that of CP, NDF, ADF and starch was not different. Digestibility of DM, CP and ADF was greater ($P < 0.05$) for PP (74, 73 and 48%, respectively) than CON (70, 68 and 39%, respectively). These results suggest greater feed efficiency with HB than with LB due to less DMI and greater digestibility. This work demonstrates that precision processing can be used to improve the utilization of barley grain with variable kernel uniformity by beef cattle.

Key Words: feedlot cattle, precision processing, ruminal pH and fermentation

400 Effect of rumen degradable energy source on performance and forage intake of steers grazing stockpiled crested wheatgrass pasture. F. Anez*[1], J. J. McKinnon[1], H. A. Lardner[1,2], G. B. Penner[1], and P. G. Jefferson[1,2], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

The objective of this experiment was to determine the effects of supplementing blended by-product pellets that differed in starch and degradable fiber content on performance of steers grazing mature crested wheatgrass (CWG). Forty-five yearling crossbreed steers (334 ± 3.5 kg) stratified by BW were randomly assigned to 1 of 9 CWG pastures (5 steers/pasture). Each pasture was randomly assigned (n = 3), in a completely randomized design, to 1 of 3 treatments: no supplement (Control); low-starch high-degradable fiber (LSHDF; 40.3% starch; 29.5% NDF on DM basis) pellet and high-starch low-degradable fiber (HSLDF; 48.6% starch; 22.8% NDF on DM basis) pellet, both fed daily at 0.6% BW. The grazing period lasted 70 d (from late-July to mid-October). Forage utilization and DMI were estimated using the double weigh (before and after grazing) technique. Forage samples were clipped every 2 wk and analyzed for DM, CP, ADF and NDF. Steers were weighed on 2 consecutive d at the beginning and end, and every 14 d throughout the trial. Ultrasound rib-fat thickness was also measured at the beginning and end of trial. Over the 70-d study, forage CP decreased from 9.9 ± 0.82 to 6.9 ± 0.59% of DM and digestible energy content decreased from 2.6 ± 0.04 to 2.2 ± 0.04 Mcal/kg DM. Treatment did not affect forage utilization ($P = 0.50$; 73.4 ± 3.15%) or DMI ($P = 0.90$; 9.0 ± 1.54 kg/d). Final BW and ADG were not different ($P > 0.05$) between LSHDF (435 ± 6.4 kg and 1.4 ± 0.10 kg/d) and HSLDF (439 ± 10.4 kg and 1.5 ± 0.14 kg/d). However, cattle fed pellets had higher ($P < 0.05$) final BW and ADG than the control cattle (402 ± 5.6 kg and 1.0 ± 0.09 kg/d). No effect of treatment ($P > 0.05$) was noted on rib fat. These results show that beef steers grazing mature CWG were limited in energy intake and that supplementation of metabolizable energy in the form of starch or degradable fiber equally improved performance.

Key Words: crested wheatgrass, by-products, grazing steers

401 Effects of sugarcane fiber digestibility and concentrate level on intake and growth of finishing Nellore bulls. B. S. Mesquita, D. O. Souza, J. F. Penso, M. H. A. Santana, J. B. S. Ferraz, and L. F. P. Silva,* *Universidade de São Paulo, Pirassununga, SP, Brazil.*

Sugarcane has low fiber digestibility, one of the main factors limiting beef cattle performance. The objective of this study was to evaluate the effects of sugarcane stalk fiber digestibility and of concentrate level on intake, growth and carcass fat of finishing Nellore bulls. Forty-eight Nellore bulls (319 ± 9.2 kg of BW) were blocked by BW and assigned to 4 treatments in a 2 × 2 factorial arrangement in a randomized complete block design. Treatments were as follows: sugarcane genotype IAC2480 (greater stalk NDF digestibility) as roughage source fed at 20 or 40% of total DM, or sugarcane genotype IAC2094 (lower stalk NDF digestibility), fed at 20 or 40% of total DM intake (n = 4 pens for each of the 4 treatments). Diets were formulated to provide daily gain (ADG) of 1.2 kg/d (40% sugarcane) or 1.4 kg/d (20% sugarcane), and contained freshly cut sugarcane as the sole forage. Sugarcane IAC2480 stalk contained 42% NDF with 15% 30h-NDF digestibility, and sugarcane IAC2094 stalk contained 41.5% NDF with 6.5% 30h-NDF digestibility. Animals were fed ad libitum maintaining a minimum of 10% orts in each pen. Dry matter intake was determined daily, and animals were weighed every 14 d after 16h of fasting. Main effects of sugarcane genotypes (CANE), of level of concentrate (CONC), and their interaction were tested by ANOVA. Feeding sugarcane with higher NDF digestibility increased dry matter intake as a percentage of BW (2.24 vs. 2.12 ± 0.08%, $P = 0.04$) and subcutaneous carcass fat (4.6 vs. 3.1 ± 0.4 mm, $P < 0.01$). There were no significant effects of level of concentrate or of CANE × CONC interaction on these variables. Regarding ADG, there was a CANE × CONC interaction ($P = 0.03$), where sugarcane with higher NDF digestibility increased ADG only when fed at 20% of DM (1.80 vs. 1.52 ± 0.09 kg/d, $P = 0.005$), and not when fed at 40% DM (1.57 vs. 1.59 ± 0.09 kg/d, $P = 0.87$). Feeding finishing bulls a diet containing sugarcane with greater stalk NDF digestibility increased DM intake and subcutaneous fat, regardless of concentrate level. Higher NDF digestibility also increased ADG, but only when fed at 20% of total DM.

Key Words: cattle, fiber digestibility, sugarcane

402 High dietary sulfur decreases apparent absorption of copper and manganese by steers. D. J. Pogge, M. E. Drewnoski,* and S. L. Hansen, *Iowa State University.*

The antagonism between S and Cu in ruminants is well established. However, the potential antagonism between high dietary S in concentrate-based diets and the divalent trace minerals Mn and Zn has not been extensively explored. Ruminal metabolism of sulfate can lead to the production of sulfide. Sulfide has the potential to bind divalent minerals and make them less available for absorption. To examine the effect of dietary S on apparent absorption and retention of Cu, Mn, and Zn, 16 steers (8 cannulated; 355 kg; and 8 unmodified; 386 kg) were used in a 2 × 2 factorial design with the 2 factors being modification status and dietary treatment. Dietary treatment consisted of a low sulfate (0.2% S; LS) wheat midd-based pellet or LS plus sodium sulfate added at 2% of DM to achieve a high sulfate (0.7% S; HS) pellet. Steers were blocked to pairs by modification status and BW and pair-fed between treatments. The HS steers were fed 110% of the previous day's intake of pellets and the LS steers were pair-fed 105% of their HS counterpart. All steers were fed chopped bromegrass hay at 5% of pellet intake. Steers were adapted to metabolism crates for 4 d, stepped up to a high concentrate diet for 7 d, and after an additional 7 d ad libitum intake period apparent mineral absorption and retention were determined over 5 d in which all urine, feces, and orts were collected. By design, DMI did not differ ($P = 0.55$) between treatments during the collection period (5.8 and 5.6 kg, for LS and HS, respectively). Apparent absorption of Cu was greater ($P < 0.05$) in LS (34.5%) compared with HS (17.9%). Apparent absorption of Mn was also greater ($P < 0.05$) in LS steers (20.4%) vs. HS steers (10.1%); however, apparent absorption of Zn did not differ ($P = 0.17$; 17.3 vs. 12.1% for LS and HS, respectively). These data suggest that high dietary S cannot only negatively affect absorption of Cu but also absorption of Mn, and because both of these minerals are essential to antioxidant enzymes long-term feeding of high S diets may increase the risk of oxidative stress in cattle.

Key Words: cattle, copper, manganese

403 Comparison of receiving strategies on feedlot performance in beef calves at weaning. K. L. Neuhold*[1], J. K. Ahola[1], C. W. Shonk[1,2], T. E. Engle[1], and J. J. Wagner[1,3], [1]*Colorado State University, Fort Collins,* [2]*Agriculture, Research, Development and Education Center, Wellington, CO,* [3]*Southeast Colorado Research Center, Lamar.*

One hundred twenty-four newly weaned Angus, Hereford, and Angus × Hereford bull and heifer calves (initial BW = 233 ± 14.9 kg) were utilized to evaluate the effects of 2 feedlot receiving management strategies at Colorado State University's Agriculture, Research, Development and Education Center in Wellington, CO on feedlot performance over the first 30 d upon arrival to the feedlot. Cattle were blocked by sex and stratified by weight, breed, and age, and assigned to one of 14 pens (8 - 10 head/pen). Pens were then assigned to one of 2 dietary treatments. Dietary treatments included: 1) dried distiller's grain-based total mixed ration (TMR) initiated upon arrival (DDG), or 2) long-stem grass hay followed by a TMR containing no DDG (HAY). Calves receiving the HAY treatment received only grass hay for the first d after arrival, long stem grass hay and TMR combination the following 2 d, and a grain-based TMR on d 4. Beginning on d 4, calves across all treatments were fed once a d and had access to iso-caloric and iso-nitrogenous diets. Calves were weighed on d 0 and 30, and DMI was determined daily. Initial BW was similar ($P = 0.99$) across treatments; however, d 30 BW was greater ($P < 0.001$) for DDG vs. HAY calves. As a result, ADG was greater ($P < 0.001$) for DDG vs. HAY calves (0.59 vs. 0.41 ± 0.042 kg/d, respectively). Gain-to-feed ratio was greater ($P < 0.05$) for DDG vs. HAY calves (0.22 vs. 0.17 ± 0.013, respectively), and feed-to-gain ratio tended ($P = 0.05$) to be greater in HAY vs. DDG calves. Daily DMI tended ($P = 0.06$) to be greater in DDG vs. HAY calves (2.70 vs. 2.35 ± 0.256 $kg \cdot hd^{-1} \cdot d^{-1}$, respectively). In summary, providing a DDG-based receiving ration to newly weaned calves upon arrival to the feedlot resulted in greater feed intake, gain, and feed efficiency over a 30 d period than traditional long-stemmed grass hay followed by a non-DDG TMR.

Key Words: feedlot performance, receiving diet, weaning

404 Determining the influence of dietary NDF concentration from bromegrass hay on performance of steers fed high sulfur diets. S. J. Morine,* M. E. Drewnoski, and S. L. Hansen, *Iowa State University, Ames.*

Feedlot cattle are often fed co-products from ethanol production that are rich in protein and energy but high in sulfur (S). Excess sulfate, when fed to ruminants, is reduced to sulfide by ruminal bacteria. Rumen sulfide can be converted to hydrogen sulfide (H_2S) in a pH dependent process. Elevated ruminal H_2S has been correlated to S toxicity. The objective of this study was to determine the effect of feeding 5 dietary concentrations of NDF from chopped bromegrass hay (66% NDF) on cattle performance, rumen pH, and H_2S concentration of steers fed a high S diet. One hundred fifty steers (359 ± 4.9 kg) were fed 1 of 5 diets that included 3.5, 5.7, 7.9, 10.1, or 11.4% added roughage NDF (rNDF) from bromegrass hay and contained 0.5% dietary S, from a combination of distillers grains and condensed corn solubles. In all diets hay was added at the expense of corn. Steers were blocked by weight into pens of 5 and then randomly assigned within block to 1 of the 5 treatments (n = 6 pens per treatment). Effective NDF was linearly increased ($P < 0.01$) with increased inclusion of rNDF. The addition of roughage did not appear to negatively affect cattle performance as ADG did not differ ($P = 0.55$) between treatments (2.01 ± 0.05 kg/d). Intake linearly increased ($P = 0.02$) with the increased inclusion of rNDF and gain to feed was linearly decreased ($P = 0.01$) with the increased inclusion of rNDF. At 6 h post-feeding ruminal H_2S concentrations were linearly decreased ($P < 0.01$; 7365, 6290, 5568, 5148, and 4528 ppm for 3.5, 5.7, 7.9, 10.1, and 11.4% rNDF, respectively) and pH was linearly increased ($P < 0.01$; 5.48, 5.64, 5.75, 5.75 and 5.79 for 3.5, 5.7, 7.9, 10.1, and 11.4% rNDF, respectively) by the increased inclusion of rNDF. Ruminal pH and H_2S data were negatively correlated ($R = -0.48$; $P < 0.01$). The results of this study suggest that inclusion of hay up to 11.4% rNDF will not decrease cattle gain and will manage the ruminal pH and decrease H_2S concentrations, thus reducing the risk of S toxicity.

Key Words: cattle, roughage, sulfur

405 Effects of method of forage finishing and cattle breed on growth performance, carcass characteristics, meat quality, and fatty acid composition. L. Shepherd*[1], R. Berthiaume[2], C. Lafreniere[3], C. Campbell[1], L. Pivotto[1], and I. Mandell[1], [1]*Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada,* [2]*Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada,* [3]*Agriculture & Agri-Food Canada, Kapuskasing, ON, Canada.*

Three methods of forage finishing (pasture, silage, hay) were used to evaluate growth performance, carcass traits, meat quality, and fatty acid composition relative to a grain finished product. 100 Angus (AN) and 100 Hereford (HE) steers were allocated to 2 research stations (each station feeding 50 head from each breed), with one location evaluating alfalfa (Alf) forages while the other station evaluated grass forages.

Regardless of location, growth performance (total gain, average daily gain, feed:gain) and carcass traits (hot carcass weight (HCW), backfat depth) were greater ($P < 0.03$) for cattle fed a high grain (HG) diet vs. forage finishing. Feeding the HG diet decreased ($P < 0.03$) lean yield vs. forage finishing. Within forage treatments, gains were greater ($P < 0.03$) for pasture vs. conserved forages due to poor nutritional quality for the hays at either location. Carcass traits were similar ($P > 0.40$) across method of forage finishing Alf, apart from lower ($P < 0.09$) HCW for conserved forages vs. pasture finishing. Carcass traits were similar ($P > 0.19$) between grass pasture- and grass silage-fed cattle, while no steers fed grass hay were slaughtered due to poor performance. A trained taste panel found HG beef to be more tender ($P < 0.09$) vs. cattle fed Alf and numerically more tender ($P > 0.12$) vs. cattle fed grass forages Forage finished beef (Alf or grass) had less beef flavor ($P < 0.02$) and increased off flavor ($P < 0.01$) vs. HG beef. Palatability traits were generally similar across method of forage finishing. Omega 3 fatty acids and PUFA were greater ($P < 0.001$) in forage finished vs. HG beef. Linolenic acid content was higher ($P < 0.013$) in grass and Alf finished beef vs. HG beef. Generally, no breed differences existed in palatability traits at either location. Linolenic acid levels were greater ($P < 0.001$) in beef from cattle fed conserved Alf vs. Alf pasture. While palatability traits may be similar regardless of method of forage finishing, differences in fatty acid levels across method of forage finishing may affect nutrient composition claims about grass-fed beef.

Key Words: beef cattle, forage finishing, palatability traits

406 Evaluation of weight gain pattern between 7 and 18 months of age of Hereford heifers and reproductive performance when mated at 18 months of age.

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The objective of this study was to evaluate the average ADG, BW, rump fat thickness (RFT) and pregnancy rate in Hereford heifers at 18 mo of age originated from a commercial cattle herd at a facility in state Rio Grande do Sul, Brazil. Three different levels of ADG (high - H, moderate - M and low - L) with 3 different combinations (LHM; HLL; MMH) were considered. These ADG levels were applied between 7 to 12 mo (P12); 12 to 15 mo (P15) and 15 to 18 mo of age (P18). The heifers were mated by natural service without synchronization of estrus for 60 d. Used to the LHM, MMH, and HLL treatments 65, 58, and 60 heifers respectively. The overall pattern of gain during the study period was different for each treatment. The animals had the same initial (171 kg) and final (312 kg) BW. The heifers submitted to the HLL treatment presented higher gains than the rest ($P = 0.09$). These animals probably presented compensatory growth. The heifers in MMH treatment, which had the highest BW at 12 mo of age, also had higher pregnancy rate than the heifers in LHM treatment. At the beginning of mating BW was similar between both MMH and LHM treatments. The combination of the BW gain in the winter (19.5 kg during 148 d or ADG of 0.131 kg/d) allowed compensatory gain in the spring and high BW gain before mating which were the factors that determined the highest pregnancy rate (94.8%) in heifers of the MMH treatment. The MMH treatment also had the highest BW (315 kg) at the end of post-weaning period. At the beginning of the mating, the RFT was different among the treatments. The pregnancy percentage was higher for heifers the MMH treatment, which had higher RFT associated with the intermediary BW gain at the beginning of the experimental period P12. The RFT at the beginning of the mating did not differ among heifers in the MMH and LHM treatments (2.19 and 1.96mm, respectively) and heifers in the HLL treatment (1.53mm) it was low, ($P < 0.05$) indicating that the backfat thickness at the mating was accumulated lately during the rearing and the fat precociously deposited during P12 could be mobilized. Considering the observed results, the MMH sequence of body weight gain between the 7 and 18 mo of age increased the pregnancy rate and the RTF of heifers mated at the age of 18 mo.

Key Words: body weight, pregnancy rate, rump fat thickness

407 Evaluation of feed efficiency and feeding behavior traits in performance tested bulls.

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Objectives of this study were to characterize feed efficiency traits and examine phenotypic relationships with feeding behavior traits in bulls. Performance, feed intake and feeding behavior traits were measured in bulls (n = 5,073) representing 11 breeds (3,335 Angus). Intake and feeding behavior traits were measured for 70 d using a GrowSafe system while fed a corn silage based diet (ME = 2.42 Mcal/kg DM). BW was measured at 14-d intervals. Residual feed intake (RFI) was calculated as the difference between actual DMI and that expected from regression of DMI on mid-test $BW^{0.75}$ (MBW) and ADG, and residual gain (RG) as the difference between actual ADG and that expected from regression of ADG on MBW and DMI. Both models included fixed effects of trial (n = 12) and breed. A 2-population distribution model was fit to $\log_{10}$-transformed interval lengths between bunk visit events to estimate meal criterion, and compute meal traits. As expected, RFI was correlated with DMI ($r = 0.52$, $P < 0.0001$) but not MBW or ADG, whereas, RG was correlated with ADG ($r = 0.72$, $P < 0.0001$) but not MBW or DMI. RFI was positively correlated with F:G ($r = 0.35$, $P < 0.0001$) and negatively correlated with RG ($r = -0.44$, $P < 0.0001$). Initial BW was weakly correlated with F:G ($r = 0.15$, $P < 0.0001$) and RG ($r = -0.11$, $P < 0.0001$) but not RFI, indicating that lighter bulls were more efficient based on F:G and RG. Feeding bout (FB) frequency and duration were correlated with RFI ($r = 0.30, 0.26$; $P < 0.001$), but were not significant or weakly correlated ($r < 0.10$) with RG and F:G. Meal criterion and duration were both correlated ($r = -0.07, 0.18$; $P < 0.0001$) with RFI, but not with RG or F:G. Bulls with low RFI spent less time at the feed bunk (118 vs 133 ± 0.80 min/d) and had fewer FB events (75 vs 89 ± 0.6 events/d) then high-RFI bulls. Low-RFI bulls had longer ($P < 0.001$) meal criterion (11.3 vs 10.6 ± 0.2 min) indicating they took longer to initiate new meals, and had longer meal durations (216 vs 233 ± 1 min/d) than high-RFI bulls. Bulls have distinctive feeding behavior patterns that contribute to between-animal variation in RFI. However, feeding behavior traits were not associated with between-animal variance in F:G or RG.

Key Words: feeding behavior, residual feed intake, residual gain

408 Ergot alkaloids decrease rumen epithelial blood flow.

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Ergot alkaloids induce vasoconstriction of peripheral and core body vasculature resulting in altered blood flow. An experiment was conducted to determine if ergot alkaloids affect blood flow to the absorptive surface of the rumen. Steers (n = 8) were pair-fed alfalfa cubes at 1.5 × NE_m and received ground endophyte-infected tall fescue seed (E+; 0.015 mg ergovaline·kg $BW^{-1}·d^{-1}$) or endophyte-free tall fescue seed (E-) via rumen cannula 2 × daily for 7 d at thermoneutral (TN; 21°C) and heat stress (HS; 32°C) conditions. On d 8 the rumen was emptied and rinsed with tap water and saline. Buffer containing VFA was incubated in the following sequence: control (CON), 0.015 mg ergovaline/kg BW (1 × EXT), and 0.045 mg ergovaline/kg BW (3 × EXT). Ergovaline in the buffer was supplied as a seed extract solubilized in methanol. For each buffer treatment there were 2 30-min incubations; a 30 min incubation of a treatment buffer with no sampling followed by removal of the buffer and incubation of an identical sampling buffer with the addition of Cr-EDTA and D_2O. Epithelial blood flow was estimated as ruminal clearance of D_2O corrected for influx of physiological water and liquid outflow. Feed intake data was analyzed as a CRD. Blood flow data was analyzed as a split plot with a whole plot factorial of seed and temperature and buffer treatment was the subplot factor using a mixed model. Feed intake decreased with dosing E+ at HS but not at TN ($P = 0.016$). Seed treatment did not affect rumen epithelial blood flow ($P = 0.73$). Inclusion of the seed extract in the buffer caused a 50% reduction in epithelial blood flow ($P < 0.0001$) but there was no difference between 1 × EXT and 3 × EXT ($P = 0.53$). The 3 × EXT tended to reduce blood flow more at TN than HS ($P = 0.11$). Chronic exposure to ergot alkaloids through dosing steers with E+ seed did not alter rumen epithelial blood flow. However acute exposure through inclusion of ergot alkaloids in the washed rumen buffer did decrease rumen epithelial blood flow indicating that gut vasculature responds to acute alkaloid exposure and nutrient absorption could be decreased.

Key Words: blood flow, washed reticulorumen

409 Feeding distillers grains as an energy source to gestating and lactating beef heifers: Effect on feedlot performance, carcass characteristics, and glucose tolerance of steer progeny.

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Angus-cross beef heifers pregnant to a single sire (n = 80) were used to assess the effects of feeding dried distiller′s grains with solubles (DDGS) as an energy source during late gestation and early lactation on feedlot performance, carcass characteristics, and glucose tolerance of male progeny. From 192 d of gestation through 118 ± 0.2 d of lactation, dams were fed either a control diet of corn silage and haylage (CON; 10% CP prepartum; 11.8% CP postpartum) or corn stover and DDGS (DG; DDGS at 1.2% BW per d; 15.7% CP) diet. Male progeny (n = 36) were weaned, commingled, and started on a step-up diet at 186 ± 0.2 d of age. At 210 ± 0.2 d of age, steers were placed in individual pens and fed a diet devoid of DDGS (12.7% CP, 1.36 kcal/kg NEg on DM basis) once daily for ad libitum consumption. Steer weights and back fat measurements via ultrasound were recorded on 21-d intervals. At 520 ± 38 kg, a subsample of 20 steers was selected for intravenous glucose tolerance testing (IVGTT). Steers were harvested at a common 12th rib fat depth of 1.41 ± 0.22 cm. Carcass characteristics were determined following a 72-h chill. Categorical and continuous data were analyzed with the GLIMMIX and MIXED procedures of SAS, respectively. Weaning wt, feedlot entry wt, slaughter wt, slaughter frame score, days on feed, and feedlot performance parameters including ADG, DMI, and G:F did not differ due to maternal diet ($P \geq 0.11$). Steer IVGTT parameters including fasted, average, and peak glucose and insulin concentrations, and area under the curve did not differ ($P \geq 0.24$) between treatments. Furthermore, HCW, back fat, LM area, KPH, yield grade, marbling score, quality grade, and proportion of Certified Angus Beef carcasses did not differ ($P \geq 0.18$) between treatments. Dressing percent, however, tended to be greater ($P = 0.08$) in DG (59.2%) than CON (58.5%) progeny. In summary, feeding DG at 1.2% of BW per d to first-parity heifers did not affect post-weaning performance, carcass characteristics or glucose tolerance of steer progeny.

Key Words: DDGS, developmental programming, steer

410 Effects of roughage concentration in dry-rolled corn-based diets containing wet distillers grains with solubles on performance and carcass characteristics of finishing beef steers.

K. E. Hales* and H. C. Freetly, *USDA, ARS, US Meat Animal Research Center, Clay Center, NE.*

Distillers grains and distillers solubles are by-products of grain fermentation used to produce ethanol and contain relatively high concentrations of NDF and ADF compared with other grains and concentrates it replaces in feedlot diets. Typical finishing diets in the US contain 8.3 and 9.0% roughage in the summer and winter months, respectively. Therefore, it is plausible that the dietary concentration of roughage can be altered when distillers grains are included in feedlot diets. The effects of roughage concentration in dry-rolled corn-based diets containing wet distillers grains with solubles (WDGS) were evaluated in MARC II steers (n = 128, initial BW = 339 ± 6.51 kg) using Calan gates. Diets consisted of 25% WDGS and the balance being dry-rolled corn and coarsely ground alfalfa hay (AH) replacing corn at 2 (AH-2), 6 (AH-6), 10 (AH-10), and 14% (AH-14) of dietary dry matter. Daily feed offered was recorded, feed refusals were measured weekly, and BW was measured on d 0, 1, 35, 70, 105, 140, 174, and 175. At harvest, camera data were collected. The data were analyzed using the Mixed procedure of SAS. The fixed effect of treatment was included in the model. Decreasing concentrations of AH in the finishing diet resulted in no differences in final BW ($P = 0.18$), but a tendency for ADG ($P = 0.06$) to be greater when steers were fed intermediate concentrations of AH (6 and 10%) than AH-2 and AH-14. Steers consuming AH-2 had a lower DMI ($P = 0.04$) than steers consuming AH-6, AH-10, or AH-14; whereas, G:F was greater for steers consuming AH-2, AH-6, and AH-10 than AH-14 ($P < 0.01$). Concentration of AH in the finishing diet did not affect HCW, LM area, marbling score, or the proportion of cattle grading USDA choice ($P \geq 0.32$); however, dressing percent was greater for steers fed AH-2 and AH-14 than AH-6 and AH-10 ($P = 0.04$). Results indicate that decreasing AH to 2% in a finishing diet based on dry-rolled corn with WDGS may not affect ADG, but does decrease DMI which results in an increased G:F. USDA is an equal opportunity provider and employer.

Key Words: cattle, distillers grains, roughage

Ruminant Nutrition: Dairy Production III

411 Impacts of feeding a citrus extract on measures of heat stress, as well as production, of high producing dairy cows during summer heat. J. M. Soderstrom*[1], P. H. Robinson[1], and J. M. Clauzel[2], [1]*Department of Animal Science, University of California-Davis, Davis,* [2]*Phodé Laboratoires, Terssac, France.*

High somatic cell counts (SCC) in milk result from degraded mammary health and negatively affect animal performance and milk quality. Citrus by-products are high in antioxidants (i.e., vitamin C) and essential oils (e.g., limonene), both of which have positive effects on animal health. We determined effects of feeding an orange extract (OE) to high producing dairy cows on measures of heat stress as well as milk production and composition, including SCC. A replicated 2 × 2 Latin square experiment was conducted with two 28-d periods on a dairy farm near Hanford (CA) in summer 2011 with 4 high group pens (i.e., cows which had cleared the fresh pen but not yet confirmed pregnant), each with ~310 early lactation multiparity cows. Total mixed rations (TMR; based on alfalfa hay, almond hulls, canola meal, distillers dried grains with solubles, corn silage, corn grain and cottonseed, with 17% crude protein (CP), 5.4% fat, 33.4% neutral detergent fiber (NDF) and 13.4% starch were identical except for inclusion of orange extract (Veo Premium, Phodé, Terssac, France) at 4 g/cow/d in the treatment TMR (OE). Due to seasonally mild ambient temperatures (i.e., highs 31–34°C; lows 16–17°C), cows showed only mild heat stress. Feeding OE had no effect on indicators of heat stress (i.e., respiration rate, panting score, rump temperature) at anytime (i.e., 02:45, 09:15, 17:30). However at 02:45 h, a higher ($P < 0.01$) proportion of OE cows were lying (vs. standing) vs. control cows (68.6 vs. 53.7%), a possible indicator of reduced heat stress. DM intake (avg. 25.3 kg/d) and whole tract digestibility of organic matter (71.9%), CP (70.3%) and NDF (51%) did not differ between treatments. Milk production (avg. 47.3 kg/d) and composition (avg. 3.54, 2.86, 4.78% fat, true protein, lactose) also did not differ, and changes in body condition and locomotion score were not affected. However, SCC for OE cows was lower ($P < 0.05$) than control (160,000 vs. 196,000). Feeding this OE to high producing California cows during moderately hot summer weather decreased SCC with no effect on other aspects of performance or indicators of heat stress.

Key Words: limonene, vitamin C, SCC

412 Meta-analysis of the effects of dietary sugar on intake and productivity of dairy cattle. C. F. Vargas*[1], C. D. Reinhardt[1], J. L. Firkins[2], and B. J. Bradford[1], [1]*Kansas State University, Manhattan,* [2]*Ohio State University, Columbus.*

A meta-analysis was performed to determine the possible effects of dietary sugar on feed intake and milk production in lactating dairy cattle. The database used in this analysis included 18 treatment comparisons from 10 studies reported between 1985 and 2011. Treatment comparisons were used only if 1) either sucrose (n = 9) or molasses (n = 9) replaced corn grain without adding fat, and 2) sugar added by treatment ranged from 2 to 5% of DM. In addition, 1 study was excluded because the SD for DMI response was more than twice the mean SD across studies. The meta-analysis included studies analyzed by both fixed effects and mixed effects statistical models. To account for the differences in SEM reported for treatment means by these approaches, studies with repeated measures that used a mixed effects model were re-analyzed to estimate fixed effects model SEM; this approach allowed for consistent weighting across studies. The meta-analysis was conducted using a random effects model. First, responses to sucrose and molasses were compared using Cochran's Q statistic, and no evidence for heterogeneity across sugar sources was found in either DMI ($P = 0.25$) or ECM ($P = 0.59$) responses. Therefore, different sugar sources were pooled for the remaining analyses. In the final data set, ECM and DMI responses to added sugar were moderately correlated (r = 0.68, $P < 0.001$). No evidence of publication bias was observed for DMI, although for ECM, the trim and fill method suggested that 2 additional studies with negative responses would be required to generate a normal response distribution. The combined data included in this analysis showed that the addition of sugar tended ($P = 0.07$) to increase DMI by 0.38 kg/d (95% confidence interval: −0.04 to +0.80 kg/d). On the other hand, no effect was detected for ECM ($P = 0.34$; 95% confidence interval: −0.29 to +0.85 kg/d). In summary, results of this analysis suggest that the addition of 2 to 5% dietary sugar may promote small increases in DMI, but do not consistently increase ECM in lactating dairy cattle.

Key Words: lactation, molasses, sucrose

413 Potential use of specific milk fatty acids to predict enteric methane emissions from lactating dairy cows. K. E. DeLand,* M. Hollmann, J. C. Ploetz, W. J. Powers, D. K. Beede, and A. L. Lock, *Michigan State University, East Lansing.*

The ability to accurately predict methane emissions is valuable for the quantitative monitoring of environmental and management impacts of livestock production. Biomarkers such as milk fatty acids (FA) may be a useful tool for the prediction of enteric methane emissions from lactating dairy cows. This study assessed if there was a relationship between the concentration or yield of specific milk FA and enteric methane emissions. Methane emissions (by gas flux in environmentally controlled rooms) and lactation performance were measured from individual lactating Holstein cows fed a TMR with 0.0% (control), 1.3, 2.7, or 3.3% coconut oil, DM basis. Compared with control, daily methane emissions declined 3.2, 37.3, and 45.5% with increased coconut oil, respectively. Milk samples were obtained from 4 milkings (d 26 and 28 of the 35-d experiment). We evaluated the relationship between the concentration (g/100 g FA) and yield (g/milking) of individual milk FA and methane emissions for the 24-h period preceding each milking. Multiple regression analysis using forward selection criteria identified significant FA that predicted methane emissions. On a FA concentration basis, the overall coefficient of determination (CD) for methane output ($R^2 = 0.86$, $P < 0.05$) was due primarily to C18:1 12*c* ($R^2 = 0.78$, $P < 0.0001$), C18:1 9*t* ($R^2 = 0.05$, $P < 0.001$), and C16:1 *iso* ($R^2 = 0.03$, $P < 0.01$). On a FA yield basis, the overall CD for methane output ($R^2 = 0.90$, $P < 0.05$) was due primarily to C13:0 *iso* ($R^2 = 0.65$, $P < 0.0001$), C18:1 12*c* ($R^2 = 0.07$, $P < 0.01$), C15:0 *iso* ($R^2 = 0.07$, $P < 0.001$), C18:1 9*t* ($R^2 = 0.05$, $P < 0.001$), and C20:5 ($R^2 = 0.02$, $P < 0.05$). Concentration of C18:2 12*c* and yield of C13:0 *iso* also were important in explaining 12-, 36-, and 48-h methane emissions, with similar CD as found for 24-h methane emissions. Results confirm a positive relationship between enteric methane emissions and C15:0 *iso*. Importantly, results suggest for the first time that C18:1 12*c* and C13:0 *iso* may be important milk FA for prediction of enteric methane emissions in lactating dairy cows.

Key Words: dairy cows, methane emissions, milk fatty acids

414 Nitrogen concentration and source alter products from fermentation of glucose by mixed ruminal microbes. M. B. Hall,* *U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI.*

Effects of N source and concentration on microbial fermentation products formed over time were evaluated. Replicated in vitro fermentations with mixed ruminal microbes were performed with 3 treatments (Ntrt): LoN (Goering and Van Soest media with 12% less N by removal of enzymic digest of casein; 0.337 g N/L), and HiNU (urea added) and HiNT (enzymic digest of casein added) both with 0.385 g N/L. Glucose (Glc) at 3 g/L was the carbohydrate substrate. Fermentation vessels were destructively sampled at 0, 0.25, 0.5, 0.75, 1, 2, and 3 h of fermentation. Data were analyzed as a randomized complete block design with the factors Ntrt, hour of fermentation (HR), the interaction, and fermentation run (random variable) in the model. Disappearance of Glc did not differ by Ntrt (Ntrt: $P = 0.92$; Ntrt x HR: $P = 0.85$) with residual Glc at < 6% of initial Glc by 2 h. Microbial N accumulation (indicative of microbial growth) differed by Ntrt x HR ($P = 0.05$) with LoN smaller than HiNU and HiNT at 2 h (2.19, 2.52, and 2.48 mg N, respectively), and LoN and HiNT greater than HiNU at 3 h (2.80, 2.69, and 2.48 g N, respectively; SED: 0.136). Microbial glycogen peaked at 2 h, then declined. Maximum glycogen mg detected were LoN:11.0, HiNU:10.7, and HiNT:10.1 (SED = 0.108; $P = 0.03$) with HiNT differing from HiNU and LoN ($P < 0.04$). Organic acid production differed among Ntrt at 0.25 and 0.5 h; mean organic acid concentrations for these 2 time points showed LoN and HiNU greater than HiNT (4.42, 4.25, and 2.83 mM, respectively; SED = 0.254; Ntrt: $P = 0.02$, Ntrt x HR: $P = 0.10$). Molar percentages of acetate, propionate, and butyrate did not differ for Ntrt or Ntrt x HR in this same time span ($P > 0.20$), however, yield of carbon in organic acids per Glc carbon that disappeared from the media differed for Ntrt ($P = 0.01$; SED = 0.004) and Ntrt x HR ($P < 0.01$; SED = 0.005) with least squares means values averaging 0.083, 0.085, and 0.062 for LoN, HiNU, and HiNT, respectively. Ntrt did not differ in maximal lactate concentrations ($P = 0.99$; LoN: 1.28, HiNU: 1.28; HiNT: 1.36 mM; SED = 0.709). The effect of N source and amount on microbial products may have implications as factors that could alter nutrient supply to the cow.

Key Words: nonfiber carbohydrate, protein, rumen fermentation

415 Interactions in rumen pool characteristics by dairy cows fed two concentrations of a novel co-product from corn wet milling with different forage sources. D. M. Shepherd*[1], J. L. Firkins[1], and P. von Behren[2], [1]*Department of Animal Sciences, The Ohio State University, Columbus,* [2]*Cargill Corn Milling, Blaire, NE.*

Increasing particle length or decreasing fragility should increase the density of the rumen mat, rumination time, and the retention time of particles in the rumen in part by trapping smaller particles. We used a novel corn wet milling co-product, termed Dairy Protein Product (DPP, coarse particle size and approximately 70% DM, 27.1% CP, 27.5% NDF, and 23.9% NSC) in diets formulated to contain 19.0% forage NDF, 17.4% CP, 20.2% starch, and 3.7% sugar. Six primiparous, rumen-cannulated Jersey cows were assigned to a 6x6 Latin square design with a 2 × 3 factorial arrangement of treatments in 6 periods of 3 wk (last week for data collection). We hypothesized for an interaction between 20 and 30% DPP with forage source (corn silage, CS, 46% NDF; CS replaced with 10% alfalfa hay, AH, 45% NDF; or CS with 7% grass hay, GH, 63% NDF). We expected that forage source would have minimal effect on production or rumen mat characteristics (from 2 rumen evacuations) when DPP was included at 20% of dietary DM, but when DPP was increased to 30%, we expected that CS+ AH would increase rumen mat consistency and associated ruminal fluid weight more than would CS alone but potentially less than CS+GH. Means were compared by pre-planned contrasts. There were no effects on production of milk or milk components, but DMI tended ($P = 0.10$) to increase when 20% DPP was included with CS and with reciprocal effects on fat-corrected milk/DMI. For CS only, DMI (16.1 vs. 14.8 kg/d) decreased ($P < 0.05$) when DPP was increased from 20 to 30% DPP; in contrast, rumen DM pool increased ($P < 0.05$) from 8.04 to 8.65 kg/d. Grass hay increased ($P < 0.05$) total and liquid pool size of rumen contents compared with AH (by 3.2 and 3.0 kg). No effects of ruminal pH were noted (averaging 5.99). In diets containing low starch (with 4% corn grain), increasing DPP from 20 to 30% requires more attention to interactions among forages with respect to fill, digestion, and passage of fiber.

Key Words: corn co-product, forage source, rumen pool

416 Fates of medium-chain fatty acids fed to lactating dairy cows. M. Hollmann*[1], M. S. Allen[1], T. H. Herdt[2,3], J. S. Zyskowski[3], K. M. Lebbin[1], J. P. Steibel[1], and D. K. Beede[1], [1]*Department of Animal Science, Michigan State University, East Lansing,* [2]*Department of Large Animal Clinical Sciences, Michigan State University, East Lansing,* [3]*Diagnostic Center for Population and Animal Health, Michigan State University, East Lansing.*

We examined fates of dietary saturated medium-chain fatty acids (FA; C8 through C14). Eight lactating Holstein cows were fed a TMR with either coconut oil (CNO) or Energy Booster (EB) supplemented at 3.35% of diet DM for 28 d in a crossover design. Concentrations of FA in rations were 0.6 or 0.0% C8:0, 1.8 or 0.1% C10:0, 13.9 or 0.3% C12:0, and 6.8 or 1.4% C14:0, for CNO or EB, respectively (total FA basis). Cows were fed ad libitum once daily at 1000 h. Rumens were evacuated and contents sampled 4 h post-feeding (d 26) and 2 h pre-feeding (d 28). Blood samples were obtained (d 17 to 20) before feeding and hourly post-feeding for 6 h. Data were analyzed by ANOVA with repeated measures. CNO reduced DMI 17% ($P < 0.001$), but did not affect weight or volume of ruminal contents. CNO resulted in reduced total FA concentration in ruminal contents, increased plasma concentration of total FA, and depressed milk fat yield (d 22 to 25) compared with EB ($P < 0.01$). CNO vs. EB increased ruminal concentrations of C8:0 and C10:0 post-feeding ($P < 0.001$), but not pre-feeding. Although apparent total tract digestibilities of these FA were nearly complete (>98%), their respective yields in milk were reduced ($P < 0.001$) and plasma concentrations were minute in CNO-fed cows. Amounts of C12:0 and C14:0 in rumen contents were greater with CNO than with EB ($P < 0.01$). Ruminal turnover rates per h were > 100% for C8, 58% for C10, 5.8% for C12, and 4.8% for C14 in CNO-fed cows. CNO increased C12:0 and C14:0 concentrations in plasma and in milk fat compared with EB. Yet, milk fat yield of C14 decreased with CNO. Apparent transfer from diet (CNO) to milk was 57% for C12 and 187% for C14. Disappearance of C8 and C10 (not accounted for in ruminal contents, plasma, feces, or milk) suggests rapid absorption and oxidation. Ruminal turnover rate and apparent total tract digestibilities of FA decreased with increased chain length from C8 to C14. Increased conversion of C14 vs. C12 into milk FA and greater increase of C14 vs. C12 in plasma FA indicate reduced uptake of C14 by extra-mammary tissue. Results suggest large differences in fate among medium-chain FA fed to lactating cows.

Key Words: β-oxidation, digestibility, partitioning

417 The effect of rumen digesta inoculation on the time course of recovery from diet induced milk fat depression in dairy cows.

D. E. Rico,* Y. Ying, A. R. Clarke, and K. J. Harvatine, *Penn State University, University Park.*

The predominant pathway and rate of ruminal biohydrogenation is dependent on the rumen environment and microbial population. Ten ruminally cannulated cows were used in a crossover design that investigated the effect of rumen digesta inoculation from non-milk fat depressed cows on recovery from diet induced milk fat depression. Two additional cows fed a control diet (32% NDF, no supplemental PUFA) were used as rumen digesta donors. MFD was induced from d 1 to 10 of each period by a low fiber and high oil diet (27% NDF and 3.0% soybean oil). On d 11 all cows were switched to the control diet treatment (trt) was no inoculation and ruminal inoculation (Inoc) with 8 kg of donor cow digesta/d from d 11 to 16. Milk yield and composition were measured every 3 d from d 10 to 28. Data were analyzed using repeated measures. The model included period, sequence, and cow nested in sequence as random effects and trt, d on diet, trt × d, and a covariate (d10 value) as fixed effects. Day was the repeated variable and cow × period was the subject. Second, a random regression model that included the random effect of cow and period, and the fixed effect of trt and trt × d, and trt × d^2 interactions were used for analysis of the rate of recovery. Both milk fat concentration and yield increased progressively during the recovery phase and trt were not different at any time points. However, in the regression analysis, there was an effect of trt and trt × d and trt × d^2 interactions for fat concentration and an effect of trt and a trt × d interaction for fat yield (All $P < 0.01$). The best fit predictions for milk fat concentration for the Con and Inoc were $1.55 + 0.161 \times d+(-0.003) x d^2$ and $0.56+0.253 \times d+(-0.005) \times d^2$, respectively. The concentration of milk fatty acids less than 16 carbons increased progressively in both trt and was higher for Inoc than Con on d 16. In contrast, milk fat concentration of *trans*-10 C18:1 and *trans*-11 C18:1 decreased progressively and was not affected by trt. Under the conditions of the current experiment, ruminal inoculation from non-milk fat depressed cows modestly accelerated the rate of recovery from diet induced milk fat depression.

Key Words: milk fat depression, biohydrogenation, CLA

418 Effect of carbohydrate conformation in hulless barley (*Hordeum vulgare* L.) on in situ rumen and in vitro intestinal nutrient availability.

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Hulless barley breeding lines varying in amylose (1 to 20% DM), amylopectin (34 to 51% DM), amylose to amylopectin ratio (Ay:Ap) (0.02 to 0.59) and β-glucan content (5 to 10% DM) have been developed at the Crop Development Centre, University of Saskatchewan. The objective of this study was to determine the effect of these new hulless barley lines (zero-amylose waxy, CDC Fibar; 5%-amylose waxy, CDC Rattan; normal-amylose, CDC McGwire and high-amylose, HB08302) on rumen degradation kinetics and in vitro intestinal nutrient digestion (CDC Copeland was included as a hulled control). Three dry Holstein cows fitted with rumen cannula were used for measuring rumen degradation of barley varieties. The estimation of intestinal digestion was determined by a modification of the 3-step in vitro procedure described by Calsamiglia and Stern with duplicate of each in situ residue. Among the hulless barley lines, HB08302 was greater ($P < 0.05$) in rumen bypass dry matter (BDM: 46.5 vs. 33.4% DM), rumen bypass starch (BST: 40.3 vs. 25.2% ST or 218 vs. 155g/kg DM) and reduced ($P < 0.05$) in effective degradability of dry matter (EDDM: 53.5 vs. 66.6% DM) and starch (EDST: 59.8 vs. 74.8% ST or 320 vs. 461 g/kg DM) compared with CDC Rattan. HB08302 was also greater ($P < 0.05$) in rumen bypass crude protein (BCP: 52.1% CP), effective degradability of neutral detergent fiber (EDNDF: 74 g/kg DM) and intestinal absorbable feed protein (IADP: 40.6% CP) but reduced ($P < 0.05$) in total digestible protein (TDP: 120 g/kg DM) than the other hulless barley lines. CDC Fibar showed greater ($P < 0.05$) effective degradability of crude protein (EDCP: 90 g/kg DM) while CDC McGwire showed reduced ($P < 0.05$) TDP (116 g/kg DM). Compared with hulless barley, the hulled CDC Copeland showed relatively greater ($P < 0.05$) BNDF (62.5% NDF or 98 g/kg DM), starch degradation rate (K_d: 17.4%/h) and EDST (75.9% ST) but reduced ($P < 0.05$) BCP (49 g/kg DM), rumen undegradable protein (RUP: 55 g/kg DM) and TDP (102 g/kg DM). In conclusion, hulless barley lines with altered carbohydrate traits have the potential to increase rumen and intestinal nutrient availability to ruminants.

Key Words: amylose to amylopectin ratio, hulless barley, rumen degradation and intestinal digestion

419 Palmitic acid increased milk yield and feed efficiency across production level of lactating cows.

P. Piantoni,* A. L. Lock, and M. S. Allen, *Michigan State University, East Lansing.*

The objective of this experiment was to evaluate the effects of palmitic acid supplementation on feed intake, digestibility, and metabolic and production responses of dairy cows with a wide range of milk production (35 to 66 kg/d) in a crossover design experiment with a covariate period. Thirty-two multiparous Holstein cows (151 ± 66 DIM) were assigned randomly within level of milk yield to treatment sequence. Treatments were diets supplemented (2% of diet DM) with palmitic acid (PALM, 99% C16:0) or control (CONT, soy hulls). Treatment periods were 21 d with the final 4 d used for data and sample collection. No interactions were detected between treatment and milk yield when all cows received a common diet during the covariate period for any response variable. Compared with CONT, the PALM treatment increased milk yield (46.0 vs. 44.9 kg/d, $P = 0.04$), milk fat concentration (3.4 vs. 3.3%, $P = 0.01$) and yield (1.53 vs. 1.45 kg/d, $P = 0.001$), and 3.5% fat-corrected milk (FCM, 44.63 vs. 42.89 kg/d, $P < 0.01$). Treatment did not affect dry matter intake (DMI, $P = 0.96$), yield and concentration of protein and lactose in milk ($P > 0.12$), or body weight ($P = 0.58$). The PALM treatment increased feed efficiency (3.5% FCM/DMI, 1.61 vs. 1.55, $P < 0.0001$) and tended to decrease body condition score (2.93 vs. 2.99, $P = 0.06$) compared with CONT. Compared with CONT, the PALM treatment increased total tract digestibility of NDF (38.7 vs. 35.4%, $P < 0.001$) and OM (67.3 vs. 66.0%, $P < 0.01$). The PALM treatment increased plasma concentration of NEFA (101.4 vs. 90.0 μEq/l, $P < 0.0001$) and the ratio of insulin to glucagon (0.092 vs. 0.083, $P = 0.05$), and tended to increase plasma concentration of insulin (11.4 vs. 10.3 μIU/ml, $P = 0.07$). Results show that palmitic acid has the potential to increase yields of milk and milk fat as well as the conversion of feed to milk, independent of production level without increasing body condition score or body weight.

Key Words: feed efficiency, milk fat, palmitic acid

420 Palmitic acid increased the yield of milk fat and improved feed efficiency across production level of cows compared with stearic acid.

J. E. Rico,* M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

The effects of dietary palmitic (C16:0) and stearic (C18:0) acids on feed intake, yield of milk and milk components, and feed efficiency of dairy cows with a wide range of milk production were evaluated in an experiment with a crossover arrangement of treatments and a covariate period. A wide range of milk production (38 to 65 kg/d) was used to determine if response to fat supplementation varied according to production level. Thirty-two Holstein cows (143 ± 61 DIM) were assigned randomly to treatment sequence within level of milk yield. Treatments were diets supplemented (2% of diet DM) with palmitic acid (PA; 99% C16:0) or stearic acid (SA; 98% C18:0). Treatment periods were 21 d with the final 4 d used for sample and data collection. The corn silage and alfalfa haylage based diets were formulated to contain 29% NDF, 17% CP, and 5.7% crude fat. The statistical model included the random effect of cow and the fixed effect of treatment and period. No interactions were detected between treatment and level of milk production when all cows received a common diet during the covariate period for any response variable. Compared with SA, the PA treatment increased milk fat concentration (3.55 vs. 3.66%, $P < 0.01$) and yield (1.59 vs. 1.68 kg/d, $P < 0.001$), and 3.5% fat-corrected milk yield (45.56 vs. 47.46 kg/d, $P < 0.001$). Treatment did not affect DMI, milk yield, milk protein yield, body weight, or body condition score (all $P > 0.10$). Milk protein concentration was lower for PA compared with SA treatment (3.24 vs. 3.29%, $P < 0.01$). The PA treatment increased feed efficiency (3.5% fat-corrected milk yield/DMI) compared with SA (1.48 vs. 1.40, $P < 0.001$). Results demonstrate that palmitic acid is more effective than stearic acid in improving milk fat concentration and yield as well as efficiency of feed conversion to milk. Responses were independent of production level and without change in body condition score or body weight. Further studies are required to test the consistency of these responses across different types of diets.

Key Words: milk fat, palmitic acid, stearic acid

421 Linseed oil reduces methane emissions from grazing dairy cows.

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Enteric methane accounts for approximately 50% of the total greenhouse gas emissions from the average Irish dairy farm as well as representing an energy loss to the animal. Lipid supplementation of the diet is an accepted mitigation strategy; however, the efficacy of individual oils is linked to their individual fatty acid composition. The objective of this study was to assess the effect of oils rich in polyunsaturated fatty acid (PUFA) on methane output, milk performance and rumen parameters of grazing dairy cows. Forty 5 Holstein Friesian cows were blocked on parity and allocated to 1 of 3 (n = 15) treatments, balanced for days in milk (mean 143 d ± 22) and pre-experimental milk yield (mean 24.6 l ± 4.8) in a randomized block design study. All animals had a daily grass allocation of 17kg dry matter (DM) plus 4kg of concentrate DM containing either 160g/kg FW of stearic acid (CO), soy oil (SO) or linseed oil (LO). Individual methane emissions were measured using the SF6 technique at 17 (PI) and 44 (PII) days post dietary introduction. Individual rumen samples were collected on d 22 and 49 for volatile fatty acid (VFA) and ammonia (NH3) analysis. Data were analyzed using the least squares procedures using the MIXED procedure of SAS. The statistical model used included the fixed effects of treatment, period and parity and appropriate interactions. Pre-experimental milk yield and days in milk were included in the model as covariates. Supplementary LO reduced ($P < 0.001$) methane emissions per kg of milk and milk solids produced compared with the CO or SO diets. Dietary LO reduced methane emissions per kg of dry matter intake ($P < 0.01$) compared with the SO diet. Dietary LO and SO supplementation increased ($P < 0.001$) milk yield and milk protein yield and had no effect on milk fat yield ($P < 0.001$) compared with the CO diet. Dietary PUFA supplementation reduced total rumen VFA concentrations ($P < 0.001$), NH3 concentrations ($P < 0.001$) and molar proportion of butyrate ($P < 0.001$) in the rumen. Dietary LO supplementation has the capacity to substantially reduce enteric methane emissions from grazing dairy cows while maintaining or enhancing milk production and composition.

Key Words: dairy cows, linseed oil, methane

422 Effects of different protein supplements on AA availability in dairy cows.

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Canola meal (CM) or by-products of ethanol production (dried distillers grain, DDG) may offer an economical alternative to soybean meal (SBM) in North American dairy rations. Several studies have shown that these protein sources can effectively replace SBM, but few studies have focused on the AA availability. The objective of this study was to determine the effects of replacing SBM by either CM, high protein corn DDG with solubles (HPDDG) or wheat DDG with solubles (WDDG) on the availability of 3 AA: His, Lys and Met. Eight Holstein cows were used in a replicated 4 × 4 Latin square with 14-d periods. Cows were fed isoN (17.4%CP) diets formulated to slightly exceed energy and protein requirements (NRC, 2001) which contained 38% grass hay and 62% corn-based concentrate including either SBM, CM, HPDDG or WDDG as the protein source. The AA availability was estimated using the variation of whole body (WB) irreversible loss rate (ILR) of each AA, determined by the isotope dilution technique (Borucki Castro et al. 2008, Animal 2:224). A pulse dose of L-[$^{15}N_3$]His (0.18 g), L-[1-^{13}C]Met (0.12 g) and L-[α-^{15}N]Lys (0.55 g) was administered into one jugular vein. Blood samples were then collected from the other jugular vein at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 13, 16, 19, 25 and 31 min after the bolus injection to determine AA enrichments. The procedure was repeated at the end of the main study following a 7-d continuous abomasal infusion of Lys (70g/d) and Met (20g/d) with cows fed the SBM diet. As required by this technique, DMI, milk and milk protein yields were not affected by treatments and averaged 23.7, 31.4 and 1.14 kg/d. Preliminary results showed no difference in the WB ILR of Met and His among the treatments (122.1 ± 7.6, 128.4 ± 6.2 g/d), suggesting a similar availability of these 2 AA across diets. WB ILR of Lys was numerically ($P = 0.20$) higher with CM (352 g/d) and lower with HPDDG (291 g/d) than with SBM and WDDG (325 and 319 g/d). In comparison with the SBM diet, Lys and Met infusions increased ($P < 0.05$) Lys and Met WB ILR by 62.2 ± 30.5 and 24.8 ± 14.5 g/d, respectively, indicating that the above method is reliable to determine changes in AA availability.

Key Words: amino acids, dairy cow, protein sources

Small Ruminant: Nutrition and Parasites

423 Nitrogen balance of growing West African Dwarf ewe fed Mexican sunflower leaf meal based diets. A. H. Ekeocha,* *University of Ibadan, Ibadan, Oyo, Nigeria.*

After a previous 84-d performance phase, a study was conducted using 16 West African Dwarf (WAD) ewes. Ewes (Initial BW 17.5 ± 0.19kg) were used in a completely randomized design to study the effects of increasing level of Mexican sunflower leaf meal (MSLM) on nitrogen balance. The experimental animals were assigned to 4 treatment groups A (O%MSLM), B(15%MSLM), C (30%MSLM) and D (45%MSLM) of 4 replicates each and were fed with grass (*Panicum maximum*) plus concentrate diet mixture of Mexican sunflower leaf meal (MSLM) and wheat bran (WB) such that 0%, 15%, 30% and 45% of WB was replaced by weight with MSLM gravimetrically. About 60% of the diet came from the concentrate while 40% came from grass. The experiment lasted for one week. Digestibility was determined using a 6-d total urine and fecal collection. Ewes were given ad libitum access to feed and water and routine vaccination and medication followed standard procedures. Parameters measured were nitrogen intake (NI), nitrogen balance (NB), nitrogen apparent digestibility (NAD) and nitrogen retention(NR). Data were analyzed using descriptive statistics and ANOVA. Concentrate DMI (CDMI) ranged from 181.8 g/d (45%MSLM) to 536.8 g/d (15%MSLM) and grass DMI (GDMI) ranged from 130.6 g/d (0%MSLM) to 215.9 g/d (30%MSLM) and this was significant ($P < 0.05$). Positive NB was observed for animals on all treatments. This suggested that the various diets were able to meet the protein need of the animals for maintenance and production. Urinary nitrogen g/d was greater ($P < 0.05$) with increasing inclusion of MSLM in the ration while protein retention increased from treatment A (0%MSLM) to treatment B (15%MSLM) (90.4 - 90.8%) and subsequently decreased from treatment B (15%MSLM) to D (45%MSLM) (90.8 - 85.0%). Data obtained for N- balance in this study ranged from 6.28 – 15.0 g/d. Animals on treatment B (15.01g/d) had the greater N-balance, and this was significantly ($P < 0.05$) greater compared with animals on treatment D (6.28g/d) but numerically more ($P > 0.05$) than observed values for animals on treatments C (9.05g/d) and A (9.32 g/d). This suggested that the fermentable OM in the WB apparently encouraged greater N digestibility and it is an indication that a favorable energy: N balance resulted from diet B. This trend was the same for nitrogen intake (7.39 – 16.5g/day) and absorbed (6.36 – 15.1 g/d). Nitrogen balance was positively related to DMI and N intake. The overall regressions were NB = 2.39 + 0.07 DMI; $R^2 = 0.93$, ($P = 0.37$) and NB = 0.72 +0.91 NI; $R^2 = 0.99$, ($P = 0.13$). This study showed that a greater level of NI and DMI improved ($P < 0.05$) N-balance. The low level of nitrogen balance in animals on treatment D could have been due to the level of feed intake. Mexican sunflower leaf meal incorporation in the diets of sheep improved nitrogen intake, balance and retention.

Key Words: nitrogen balance, West African dwarf ewe, Mexican sunflower leaf meal

424 Excess iodine intake by the ewe in late pregnancy programs on the lamb for reduced immunoglobulin G absorption. T. M. Boland,* *University College Dublin, Lyons Research Farm, Newcastle, Co. Dublin, Ireland.*

The lamb is born hypoimmunocompetent as the placenta prevents the in utero transfer of antibodies from mother to offspring. Therefore, the lamb is dependent on the postnatal absorption of antibodies from colostrum to confer disease resistance in early life. Several maternal and nutritional factors influence this transfer, but perhaps none so dramatically as high level iodine intake by the pregnant ewe in late gestation. Several studies were conducted over several years with the objective of determining the mechanisms involved in the reduced antibody transfer following high level iodine supplementation. This abstract represents a synthesis of these studies to better describe this phenomenon. The lamb's ability to absorb colostral immunoglobiulin G (IgG) is greatly impaired by high (11 to 40 mg/ewe/day) level iodine intake by the pregnant ewe during the last 6 weeks of pregnancy. While these levels of intake are in excess of requirements they do represent the voluntary iodine intake of ewes when offered free access mineral blocks. Vitamin E absorption from colostrums is affected in a similar manner. The response to this high level iodine intake is rapid with supplementation during the final 2 weeks of pregnancy sufficient to produce the response. A 2 week supplementation period earlier in pregnancy has no effect. This is a dose dependent response with greater reductions seen at higher levels of intake. The lamb is preprogrammed in utero for this effect and the quality or availability of colostral IgG is unaffected by iodine supplementation. In the small intestine, the primary site of IgG absorption there are alterations in mRNA expression of several genes, namely β2-microglobulin (B2M) and a lower expression of upstream stimulator factor 2 (USF2), interleukin-4 (Il-4) and thyroid hormone receptor β (THRβ) ($P < 0.05$) potentially mediated through alterations in thyroid hormone metabolism. These findings indicate the pathway involved in the observed reduction in IgG absorption and the need for a downward revision (to approximately 40% of current values) of the iodine toxicity levels for ewes during late pregnancy.

Key Words: iodine, IgG, lambs

425 Effects of different NFC/NDF ratios of TMR on ruminal pH and VFA in meat sheep. J. Liu,* Q. Y. Diao, Y. Tu, Y. G. Zhao, X. H. Gao, and L. H. Zhao, *Key Laboratory of Feed Biotechnology of Ministry of Agriculture/Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China.*

This study examined the effect of different NFC/NDF (nonfiber carbohydrates/NDF) ratios of TMR (total mixed ration) on ruminal pH and VFA in meat sheep. Twelve crossbred rams (Dorper♂ × Thin-tailed Han♀) fitted with ruminal cannulas and BW of 47.2 kg (±1.01 kg) at the start of trial were used in an incomplete 12 × 4 Latin square arrangement. Period length was 16 d, and the first 14 d of each experiment were for ration adaption, with sampling during d 15 to 16 of each period. The rams were fed rations with different NFC/NDF ratios, which the ratios were 0.25 (1), 0.34 (2), 0.36 (3), 0.52 (4), 0.60 (5), 0.80 (6), 0.87 (7), 1.13 (8), 1.30 (9), 1.58 (10), 2.17 (11), and 2.49 (12), respectively. Diets were fed as pelleted TMR once daily at 08:00. The amount of feed offered was restricted to 1.2 kg/d. Ruminal fluid was sampled from rams at 08:00, 14:00, and 20:00 on d 15 and at 02:00, 05:00, 11:00, 17:00, and 23:00 on d 16 of each period. Data were analyzed using the GLM procedure of SAS software. The results showed that, with increasing NFC/NDF ratios, ruminal pH decreased ($P < 0.01$), total VFA and butyrate percentage changed with cubic curve ($P < 0.05$), percentage of propionate, valerate and isovalerate in rumen increased ($P < 0.01$), while acetate percentage and A/P (acetate/propionate) ratio decreased ($P < 0.01$). It was concluded that NFC/NDF ratios of TMR had significant effect on ruminal pH and VFA. Increasing dietary NFC/NDF ratios decreased ruminal pH, acetate percentage and A/P ratio and increased percentage of propionate, valerate and isovalerate in rumen.

Key Words: NFC, rumen fermentation, sheep

426 Protein supplementation of low-quality forage: Effects of amount and frequency on intake and nutrient digestibility by lambs. M. L. Van Emon*[1,2], C. S. Schauer[2], and D. W. Bohnert[3], *[1]Department of Animal Sciences, North Dakota State University, Fargo[2]Hettinger Research Extension Center, North Dakota State University, Hettinger, [3]Eastern Oregon Agricultural Research Center, Oregon State University, Burns.*

The objectives of this research were to determine the effects of protein supplementation and frequency on intake and nutrient digestibility by lambs. Seven lambs were utilized in a 4 × 7 incomplete Latin square design. Dietary treatments were arranged in a 2 × 3 factorial design (2 levels of CP and 3 supplementation frequencies); CON = unsupplemented control; D = supplemented daily 0.28% of BW of soybean meal (SBM); 5D = supplemented 1.4% of BW of SBM once every 5 d; 10D = supplemented 2.8% of BW of SBM once every 10 d; 1/2 D = supplemented at 50% of D; 1/2 5D = supplemented at 50% of 5D; 1/2 10D = supplemented at 50% of 10D. Full CP refers to D, 5D, and 10D and half CP refers to 1/2 D, 1/2 5D, and 1/2 10D dietary treatments. Lambs were supplemented with SBM immediately before feeding of low-quality forage (Chewings fescue grass seed straw). Each experimental period was 30 d, with intake measured d 19 to 28. Feces, urine, and blood were collected d 21 to 30. Straw and SBM DMI, total DMI, straw OM intake, OM intake, ADF intake, and NDF intake were not different ($P \geq 0.26$) due to supplementation. Supplementation increased ($P \leq 0.02$) DM, OM, and NDF digestibility compared with the CON. The CON lambs had reduced ($P \leq 0.002$) N intake, urine N excretion, N balance, N digestibility, and digested N retained compared with supplemented lambs. Plasma urea N was increased in the supplemented lambs ($P = 0.004$) compared with the CON lambs as well as for full CP compared with half CP lambs ($P = 0.03$). Lambs supplemented with full CP had increased ($P \leq 0.03$) urine N excretion and N digestibility compared with the half CP lambs; however, digested N retained was not different ($P = 0.94$) due to supplementation amount. As supplementation frequency decreased, N digestibility was also reduced ($P = 0.01$). Both DM and OM digestibility increased ($P \leq 0.04$) as supplementation interval increased. These results suggest that increasing the supplementation interval may be utilized to maintain intake, digestibility, and reduce the labor costs associated with more frequent supplementation.

Key Words: lambs, nitrogen balance, supplementation frequency

427 Effect of feeding differently processed sweet sorghum (*Sorghum bicolor* L. Moench) bagasse based complete diet on nutrient utilization and microbial N supply in growing ram lambs. N. Nalini Kumari[1], Y. Ramana Reddy*[1], M. Blummel[2], T. Monika[1], B. V. S. Reddy[3], and Ch. Ravinder Reddy[3], *[1]S.V. Veterinary University, Tirupati, Andhra Pradesh, India, [2]International Livestock Research Institute (ILRI), Patancheru, Andhra Pradesh, India, [3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India.*

This study was carried out to identify appropriate processing method for efficient utilization of sweet sorghum bagasse (SSB), an agro-industrial by product of bio-ethanol industry after blending with concentrate in sheep. The SSB based complete diet with roughage to concentrate ratio of 50:50 was processed into mash (SSBM), expander extruded (SSBP) and chop form (SSBC) and evaluated in a growth- cum-metabolism trial using growing ram lambs in comparison to sorghum stover based complete diet (50:50) in mash form (SSM). Mash form of diet is prepared by grinding the roughage and concentrate portion of the ration after batching through hammer mill using 8mm sieve and mixing the grind material in a horizontal mixer. Expander extruded pellets are prepared by using expander extruder which combines the futures of expanding (application of moisture, pressure and pressure) and extruding (pressing the feed through constrictions under pressure). Twenty-four growing Nellore × Deccani ram lambs (10.6 ± 0.23 kg BW) were randomly divided into 4 groups of 6 animals each in a completely randomized design and the experimental complete diets were allotted at random to each group. A metabolism study was conducted at the end of the growth trial of 180 d to assess the nutrient utilization, and energy, nitrogen (N), calcium (Ca) and phosphorus (P) balance. The daily intestinal flow of microbial nitrogen (g/d) was calculated from total urinary purine derivatives (PD) (mmol/d). The average DMI (g/d or g/kg$^{0.75}$) was greater ($P < 0.01$) in lambs fed SSBP diet than those fed SSBC, SSBM and SSM diets. The lambs fed expander extruded (SSBP) diet could digest more ($P < 0.01$) DM, OM, CP ($P < 0.01$) than those fed SSBC, SSBM and SSM diets. Cellulose digestibility was greater ($P < 0.05$) in lambs fed SSBP diet than those fed SSM and SSBC diets. The intake of ME was more ($P < 0.01$) in lambs fed SSBP diet but comparable among SSM, SSBC and SSBM diets. The SSBP diet had greater ($P < 0.01$) DCP content compared with SSM, SSBC and SSBM diets, whereas the ME ($P < 0.05$) content was greater than SSBC and SSM diets. The DCP and ME values were comparable between SSBM and SSM diets. There was greater N, P ($P < 0.05$) and Ca ($P < 0.01$) balance in lambs fed SSBP diet compared with those fed the other 3 diets. Expander extrusion of SSB based complete diet resulted in improved ($P < 0.01$) efficiency of microbial protein synthesis. It is concluded from the results of the present study that, sweet sorghum bagasse is comparable with that of sorghum stover in nutritional value and processing SSB based complete diet into expander extruded pellets improved the nutrient utilization and microbial protein synthesis in growing sheep.

Key Words: sweet sorghum bagasse, processing, nutrient utilization

428 Effect of the dietary cation-anion difference on the lactation performances of dairy ewes at early-mid lactation. M. M. Youssef, G. Caja,* A. A. K. Salama, A. Ait-Saidi, and E. Albanell, *Grup de Recerca en Remugants (G2R), Universitat Autonoma de Barcelona, Bellaterra, Barcelona, Spain.*

Lactating ewes from 2 dairy breeds (Manchega, n = 20, Lacaune, n = 20) at 82 ± 3 DIM were used to study the lactational effects of diets varying in dietary cation-anion difference taking into account S (DCAD:S). Ewes were allocated in balanced groups of 5 ewes according to breed, BW and milk yield (Manchega, 68.3 ± 1.7 kg BW, 0.84 ± 0.05 L/d; Lacaune, 71.8 ± 2.1 kg BW, 1.46 ± 0.09 L/d), to which the dietary treatments were randomly assigned. Diets were fed for 8 wk and consisted of a total mixed ration (forage-to-concentrate ratio = 60:40) with 4 different DCAD:S values (22.5, 31.9, 45.9 and 64.9 mEq/100 g DM) formulated by adding anionic or cationic salts. Individual intake was calculated using polyethylene glycol 6000 as indigestible marker. Milk yield and milk composition were recorded weekly and biweekly, respectively. Blood and urine samples, for studying acid-base balance, were taken at wk 4 and 8, and wk 8 respectively. There were no effects of DCAD:S on feed intake, but milk yield showed a positive linear response to DCAD:S ($P < 0.001$). Effects of DCAD:S on milk composition differed by breed, showing a negative linear response in Lacaune ewes ($P < 0.01$) and no variation in Manchega. There was no DCAD:S effect on blood acid-base indicators (pH, HCO3—, pCO$_2$, AGap, BEx), indicating that ewes were in a neutral stage, but blood glucose and urea showed positive and negative linear effects of the treatments ($P < 0.001$), respectively. Blood fixed ions (Na$^+$, K$^+$, and Cl$^-$) did not vary and urine pH varied in a linear and positive manner by DCAD:S treatments ($P < 0.001$). Urinary urea and minerals showed different responses to

DCAD:S according to breed, with negative effects on urea, Ca and S ($P < 0.05$), and positive effects on Na ($P < 0.001$), which agreed with their respective intakes and with a metabolic stage of Ca mobilization. According to the obtained results, cationic diets (DCAD:S ~60 mEq/100 g DM) are recommended for lactating dairy sheep, which is markedly greater than previously reported in dairy cows and in dairy goats.

Key Words: dairy sheep, DCAD, electrolytic balance

429 Factors affecting dry matter intake of grazing goats in the Brazilian rangelands. M. A. D. Bomfim*[1,2], L. O. Tedeschi[2], and N. F. De Paula[3,2], [1]*Embrapa Goats and Sheep, Sobral, Ceara, Brazil,* [2]*Texas A&M University, College Station,* [3]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Feed intake of grazing goats is a critical factor to determine their nutrient requirements. Research has shown that DMI varies with BW when diet DM digestibility (DMD) is lower than 66%, but other factors may affect DMI, such as pasture or environmental variables. A DMI database of grazing goats under the Brazilian rangeland conditions was built from 10 studies and had 61 data points. This database was used to determine key variables that could explain the variation in DMI. The recorded variables were age, BW, ADG (g/d), DMI (g/d), pasture area (AREA, ha), stocking rate (SR, goat/ha), pasture offer (PO, kg/goat/d), forage availability (FA, kg/ha), legume (LEG, % forage), pasture CP (PCP, %DM), pasture DM (PDMD) and OM digestibility (POMD), supplement CP (SCP, %DM) and ME (SME, Mcal/kg), supplement DMI (SDMI, g/d), minimum and maximum temperatures, and relative humidity (RH). The OM intake (OMI) was converted to DMI assuming an average of pasture ash content of 11.5% DM obtained from several publications. A stepwise regression was performed to identify the variables that explained the variation in the DMI. Then, a random coefficient model was used to obtain the fixed effect coefficients of the selected variables by assuming study as a random variable. The BW, FA, LEG, and their interactions explained more than 88% of the variation in the DMI. The study-variation free multiple regression was DMI (g/d) = $708.3 - 7.91 \times \mathrm{BW} - 0.172 \times \mathrm{AVAIL} + 0.00875 \times \mathrm{BW} \times \mathrm{AVAIL} - 6.8 \times \mathrm{LEG} + 0.304 \times \mathrm{BW} \times \mathrm{LEG}$ (n = 26, root of mean square error (RMSE) = 79.4 g/d, $R^2 = 0.883$). When only BW was used, approximately 75% of the variation in the DMI was explained and the study-variation free polynomial regression was DMI (g/d) = $368.9 - 6.56 \times \mathrm{BW} + 0.6 \times \mathrm{BW}^2$ (n = 61, RMSE = 104.5 g/d, $R^2 = 0.75$). Our results suggested that although BW was able to explain the majority of the variation in the DMI of these grazing goats, additional variation could be explained when forage availability and legume in the pasture were used. Although our database included most of the research carried out under these conditions, more studies are needed to confirm our findings.

Key Words: caatinga, caprine, ingestion

430 Effects of diet on carcass quality and consumer taste panel acceptance of intact or castrated hair lambs. J. D. Kohler*[1], W. W. Miller[1], J. L. Vest[1], J. M. Burke[2], M. A. Brown[3], K. R. Maddock Carlin[4], M. D. Hudson[1], and E. L. Walker[1], [1]*Missouri State University, Springfield,* [2]*Dale Bumpers Small Farms Research Center, Booneville, AR,* [3]*USDA ARS Grazinglands Research Laboratory, El Reno, OK,* [4]*North Dakota State University, Fargo.*

Forty hair-type lambs were examined in a 70-d study to determine the effects of gender (castrate; C vs. intact; I) and forage type on carcass traits and sensory acceptability. Lambs were procured from a single source in Missouri and one-half were randomly castrated. Lambs were randomly assigned to treatment and housed in individual pens. Equal number of each gender were assigned to 1 of 2 isonitrogenous dietary treatments: alfalfa (*Medicago sativa*; AL) or sericea lespedeza (*Lespedeza cuneata*; SL). Lambs were slaughtered and carcasses fabricated 48 h postmortem. Wholesale loins were split, vacuum packaged, and randomly assigned to an aging time of 48 h or 14 d before freezing. Minolta color scores were taken on the lateral surface of the loin after 15 min bloom time. A consumer taste panel was conducted using 64 untrained panelists. Approximately 13.5 cm of the loin was cooked to 71°C, cut into 12.7-mm x 12.7-mm pieces, and served at room temperature. Panelists scored samples for color, aroma, texture, aftertaste, juiciness, and overall appeal (1 = strongly disliked and 8 = highly desirable). Data were analyzed using Proc Mixed. The model included the fixed effects of gender, forage, panelist gender, and postmortem aging and all interactions. Non-significant interactions were removed. Initial BW was not different ($P = 0.89$). At slaughter, I lambs were 4.36 kg heavier and had greater HCW (18.8 vs. 16.6 kg; $P \leq 0.05$) than C lambs. Castrate lambs had greater ($P \leq 0.05$) a* and b* values than I lambs. Color was rated highest for C than I lambs (5.4 vs. 5.0; $P \leq 0.01$). Aging for 14 d had a positive effect on texture and aftertaste ($P \leq 0.05$) and there was a diet by lamb gender interaction on texture ($P \leq 0.01$). Female panelists preferred the aroma of AL vs. SL lambs (5.3 vs. 4.9; $P < 0.04$) and male panelists had a greater acceptance of aftertaste than females (5.2 vs. 4.8;$P = 0.017$). Castrate lambs fed AL were juicier and with a more desirable aftertaste (5.3 vs. 4.9; $P = 0.07$). Overall, male panelists preferred lamb more than females (5.4 vs. 4.9; $P = 0.002$). Consumer acceptance of lamb is influenced by diet, gender, and aging of lamb.

Key Words: lambs, carcass quality, consumer panel

431 Exploring the combined effects of dietary tannins and saponins on sheep infected with *Haemonchus contortus*. G. Copani[1], H. Hall[2], J. Miller[3], A. Priolo[1], and J. Villalba*[2], [1]*University of Catania, Catania, Sicily, Italy,* [2]*Utah State University, Logan,* [3]*Louisiana State University, Baton Rouge.*

The feeding behavior of lambs and the anthelmintic properties of tannins and saponins when offered in single rations or as a choice between rations were determined. Thirty 5 lambs were randomly assigned to 5 groups (7 lambs/group) and fed for 12 d: beet pulp (Group BP); BP + 8% quebracho tannins (Group CT); BP + 1.5% quillaja saponins (Group SAP), or a choice between BP + 8% quebracho tannins and BP + 1.5% quillaja saponins (groups CH-P parasitized and CH-NP non-parasitized). After this period, lambs in all groups, except those in CH-NP, were dosed with 5,000 and 27 d later with 8,000 infective larvae of *Haemonchus contortus*. After 23 d, all lambs were exposed to their respective diets for 12 d. Feed intake and fecal egg counts (FEC) were analyzed as a split-plot design with lambs (random factor) nested within group and day as the repeated measure. Lambs in BP, CH-P and CH-NP ate more feed than lambs offered just tannins (CT) or saponins (SAP) in single rations ($P < 0.05$). Groups offered choices (CH-P and CH-NP) did not differ in food intake ($P > 0.05$) and preferred the saponin- over the tannin-containing ration ($P < 0.05$). Before exposure to the experimental diets, groups had similar FEC ($P > 0.05$). In contrast, after being exposed to the experimental diets for 12 d, lambs in CT and SAP showed lower FEC than lambs in BP and in CH-P ($P < 0.05$). Thus, even when lambs exposed to a choice of rations containing tannins and saponins consumed more total feed than animals exposed to single rations, the effect at reducing FEC was less effective, suggesting that a combination of saponins and tannins have synergistic effects on food intake but antagonistic effects on parasitic loads.

Key Words: plant secondary compounds, food choice, endoparasites

432 Effect of feeding sericea lespedeza pellets on *Haemonchus contortus* in goats. D. S. Kommuru*[1], T. H. Terrill[1], N. C. Whitley[2], J. E. Miller[3], and J. M. Burke[4], [1]*Fort Valley State University, Fort Valley, GA,* [2]*North Carolina A&T State University, Greensboro,* [3]*Louisiana State University, Baton Rouge,* [4]*USDA/ARS/DBSFRC, Booneville, AR.*

Due to increased prevalence of anthelmintic resistance in sheep and goat gastrointestinal nematodes (GIN), there is a critical need for alternative control methods. Sericea lespedeza (SL; *Lespedeza cuneata*) has been shown to have activity against small ruminant GIN, but the mechanism of action has not been determined. Three experiments (Exp) with Spanish or Boer crossbred goats were designed to study the effect of feeding SL leaf meal pellets fed for 10% orts in confinement on *Haemonchus contortus* larvae during establishment (Exp 1; 75% SL; mature bucks group fed; n = 8/treatment) and after establishment (Exp 2; 75% SL; mixed sex kids individually fed; n = 18/treatment) or fed at 0.9 kg/head/day while grazing (Exp 3; 75 and 95% SL; young bucks; n = 10/treatment). Control animals in each study were given commercial forage-based pellets. A total of 5 adult female *H. contortus* recovered from the abomasum of 2 animals from each treatment group in each experiment were examined for evidence of surface damage using scanning electron microscopy. There was no evidence of damage on worms processed from Exp 1, indicating little effect of feeding SL pellets on establishment of *H. contortus* larvae in mature goats. There were constricted folds and a disheveled cuticular surface on 2 worms (40%) and damage on the cuticular surface on one worm (20%) from the 75% SL leaf meal pellet treatment group in Exp 2, with no damage observed on control worms. In Exp 3, all 5 worms (100%) observed from both the 75% and 95% SL leaf meal pellet treatment goats (but not control goats) showed a disheveled surface. As previously reported, fecundity of worms in Exp 2 and 3 was reduced ($P < 0.05$) by SL, and total adult worm numbers were reduced ($P < 0.05$) by SL in Exp 3. Together, this work suggests that SL may have a direct effect on the cuticle of female *H. contortus*.

Key Words: goats, *Haemonchus contortus*, sericea lespedeza

ADSA-ASAS Northeast Section Symposium: The Future of Animal Agriculture Programs in the Northeast in the Face of Reducing Animal Holdings on Campus

433 The challenges associated with sustaining livestock farms for undergraduate teaching programs. T. Etherton,* *The Pennsylvania State University, University Park.*

It is extraordinarily important to provide animal science majors access to dynamic hands-on learning experiences with animals used in animal agriculture. This is particularly important as the proportion of students enrolling in animal science degree programs from urban/suburban areas grows. This shift in student demographics is occurring in the Northeast in an era where budget cuts have reduced or eliminated livestock farms at many universities. Consequently, we are navigating an era where regionally (and nationally) the number of universities that provide students learning opportunities in a “full-service” manner (i.e., maintaining farms that house beef, dairy, horses, poultry, sheep, and swine) has dramatically decreased. This reality raises many questions, including how will Colleges that elect to sustain dynamic full-service educational, research and extension programs continue to fund farms? This presentation will address strategies that universities need to use to continue to meet the funding needs (which are rapidly increasing) associated with providing full-service learning programs involving farms. In addition, an important part of the presentation will be directed to the matter of providing, and funding, a robust learning experience for the growing cohort of animal science students who wish to pursue important career interests that focus on other animal species including cats and dogs.

Key Words: farms, funding, undergraduate education

434 Budgeting for teaching programs in animal science with shrinking resources. M. G. Hogberg,* *Iowa State University, Ames.*

The cost of operating teaching programs in animal science programs have always been higher than our sister departments in colleges of agriculture. This has been due to many of our courses being laboratory intensive and the cost of maintaining university farms as teaching laboratories. As budget resources shrink, the cost of operating farms draws attention of college administrators. Departments are increasingly being asked to justify the cost of teaching farms. In this paper there will be a discussion on increasing the student educational experience as one means to justify the use of the farms as well as how to increase the funding through course fees and per diems to help pay for the cost of operations.

Key Words: teaching costs, university farms

435 Who are the animal science customers of the future? An industry perspective. D. E. Putnam,* *Balchem Corporation, New Hampton, NY.*

The future of animal science programs, particular the future of having animal holdings on campus is uncertain. There is a lack of connectivity with the largest source of funding for most institutions, which is state level, and the customers that benefit from the activities, which are national and global. Indeed, from an industry perspective regarding a university, the state or regional boundary has little meaning. What are most relevant are core competencies, how well these relate to market needs and other sources for similar information or services. This is ultimately true whether the entity is an animal producer or one of the associated industries such as animal health. Thus, while historically, a state or regional industry segment, including its students and recipients of research and extension information, was the primary customer for a given university animal science program, this has changed. A significant consolidation of all industry segments has occurred, significantly altering the number of potential customers for a given university animal science program. Yet the ease of global transfer of information has eroded the natural barriers to competition for a university, making the best programs increasingly relevant and the pressure on others to be relevant more intense. The endpoint of these changes is an overcapacity of animal science programs relative to the needs of a smaller customer base. Therefore, costs must be aligned with the value created. This problem creates an opportunity and need for interstate, multi-institutional collaboration and perhaps, consolidation. This should be done with strategic intent, choosing carefully what core competencies will be created, which customers will be targeted to serve and how this program will withstand competitive forces. Strong programs focused on clear research and educational core competencies will appeal to students and industry customers alike, all the while being enabled to maintain and enhance basic research and overall scholarly endeavors. These customers will be drawn from a larger geography yet will be well poised to extract the value from a high quality animal science program, in turn ensuring future growth for successful programs.

Key Words: animal science, customers, students

Animal Health IV

436 I. Demographic trends in livestock inventory and number of operations in the United States. G. M. Schuenemann* and W. P. Shulaw, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

Food animal veterinary services are important to support rural communities in the US; however, the veterinary supply (shortage) has recently been a source of debate in the academia and representative organizations. The objective of the present study was to estimate the trends of livestock inventory (dairy, beef, sheep, and swine) and the number of operations from 1982 to 2010 in the US. The livestock inventory and the number of operations are the main source of income that supports food animal veterinary practices in rural areas. Over time they provide a description of industry trends and serve as data points or baseline for comparisons for service providers (e.g., veterinarians), input suppliers, producers, and government among others. Historical data collected by the National Agriculture Statistical Services (NASS) were used in the present study. Livestock inventory (millions of heads) by county and the numbers of operations by group size (≤99, 100–499, and ≥500 head) were estimated for 1982 and 2010. The data collected at each point in time was compared to assess the changes (%) between 1982 and 2010 in inventory and the numbers of operations. A reduction in inventory was observed for beef (18.4%), dairy, (15.1%) and sheep (58.4%) while the inventory for swine increased (56%) from 1982 to 2010. Regardless of group size, the overall numbers of operations was reduced for beef (10.4%), dairy (40.2%), sheep (30.7%), and swine (33.6%). The livestock industry has lost about 50% (21–66% range) of small (≤99 head) beef, dairy, sheep and swine operations from 1982 to 2010. For the same period, the proportion of operations with ≥500 head has steadily increased for dairy (250% up) and beef (600% up) herds. Fewer producers of larger size characterized the US livestock industry in 2010 as compared with 1982. The effect of the livestock industry consolidation on the designated food animal veterinary shortage situations in rural areas needs further investigation.

Key Words: livestock inventory, food animal veterinary practice, rural area

437 II. Effect of trends in livestock inventory and number of operations on food animal veterinary practices in the United States. G. M. Schuenemann* and W. P. Shulaw, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

The number livestock operations and inventory are the main source of income for food animal veterinary practices across rural areas in the US. The objective of the present study was to compare the trends of livestock (dairy, beef, sheep, and swine) inventory (head) and the number of operations by group size (≤99, 100–499, and ≥500 head) from 1982 to 2010 with the designated areas of food animal veterinary shortage for 2010 in the US. Historical data collected by the National Agriculture Statistical Services (NASS) and the Veterinary Medicine Loan Repayment Program (VMLRP; USDA-AFRI, Animal Health) were used in the present study. The VMLRP reported the state-designated veterinary shortage situations by county for 2010 in the US. Type I (Private practice, food animal medicine with at least 80% time) and type II shortage situations (Private practice, rural areas, food animal medicine with at least 30% time) were considered. According to the VMLRP, an estimated 187 shortage areas (628 counties) were reported in 2010. According to the NASS, the inventory and number of operations (≤99 head) has steadily declined from 1982 to 2010 for cattle and sheep, but has increased for swine (56% up). Fewer producers with larger size of operations characterized the US livestock industry in 2010. When data for 2010 from the NASS and the VMLRP were compared, about 30% (Type I) and 52% (Type II) of the counties with veterinary shortage situations had ≤12,000 head of livestock (all cattle, sheep, and swine combined) to support food animal veterinary practices. In 1982, about 3% (Type I) and 13% (Type II) of the counties with shortage situations in 2010 had ≤ 12,000 head of livestock to support food animal veterinary practices. Both livestock inventory and number of operations are vital to support food animal veterinary practices. The livestock industry consolidation (steadily decline in livestock inventory and in the number of operations with ≤ 99 head) may contribute, at least in part, to those designated food animal veterinary shortage situations. The livestock industry consolidation and the food animal veterinary shortage situations warrant further investigation.

Key Words: livestock inventory, food animal veterinary practice, rural areas

438 Estimation of genetic parameters for hoof lesions in Canadian Holstein cows. N. Chapinal*[1,2], A. Koeck[3], S. Mason[4], A. Sewalem[5,6], D. Kelton[1], and F. Miglior[5,6], *[1]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [2]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [3]Centre for Genetic Improvement of Livestock, Department of Animal & Poultry Science, University of Guelph, Guelph, ON, Canada, [4]Alberta Milk, Edmonton, AB, Canada, [5]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada, [6]Canadian Dairy Network, Guelph, ON, Canada.*

Impaired hoof health is one the most important welfare and economic problems in modern dairy herds. No direct genetic selection for resistance to hoof lesions has been done so far. The objective of this study was to estimate the genetic parameters of hoof lesions for Holstein cows from Alberta, British Columbia, and Ontario (Canada). Hoof lesions were routinely recorded by 18 different hoof trimmers in 365 different herds from 2004 to 2011. A total of 35,059 records from 27,267 cows were used in this study. Lesions were divided into infection (dermatitis, heel erosion and foot rot), horn lesions (ulcers, hemorrhages and white line disease) and other lesions (e.g., interdigital hyperplasia, fissures). One-trait (any lesion in any hoof), 2-trait (any lesion in the front and rear hooves), and 4-trait (front and rear infection, and front and rear horn lesions) linear animal model were used. For the analyses, the statistical model included the fixed effects of parity (1 to 6), hoof trimmer, and stage of lactation, and the random effects of herd-year-season, permanent environment, animal and random error. Variance components were estimated with REML procedure using a DMU software package. The heritability estimates were: a) 0.06 for the occurrence of any lesion, b) 0.02 and 0.07 for the occurrence of any front and rear lesion, respectively, and c) 0.02, 0.01, 0.08 and 0.05 for the occurrence of front infection, front horn lesion, rear infection and rear horn lesion, respectively. The genetic correlation between the occurrence of any lesion in the front and rear hooves was 0.53. The genetic correlations between the occurrence of front and rear infection and the occurrence of front and rear horn lesion were 0.78 and 0.58, respectively. In conclusion, hoof lesions traits showed genetic variation that needs to be included in routine genetic evaluation for lameness resistance. Standardized hoof health data collection by hoof trimmers should be encouraged. Further analysis using additional hoof health data and conformation traits is in progress.

Key Words: dermatitis, sole ulcer, lameness

439 An international overview of the recording and use of functional traits in dairy cattle breeding and management.

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An important component in the development of sustainable dairy production systems is the maintenance of cow health and functionality. Genetic selection has resulted in substantial increases in cow productivity over the past 50 years, but health and fertility are increasingly important determinants of individual profitability. Breeding goals and selection programs are changing worldwide to reflect this shift toward greater functionality. Standardized trait definitions, recording practices and data analyses are needed to ensure that data and genetic evaluations are comparable across countries, but such efforts have proven to be difficult in practice. The International Committee for Animal Recording's Functional Traits Working Group (FTWG) has worked for several years to develop a standard defining best practices for the recording, evaluation, and genetic improvement of functional traits in dairy cattle. A review of past, current, and planned activities in many countries allowed the FTWG to identify key areas in which standards were needed. In addition to indicator traits like somatic cell score for mastitis, direct measures of health and disease will provide valuable information for genetic evaluations. Other traits, such as feed intake, may be developed and used to improve cow functionality. Guidelines for new traits must account for new sources of information and the needs of parties involved in data recording. Technical developments should be reviewed regularly to ensure that data represent the entire population, collection costs to producers and recording bodies are reasonable, and high-quality records suitable for use by management systems and genetic evaluation programs are obtained. A network of experts is needed to support the FTWG's efforts in compiling and updating the guidelines, exchanging information and experiences, and meeting the future needs of the dairy industry. A survey to assess current practices relating to the collection and evaluation of functional data has been distributed internationally.

Key Words: health traits, dairy management, data recording

440 Effect of intrauterine dextrose therapy on reproductive performance of lactating dairy cows with clinical endometritis.

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The objective was to assess the effect an intrauterine infusion of 50% dextrose in water (DEX) on clinical cure and reproductive performance of lactating dairy cows diagnosed with clinical endometritis (CE) compared with untreated control cows (CON). Cows (n = 1122) 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 2 treatment groups: 1) CON (n = 159) or 2) 200 mL DEX (n = 154). Fourteen days post-therapy (at 40 ± 3 DIM), treated cows were re-examined to assess treatment responses (cure). All cows 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) or Cosynch (GnRH-7d-PGF2α-72 h-GnRH^{+}TAI) 12 d later. Cows displaying signs of standing estrus any time during the OV 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. The proportion of cows that cured (GLIMMIX) and pregnancy up to 250 DIM (PHREG) were assessed. DIM at first service, milk yield at first service, BCS at treatment, rectal temperature at treatment were not different between groups. Cows with CE had greater cervical diameters at the time of treatment compared with cows without CE (n = 809). The proportions of cows that cured (vaginoscopy score of 0) was greater for DEX (48.4%) compared with CON cows (29%; $P < 0.05$). The probability of pregnancy was greater for DEX (HR = 0.74) compared with CON cows (HR = 0.60; $P < 0.05$). The median time to pregnancy was shorter for cows without CE (89 d), or DEX (117 d) compared with CON cows (135 d). The use of intrauterine DEX alone or as an adjunct of antibiotic therapy for the treatment of cows diagnosed with CE or metritis needs further investigation.

Key Words: endometritis, intrauterine dextrose, pregnancy

441 Efficacy of two herbal remedies as alternatives to antibiotic dry cow therapy: Preliminary microbiology results.

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Mastitis is a costly disease for the dairy industry. It is normally treated using antibiotics either for clinical cases of mastitis or for prevention in nonlactating cows. The aim of dry period preventive therapy is to eliminate existing infections and to prevent new infections from occurring pre-calving. This study evaluated the effectiveness of 2 herbal remedies as dry period treatments: Phyto-Mast (Penn Dutch Cow Care, Narvon, PA) and Cinnatube (New AgriTech Enterprises, Locke, NY). If proven effective, those treatments could potentially reduce antibiotic usage on all dairy farms. Data were taken from 3 private and one research herd over 2 years. Five intramammary dry treatments were assessed: 1) Phyto-Mast; 2) Cinnatube; 3) Phyto-Mast plus Cinnatube; 4) no treatment; 5) Penicillin dihydrostreptomycin plus teat sealant (Conventional). Milk samples were aseptically collected from each functional quarter of each cow (n = 264) before treatment and once within 3 to 10 d post-calving. Microbiological content was assessed using methods consistent with those of the National Mastitis Council. A mixed linear model was used to obtain least squares means and comparisons between treatments were obtained using the Tukey-Kramer adjustment. A cure was defined as the absence of a microbiological species that was present pre-treatment. The scope of the analysis is limited by the positive fact that 130 cows had no infection present pre-treatment and no infection post-calving. Results are given as least squares means ± se. There were no differences among treatments for percentage of quarters per cow with new infections: Conventional 2.8 ± 2.0%, Cinnatube 12.1 ± 4.4%, no treatment 16.0 ± 5.4%, Phyto-Mast plus Cinnatube 16.8 ± 5.7%, Phyto-Mast 17.2 ± 5.8%. For percentage of quarters per cow cured, analyzed from the subset of cows with infections pre-calving (n = 134), there were no differences among treatments: Phyto-Mast 23.4 ± 8.9%, Phyto-Mast plus Cinnatube 21.0 ± 7.9%, no treatment 18.8 ± 7.8%, Cinnatube 15.6 ± 6.7%, Conventional 15.0 ± 12.6%. Though no dry cow treatment was significantly more effective in this trial, the proportion of non-infected cows was encouraging.

Key Words: mastitis, organic, dairy

442 Comparison of low versus high calcium "anionic" diets for prevention of hypocalcemia and milk fever. J. P. Goff*[1] and R. L. Horst[2], [1]*Iowa State University, Ames,* [2]*Heartland Assays, Ames, IA.*

Three questions were addressed with this study. 1) Is it necessary to increase diet Ca when using anions to reduce DCAD to prevent periparturient hypocalcemia? 2) Can adding anions to a "low" Ca diet further reduce hypocalcemia around calving? 3) Are anions effective even if urine pH is not reduced all the way to the target pH of 6.2–6.8? Sixty Holstein cows entering their 2nd or greater lactation were assigned to 1 of 3 treatments. A high wheat straw-corn silage, 1.46 Mcal NEl/kg diet was utilized that was 1.44% K, 0.11% Na and 0.25% P. A high Mg, low Ca, No anion, a high Mg, low Ca, Anion, or a moderate Mg, high Ca, Anion supplement was added to the basal diet to create diets (see Table 1). Diets were fed for at least 2 weeks before calving and plasma Ca was determined weekly and within 7 h after calving and again at 24 ± 7 h after calving. Dry matter intake before calving was similar across all treatments with cows averaging 13.4 kg/d from 14 to 3 d before calving. The pH of urine collected during the wk before calving and blood Ca concentrations (mg/dl) (Mean + SEM) close to calving (Time 0 and 24 h) are presented (see Table). Plasma Ca was significantly improved (ANOVA, $P < 0.05$) at calving by both Low and Hi Ca anion supplementation – despite the fact that anions were not added in high enough quantity to decrease urine pH to the "target pH." Use of anions to prevent hypocalcemia does not require addition of Ca to the diet. The effectiveness of a "low calcium" diet to prevent hypocalcemia can be improved by adding anions.

Table 1. Diet composition; urine pH and plasma Ca observed

Treatment	% Ca	% Mg	% Cl	DCAD (mEq/kg)	Urine pH	Plasma Ca Time 0	Plasma Ca at 24 h
Lo Ca, No Anion	0.46	0.65	0.44	+162	8.20 ± 0.06	7.17 ± 0.31	7.44 ± 0.34
Lo Ca, Anion	0.46	0.66	1.24	−61	7.07 ± 0.17	7.95 ± 0.24	8.09 ± 0.24
Hi Ca, Anion	0.78	0.48	1.26	−68	7.41 ± 0.17	8.05 ± 0.27	7.98 ± 0.35

Key Words: milk fever, DCAD, hypocalcemia

443 Variation in metabolic, hematologic, and innate immunologic parameters in early postpartum dairy cows is not largely influenced by dairy, days in milk, or parity. M. D. Sellers,* A. R. Pepper-Yowell, D. L. Hanson, C. R. Nightingale, C. J. Cobb, B. S. Obeidat, and M. A. Ballou, *Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

The objective was to partition total variation in metabolic, hematologic, and immune variables in early postpartum dairy cows among dairy, days in milk (DIM), and parity (LACT). Two hundred forty Holstein cows, 2–8 DIM and 2nd-8th LACT, from 8 dairies were sampled across 5 d (BLK; n = 6 cows/dairy/day). Metabolic measurements included plasma nonesterified fatty acids, β-hydroxybutyrate, glucose, and urea nitrogen concentrations. Hematologic measurements included total leukocytes and differentials, and immunologic measurements included neutrophil oxidative burst capacity to an *Escherichia coli*, neutrophil L-selectin expression, plasma haptoglobin concentration, rectal temperature, as well as tumor necrosis factor-α and interferon-γ concentrations in stimulated whole blood cultures with lipopolysaccharide and phytohemagglutinin, respectively. Type III sums of squares were estimated using PROC Mixed with the fixed effects of DIM, LACT, and the random effects of dairy and BLK. No differences were observed in regard to DIM ($P > 0.22$) or LACT ($P > 0.14$). Data are reported as η^2, representing the proportion of the total sums of squares for each effect. For metabolic parameters, DIM accounted for an average of 2.2% of total variation, LACT an average of 2.9%, and dairy an average of 4.3%, with residual variation accounting for an average of 75.1%. For hematologic parameters, DIM accounted for an average of 3.4% of total variation, LACT an average of 2.8%, and dairy an average of 4.2%, with residual variation accounting for an average of 85% of total variation. For immune parameters, DIM accounted for an average of 3.1% of total variation, LACT an average of 2.7%, and dairy an average of 9.8%, with residual variation accounting for an average of 78.1% of total variation. Differences among dairy, DIM, and LACT did not explain a large portion of the total variation across each class of variables; whereas residual effects likely associated with genetics, metabolic status, and health status contributed to the majority of the total variation.

Key Words: immune, metabolic, transition cow

444 Production and metabolic response of lactating dairy cows supplemented with a dietary antioxidant to intramammary infusion of lipopolysaccharide during thermoneutral and heat stress conditions. A. L. Kenny*[1], Y. M. Yang[2], N. M. Barkley[1], R. R. Rodrigues[1], G. I. Zanton[2], and M. R. Waldron[1], [1]*University of Missouri, Columbia,* [2]*Novus International Inc., St. Charles, MO.*

The response to intramammary lipopolysaccharide (LPS) infusion during heat stress in 24 lactating dairy cows fed the antioxidant Agrado Ultra (dry blend of ethoxyquin and propyl gallate) was investigated. Holstein cows (153 ± 5 d in milk) were randomly assigned (complete block design) to 1 of 2 treatments: Control (soy hulls 6.1 g/cow/day; n = 12) or AOX (AGRADO Ultra 6.1 g/cow/day; n = 12). Cows were housed in a free stall barn until d 14 of treatment and then housed in environmentally controlled rooms for 7 d at thermoneutral temperature (TN; d 15 to 21; Constant 20°C) and then 14 d of programmed 12-h cyclical heat stress (HS; d 22 to 35; Mean THI range 72.5 ± 0.1 to 81.3 ± 0.5). On d 20 (TN) systemic plasma and quarter milk was sampled and sterile saline (10 mL) infused into the right front quarter of the mammary gland and LPS (100 ng/10 mL saline) into the right rear quarter. Rectal temperature, respiration rate were measured, and systemic plasma and milk from the 2 quarters were sampled 1, 2, 3, 4, 6 and 12 h after infusion. This process was repeated on d 34 (HS) using the left quarters. Data were analyzed using SAS by mixed model ANOVA with repeated measures. Data collected at 0 h were used as covariates if found to be significant. Rectal temperature and respiration rate increased during HS ($P < 0.01$) and somatic cell count was greater in the LPS quarter than the saline quarter ($P < 0.01$). All milk components changed over time ($P < 0.01$) and between TN and HS ($P < 0.01$); however, these responses were similar for both saline and LPS quarters. The saline quarter of control cows had a greater percent of milk lactose ($P = 0.03$) and a tendency ($P = 0.08$) for fewer somatic cells than the saline quarter of AOX cows. All other responses of milk components and metabolites to LPS infusion were similar between control and AOX ($P > 0.05$). The addition of antioxidant to the diet of lactating dairy cows did not alter the response of plasma metabolites or milk components to intramammary infusion of LPS.

Key Words: dairy, antioxidant, lipopolysaccharide

445 Potential risk of western juniper-induced abortion in beef cattle.

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Ponderosa pine needles are known to induce late term abortions in cattle. Labdane acids including isocupressic acid (ICA) and agathic acid are the compounds responsible for initiating the abortions. Current research results suggest that an ICA concentration of 0.5% is required for pine needles to be a risk for inducing abortions, while pine needles that contain >1% ICA pose a significant risk. However, stage of pregnancy, amount consumed, snow cover, temperature and other issues contribute to the overall risk. Research on ponderosa pine needles has demonstrated large variation in the concentrations of the abortifacient compounds, both geographically and seasonally. Concentrations vary from location to location as well as seasonal fluctuations in some areas throughout the year. This variability results in differential potential for pine needle-induced abortions to occur depending upon the location and the time of the year. Several other trees, including many species of pine, juniper, cypress and cedar contain either isocupressic acid or agathic acid at concentrations sufficient to be a risk for causing abortions in late term pregnant cattle. In this study, we present data that western juniper (*Juniperus occidentalis*) trees contain compounds known to be abortifacient in cattle and that consumption of large amounts of bark in the third trimester of gestation can induce abortions. We also examined the geographical variation in the labdane acid content of western juniper trees by measuring the labdane acid content of bark, needles, and berries from western juniper trees from 6 different locations in Baker County, Oregon. The berries had a higher concentration of labdane acids than needles ($P < 0.001$) and bark ($P < 0.001$). Interestingly, bark had a higher concentration of labdane acids than needles ($P < 0.001$). However, there was no difference in the concentrations of labdane acids from location to location for berries ($P = 0.33$), needles ($P = 0.13$), or bark ($P = 0.15$). These results indicate that there is a similar risk for western juniper trees to cause late term abortions in cattle across Baker County, Oregon.

Key Words: juniper-induced abortion, western juniper, abortifacient

446 Assessment of daily milk fat and protein composition and the milk fat-protein ratio early postpartum as a predictor for subclinical ketosis in dairy cows.

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Objectives were to determine milk fat percentage (%), milk protein % and fat-protein ratio cut-off values (Cv) to predict subclinical ketosis (SCK) during early lactation. A total of 209 cows were enrolled in the study. Daily milk samples were analyzed using AfiLab milk analyzer from Afikim milk system and the daily average % of fat and protein in milk, and the milk fat-protein ratio were calculated for the first 12 d in milk (DIM). Blood samples were collected at 4, 7 and 12 DIM to evaluate the concentration of β-hydroxybutyrate (BHBA). Concentration of BHBA > 1.2 mM was the criterion to determine SCK. The receiver-operating characteristics analysis using MedCalc software was deployed to calculate Cv of milk fat %, milk protein %, and fat-protein ratio for each day before and on the same day when BHBA was measured. A Cv was selected based on the best-combined sensitivity (Se, %) and specificity (Sp, %). Milk fat % at 3 DIM predicted SCK at 4 DIM (Cv > 4.96%, Se = 65.3 and Sp = 69.2). Likewise, milk fat % at 4 (Cv > 4.57%, Se = 78.6 and Sp = 52.2), 7 (Cv > 4.68%, Se = 74.6 and Sp = 60.5) and 12 (Cv = 4.35%, Se = 63.0 and Sp = 76.6) DIM predicted subclinical at 4, 7 and 12 DIM, respectively. Milk fat protein at 7 DIM predicted subclinical ketosis at 7 DIM (Cv < 3.47%, Se = 65.3 and Sp = 69.2). Milk fat-protein ratio on d3 postpartum predicted subclinical ketosis at 4 DIM (Cv > 1.36, Se = 50.0 and Sp = 78.0). Moreover, milk fat-protein ratio at 4 (Cv > 1.31, Se = 69.1 and Sp = 61.6), 7 (Cv > 1.40 Se = 68.7 and Sp = 77.4) and 12 (Cv > 1.56, Se = 40.8 and Sp = 93.7) DIM predicted SCK at 4, 7 and 12 DIM, respectively. Milk composition in the first 12 DIM can be used to predict SCK; however, the Se and Sp of cut-off values were moderate. Thus, because of limited Se or Sp, milk composition in the first 2 weeks postpartum can aid on the diagnosis, but should be used concurrent with other methods to identify cows with SCK.

Key Words: subclinical ketosis, milk composition, dairy cows

Breeding and Genetics: Advances in Genomic Methodology

447 Iterative combination of national phenotype, genotype, pedigree, and foreign information. P. M. VanRaden,* *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Single step methods can combine all sources of information into accurate rankings for animals with and without genotypes. Equations that require inverting the genomic relationship matrix G work well with limited numbers of animals, but equivalent models without inversion are needed as numbers increase. An equivalent model that includes extra equations to solve for the added contribution of genomic information was applied to national Jersey data. The extra equations solved for $G\gamma = u$ and $A_{22}\phi = -u$, where A_{22} contains pedigree relationships for genotyped animals and u contains genomic estimated breeding values (GEBV) from the previous iteration. Solutions for γ and ϕ were then added when solving for u. Multi-trait across country evaluations (MACE) were deregressed and inserted as extra records containing foreign information. The methods were tested on US Jersey yield data containing 4.4 million lactation records, 4.1 million animals in the pedigree, 16,852 genotyped animals, and 7,072 bulls with foreign MACE records. Heritability was reduced from 0.35 in official evaluations to 0.23 to mimic the effect of cow adjustments. For genotyped young bulls, single-step evaluations were correlated by 0.966 to multi-step evaluations. Both had the same reliability when tested using 4 year truncated data to predict deregressed proofs from the last 4 years, but regressions for single-step evaluations were closer to expected values. The weight on ϕ was reduced to 0.8 in the single step method and polygenic variance was increased to 20% in the multi-step method, both to improve the regressions. Convergence was much slower when the same algorithm was applied to Holstein data, and correlations were poor even after thousands of iterations. The number of Holstein genotypes was 135,724, with 65 million lactation records and 50 million animals in the pedigree. Second order Jacobi iteration was used in this study, but preconditioned conjugate gradient algorithm should be faster. More efficient strategies are needed because algorithms that work well on small or medium-sized data sets may not handle very large populations.

Key Words: single step methods, genomic evaluation, mixed model equations

448 Adaptation of BGF90 package for genomic computations. I. Misztal*[1], A. Aguilar[3], S. Tsuruta[1], and A. Legarra[3], *[1]University of Georgia, Athens, [2]INIA, Las Brujas, Canelones, Uruguay, [3]INRA, UR631 Station d'Amélioration Génétique des Animaux (SAGA), Castanet-Tolosan, France.*

The BGF90 package is a tool for mixed model analyses. The original package contains programs for renumbering, BLUP, variance components estimation, accuracy approximation and visualization. A renumbering program (RENUMF90) prepares data files for application programs, prunes pedigrees and can support national data sets. BLUP programs are for equations in memory (BLUPF90) and iteration on data (BLUP90IOD). Parameter estimation is via REML (REMLF90 and AIREMLF90) or Bayesian methods (GIBBS*F90), which are able to support large number of traits (20+). Samples from GIBBS* programs can be analyzed by POSTGIBBSF90, and accuracies of predictions can be approximated by ACCF90. Specific programs are available for threshold-linear models. Nearly all programs were updated to support the genomic information and several new programs were added. Program PreGSF90 analyzes the SNP information, provides basic quality control, creates a genomic relationship matrix using a large variety of options, and combines pedigree and genomic relationship matrices for a single-step methodology. Computations with PreGSF90 are optimized for parallel processing; preparing matrices for 30k animals with 50k SNP takes about 1 h. PreGSF90 can be run separately or as part of application programs. PostGSF90 converts GEBV to SNP effects, displays Manhattan plots possibly using moving averages, and estimates variances of SNP effects. Program PredF90 predicts GEBV based only on estimates of SNP effects obtained from PostGSF90. Most of the programs are available online at nce.ads.uga.edu. The package can be used for genomic predictions (including national data sets), parameter estimation (including GBLUP and G-REML), and GWAS. Unequal variances for SNP effects similar to those in BayesA and subsequently "Manhattan" plots can be obtained by iterating on postGSF90 and possibly one of BLUP programs; no deregression is required and complex models may be used. Classical GWAS can be carried out with BLUPF90 fitting one SNP at a time as fixed regression and an animal effect with a genomic (or combined) a relationship matrix. The package has been used for genomic analyzes of models with up to 10 million animals, 18 traits, 40k genotypes and 400k SNP. The updated package simplifies genomic analyses in breeding applications.

Key Words: genomic selection, genome wide association, software

449 Methods to include foreign information in national evaluations. P. M. VanRaden and M. E. Tooker,* *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Genomic evaluations (GEBV) with higher reliability often result from including genotypes and phenotypes from foreign bulls in the reference population. Multi-step methods evaluate domestic phenotypes first using only pedigree relationships (EBV), then add foreign data available from multi-trait across country evaluations (MACE), then compute GEBV for genotyped animals, and finally propagate information from GEBV to EBV of non-genotyped relatives. An alternative is to include domestic and foreign phenotypes together so that GEBV and EBV for all animals can be computed in a single step. The MACE EBV could be treated as a correlated trait, but previous research indicates that including these as the same trait with their lower reliability (REL) is sufficient. To include foreign data, the bull's deregressed proof (DRP) was obtained from the MACE EBV as: DRP = PA + (EBV - PA)/REL, where PA is the parent average from MACE. For bulls with both domestic and foreign daughters, domestic EBV was used instead of PA to compute DRP, and domestic daughter equivalents (DE) were subtracted from the total. Remaining DE were added to diagonals of the mixed model equations and were used to compute REL. This strategy included 1 extra record per bull and differed from previous methods that included 1 record for each foreign daughter. For multi-trait models, diagonal matrix D contained the DE for each trait of a bull. The vector of DRP was premultiplied by $D^{.5}T^{-1}D^{.5}$, where T is the genetic covariance matrix among traits, and $D^{.5}T^{-1}D^{.5}$ was added to the mixed model equations. A mean for the DRP was included in the model because the base is not fixed during iteration, only after convergence. The methods were tested using national Holstein data for 25 million cows, MACE data for 88,000 bulls, and a pedigree file of 52 million animals. For bulls with only foreign daughters, correlations between MACE EBV and national EBV after including the foreign data were 0.991 to 0.994 for yield traits, 0.986 for somatic cell score, 0.973 for single-trait productive life, and 0.974 for daughter pregnancy rate. This simple approach is reasonably accurate for including foreign data in national evaluations.

Key Words: MACE, foreign daughters, genomic evaluation

450 Characteristics and use of the Illumina BovineLD BeadChip. G. R. Wiggans*[1], P. M. VanRaden[1], T. A. Cooper[1], C. P. Van Tassell[2], T. Sonstegard[2], and B. Simpson[3], [1]*Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD,* [2]*Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD,* [3]*GeneSeek, Lincoln, NE*

Genotypic information from the 6,909-SNP Illumina BovineLD (LD) Genotyping BeadChip, which replaced the Illumina GoldenGate Bovine3K (3K) Genotyping BeadChip, have been included in US genomic evaluations since November 2011. Of 73 LD single nucleotide polymorphisms (SNP) not used in genomic evaluation, 35 were from the Illumina BovineSNP50 (SNP50) Genotyping BeadChip, and 38 (13 mitochondrial, 9 Y-chromosome, and 16 X-chromosome SNP to improve genome coverage) were from the Illumina BovineHD (HD) Genotyping BeadChip. As of February 2012, the USDA national genotype database for dairy cattle included LD genotypes for 19,515 animals (550 males). Call rate for LD SNP used in genomic evaluation was 99.4%. The 9 Y SNP were highly effective in sex validation (call rate of 98% for males and 0.5% for females). Rate of parent-progeny conflicts on a SNP basis was similar to that for SNP50 SNP. Imputation accuracy averaged 98.9% for Holsteins, 98.3% for Jerseys, and 97.9% for Brown Swiss for LD genotypes compared with 95.9, 94.6, and 93.9% for 3K genotypes. To calculate reliability of genomic evaluations, the fraction of correctly imputed SNP was estimated as a function of the number of low-density SNP that were not missing and the number of animals with SNP50 genotypes. Reliabilities for LD genotypes were about 5 percentage points higher than for 3K genotypes. Using the add-on capability of the LD chip, the GeneSeek Genomic Profiler (GGP) for Dairy Cattle BeadChip was developed with 8,655 SNP. The additional SNP were for proprietary single-gene tests, detection of haplotypes that affect fertility, imputation of microsatellite alleles to facilitate parentage validation, and improved imputation by including more 3K SNP. The GeneSeek Genomic Profiler 80K (GGP-80) also was developed with around 80,000 SNP. The added SNP were SNP50 and HD SNP with the largest effects on primarily the net merit index. Consideration also was given to spacing as well as maintaining around 30,000 SNP50 SNP for imputation accuracy. The GGP and GGP-80 genotypes are expected to further improve accuracy of imputation and genomic evaluation because of the additional SNP.

Key Words: genomic evaluation, beadchip, SNP

451 Partitioning genetic (co)variances leading to alternative derivation of single-step type genomic prediction equations allowing joint estimation of GEBV and SNP effects. N. Gengler*[1], G. Nieuwhof[2], K. Konstantinov[2], and M. Goddard[3,4], [1]*ULg - Gembloux Agro-Bio Tech, Gembloux, Belgium,* [2]*ADHIS, Bundoora, Australia,* [3]*DPI, Bundoora, Australia,* [4]*University of Melbourne, Melbourne, Australia.*

Interest in single-step type procedures to do genomic prediction is growing because of its numerous advantages especially its robustness and its simplicity. Current derivations of single-step equations modify relationships among animals replacing for genotyped animals on an inverted scale, pedigree based by modified, partially genomic based, relationships. From an theoretical standpoint these methods are all based on assumptions and use a hidden underlying hypothesis that modified relationships are obtained as linear combination of strictly genomic and pedigree based relationships, therefore implicitly "weighting" SNP and polygenic effects. Alternative equations were recently proposed de-absorbing the genomic relationships out of the equations. This derivation did not change basic assumptions, but was derived using a matrix of relationship differences. This presentation will show a new and alternative derivation of single-step type genomic prediction equations allowing joint estimation of GEBV and SNP effects based on the partitioning of genetic (co)variances. The method was derived from a random mixed inheritance model where SNP and residual polygenic effects are jointly modeled. The derived equations were modified to allow non-genotyped animals and to estimate directly and jointly GEBV and SNP effects. Equations resemble recently proposed alternative single-step equations but were derived differently and are based on completely different assumptions and avoid certain issues in de-absorbing derivation linked to the matrix of relationship differences by using (co)variances. Several other advantages of the new equations are that weighting of SNP and polygenic effects becomes explicitly and that SNP effects are also estimated. This method makes better use of High-Density SNP panels and can be easily modified to accommodate other genetic effects as major gene effects or copy-number variant based effects. Finally these alternative equations combine advantages of single-step and of explicit SNP effect estimation based methods. Additional research is required to test and validate the proposed method.

Key Words: genomic prediction, single-step method, alternative equations

452 Use of canonical discriminant analysis for detecting selection signatures in cattle. R. Steri, C. Dimauro, S. Sorbolini, G. Marras, M. Cellesi, G. Gaspa, and N. P. P. Macciotta,* *Dipoartimento di AGRARIA, Università di Sassari, Sassari, Italia.*

The development of high throughput SNP platforms for several livestock species allows to study genetic variability both within and between breeds. Several techniques have been used to exploit information derived by these new tools, including principal component analysis (PCA). However, results are not easy to interpret in terms of markers, or genomic regions, linked to phenotypic traits. To explain the biological meaning of multivariate approach, canonical discriminant analysis (CDA) could be proposed. CDA is based on PCA applied on within-between (co)variance ratio matrix of predefined groups instead the (co)variance matrix. The new orthogonal variables maximize the differences among groups on the basis of variances within each groups. The biological meaning of canonical variables (CANi) can be inferred by the canonical coefficients (loadings) that represents the correlations between CAN and the original variables. In the present work, CDA was used to analyze a total of 2,627 bulls of Italian Holstein (IH; 1000), Italian Brown (IB; 755), Italian Simmental (IS; 493) and Piemontese (IP; 379). Thus CDA was used to study genetic differences between 2 dairy, one beef and one dual-purpose cattle breeds. Animals were genotyped with the 50k SNP panel. The analysis was carried out separately for the 29 autosomes. The separation among breeds was always clear. On average, the CAN1 explained about 50% of the total variability and was able to discriminate between IH and all the other breeds. This result, probably, underline the high selection pressure exerted on this population. CAN2 and CAN3, explaining on average 25% each, usually separated dairy breeds (IH and IB) from the IP, whereas the IS tended to be located in an intermediate position. Structure of the new variables shows genomic regions associated with extreme loadings value. Considering only values exceeding the 0.99 quantile as an empirical threshold, we found 743 SNPs across the whole genome that can be considered involved in differences among breeds. Interesting clustered signals were found near ABCG2 for CAN1, MSTN, LEPR and MC1R for CAN2 and LEP and KIT for CAN3.

Key Words: SNP, canonical discriminant analysis, selection signatures

453 Genome-wide association mapping including phenotypes from relatives without genotypes. H. Wang*[1], I. Misztal[1], I. Aguilar[2], A. Legarra[3], and W. Muir[4], *[1]Department of Animal and Dairy Science, University of Georgia, Athens, [2]Instituto Nacional de Investigación Agropecuaria, INIA Las Brujas, Canelones, Uruguay, [3]INRA, UR631 Station d'Amélioration Génétique des Animaux (SAGA), Castanet-Tolosan, France, [4]Department of Animal Science, Purdue University, West Lafayette, IN.*

The purpose of this study was to extend single-step GBLUP (ssGBLUP) to genome wide association analysis (GWAS). The ssGBLUP is a procedure that calculates breeding values (GEBVs) based on combined pedigree, genomic and phenotypic information. The procedure achieves these goals by blending traditional pedigree relationships with those derived from genetic markers. In this study, GEBVs were converted to marker (SNP) effects. Unequal variances for markers were incorporated by deriving weights from SNP solutions, and incorporating the calculated weights into a new genomic relationship matrix. Improvements on the SNP weights were obtained iteratively either by recomputing the SNP effects only or also by recomputing the GEBVs. Efficiency of the method was examined using simulations for 10 replications with 15,800 subjects across 6 generations, of which 1500 were genotyped with 3000 SNP markers evenly distributed on 2 chromosomes. Heritability was assumed 0.5 all due to 30 QTL effects that were simulated based on Gamma distribution across genome. Comparisons included accuracy of breeding values and cluster of SNP effects of ssGBLUP and BayesB with several options for each procedure. For genomic evaluation, an accuracy of prediction of 0.89 (0.01) was obtained by ssGBLUP after only one iteration, which was slightly higher than BayesB of 0.88 (0.02), but required only a small fraction of time. Power and precision for GWAS applications was evaluated by correlation between true QTL effects and the sum of m adjacent SNP effects, where m varied from 1 to 40. The highest correlations were achieved with m = 8 and were 0.82 (0.02) for ssGBLUP, and 0.83 (0.07) for BayesB with m = 16 according to marker density and extent of linkage disequilibrium in simulated population. Computing time for ssGBLUP took about 2 min while BayesB took about 5 h. Therefore, ssGBLUP with marker weights is 2 orders of magnitude faster than the next best procedure, accurate, and easy to implement for GWAS applications. In particular, ssGBLUP is applicable to GWAS with complex models including multitrait, maternal and random regression.

Key Words: genomic evaluation, genome-wide association mapping, single step procedure

454 Genotyping by sequencing (GBS): A novel, efficient and cost-effective genotyping method in cattle. M. De Donato*[1,2], S. O. Peters[1,3], S. E. Mitchell[4], T. Hussain[1,5], and I. G. Imumorin[1], *[1]Department of Animal Science, Cornell University, Ithaca, NY, [2]IIBCA, Universidad de Oriente, Cumana, Venezuela, [3]Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [4]Institute for Genomic Diversity, Cornell University, Ithaca, NY, [5]Institute of Biochemistry and Biotechnology, University of Veterinary and Animal Sciences, Lahore, Pakistan.*

High-throughput genotyping methods have increased the analytical power to study complex traits by increasing the resolution and ultimately identifying the changes responsible for phenotypic differences in economic traits. However, high cost has prevented large scale use for animal improvement. In this study, we applied a recently published method for genotyping plants to 7 taurine and indicine breeds of cattle from the US and Africa, to determine the efficiency and feasibility of this method in cattle. Genomic DNA from each animal was individually digested with *Ape*KI and *Pst*I. Each sample was then ligated to adaptors containing one of 96 unique bar codes. Samples were then pooled and sequenced in a single lane on the Illumina HiSeq 2000. *Ape*KI GBS libraries produced more than 1.37 million unique reads, but had low number of SNPs, low call rate and too many reads with multiple locations in the genome, so this data was not analyzed any further. *Pst*I libraries produced about 500,000 unique reads, 93.9% of which were tags with at least 64 bases with no "Ns," with a significantly lower number of non-unique reads. On average, 1.14 million reads were produced per animal. A total of 62,295 SNPs were detected throughout all autosomes with an average distance of 39.9 kb, as well as 1,402 SNPs on the X chromosome at an average distance of 106.1 kb. The average marker density per autosome was highly correlated with size (CC = 0.797, $r^2 = 0.635$) with more markers per Mb in smaller chromosomes. Average SNP call rate in the genotyped individuals was higher than 0.70 in 81.5% of all loci, and the average minor allele frequency was 0.223 ± 0.001. Average observed heterozygosity per individual ranged from 0.046 to 0.294, with 0.064 as the lowest found in the Nigerian Sokoto Gudali breed (indicine) and the highest of 0.197 in Brangus (indicine × taurine). This technique has shown to be a novel, flexible, cost effective and sufficiently high-throughput, yet requiring no previous knowledge of the population, genome structure or diversity and can provide different levels of marker density depending on the resolution or cost desired.

Key Words: cattle, genotyping, NGS

455 Models' predictive ability of breeding values for a small data set of genotyped animals. F. M. Rezende*[1], J. B. S. Ferraz[1], F. V. Meirelles[1], J. P. Eler[1], and N. Ibañéz-Escriche[2], *[1]Faculdade de Zootecnia e Engenharia de Alimentos-Universidade de São Paulo, Pirassununga, São Paulo, Brazil, [2]Genètica i Millora Animal-IRTA, Lleida, Cataluña, Spain.*

The aim of this study was to compare the breeding values' predictive ability of 3 different models for a small data set composed by 3,149 animals genotyped for 106 SNP markers, for which adjusted phenotype and pedigree information were available. The 106 SNP are causal mutations or are located in transcript or promoter regions of *Bos taurus* genes. A data set composed by 83,404 Nellore beef cattle animals measured for production traits and their pedigree, contained a total of 116,652 animals, were used to estimate fixed and random effects solutions on single traits analysis by MTDFREML software, under animal model. The direct additive effects estimated from that analysis were assumed to be the "true" breeding values for those animals. The individual records for all traits were adjusted for fixed and random effects solutions, except for the direct additive effect. The adjusted phenotypes, composed by the direct additive and residual portions of raw phenotype, were used as dependent variables in tested models. Model 1 included only polygenic effects, model 2 included only markers effects and model 3 included both polygenic and markers effects. These analyses were performed by TM software. The models' predictive ability was verified by Spearman rank correlation coefficient, estimated by PROC CORR from SAS, between the animals' rank based on breeding values estimated on models 1, 2 and 3 and the rank based on "true" breeding value. The correlation coefficients estimated for models 1, 2 and 3 were 0.47, 0.22 and 0.66 for weaning weight, 0.53, 0.36 and 0.83 for post weaning gain, 0.57, 0.31

and 0.94 for scrotal circumference and 0.57, 0.29 and 0.84 for muscle score, respectively. The estimates of rank correlation coefficients lead to the same inferences for all analyzed traits. The reduced number of genetic markers available was not enough to retain a large proportion of additive effects contained in the adjusted phenotypes, as indicated by the lower values of rank correlation for model 2. The outcomes for model 3 suggested that for a small data set and a reduced set of genetic markers, the additive effects were better estimated when markers and polygenic effects were considered together, what suggests that marker assisted selection can be useful for Nellore populations.

Key Words: Marker assisted selection, SNP markers, *Bos indicus* cattle

456 Improving efficiency of inferring genetic architecture parameters in whole genome prediction models. W. Yang* and R. J. Tempelman, *Michigan State University, East Lansing.*

The reliability of whole genome prediction models (WGP) based on using high density single nucleotide polymorphism (SNP) panels critically depends on knowledge and/or reliable estimation of key hyperparameters that partly specify genetic architecture for the traits of interest. These hyperparameters include π, the proportion of SNP not associated with the trait as well as df and s^2. These latter 2 are, respectively, the degrees of freedom and scale parameter for the Student t density, often used to characterize the distribution of SNP effects in BayesB ($\pi > 0$) and BayesA ($\pi = 0$) models. Estimation schemes, however, based on the use of Markov Chain Monte Carlo (MCMC) methods have been plagued by poor mixing, in part because of the high correlation between df and s^2 in current univariate (UNI) sampling approaches. We consider 2 alternative approaches based on Metropolis-Hastings sampling schemes; one based on univariate draws from each of df and scale (UNIMH) and the other based on bivariate draws of the 2 parameters (BIVMH). We tested these 3 sampling methods on 6 replicated data sets, each analyzed at 3 different SNP marker densities with average pairwise LD levels of r^2 = 0.17, 0.25 and 0.32 . The BIVMH and UNIMH methods had significantly higher computational efficiencies for estimating df and scale compared with UNI ($P < 0.001$) in BayesA and BayesB implementations at all LD levels with the BIVMH outperforming UNIMH for s^2 in BayesA only. For BayesA, these efficiencies were 3–7 times greater in BIVMH and UNIMH relative to UNI whereas they were 5–35 times greater in BayesB with the largest gains being attained at higher LD levels. One ominous result is that the effective number of independent samples (ESS) from MCMC on estimating df and s^2decreases substantially with increasing marker densities such that reliable inference from higher density SNP marker panels require not only greater computing time per MCMC cycle but also greater total number of cycles as well. We also demonstrate how sensitive the accuracy of WGP is to misspecification of these key hyperparameters.

Key Words: genomic prediction, Bayesian inference, genetic architecture

457 A multi-compartment model for genomic selection in admixture populations. E. Hay,* S. Smith, and R. Rekaya, *University of Georgia, Athens.*

Currently, genome wide association studies and genomic selection (GS) are often conducted using purebred populations. Estimation and often validation of SNP are carried out using a select elite set of purebred animals (i.e., proven sires). This process was successful when estimated SNP effects were used to predict genomic breeding values on animals of the same breed. But it fails at different degrees when these SNP estimates are used for genomic prediction in other breeds or crossbred animals. Current approaches for dealing with admixed and crossbred populations in GS rely on using different groups of pooled animals in training and validation sets, hence are data dependent and often lead to reduction in accuracies for animals in pure breed populations. In admixture populations or in presence of crossbred animals, pooled databased methods assume SNP effects are the same across breeds or sub-populations. This assumption is seldom true due to several parameters such as minor allele frequency, strength of LD between markers and QTLs, and linkage phase between marker and QTL alleles change across sub-populations. To deal with this problem, we proposed a multi-compartment model where the effect of a SNP could be different between breeds and parameterized as a function of its effect on one of the breeds in pooled population through a one to one mapping function. An admixture population consisting of 2 lines (A and B) of birds was used to test our proposed method. It consisted on 2807 birds (1989 for A and 818 for B) genotyped for around 57 k SNPs. Three analyses were conducted: 1) each line analyzed separately (M1); 2) pooled data (M2); 3) pooled data using our multi-compartment model (M3). For M1, accuracy (correlation between EBVs and GEBVs) was 0.69 and 0.68 for line A and line B, respectively when training and validation were conducted within the same line. These accuracies dropped to 0.15 and 0.21 when training and validation were conducted in different lines. Using M2 (training and validation on pooled data), the accuracy decreased to 0.53. Using our method (M3), the accuracy was 0.59 or 11% increase compared with M2.

Key Words: genomic selection, admixture, SNP

458 Bayesian integration of external information into the single step approach for genomically enhanced prediction of breeding values. J. Vandenplas*[1,2], I. Misztal[3], P. Faux[1], and N. Gengler[1], [1]*University of Liege - Gembloux Agro-Bio Tech, Gembloux, Belgium,* [2]*National Fund for Scientific Research, Brussels, Belgium,* [3]*University of Georgia, Animal and Dairy Science Department, Athens.*

An assumption to compute unbiased estimated breeding values (EBV) is that all information, i.e., genomic, pedigree and phenotypic information, has to be considered simultaneously. However, current developments of genomic selection will bias evaluations because only records related to selected animals will be available. The single step genomic evaluation (ssGBLUP) could reduce pre-selection bias by the combination of genomic, pedigree and phenotypic information which are internal for the ssGBLUP. But, in opposition to multi-step methods, external information, i.e., information from outside ssGBLUP, like EBV and associated reliabilities from Multiple Across Country Evaluation which represent a priori known phenotypic information, are not yet integrated into the ssGBLUP. To avoid multi-step methods, the aim of the study was to assess the potential of a Bayesian procedure to integrate a priori known external information into a ssGBLUP by considering simplifications of computational burden, a correct propagation of external information and no multiple considerations of contributions due to relationships. To test the procedure, 2 dairy cattle populations (referenced by “internal” and “external”) were simulated as well as milk production for the first lactation of each female in both populations. Internal females were randomly mated with internal and 50 external males. Genotypes of 3000 single-nucleotide polymorphisms for the 50 males were simulated. A ssGBLUP was applied as the internal evaluation. The external evaluation was based on phenotypic and pedigree external information. External information integrated into the ssGBLUP consisted to external EBV and associated reliabilities of the 50 males. Results showed that rank correlations among Bayesian EBV and EBV based on the joint use of external and internal data and genomic information were higher than 0.99 for the 50 males and internal animals. The respective correlations for the internal evaluation were equal to 0.50 and 0.90. Thereby, the Bayesian procedure can integrate external information into ssGBLUP.

Key Words: Bayesian, genomic, single step

459 Conceptual comparison between standard multiple-trait and structural equation models in animal breeding applications.

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Structural equation models (SEM) are multivariate specifications capable of conveying causal relationships among traits. Although these models offer insights into how phenotypic traits relate to each other, it is unclear how SEM can improve multiple trait selection. This is a major issue, ultimately defining how SEM can serve animal breeding. Here, we explored concepts involved in SEM, seeking for benefits it could bring to breeding programs, relative to the standard multi-trait models (MTM) commonly used in practice. Genetic effects pertaining to SEM and MTM have distinct meanings. In SEM, these represent genetic effects acting directly on each trait, without mediation by any other instances of the multiple-trait set under study; in MTM they represent overall genetic effects on each trait. Hence, by using a SEM, it is possible to disentangle the overall genetic components into direct and indirect effects. However, in breeding programs one is interested in selecting candidates that produce offspring with best phenotypes, regardless of how traits are causally associated, and overall additive genetic effects are predictive of offspring phenotypes. So, there is no loss of information by using MTM based predictions, even if there are causal associations among traits. Conversely, the extra knowledge provided by causal information may give the ability of predicting effects of external interventions. One may be interested in selecting for a scenario where interventions are performed, e.g., artificially defining the value of a trait, blocking causal associations, or modifying their magnitudes. By knowing SEM genetic effects and mirroring interventions on the causal structure of the model, predictions for these scenarios are possible from data recorded without the interventions. MTM, on the other hand, do not provide information for such predictions. As livestock production involves many interventions, SEM may be then advantageous in many settings.

Key Words: multiple-trait models, selection, structural equation models

Breeding and Genetics: Beef Cattle Breeding I–Production Traits

460 Incorporation of external EBV into the American Gelbvieh Association carcass national cattle evaluation.

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The goal of this project was to incorporate prior genetic knowledge on Angus and Red Angus sires whose progeny are being registered in the American Gelbvieh Association (AGA) to better account for selection on these sires and to improve carcass EBV prediction for their crossbred progeny. External EBV (EEBV) for carcass weight (CWT), rib eye area (REA) and marbling score (MARB) were obtained from the American Angus Association (n = 5,472) and Red Angus Association of America (n = 3,482). EEBV for CWT and REA were added to the AGA model containing actual CWT, REA, and ultrasound REA (UREA). EEBV for MARB were added to the AGA model containing actual MARB and percent intramuscular fat (IMF). Prior to their inclusion, EEBV were deregressed for accuracy. Models currently used by the AGA for the prediction of carcass EPD were preserved. Heritability of the EEBV and genetic correlations between the EEBV and traits in the existing models were the only parameters estimated. A simple mean was the sole EEBV fixed effect included. Heritability estimates for the EEBV were found to be 0.23 ± 0.01, 0.28 ± 0.01 and 0.18 ± 0.01 for CWT, REA and MARB, respectively. Genetic correlations between external CWT EBV and actual CWT, external REA EBV and actual REA, external REA EBV and UREA, external MARB EBV and actual MARB, external MARB EBV and IMF were found to be 0.35 ± 0.15, 0.33 ± 0.15, 0.39 ± 0.06, 0.53 ± 0.15 and 0.49 ± 0.05, respectively. Angus animal EPD correlations between models with EEBV and those without were 0.94, 0.95 and 0.78; Gelbvieh EPD correlations were 0.98, 0.996 and 0.98; EPD correlations for all animals were 0.95, 0.98 and 0.90 for CWT, REA and MARB, respectively. Inclusion of the EEBV resulted in an increased EPD spread for the suite of AGA carcass EPD. For Angus animals and their progeny, this spread was increased by 43%, 25% and 101%; EPD spread increase for all animals was 6.3%, 3.4% and 44.8% for CWT, REA and MARB, respectively. This procedure resulted in positive and moderately high genetic correlations between the EEBV and corresponding traits in the current evaluation. This procedure resulted in the models more appropriately evaluating external Angus sires in the AGA carcass evaluation.

Key Words: beef cattle, genetic evaluation

461 Across-population estimation of heritability of carcass traits in beef cattle: Meta- vs. mega-analyses.

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Across-population estimation of genetic parameters is a challenge because populations are heterogeneous and the distribution of individual estimates over populations may be multi-modal. Two types of statistical methods can be used to combine estimates from many populations. Meta-analysis combines summary results from populations, whereas mega-analysis pools data from multiple populations into a single data set. We compared these approaches in estimation of heritability of 6 carcass traits [marbling score (MBS), back fat thickness (BFAT) at 12th rib, hot carcass weight (HCW), ribeye area (REA), yield grade (YG) and Warner-Bratzler shear force (WBSF)] using 15,016 cattle (2,964 phenotyped) from 4 populations sired by Angus, Hereford, Limousin or Simmental. We fitted fixed-effects (FMA) and random-effects (RMA) meta-analytical models in a frequentist framework. FMA viewed populations as homogeneous for any of the traits; RMA postulated a normal distribution of heritability values across populations. Further, a Bayesian non-parametric model with a Dirichlet process prior (DPP) was fitted, to avoid the normality assumption implied in RMA. In the mega-analysis, heritability was estimated with an animal model, pooling data over the 4 populations. Heritability was 0.42 (MBS), 0.24 (BFAT), 0.35 (HCW), 0.28 (REA), 0.29 (YG), and 0.12 (WBSF) using mega-analysis, and 0.31 to 0.39 (MBS), 0.21 to 0.34 (BFAT), 0.33 to 0.39 (HCW), 0.27 to 0.41 (REA), 0.31 (YG), and 0.17 to 0.20 (WBSF) with the meta-analysis models. In general, heritability estimates from RMA and DPP models agreed, but differed slightly from those obtained with FMA for all traits, except YG. When population heterogeneity is evident, meta-analysis using FMA (possibly mega-analysis too) appears suboptimal, whereas RMA and DPP can potentially capture the distribution of heritability estimates over populations.

Key Words: heritability, mega-analysis, meta-analysis

462 Accuracies with different genomic models for traits with maternal effects.

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Several methods were compared for the accuracy of evaluation using phenotypic, pedigree and genomic information for a trait influenced by a maternal effect. A simulated population included 15,800 animals in 5 generations. Genotypes from 3k SNP were available for 1500 animals in the last 3 generations. All animals except 300 in the last generation had phenotypes. Simulations were by an animal model with direct (heritability 0.32) and maternal (heritability 0.13) effects, mimicking weaning weight in beef cattle. Models of analysis were regular BLUP, single-step GBLUP (ssGBLUP), BayesC with deregressed proofs (BayesC-D) and BayesC using phenotypes and ignoring the maternal effects (BayesC-ph). For all animals, the accuracies with ssGBLUP were 0.01 (0.04) higher than with BLUP. For genotyped animals, the direct (maternal) accuracies for males were 0.71 (0.43) for BLUP, 0.79 (0.60) for ssGBLUP, 0.70 (0.48) for BayesC-D, and 0.63 for BayesC-ph. For females, the same accuracies were 0.68 (0.54) for BLUP, 0.76 (0.65) for ssGBLUP, 0.69 (0.56) for BayesC-D, and 0.65 for BayesC-ph. For genotyped animals in the last generation, the direct (maternal) accuracies were similar for males and females and were 0.50 (0.38) for BLUP, 0.69 (0.58) for ssGBLUP, 0.62 (0.48) for BayesC-D, and 0.54 for BayesC-ph. Accuracies by BayesC-D were lower than those by ssGBLUP because of approximations involved in deregressions, lack of accounting for parental average that is done automatically by ssGBLUP, and by sequential rather than simultaneous fitting of genomic and nongenomic information. Low direct accuracies by BayesC-ph were additionally due to ignoring phenotypes on ungenotyped animals and ignoring the maternal effect. Highest accuracy of prediction with the genomic information occurs when the information on all ungenotyped but related individuals is included and when all sources of information (phenotypic, pedigree and genomic) are considered jointly. The accuracy with a procedure that uses simplified models and ignores information from ungenotyped animals can be lower than that by BLUP.

Key Words: beef cattle, genomic selection, single-step procedure

463 Cumulative discounted gene expression for economically relevant traits for terminal and maternal purpose in cattle production system. X. Zeng,* B. W. Brigham, S. E. Speidel, D. H. Crews, and R. M. Enns, *Colorado State University, Fort Collins.*

The objective of the study was to estimate the cumulative discounted gene expressions (CDGE) for birth, slaughter, annual and end-of-cow-life traits in terminal and maternal purpose Angus cattle. CDEG were not calculated to annual and end-of-cow-life traits for terminal sire. The overarching goal of the project is to develop prototype producer-specific selection indexes based on production characteristics in the intermountain region of the US. The discounted gene-flow principle was used to estimate CDGEs. The parameters used in equations to calculate the CDGEs were estimated from 10,007 individual records and 27,165 pedigree records from the Angus herd at the John E. Rouse Beef Improvement Center of Colorado State University. There were 313 sires with generation interval of 3.30 years involved in the study, as well as 2,160 dams with generation interval of 5.32 years. The planning horizon, cull age of cow and discount rate were set as 20 years, 12 years old and 0.03 as the base situation to estimate CDGE. The result contained 14 CDGEs for 4 kinds of animals, each of which included different categorical traits. n the base situation, the CDGE of annual cow traits were 4.29, 6.93 and 29.01 for terminal female, self-replace female and sire breeding replacement females. The range of CDEG for slaughter traits is 20.39 to 35.00 from terminal sire to sire breeding replacement females, while 1.90 to 4.72 from terminal female to self-replacing female. For self-replacing female, the CDEGs of traits expressed at different time and frequency were 6.93, 6.15, 1.35 and 4.72 for annul, birth, end-of cow-life and slaughter traits, with a range of 1.35 to 6.93. Sensitivity analysis was adapted to test the effect of different levels of discount factors from 0 to 2.0. Results of the study indicated that different purpose of calves lead to large differences in gene expression. Thus, when adjustments are made to economic values, the relative economic importance may change for the economically relevant traits in a breeding objective.

Key Words: cumulative discounted gene expression, discounted gene-flow, economic value

464 Cluster and meta analyses of genetic parameters for feed intake traits in beef cattle. I. D. P. S. Diaz[1], D. H. Crews Jr.*[2], and R. M. Enns[2], *[1]Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil, [2]Colorado State University, Fort Collins.*

A lot of studies have been estimated genetics parameters for different measures of feed efficiency so it has becoming important to summarize all the different parameters found on publication and to get an average of these results. In this study feed efficiency data from 62 studies were used to estimate the pooled heritability and the pooled genetic correlation estimates among average daily gain (ADG); residual feed intake (RFI); metabolic body weight (MBW); feed conversion ratio (FCR) and dry matter intake (DMI) of beef cattle. A meta-analysis approach was applied following a cluster analysis of the heritability estimates. The total data sample had 177 heritability estimates and 149 genetic correlation estimates collected from studies published from 1961 to 2011. The cluster analysis was conducted using the Ward method within trait. Pooled heritability estimates were calculated for each cluster within each trait and for all the clusters together. For all traits 2 clusters were obtained, however for each trait the key variable that separated the groups was different. With this approach, the homogeneity between the studies could be evaluated and if present, a random model was chosen to calculate the variance between studies. In this study the variance was calculated using restricted maximum likelihood. Heterogeneity was found among the studies for all traits. Pooled heritability estimates for ADG, DMI, RFI, MBW and FCR were 0.32 ± 0.04; 0.39 ± 0.03; 0.31 ± 0.02; 0.31 ± 0.03 and 0.26 ± 0.03, respectively. Pooled genetic correlation estimates ranged from −0.15 to 0.67 among these traits. These pooled genetic parameter estimates could be used to solve genetic prediction equations in populations where data are insufficient for variance components estimation.

Key Words: feed efficiency, multivariate analysis

465 Marbling change patterns of rib eye area by slaughter age using random regression sire model. K. Kato,* Y. Nakahashi, and K. Kuchida, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Japan.*

Japanese Black cattle (Wagyu) are the predominant beef breed due to high marbling. Degree of intramuscular marbling is measured at the 6th to 7th rib section, and graded according to the beef marbling standard (BMS, 1 to 12) in Japan. Currently the slaughter age of this breed is about 29 mo on average. However, it is required to shorten the length of fattening because of increasing the feeding costs. The objectives of this study were to investigate sire differences in marbling change patterns of rib eye area by slaughter age in Japanese Black cattle using regression within sire, and to find the appropriate slaughter age. Data were 18,350 carcass records (steer: 13,218, heifer: 5,132) collected between April in 2000 and December in 2010 in Hokkaido, Japan. Statistical analysis was performed using AI-REML procedure. The random regression model included year, month, sex and farm as fixed effects, slaughter age (linear and quadratic) as fixed regression, and random sire effects was fitted with a k-th ($k = 0, 1, 2$) order Legendre polynomials of slaughter age. The breeding value of sire for each age was predicted by BLUP of random regression coefficients. Estimated sires were totally 753. Estimated breeding value (EBV) of BMS increased with the age until the peak, and then decreased. The different regression curves and the peaks among sires were shown. For top 5 sires in service number, EBV of BMS ranged 1.0~1.4, 1.0~2.1, 1.0~1.2, 0.9~1.2 and 0.5~1.3, respectively Therefore, it is thought that fattening farmer can decide the slaughter age appropriately and carcasses can show their ability maximally.

Key Words: marbling, slaughter age, random regression

466 Estimation of heterotic effects on stayability in beef cattle. E. M. Huff*[1], B. W. Brigham[1], S. Willmon[2], and R. M. Enns[1], *[1]Department of Animal Science, University of Colorado, Fort Collins, [2]American Gelbvieh Association, Westminster, CO.*

Stayability in beef cattle is defined as the probability that a cow remains in the herd until age 6 given that she has calved as a heifer. In some breeds with total herd reporting, those cows are required to calve every year. Profitability of the herd is affected by stayability by decreasing the need for replacements by increasing the number of cows that reach the typical breakeven age of 6. Stayability is a binary trait on the observed scale and is considered a lowly heritable trait. General consensus is that lowly heritable traits should be subject to higher levels of heterosis in crossbreeding programs and has shown to have a large effect on cow longevity. Therefore, heterosis should have a positive effect on the cows' ability to remain in the herd until age 6. The objective was to estimate maternal and individual heterosis values for stayability. Data obtained from the American Gelbvieh Association and included a total of 103,022 animals, with 20,173 being purebred Angus, 6,223 purebred Red Angus, 47,549 purebred Gelbvieh, and the rest being a combination of crossbred animals. Variance components and fixed heterosis effects were estimated from an animal model using a probit threshold link function. The model included contemporary group as a fixed effect and breed percentage as a linear covariate. Contemporary groups were required to have variation within the group and to have at least 5 observations. After initial analysis Red Angus and Angus cattle were combined due to there not being a significant difference between the 2 breeds. Two models were run with different backcross covariates, model one included only individual backcross and model 2 included individual and maternal backcross. Heterosis was estimated to be 35.78% for the individual with the first model. For the second model individual heterosis was estimated to be 31.77% and 11.85% was the estimate for maternal heterosis. The results from this experiment indicate that stayability is affected by heterosis and that these effects should be accounted for in cattle evaluation using pure and crossbred data.

Key Words: heterosis, stayability, beef cattle

467 Comparison of single breed and admixed reference populations for across-breed prediction of direct genomic breeding values in Red Angus beef cattle. M. Saatchi*[1], R. D. Schnabel[2], J. F. Taylor[2], and D. J. Garrick[1,3], [1]*Department of Animal Science, Iowa State University, Ames,* [2]*Division of Animal Science, University of Missouri, Columbia,* [3]*Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand.*

The objective of this study was to derive and evaluate the accuracy of direct genomic breeding values (DGV) for Red Angus beef cattle using single breed and admixed reference populations. Seven traits (birth, weaning and yearling weights; calving ease direct and maternal; marbling; rib eye area) were evaluated using 2,359 Black Angus, 891 Hereford and 1,655 Limousin genotyped individuals as a reference population, separately and admixed. Genotyping used the Illumina BovineSNP50 assay. Deregressed estimated breeding values (DEBV) were used as observations in a weighted Bayesian analysis to estimate marker effects used in DGV calculation. Accuracy of DGV was the correlation between DEBV and DGV in a sample of 90 Red Angus sires. The single breed reference populations accuracies of DGV were, in general, higher for marker effects predicted in Black Angus, followed by Hereford, and finally Limousin, reflecting the genetic distances between the breeds. The use of admixed reference populations produced more accurate DGV (average accuracies over all traits were 0.24, 0.19, 0.13 and 0.06 when marker effects were predicted in admixed, Black Angus, Hereford and Limousin, respectively). Incorporating 86 additional Red Angus (different animals from validation individuals) and 102 Simmental individuals into the admixed training population dramatically increased the accuracies of DGV, averaging 0.43 over all studied traits. These DGV show promise for routine use by Red Angus breeders to predict the genetic merit of their animals at a young age. Red Angus breeders will benefit most from the use of an admixed reference population which includes Red Angus.

Key Words: admixed reference population, genomic breeding values, Red Angus

468 Adipose and muscle tissue expression of two genes (*NCAPG* and *LCORL*) located in a chromosomal region associated with cattle feed intake and gain. A. K. Lindholm-Perry,* A. K. Sexten, L. A. Kuehn, L. A. Rempel, J. R. Miles, R. A. Cushman, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

A region on bovine chromosome 6 has been implicated in cattle birth weight, growth, and length. Non-SMC conodensin I complex subunit G (*NCAPG*) and ligand dependent nuclear receptor corepressor-like protein (*LCORL*) are positional candidate genes within this region. We previously identified genetic markers in both genes that were associated with average daily gain and feed intake in a crossbred population of beef steers. Two markers within *LCORL* were validated in a second, unrelated population of steers. We also detected associations between these markers and hot carcass weight, adjusted fat thickness and ribeye area suggesting that one or both of these genes play a role in lean muscle growth and reduced fat deposition. The purpose of this study was to determine whether the transcript abundance of either of these genes in adipose and muscle tissues was associated with variation in beef cattle feed intake, residual feed intake and average daily gain phenotypes. Transcript abundance for *NCAPG* and *LCORL* in adipose and muscle tissue was measured by quantitative PCR from heifers (adipose only, n = 88), cows (n = 85 muscle, n = 18 adipose) and steers (n = 12). Phenotypic correlations among expression levels and measures of growth, feed intake, and efficiency were derived and tested for significance. The levels of *NCAPG* and *LCORL* gene expression in adipose tissue were not correlated to gain, feed intake or residual feed intake in steers, heifers or cows. However, transcript abundance of *NCAPG* in the muscle tissue of cows was correlated to BW gain ($r = 0.31$; $P = 0.004$) while muscle gene expression levels of *LCORL* were correlated with dry matter intake in steers ($r = -0.57$; $P = 0.03$). These data corroborate the genetic associations with gain and feed intake within this region and represent biological activity of these genes in the muscle tissue of cattle. The data also suggests that sex, age and/or nutrition-specific interactions may affect the expression of *NCAPG* and *LCORL* in beef cattle. USDA is an equal opportunity provider and employee.

Key Words: beef cattle, gene expression

469 Identification of single nucleotide polymorphisms for feed efficiency and performance in crossbred beef cattle. M. K. Abo-Ismail*[1], G. Vander Voort[1], E. J. Squires[1], K. C. Swanson[1,2], J. Thomson[3], B. Karisa[3], G. Plastow[3], S. Moore[3], and S. P. Miller[1,3], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada,* [2]*Animal Sciences Department, North Dakota State University, Fargo,* [3]*Faculty of Agricultural, Life and Environmental Sciences, University of Alberta, Edmonton, AB, Canada.*

Novel genomics approaches offer opportunities to select for efficient cattle to reduce feed costs. The objectives of this study were to: (1) identify new SNPs for residual feed intake (RFI) and performance traits within the candidate genes identified in a genome wide association study (GWAS); (2) estimate the proportion of variation in feed efficiency traits explained by the detected SNPs; (3) estimate the effect of detected SNPs on carcass traits to avoid undesirable correlated effects on other economically important traits when selecting for feed efficiency; and (4) map the corresponding genes to biological mechanisms and pathways. A total number of 339 SNPs corresponding to 180 genes were tested for association with phenotypes using a single locus regression (SLRM) and genotypic model on 726 and 990 crossbred animals for feed efficiency and carcass traits, respectively. Strong evidence of associations for RFI were located on chromosomes 8, 15, 16, 18, 19, 21, and 28. The strongest association with RFI ($P = 0.0017$) was found with a newly discovered SNP located on BTA 8 within the ELP3 gene. In addition, SNPs rs41820824 and rs41821600 on BTA 16 within the gene HMCN1 showed strong evidence of association with RFI ($P = 0.0064$ and $P = 0.0033$, respectively). A newly identified SNP located on BTA 18 within the ZNF423 gene provided strong evidence for association with RFI ($P = 0.0028$). Several SNPs provided strong evidence of association with other feed efficiency, performance, and carcass traits using the SLRM and genotypic model. Genomic estimated breeding values (GEBV) from 98 significant SNPs were moderately correlated (0.47) to the estimated breeding values (EBVs) from a mixed animal model. The significant SNPs (98) explained 18.06% of the phenotypic variance of RFI. Functional analysis for the corresponding genes to significant SNP for feed efficiency traits suggested 35 and 39 biological processes and pathways respectively with majority in ion and cation transport, phosphorus metabolic process, and regulation of transcription. The newly discovered SNPs should be validated in another population before incorporation in a DNA testing panel to evaluate the genetic merit of beef cattle for feed efficiency industry-wide.

Key Words: single nucleotide polymorphisms, feed efficiency, beef cattle

470 Withdrawn by author

471 Genetic and environmental influences on movement patterns of beef cattle grazing foothill rangeland.

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A study was conducted in foothill rangelands of Montana to evaluate the effects of genotype and environment (or early learning) on grazing distribution. Based on 5 years of observations, 5 of 180 cows that used the highest and steepest terrain (hill climbers) and 5 cows that used the most gentle terrain near water (bottom dwellers) were used as donor-dams for embryo transfer. A single unrelated Simmental sire was used in these matings. Recipient cows were classified as hill climbers (HC) and bottom dwellers (BD) based on 4 years of observation from a separate herd of 98 cows. This resulted in 2x2 factorial study with donor and recipient as factors and HC and BD as levels within each factor. During the summer of 2011, 18 of these cows (6 to 8 years of age) were tracked at 10-min intervals by global positioning system technologies in a 336 ha pasture. Distance to water, elevation, slope and a normalized average of these terrain attributes from recorded cow locations were averaged and evaluated using a statistical model that included donor, recipient and the donor*recipient interaction. A separate analysis compared breed groups irrespective of the donor and recipient classifications. We were unable to detect any differences between HC and BD recipients for any measure of grazing distribution. We observed a tendency ($P = 0.08$) for cows from HC donors (490 ± 13 m) to be farther from water than those from BD donors (456 ± 11 m), but we did not detect any differences ($P > 0.10$) between HC and BD donors for other measures of distribution. No interactions between donors and recipients were detected ($P > 0.10$). Tarentaise maternally influenced cows walked farther per day ($P = 0.03$) and were farther from water ($P = 0.01$) than Hereford maternally influenced cows. Grazing use of foothill rangeland appears to be affected to some degree by genetic factors, but the mechanism of this influence requires further study.

Key Words: genotype, early learning, behavior

Cell Biology Symposium: Molecular Basis for Feed Efficiency

472 Unique roles for agouti proteins and melanocortin signaling in lower vertebrates. C. Zhang[1,2], P. M. Forlano[3], and R. D. Cone*[1], *[1]Department of Molecular Physiology and Biophysics, Vanderbilt University School of Medicine, Nashville, TN, [2]Department of Cell and Developmental Biology, Oregon Health Science University, Portland, [3]Department of Biology and The Aquatic Research and Environmental Assessment Center, Brooklyn College of The City University of New York, Brooklyn.*

The agouti proteins and the central melanocortin circuits have been identified in all vertebrate species studied, from the most primitive fish to humans. These circuits regulate energy storage in adipose depots and somatic growth from fish to humans as well. However, deletion of the MC4R has only modest effects on somatic growth and reproduction in mammals, but large effects on larval teleosts, suggesting a fundamental difference in the neuroendocrine function of central melanocortin signaling in lower vertebrates. We have shown in a teleost that the hypothalamic proopiomelanocortin and AgRP neurons are hypophysiotropic, projecting to the pituitary to coordinately regulate multiple pituitary hormones. Indeed, AgRP-mediated suppression of MC4R appears essential for early larval growth. This identifies the mechanism by which the central melanocortin system coordinately regulates growth and reproduction in teleosts, and suggests it is an important anatomical substrate for evolutionary adaptation. Plasticity in growth and reproductive behavior is found in many vertebrate species, but is common in male teleost fish. Typically, "bourgeois" males are considerably larger and defend breeding territories while "parasitic" variants are small and use opportunistic breeding strategies. The P locus mediates this phenotypic variation in *Xipophorus* and encodes variant alleles of the melanocortin-4 receptor (MC4R), also explained mechanistically by our findings. These data also suggest potential commercial applications in lower vertebrates for the regulation of growth, and potentially feed efficiency as well, since inhibition of MC4R significantly stimulates early growth.

473 The physiological basis defining feed efficiency differences in pigs selected on residual feed intake. N. K. Gabler,* J. K. Grubbs, A. Harris, S. M. Cruzen, E. Huff-Lonergan, J. F. Patience, J. C. M. Dekkers, and S. M. Lonergan, *Iowa State University, Ames.*

In recent years, much attention has been given to feed efficiency in livestock production due to the rising costs of feed and other inputs. However, compared with growth and development, our understanding of the molecular biology and physiology regulating feed efficiency (FE) in swine is relatively limited. Residual feed intake (RFI) is a unique way to measure FE computed as the difference between the amount of feed a pig actually consumes and what it is expected to consume, based on its rate of growth and backfat. Therefore, selecting pigs for lower RFI results in animals that require less feed for a given rate of growth. The main biological factors that contribute to differences in RFI may include physical activity, feed intake patterns and behavior, stress, nutrient digestibility and efficiency of utilization, composition of gain and metabolism. In other words, both the maintenance and growth components of nutrient and energy utilization may be involved. In particular, the contributions of protein turnover, mitochondrial leakage and ion pump activity (i.e., Na^+, K+-ATPase) may provide the primary basis for divergence FE. Results from our lines of pigs that have been selected for high versus low RFI show that changes in body composition may help explain some of the variation observed in RFI divergence. Our data also suggests that a significant part of RFI variation may also be related to the level of protein turnover and degradation rates. These differences could be linked to mitochondrial function and oxidative stress in muscle and liver tissues. Furthermore, increased ion pump activity may contribute to reduced FE in pigs selected for high RFI, as maintaining high ion pump activity and membrane potentials are energetically expensive processes in metabolism. Altogether, this paper will discuss the molecular and physiological explanations for the observed phenotype in response for selection based on RFI. This project was supported by USDA-AFRI Competitive Grant #2010–65206–20670 and the Iowa Pork Producers Association.

Key Words: pig, feed efficiency, residual feed intake

474 Genetics of feed efficiency in dairy and beef cattle. D. P. Berry*[1] and J. J. Crowley[2], *[1]Teagasc, Moorepark Dairy Production Research Center, Fermoy, Co. Cork, Ireland, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

Increasing food production for the growing human population off a decreasing land-base will require greater efficiency of production. Feed efficiency in cattle can contribute to this, and breeding, which is cumulative and permanent, is one likely vehicle to achieving efficiency gains within animal. A meta-analysis of up to 25 studies in growing cattle clearly showed that genetic variation in feed efficiency exists with a pooled heritability for residual feed intake and feed conversion efficiency of 0.34 ± 0.01 (range of 0.14 to 0.62) and 0.25 ± 0.01 (range of 0.06 to 0.46), respectively. However, what is not clear from the literature is what is the best breeding strategy to ensure food security, long-term—a conflict exists between focusing on improving feed efficiency per day or efficiency of an entire sector. Also, the studies to-date that highlight the importance of feed efficiency in breeding programs seem to ignore selection index theory that most of the variation in feed intake can actually be accounted for by other performance traits. Selection index calculations on a genetic covariance matrix between feed intake, liveweight and average daily gain generated from a meta-analysis of up to 12 studies showed that 84% of the genetic variation in feed intake could be explained by these traits. Therefore the marginal benefit of collecting feed intake data appears to be low. There is now sufficient information available to develop a roadmap on how best to direct research to ensure long-term food security for a growing human population.

Key Words: cattle, genetic, efficiency

475 Feed efficiency: Mitochondrial function to global gene expression. W. G. Bottje* and B.-W. Kong, *Department of Poultry Science, Center of Excellence for Poultry Science, University of Arkansas, Fayetteville.*

There is evidence that links mitochondrial function and biochemistry with the phenotypic expression of feed efficiency (FE, gain:feed). Consistent findings observed in low FE in several tissues were evidence of increased protein oxidation or oxidative stress that probably resulted from increased mitochondrial reactive oxygen species (ROS) generation. As ROS are well known to act as second messengers, gene expression in the low FE phenotype could be hypothesized to be due to inherent gene expression that is modulated by increased mitochondrial ROS production. Studies have been conducted to assess global gene expression in breast muscle associated with the phenotypic expression

of FE. In these studies, RNA samples were obtained from broilers that exhibited either high FE (0.65 ± 0.01) or low FE (0.46 ± 0.01) (n = 6 per group). Global RNA expression was investigated using a 44K chicken oligo microarray that was validated by comparison to values obtained by qRT-PCR for 33 different genes. A 1.3 fold cutoff value for expression resulted in over 750 genes that were differentially expressed in muscle between the high and low FE phenotypes. An online software program (Ingenuity Pathway Analysis) was used to group genes by function, gene networks and into established biochemical (canonical) pathways to facilitate data interpretation. The results indicate that animals exhibiting a high FE phenotype had increased expression of genes associated with anabolic activities and signal transduction-cascade mechanisms that would appear to favor cell growth, development and differentiation. AMP kinase (AMPK) that senses coordinates energy production to meet cell energy needs was also upregulated in the high FE phenotype. In contrast, animals exhibiting a low FE phenotype exhibited upregulation of many genes associated with actin-myosin filaments that would be involved in cytoskeletal architecture and/or muscle development. Several stress-related or stress responsive genes (e.g., heat shock proteins, superoxide dismutase) were also upregulated that might be attributed to higher ROS production. Although these studies are limited mRNA expression in muscle, the results provide additional information to help in understanding the cellular basis of feed efficiency.

Key Words: feed efficiency, bioenergetics, gene expression

Companion Animals Symposium: Impact of Anthropomorphism on Companion and Captive Animal Husbandry

476 Capitalizing on human health trends to improve feline health and wellbeing. M. R. Lappin,* *Department of Clinical Sciences, Colorado State University, Fort Collins.*

For some pet owners, their cat(s) is(are) treated like other 2-legged family members. In these situations, the veterinarian can be as vital a member of the family as the pediatrician or family practitioner who guide human health decisions. These owners tend to be well read and are easy influenced by electronic and other media. In my opinion, human health trends generally improve feline health and wellbeing. However, information derived from the human health care system can also hamper feline health care. In this lecture, a case-based approach will be used to provide examples of both potential outcomes. For example, in an attempt to provide cats the safest possible environment, many owners restrict the cat's access to the outdoors. This housing trend combined with over-feeding has led to an epidemic of feline obesity and related problems such as diabetes mellitus. Increased recognition of the human obesity problem by pet owners in North America has led to an increase in recognition of the problem in cats and makes directing the cat owner toward providing a more positive lifestyle for their cat much easier. The widespread use of supplements such as glycosaminoglycans to enhance the wellbeing of humans has also lead to improvement in feline health. For example, degenerative joint disease is more common in cats than is commonly believed. The resultant discomfort decreases activity levels and can potentiate the feline obesity problem. The increased recognition of the benefits of glycosaminoglycans in humans has made it much easier to convince owners to complete diagnostic evaluations of cats exhibiting inactivity and to appropriately manage degenerative joint disease. Last, due to a perceived increased risk of autism in vaccinated children and injection site sarcoma in cats, some cat owners are now fearful of vaccines of all types for cats. This problem dramatically lessens numbers of feline veterinary visits, which provide many benefits other than just vaccination.

477 Effect of anthropomorphism on companion and captive animal husbandry. T. M. Edling,* *Petco Animal Supplies Inc., San Diego, CA.*

The objective of this presentation is to demonstrate how anthropomorphism affects companion and captive animals, specifically those within the pet industry. Anthropomorphism is a double-edged sword. From the point of view of the veterinarian, the pet product manufacturer, service providers and retailers, we all embrace the fact that pet owners actively anthropomorphize their animals. We love that most people in the United States consider their pets to be part of their families and consider themselves to be "pet parents." In fact, we promote that pet owners place human attributes on their animals and we play to the emotions that relationship elicits to encourage owners to purchase products and services. The other edge of the sword cuts backward as we consider animals that are treated like human children. Those animals are fed inadequate diets of "people food," kept in habitats that are designed to fit fashionably into a home but are dysfunctional and inappropriate for the animal and placed in social situations where a human would be comfortable but are not ideal for an animal. It is vitally important that those of us who understand the husbandry needs of companion and captive animals educate the public as well as the marketing and merchandising leaders in the pet industry. With the proper influence, we can help ensure the products and services available to pet owners will provide the best possible outcome and anthropomorphism is kept in check.

Key Words: anthropomorphism, animal husbandry, companion and captive animals

478 Companion animal and captive animal husbandry: The balance between what animals need and what people think they need. M. S. Edwards,* *California Polytechnic State University, San Luis Obispo.*

Air, food, water, and shelter are described as fundamental animal needs. Species-specific adaptations enable animals to satisfy their unique needs. Those unable to meet their needs are removed, along with their genetics, from populations through natural selection. Animals maintained in human managed environments are dependent upon their caregivers for these needs, in appropriate type, quantity and quality. Selections made by human caregivers are not always consistent with species, or individual, requirements and may result in clinical or subclinical disease, reduced longevity and/or productivity. When considering appropriate nutrition (i.e., food, water), requirements are defined as the lowest nutrient intake that maintains a defined level of nourishment for a specific adequacy indicator (Jones and Varady, 2007). It is the exception that species are offered the identical compliment of foods consumed by their native range counterparts. Regardless of environment, species require nutrients contained within consumed foods, not the foods themselves. Nutrients, including those catabolized for energy, may be effectively delivered using multiple methods. Polar bears feed primarily on ringed and bearded seals, but seasonally shift to alternative nutrient sources, including caribou, arctic charr, several berry species, and human garbage (Dyck and Kebreab, 2009). In managed environments, nutrients supporting polar bears are effectively delivered using available ingredients, nearly all of which are not consumed by the species in its native range. The apparent disconnect between animal requirements and what human caregivers perceive as needed is best demonstrated by the current incidence of companion animal obesity. In the United States, 53% of adult dogs, 55% of cats, and 32% of horses are overweight or obese (APOP, 2012; Thatcher et al., 2008). These are animals whose needs are dependent on a human population, 68% of which are overweight or obese (Flegal et al., 2010). Wildlife species maintained in human managed environments are also susceptible to these trends, although objective population data has not been compiled. An effort to educate animal caregivers regarding species needs, and how they distinctly differ from their own, should be an objective of responsible animal management.

Key Words: requirements, husbandry, obesity

479 Antimicrobial cathelicidin peptides: What are they and how do they help protect the dog? T. Melgarejo* and F. Blecha, *Kansas State University, Manhattan.*

Cathelicidins, a group of cationic peptides found mainly in leukocytes and epithelial cells, play a central role in the innate immune defense against infection. These host defense peptides (HDPs) have been reported in several animal species; however, our team was the first to identify a HDP in the neutrophil granules of the domestic dog. This finding recently led to the patent of a canine cathelicidin (K9CATH) peptide and its functional analogs. The mature K9CATH peptide exhibits broad antimicrobial activity against gram-negative and gram-positive bacteria, fungi as well as certain intra-cellular parasites. Through computational optimization we have moreover succeeded in further enhancing the biological activity and stability of the synthetic K9CATH peptide. The potency and broad antimicrobial activity of K9CATH support that this peptide acts as a key player in the innate immune response of the dog. In light of increasing antibiotic resistance it is important to identify natural compounds that may serve as model molecules for the development of novel antimicrobials with application against clinically relevant infections in veterinary medicine. We are currently investigating the use of K9CATH analogs as potential therapeutic agents for common pathologies in dogs, such as urinary tract infections, yeast and bacterial dermatitis, and chronic otitis.

Key Words: dog, canine, antimicrobial

480 New findings in the obligate carnivore-omnivore debate: Regulation of macronutrient intake in cats and dogs. A. K. Hewson-Hughes*[1], V. L. Hewson-Hughes[1], A. Colyer[1], A. T. Miller[1], S. M. McGrane[1], S. R. Hall[1], R. F. Butterwick[1], S. J. Simpson[2], and D. Raubenheimer[3], *[1]Waltham Centre for Pet Nutrition, Waltham-on-the-Wolds, Leicestershire, UK, [2]University of Sydney, Sydney, Australia, [3]Massey University, Auckland, New Zealand.*

Animals in the wild are faced with a variety of food sources that differ in nutritional content (quality) and availability from which they must compose a diet to meet their nutrient requirements. While many herbivores and omnivores have been shown to balance their intake of macronutrients [protein (P), fat (F) and carbohydrate (C)] when faced with nutritionally variable foods, study of this ability has been relatively neglected in predators, largely on the assumption that prey are less variable in nutrient composition than the foods of herbivores and omnivores and such mechanisms therefore unnecessary. The mammalian order Carnivora is of particular interest for the study of macronutrient regulation since it includes our major companion animals, cats and dogs which have predator heritage but today are largely provided with food by their owners. We carried out studies in adult domestic cats and adult dogs representing 5 breeds from toy to giant to determine whether these ′domestic predators′ regulate macronutrient intake. Cats and dogs were provided with a choice of 3 different foods (each in a separate bowl and each food containing different amounts of P, F and C) from which they could self-select the amount of each food they consumed to compose a diet. Each of the foods was offered in excess of energy requirements and if any animal consumed all of one or more foods the amount offered was increased to ensure that the diet composed was not influenced by food availability. From the amount of each food consumed we calculated the overall amount of energy consumed from each macronutrient and expressed this as a proportion of the total energy intake. Cats composed a diet from the 3 foods offered of ~52% of energy from protein (95% confidence interval (CI) 47.7, 56.1%), 36% from fat (33.0, 37.6%) and 12% from carbohydrate (7.5, 18.2%). The different breeds of dogs regulated intake to a remarkably similar %P:F:C balance of ~30% (CI 27.3, 30.9):63% (62.0, 64.6%):7% (6.4, 7.9) suggesting that the mechanisms regulating food intake have been strongly conserved in these dogs despite rapid (artificially selected) changes in other phenotypic traits such as size. These studies indicate that domesticated mammalian carnivores are able to regulate food selection and intake and so balance their macronutrient intake to specific intake targets.

Key Words: macronutrient regulation, companion animals, carnivore nutrition

Dairy Foods Symposium: Bioactive Components in Milk and Dairy Products: Recent international perspectives and progresses in different dairy species

481 Bioactive components in cow milk and products. H. J. Korhonen,* *MTT Agrifood Research Finland, Jokioinen, Finland.*

Milk is considered a nutritionally perfect food for newborn mammals. Furthermore, scientific evidence is continuously accumulating on the health-promoting effects of different milk components. These components encompass proteins, peptides, carbohydrates and lipids, glycolipids and other minor biomolecules. Their biological properties and functions are already reasonably well established and this knowledge has laid the basis for use of bioactive cow milk components as ingredients for functional foods. Industrial or semi-industrial scale processing techniques are available for fractionation and isolation of such components from colostrum and milk. Biomining and marketing of native dairy-derived functional ingredients is now emerging as a new lucrative business sector for the dairy industry and specialized bio-industries. A few milk protein and peptide-based products as well as growth factors have already been commercialized. It can be envisaged that more similar products will be launched on worldwide markets in coming years. Such products could be targeted to specific target groups so as to maintain good health status, improve performance, or prevent diet-related metabolic diseases.

Key Words: milk, bioactives, ingredients

482 Bioactive components in buffalo milk and products. M. Guo,* *University of Vermont, Burlington.*

Buffalo are the second largest source of milk supply in the world; world production of buffalo milk exceeds 75 million metric tons per year and is increasing steadily at about 3 percent per year. Because buffalo milk has higher total solids compared with bovine milk, it accounts for about twice the food contribution implied by the volume of buffalo milk produced yearly. Buffalo milk may contain almost all the bioactive compounds found in bovine milk, e.g., proteins, peptides, fatty acids, vitamins, and other bioactive compounds. Buffalo milk has higher levels of total protein, medium chain fatty acids, CLA, and contents of retinol and tocopherols than those in bovine milk. Some components may only be present in buffalo milk such as gangliosides. Because of the differences in compositional and physiochemical properties between buffalo and bovine milk, processing technology and equipment designed for cow's milk may not be suitable for buffalo milk processing. However, it has been approved that buffalo milk can be utilized for manufacture of a wide variety of functional dairy products with limited modifications in processing technology.

Key Words: bioactive, components, buffalo

483 Bioactive components in goat milk and products. Y. W. Park,* *Fort Valley State University, Fort Valley, GA.*

Milk contains a wide variety of heterogeneous mixture of chemical and bioactive compounds, which play integral roles in human health and nutrition. Once these components are liberated from milk and dairy products, they exhibit various physiological effects in the body, including gastrointestinal, cardiovascular, endocrine, immune, and nervous systems. Functionalities of bioactive peptides include antimicrobial, antihypertensive, antithrombotic, antioxidative, hypocholesterolemic, antiappetizing, immunomodulatory and mineral binding activities. Bioactive compounds in caprine milk have not been well explored compared with human and bovine milk. Quantification of bioactive components in different species milk has been difficult, due to their biochemical complexities, the small concentrations, the need to develop special methods to quantify, the compartmentalization of some of the agents, and the dynamic effects of maternal factors on the concentrations. A myriad of milk-derived bioactive peptides have been reported. Immunomodulatory peptides, as one example, include αs1-CN f194–199 (αs1-immunocasokinin) and β-CN f193–202, f63–68, f191–193 (immunopeptides), that are synthesized by hydrolysis with pepsin-chymosin. Casein fractions of goat milk proteins, such as α-, β- and k-CN, are sources of bioactive components, which contain the peptides Tyr-Gln-Glu-Pro, Val-Pro-Lys-Val-Lys, and Tyr-Gln-Glu-Pro-Val-Leu-Gly-Pro-* from β-CN, as well as Arg-Pro-Lys and Arg-Pro-Lys-His-Pro-Ile-Lys-His-* from αs1-CN, that exhibit ACE-inhibitory activity. Goat milk has therapeutic, hypoallergenic and nutritional advantages over cow milk due to its specific bioactive protein, fatty acids and mineral compositions. The short and medium chain fatty acids (MCT) in goat milk have several bioactive functionalities in digestion, metabolism, treatment of lipid malabsorption syndromes. Other bioactive components in goat milk include CLA, gangliosides, glycolipids, glycosphingolipids and cerebrosides, alkylglycerol, phospholipids, growth factors, hormones, immunoglobulins, oligosaccharides, lactose-derivatives, lactoferrin, lysozyme, nucleosides, nucleotides, minerals, and vitamins.

Key Words: goat milk, products, bioactive components

484 Bioactive components in sheep milk and products. M. A. de la Fuente* and M. Juarez, *Instituto de Investigacion en Ciencias de la Alimentacion, Madrid, Spain.*

Although in quantitative terms the production of sheep milk is of marginal importance compared with cow milk, it is of particular interest in certain areas of the world and has special relevance for arid and semi-arid regions. Most sheep milk produced in the world is processed into dairy products, mainly cheese. The specific composition of milk of sheep makes it especially valuable nutritionally and for consumer health since it generally contains higher total solids and major nutrient contents than goat and cow milk. Sheep milk is an excellent source of high-quality protein, calcium and lipids. It also became apparent during the last years, that some milk compounds possess biological properties beyond their nutritional significance that can be utilized as ingredients for health-promoting functional foods or as nutraceuticals. Milk lipids contain several components that have demonstrated healthy properties. The most important is the rumenic acid, an isomer of the conjugated linoleic acid (CLA). Data from in vitro studies and animal models suggest that rumenic acid is responsible for CLA anticarcinogenic and antiatherogenic properties, as well as a multiplicity of potentially beneficial effects on human health. Enzymatic hydrolysis of milk proteins during gastrointestinal digestion and/or milk processing can release fragments, known as bioactive peptides, able to exert specific biological activities, such as antihypertensive, antimicrobial, opioid, antioxidant, immunomodulatory, or mineral binding. With the research tools available nowadays, the presence of these components with biological activity has been demonstrated in cow but less is known about ovine milk. This presentation will discuss current knowledge of the main natural bioactive substances contained in sheep dairy products mostly linked to the lipid and protein fractions. Emphasis will be put on fatty acids as CLA and bioactive peptides, which can favorably contribute to human nutrition.

Key Words: sheep milk, dairy, conjugated linoleic acid

485 Biosynthesis and secretion of bioactive compounds in milk in relation to genetic, molecular, and endocrine mechanisms. R. M. Akers,* *Virginia Tech, Blacksburg.*

Research and general interest in bioactive components in milk and milk products has exploded in the past decade. A simple PubMed search of primary scientific journal articles using the key word bioactive shows returns of 714, 1524, and 2,751 for the years 2000, 2005, and 2010, respectively. In this review, I explore the sources of bioactive components in mammary secretions and pathways which allow for synthesis, secretion and/or transport of bioactive materials into milk and mammary secretions. In the past decade understanding of regulatory processes that affect secretion of lipids and proteins in multiple cell types has also increased. Some of these proposed mechanisms have also been examined in mammary secretory cells. A prime driver of alterations in the composition of mammary secretions e.g., the change from colostrum-like to mature milk is the state of biochemical and structural differentiation of the mammary alveolar cells. Thus understanding factors which initiate and maintain the differentiated state of these cells directly correlates with the composition of milk and therefore the presence of various bioactive components. Gene profiling, proteomic measurements and other molecular tools have made it clear that the various cells within the mammary gland (ductal and alveolar epithelial cells, myoepithelial cells, endothelial cells, fibroblasts, adipocytes, macrophages, plasma cells etc.) are capable of producing a variety of bioactive agents including hormones, growth factors, and derivatives unimagined until recently. It is important to remember that milk and mammary secretions are first and foremost biological fluids. The lactocrine hypothesis to explain how the mammary gland and its secretions can act to control neonatal development is gaining much support. It is rather ironic that while we have long appreciated the nutrient value of mammary secretions, a nearly perfect food, we are seemingly only now beginning to appreciate the rich diversity of the bioactive agents in milk and milk products.

Key Words: bioactive, mammary, milk

Forages and Pastures II

486 Corn hybrid and plant density effects on corn silage quality and yield.

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The objective of this study was to evaluate corn hybrid, plant density, and harvest time effects on corn silage quality and yield. Five moderately early maturity corn hybrids (MEM; Hoegemeyer Hybrids) and 5 moderately late maturity corn hybrids (MLM; 1, Pioneer; 4, Hoegemeyer Hybrids) were planted at 4 populations (49,421, 64,247, 79,073, and 93,900 plants/ha) in a split plot design with 3 replications per hybrid × population combination. Five competitive corn plants were cut 15 cm above ground level and collected at 2 harvest dates (September 1, EH; September 15, LH). Grain, husk, and cob fractions were compiled. The remaining tissues (stalk, leaf, and shank) were chopped through a wood chipper, weighed, mixed, and subsampled at time of collection. There were interactions ($P \leq 0.001$) between hybrid, plant density, and harvest time for grain yield, grain percentage of total DM yield, and NDF concentration of the chopped subsample. Mean and standard deviation of grain yield was 12.0 ± 1.6 Mg/ha (range of 8.5 to 15.9 Mg/ha) for MEM hybrids and 12.5 ± 1.7 Mg/ha (range of 8.1 to 15.6 Mg/ha) for MLM hybrids. Grain yield as a percentage of total DM yield was 52.8 ± 3.3% (range of 42.1 to 59.2%) for the MEM hybrids and 50.6 ± 2.8% (range of 42.3 to 55.8%) for the MLM hybrids. Neutral detergent fiber concentration of the chopped subsample was 59.6 ± 5.1% (range of 50.4 to 70.7%) for the MEM hybrids and 61.7 ± 5.0% (range of 50.7 to 74.1%) for the MLM hybrids. Grain yield for corn planted at 49,421, 64,247, 79,073, and 93,900 plants/ha was 10.4, 12.5, 12.8, and 13.3 Mg/ha, respectively. Grain yield as a percentage of total DM yield was 49.7, 52.0, 52.8, and 52.4% for plant densities of 49,421, 64,247, 79,073, and 93,900 plants/ha, respectively. Chopped subsample NDF concentration was 57.3, 59.1, 62.7, and 63.4% for plant densities of 49,421, 64,247, 79,073, and 93,900 plants/ha, respectively. Grain yield as a percentage of total DM yield was 51.2 and 52.2% for EH and LH, respectively. Chopped subsample NDF concentration was 62.5% for EH and 58.8% for LH. Data from this study illustrate that corn hybrid, plant density, and harvest time affect corn silage yield and fiber characteristics.

Key Words: corn, corn silage, plant density

487 Characterization of aerobic deterioration of corn silage treated with stabilizers.

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We determined how spoilage alters the nutritive value of corn silage and evaluated the ability of TMR-mate (TMR-M, containing a blend of antifungal organic acids, 0.3% wet weight basis) and a feed additive, Omnigen-WYC, (O-WYC, containing potassium sorbate and other ingredients, 0.176% wet weight basis) to slow this process. Five replicated 20 L buckets with 5 cm diameter holes drilled throughout the bucket were prepared for each treatment, and filled with 6 kg of untreated or treated silage with one of the 2 additives. Bucket silos were exposed to air at 22°C. Samples from each bucket were taken at time 0 and every 24 h for 5 d. Core temperatures were measured every 15 min and aerobic stability was calculated as the number of h before the silage mass increased 2°C above baseline. Data were analyzed as a 3 × 6 factorial arrangement of treatments with the main effects of additive and time of sampling and their interaction. In general, the chemical composition and numbers of yeasts remained constant for all treatments through 2 d of exposure. The general tendencies observed relative to time of exposure were an increase ($P < 0.01$) in pH, ammonia-N, numbers of yeasts, DM, CP, and NDF. Decreases ($P < 0.01$) in concentrations of lactic and acetic acids, ethanol, water-soluble carbohydrates, and soluble protein occurred with time. Concentrations of lactic and acetic acids decreased ($P < 0.01$) by more than 80% of initial values after 3 and 5 d, respectively. Loss of DM did not differ among treatments but averaged 11.2% after 3 d and 27.5% after 5 d. At 3 d of exposure, the number of yeasts was 6.42 $\log_{10}$ cfu/g in untreated silage but less ($P < 0.01$) in treated silages (average of 4.91 $\log_{10}$ cfu/g). Similarly, silage pH was higher (5.75, $P < 0.01$) in untreated silage than in treated silage (average of 4.75). Treatment with O-AF and TMR-M improved ($P < 0.01$) aerobic stability (average 53 h) compared with untreated silage (44 h). The extent and duration of heating was lower for silage treated with O-AF than TMR-M. The additives in this study moderately improved the aerobic stability of corn silage.

Key Words: aerobic stability, silage

488 Exogenous fibrolytic enzyme effects on preingestive fiber hydrolysis and release of sugars and phenolics from bermudagrass haylage.

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The objective was to examine the effects of 12 exogenous fibrolytic enzyme (EFE) on hydrolysis of the fiber in a 4-wk regrowth of Tifton 85 bermudagrass haylage. The endoglucanase (EN) and xylanase (XY) activities (μmol/min/g) of the enzymes ranged from 9 to 3624, and 86 to 29301, respectively. The EFE were diluted in citrate–phosphate buffer (pH 6) containing sodium azide (0.02% w/v) antimicrobial agent and applied in quadruplicate to ground bermudagrass haylage (67.3, 33.5, 3.4 and 18.7% NDF, ADF, ADL, and CP, respectively) at manufacturer–recommended rates. The suspensions were incubated at 25°C for 24 h before addition of 30 mL of water, shaking for 1 h, and filtration of contents through Whatman 451 paper. The model included the fixed effect of enzyme. Compared with the Control (buffer and substrate alone), 10 EFE released more water-soluble carbohydrates (WSC, %; 3.69 ± 1.12 vs. 2.28 ± 0.04; $P < 0.01$), 10 released more ferulic acid (FER, μg/g; 263 ± 64 vs. 198 ± 2.3; $P < 0.01$), 8 released more *p*-coumaric acid (μg/g; 178 ± 13 vs. 162 ± 1.3; $P < 0.05$), and 3 solubilized more DM (%; 24.1 ± 0.5 vs. 22.0 ± 0.5; $P < 0.05$). Furthermore, compared with the control, 4 EFE-treated substrates had lower NDF (%; 64.0 ± 1.1 vs. 67.3 ± 0.6; $P < 0.05$), 5 had lower hemicellulose (31.4 ± 1.2 vs. 33.8 ± 0.45; $P < 0.01$), 1 had lower ADF (31.9 ± 0.4 vs. 33.5 ± 0.4; $P < 0.01$) and 1 had lower cellulose (28.6 ± 0.4 vs. 30.1 ± 0.4; $P < 0.01$). Prediction equations with independent variables including enzyme protein content (PR, mg) and EN, exoglucanase (EX), β-glucosidase, (BG), XY and ferulic acid esterase activities applied explained ($P < 0.01$) 64, 72, 99 and 93% of variation in NDF, HEM, WSC (%), and FER (μg/g), respectively. The greatest ($P < 0.01$) contributors to the R^2 for predicting NDF, WSC, and FER were EN (0.34) and BG (0.15), EN (0.65) and PR (0.14), and EN (0.17) and XY (0.71), respectively. Several promising EFE candidates that can hydrolyze bermudagrass fiber before ruminal degradation were identified as well as the critical enzyme activities responsible for such hydrolysis.

Key Words: forage, enzyme, fiber

489 Indigestible NDF in predictions of grass and red clover silage digestibility.

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The objective of this study was to correct indigestible NDF (iNDF) for the loss of lignin to improve predictions of forage OM digestibility. Samples of silages, iNDF and feces were analyzed for acid detergent lignin (ADL). Feed and fecal samples were from grass and red clover silages with in vivo digestibility determined in sheep fed at maintenance level using the total fecal collection method. Silages were harvested at different maturities from primary growth (n = 12) or secondary growth (n = 14) of timothy-meadow fescue (n = 15) or red clover (n = 11) swards. Indigestible NDF was recovered from 288-h in situ incubation in the rumen of 3 lactating dairy cows. Acid detergent lignin was determined in all samples by solubilization of cellulose in sulfuric acid after extraction with acid detergent. Indigestibility of ADL was determined by the Lucas test, where indigestible ADL was calculated from the concentrations of ADL in feces or iNDF. Hypothesis testing was conducted based on the parameters 95% confidence intervals. The slopes of the Lucas test for grass and red clover silages, and for first and second cut silages based on fecal samples did not differ ($P > 0.05$), and indigestibility of ADL (0.97 ± 0.069) was not different from 1 across all silages ($P < 0.05$). Indigestibility of ADL recovered in iNDF was different for grass and red clover silages (0.55 vs. 0.81; $P < 0.05$). Further, intercepts of the regression lines based on recovery of ADL in iNDF were not different from 0 ($P \geq 0.06$) and slopes were smaller than 1 ($P < 0.05$). Correcting individual samples for the loss of ADL in predictions of OM digestibility from iNDF lowered root mean square error (RMSE) from 0.0194 to 0.0179. With a general correction based on an indigestibility of 0.55 or 0.81 for grass and red clover silages RMSE increased to 0.0223. It is concluded that despite the losses of ADL in iNDF determination it is not practical to correct iNDF concentration on an individual sample level.

Key Words: acid detergent lignin, digestibility, indigestible neutral detergent fiber

490 The effect of inoculants containing *Lactobacillus buchneri* on the fermentation of alfalfa silage harvested at two dry matters.

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The objective of this study was to evaluate the effects of microbial inoculants with *Lactobacilllus buchneri* on the fermentation of alfalfa silage. Alfalfa was wilted to 33 (low) and 50% (high) DM. Forage was chopped and treated in piles (4 each) with nothing (C), *L. buchneri* 40788, application rate of 4×10^5 cfu/g of wet forage (LB; Lallemand Animal Nutrition, Milwaukee, WI), LB and *Pediococcus pentosaceus* 12455 (1×10^5 cfu/g; LBP), or LB and *L. plantarum* MTD1 (1×10^5 cfu/g, Ecosyl Products Ltd., Stokesly, UK; LPLB). Forages were packed and stored in lab silos at 22°C for 3, 7, 14 and 90 d. Data were analyzed in a factorial arrangement of treatments with main effects of treatment and time and their interactions. Significance was declared when $P < 0.05$. At both DM, after 3 d of ensiling, the pH declined markedly ($P < 0.01$) and to the same extent for LBP and LPLB, and to a lesser extent for LB compared with C. The drop in pH was more marked ($P < 0.01$) in low vs. high DM silages. After 90 d, LB had lower ($P < 0.01$) concentrations of lactic acid when compared with C. Inoculation of high DM alfalfa did not affect the concentration of lactic acid at d 90. Regardless of DM, inoculation did not statistically increase acetic acid. In particular, treatment with LBC resulted in greater concentrations ($P < 0.04$) of this compound relative to C in both DM. Treatment with LB and LPLB resulted in greater concentrations ($P < 0.01$) of propionic acid when compared with C but only in low DM silages. Inoculation resulted in silages with lower concentrations ($P < 0.01$) of ethanol when compared with C in low DM silages. In high DM silage, only LPLB decreased ethanol relative to C. Treatment with *L. buchneri* altered silage fermentation but the changes were dependent on what organism it was combined with and the DM content of forage.

Key Words: silage, alfalfa

491 Alfalfa/grass mixtures yield more DM, CP, NDF, and dNDF than alfalfa in monocultures.

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Alfalfa and alfalfa/grass mixture trials were seeded in 1x7 M replicated plots near Hutchinson, MN on 25 August 2008, and near Underwood, MN on 29 August 2008 to compare agronomic and nutrient differences. Treatments included binary mixtures of alfalfa (ALF) with 9 different perennial grasses, and alfalfa seeded alone. Three different ALF varieties were tested alone and in binary mixtures with 2 varieties of each of the 9 grass species. Four harvests cut to a 10 cm residual were obtained in 2011 (third production year) at both locations. At each harvest, subsamples of chopped herbage of selected treatments were oven-dried, ground, and analyzed for forage quality via NIRS Consortium equations at the UW Forage Testing Lab. Parameters measured included CP, NDF, 48-h NDF digestibility, ADF, and ADL. Values for RFQ, RFV, milk per ton, milk per acre, and digestible fiber yield were also calculated. At Underwood, binary mixtures of alfalfa/tall fescue or alfalfa/orchardgrass produced significantly higher amounts of NDF and dNDF compared with monocultures of alfalfa. Alfalfa/tall fescue mixtures also produced significantly greater amounts of DM and numerically greater amounts of CP. At Hutchinson, binary mixtures of alfalfa/orchardgrass produced significantly greater amounts of DM, NDF and dNDF when compared with alfalfa alone. Binary mixtures of alfalfa/tall fescue also produced significantly greater amounts of DM and numerically greater amounts of NDF and dNDF compared with alfalfa alone. Yield of CP was similar across treatments at Hutchinson. Alfalfa/grass mixtures offer agronomic and nutrient advantages compared with alfalfa monocultures.

Table 1. 2011 total-season DM, CP, NDF and dNDF-yields of alfalfa/grass mixtures at Hutchinson (H) and Underwood (U), Minnesota

	DM Yld	CP Yld	NDF Yld	dNDF Yld
Mixture	Tons DM/ a	lb CP/a	lb NDF/a	lb dNDF/a
Alf/Tall Fescue - U	**5.87**	**5.87**	**5530**	**2670**
Alf/Orchardgrass - U	5.41	2330	**5070**	**2490**
Alf/Orchardgrass -H	**4.03**	1670	**4530**	**2430**
Alf/Tall Fescue-H	**4.01**	1650	3920	2030
Alfalfa Alone-U	4.89	2290	4130	1710
Alfalfa Alone-H	3.60	1530	3460	1720

Bolded values: $P < 0.05$ differs to the largest value by location within the same data column.

Key Words: alfalfa, grass, dNDF

492 Effect of land clearing and tillage methods on weed incidence under maize-cassava inter-cropping system.

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Agricultural activities have been identified as the most common causes of land transformation. Such transformation results in changes in ecological features, such as weed flora succession. It is in view of this that this work was carried out to evaluate the effect of land clearing and tillage methods on weed incidence under maize-cassava intercropping system. The experiment was carried out at the International Board for Soil Research and Management experimental site, Epemakinde, Nigeria. (40 45° E, 60 45° N) after 3 cropping years. The treatments consist of 3 land clearing methods thus, given a split plot fitted into randomized complete block design. The 3 land clearing methods: slash and burn (SB), bulldozed not windrowed (BNW) and bulldozed windrowed (BW) are the main treatments while the 4 tillage methods namely (zero, conventional, traditional, and minimum tillage) constituted the sub-treatments. Data were collected on weed incidence at 6 and 16 weeks after planting (WAP). The result indicates that weed coverage at WAP were not different ($P > 0.05$) among the land clearing treatments, although SB had the least weed coverage (55.5%) ($P > 0.05$) on the average representing 9.2% and 8.9% lower than those of BW (60.63%) and BNW (60.46%). Zero tillage and traditional practices had the highest weed coverage of 86.11% and 82.17% respectively, representing 207.5% and 193.5% increase over conventional tillage (28.00%). In conclusion, slash and burn under minimum tillage and conventional tillage treatments, which gave a reduced weed problem, appears a better option.

Key Words: land clearing, tillage methods, weed incidence

493 Agronomic characteristics of pearl millet genotypes for forage production in southwestern Nigeria.

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This study was conducted to evaluate 10 selected *Pennisetum glaucum* (L.) R. Br. genotypes for forage production in Abeokuta, South - Western Nigeria. The experiment was laid out on the field in a randomized block design. The land area of 555m ^{2} was divided into 30 plots of 3m by 2.5m each with spacing of 1m between plots. Ten genotypes of pearl millet were randomly planted at a spacing of 75 × 25 cm into 10 plots per block and replicated 3 times. Weekly observations were taken on the tiller number, number of leaves on main and secondary tillers, crown spread and leaf area from the 2nd week after planting (WAP) and plant height was taken up to 22 WAP. There were significant differences in the plant height, number of tillers and leaves, leaf area and crown spread on the pearl millet genotypes. Bunkure, Mokwa, Maiwa UI 25–2, Maiwa UI 28–1, Maiwa UI 94–2 and Dauro reached their maximum heights of 275.00 cm to 417.30 cm at 22WAP with Bunkure having the highest plant height of 417cm. Dauro and Mokwa had the highest ($P < 0.05$) leaf area at 7WAP. Dauro, Maiwa UI 94–2, Maiwa UI 25–2 and Mokwa had the highest ($P < 0.05$) number of leaves on primary and secondary tillers from 8WAP to 10WAP. Bunkure had highest number of leaves on secondary tillers, though produced fewer primary leaves. It can be concluded that Bunkure, Mokwa, Dauro, Maiwa UI 25–2 and Maiwa UI 94–2 pearl millet genotypes planted between May and October which exhibited late maturity and had the highest number of leaves, are the most desirable for forage production in Abeokuta, southwestern Nigeria.

Key Words: pearl millet, genotypes, forage

494 Influence of sample preparation technique on masticate fiber content collected from esophageally fistulated cattle.

K. L. Gillespie,* J. A. Musgrave, L. A. Stalker, T. J. Klopfenstein, and S. K. Pruitt, *University of Nebraska, Lincoln.*

Diet samples collected using esophageally fistulated cattle are representative of nutrients consumed by grazing cattle. However, preparation methods may alter the nutrient composition of the masticate sample. Meadow, hay, and upland range diet samples collected using esophageally fistulated cows were used to determine the effect of squeezing masticate samples on NDF content. In study 1, nine 1-ha Sandhills upland range paddocks were each sampled twice throughout the grazing season using 3 esophageally fistulated cows each collection day. Samples were collected at 12-d intervals from May 18 to June 11 and at 28-d intervals from June 12 to August 26. In study 2, 12 esophageally fistulated cows were offered 428 g (DM) vegetative grass harvested immediately before presentation from a subirrigated meadow, and, after collection of the masticate, they were offered 1,032-g (DM) hay harvested the previous summer from a subirrigated meadow. In all studies, esophageal plugs were removed, cows were fitted with screen bottom bags and allowed to graze, and following collection, masticate samples were divided and left unsqueezed (UNSQZ) or hand squeezed until no saliva could be extracted (SQZ). Samples were frozen, lyophilized, ground to pass a 1-mm screen, and analyzed for NDF. Representative samples of the clipped meadow and hay offered in study 2 were collected, ground through a 1-mm screen, and analyzed. In study 1, squeezing increased ($P < 0.01$) NDF content from 65.9% (UNSQZ) to 69.7% (SQZ). In study 2, squeezing increased ($P < 0.01$) NDF content of clipped meadow from 43.9% (UNSQZ) to 52.0% (SQZ), and hay from 67.3% (UNSQZ) to 71.2% (SQZ). Fresh, vegetative masticate samples were affected most by squeezing. There was no significant difference ($P = 0.27$) between NDF content of hay offered at 66.2% and UNSQZ masticate sample collected at 67.3%. However, meadow sample NDF significantly increased ($P < 0.01$) under both methods, from 40.0% originally to 43.9% UNSQZ and to 52.0% SQZ. Cell solubles may be lost with saliva through screen bottom bags and further losses occur with squeezing. Squeezing masticate samples markedly increases NDF content of samples collected with esophageal fistulated animals.

Key Words: NDF, forage diet sample, fistulation

495 Influence of pre-collection diet and squeezing on crude protein content of masticate collected from fistulated cattle.

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In study 1, 12 esophageally fistulated cattle were maintained on 2 pre-collection diets: HI (24% CP, n = 6) or LO (7.7% CP, n = 6) for 8 d. On d 9, the esophageal plug was removed, screen bottom bags were attached and all cattle were presented with 428 g (DM) vegetative grass (VEG; 24% CP, 40% NDF) which had been harvested from subirrigated meadow immediately before presentation. Following VEG collection, all cows were presented with 1032 g (DM) hay (HAY; 7.7% CP, 66% NDF) harvested from subirrigated meadow the previous summer. Blood samples were collected via coccygeal venipuncture and analyzed for BUN content. In study 2, 3 esophageally fistulated cows sampled Sandhills upland range 12 times from May 21 to August 18. In study 3, 5 ruminally fistulated steers were fed vegetative smooth bromegrass harvested immediately before presentation. In all 3 studies, masticate samples were divided and each was either squeezed by hand until no more saliva could be removed (SQZ), or un-squeezed (UNSQZ). All masticate samples were immediately frozen and stored until lyophilized and analyzed for CP content. In study 1, pre-collection diet did not affect ($P = 0.49$) CP content of masticate. Type of forage offered (VEG vs. HAY) interacted ($P = 0.01$) with preparation technique, where CP was lost when VEG samples were squeezed (20.0 vs. 21.5% CP for SQZ vs. UNSQZ, respectively; $P < 0.05$) but not when HAY samples were squeezed (7.6 vs. 7.6% CP for SQZ vs. UNSQZ, respectively; $P > 0.05$). BUN levels tended to be higher for HI cows (27.6 ± 4.0 vs. 23.5 ± 3.2 mL/dL; HI vs. LO, respectively; $P = 0.08$). In this case, total amount of salivary contamination may not have been enough to influence CP content of the masticate. In study 2, there was no difference in CP between SQZ and UNSQZ (9.5 and 9.6%; $P = 0.66$) samples. In study 3, the difference in CP between SQZ and UNSQZ (18.6 and 20.1%) samples was not statistically separable ($P = 0.16$). Previous diet did not affect CP level of masticate and squeezing affected CP levels of high quality forage but had little effect on lower quality forage.

Key Words: grazed diet, diet collection, sample preparation

496 Variability and implications of indigestible neutral detergent fiber in C3 and C4 forages.

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Rates of NDF digestion are used within models such as the CNCPS and CPM Dairy to determine optimal rations for dairy cows. These models multiply ADL by 2.4 to estimate the indigestible NDF (iNDF). The resulting iNDF can be used to estimate the rate of digestion for the potentially digestible NDF (kd, pdNDF). However, recent work in C3 forages has found considerable variability in the ratio iNDF/ADL, resulting in profound effects on the calculated pdNDF, kds and the supply of energy and microbial protein. The objectives of this work were to further characterize the variability of this ratio in C3 and C4 species grown in Queensland, Australia, and to suggest better equations to predict iNDF. One hundred and 40 forages or forage mixtures were selected out of 240 sampled across Queensland during winter 2011 to represent a wide spread of NDF content, forage groups and species. Samples were analyzed for ADL, NDF and iNDF, and results were grouped for single species. Long-term in vitro fermentations were conducted for 240 h to reach the maximum extent of digestion to determine iNDF. Within and across forage groups, the iNDF/ADL ratio ranged from 1 to 9.6, with lower values ($P < 0.05$) for C3 species (3.05 ± 1.47) compared with C4 ones (5.01 ± 1.75). Only for ryegrass, iNDF appeared similar (2.53 ± 0.76, $P = 0.33$) to that estimated using the 2.4 ratio, with, however, 75% of the samples having ratios numerically lower than 2.4 and therefore lower actual iNDF and kd. The attempt to predict iNDF within species based on the relationship between ADL/NDF and the ratio, through exponential equations, resulted in R^2 values between 0.15 and 0.85. This suggests that the 2.4 ratio when applied indiscriminately has potentially large errors and simply using C3 and C4 classification will not solve this issue, but possibly a grouping tht is species-specific may be more appropriate. A wider data set across species, agronomic and environmental conditions is needed to see if generalized equations with more acceptable error terms can be devised. The project was partially funded by Dairy Australia.

Key Words: indigestible NDF, fiber, rate of digestion

497 Fecal NIRS relationship with intake and diet digestibility of grazed Bahiagrass by cows determined by n-alkanes.

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The objective of this study was to determine if fecal analysis by NIRS could be used to calibrate for intake determined by the alkane ratio technique in grazing cows. Dry matter intake (DMI; g/kg BW) and diet digestibility (D) was estimated in cows of various breeds in 7 trials over 7 years during different seasons. Nine to 12 cows were used in each trial and on d-1, each received a bolus that delivered a prescribed amount daily of both C_{32} and C_{36} n-alkanes as external markers. The bolus was designed to deliver 300 mg of marker each day over about 21 d. In 4 of the trials, actual payout was determined by collecting feces until dosed marker was not detected. Fecal samples were collected daily from the ground as marked cows defecated in presence of an observer, lyophilized, scanned by NIRS (400–2500 nm), and analyzed for n-alkane concentration following ethanolic KOH extraction and cleanup. Diet D was estimated by the ratio of naturally occurring plant cuticular wax n-alkanes (odd-chain C_{27}-C_{37}) in the forage and feces. Intake was estimated by the ratio of daily dose of external marker and fecal marker concentration corrected for forage C_{32} or C_{36}. Bahiagrass contained sufficient C_{31}, C_{33}, and C_{35} for use as markers and concentration in feces varied both within trial and across trials providing variation in D. Calibration equations were developed by PLS regression of DMI and D on fecal spectra. The equations were then used to predict values on the same spectra to determine if structural bias occurred within the data set among trials and breeds within trial. Differences between alkane estimated DMI (31.6 ± 13.6) and D (65.2 ± 7.0) and NIRS estimated DMI (31.1 ± 8.3) and D (65.5 ± 4.7) were significant ($P < 0.001$) among trials but not different due to breed within trial. When alkane estimated D was regressed on NIRS predicted D, slopes differed among trials ($P < 0.0001$) and breed within trial ($P < 0.01$). However, slopes for DMI differed among trials ($P < 0.001$) but not breed ($P = 0.60$). We suggest that NIRS can be used as a double sampling technique with n-alkanes for estimating DMI and diet D on large numbers of animals.

Key Words: grazing intake, diet digestibility, fecal NIRS

498 Dry season nutrient availability of vegetation species selected by the African elephant (*Loxodanta africana*) in the Pongola Game Reserve, South Africa.

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African elephants were reintroduced to the Pongola Game Reserve (PGR), South Africa, in 1997, via translocation. Fourteen elephants established the original population and it has since grown to over 50 individuals. Elephant conservation and management has continued to increase in importance throughout the southern African countries, and along with efforts of Space for Elephants, the PGR currently monitors herd health and behavior, but information on herd nutritional status is lacking. The purpose of this research was to collect samples of plant species consumed by the elephants and analyze the chemical composition and adequacy of the general diet using horse nutrient requirements. Body condition score was assessed to determine if animals were losing condition due to lack of nutrition. Collection of plant samples occurred during the dry season in July 2011. Nutrient analyses included DM, ash, crude protein, EE, ADF, NDF, ADICP, NDICP, hemi-cellulose, CHO content, macro and micro minerals; DE was estimated using horse energy calculations; GE, ME, TDN, and estimated digestibility were calculated using NRC Beef 2000. Fecal samples were also collected and analyzed for fiber and mineral content. Estimated DE averaged 1.63 Mcal/kg for grasses, 3.01 Mcal/kg for *Aloe marlothi*, and 2.18 Mcal/kg for tree species. Grasses averaged 2.98% CP, 47.0% ADF, and 76.8% NDF, on a dry matter basis. Aloe averages 16.0% CP, 19.7% ADF, and 25.5% NDF. Tree species averaged 8.8% CP, 37.0% ADF, and 52.7% NDF. Results of this study suggest that crude protein and phosphorus (average 0.11% of DM) are available in marginal amounts and lactating female elephants and the bulls with the highest energy requirements are at risk of losing body condition. Therefore, further population control methods or herd size reduction may be required to sustain the population and avoid detrimental environmental damage from over-exploitation.

Key Words: African elephant, nutrition, chemical composition

Horse Species II

499 Estimation of ideal body weight in horses and ponies using morphometric measurements. K. Martinson*[1], R. Coleman[2], J. Earing[1], A. Rendahl[1], and M. McCue[1], [1]*University of Minnesota, St. Paul,* [2]*University of Kentucky, Lexington.*

As the incidence of equine metabolic syndrome and obesity become more prevalent in the equine population, owners, veterinarians, and professionals need information to more effectively manage equine body weight. Body condition score (BCS) is used to measure body fat or adiposity in specific areas of the body, however, ideal body weight for equines is currently unknown. The objective of this study was to determine if ideal equine body weight could be derived based on body measurements unaffected by adiposity. Six hundred and 40 non-pregnant adult equines, ≥ 3 years of age, and ≥ 112 cm in height were measured and weighed at 2 non-breed specific equine shows in September 2011 in MN. For all equines, 2 personnel assessed BCS on a scale of 1 (poor) to 9 (extremely fat), one person measured wither height at the third thoracic vertebra, and 2 personnel measured body length from the point of buttock to the point of the shoulder. Girth and neck circumference, age, sex, and breed were also recorded, and equines were weighed on a portable livestock scale. Equines had a BSC range of 2 to 8 (mean = 5.6), mean age of 12 years, and the dominant breed and sex were Quarter Horses (n = 345) and geldings (n = 345), respectively. Of the 640 equines, 253 and 236 were given a BSC of 5 and 6, respectively, and were used to predict ideal weight. A linear regression for ideal weight was fit using body length and height as predictors. Neck ($P < 0.001$) and girth ($P < 0.001$) circumference affected model fit, however, these measurements are biased by adiposity and were removed from the model. Age ($P = 0.734$) and sex ($P = 0.337$) did not affect model fit. Body length ($P < 0.001$) and wither height ($P < 0.001$) accurately predicted ideal body weight ($R^2 = 0.86$). Breed ($P < 0.001$) affected the model, however, including that factor resulted in a minimum improvement in model fit ($R^2 = 0.88$). Morphometric measurements can be used to predict ideal equine body weight resulting in useful information for health and nutritional management of equines.

Key Words: body condition score, body length, height

500 Influence of maternal plane of nutrition and arginine supplementation on mares and their foals: Glucose and insulin dynamics. A. E. Hanson*[1], K. N. Winsco[1], J. A. Coverdale[1], C. J. Hammer[2], and A. N. Wolford[1], [1]*Texas A&M University, College Station,* [2]*North Dakota State University, Fargo.*

The objective was to determine if supplemental dietary arginine can mitigate the effect of maternal over-nutrition on mare and foal glucose and insulin dynamics. Thirty-two mares (468 to 668 kg BW; 3 to 19 yr) were blocked by expected foaling date and randomly assigned to treatments. Treatments were arranged as a 2 × 2 factorial with 2 planes of nutrition, moderate (Mod; 0.5% BW AF grain/d) or high (High; 1% BW AF grain/d) and 2 levels of L-arginine supplementation, 0.21 g/kg/d (Arg) or no supplemental Arg (Con; L-alanine to maintain isonitrogenous diets). Treatments began 110 d before expected foaling and terminated at parturition. Mares were housed by block, allowed ad libitum access to water and coastal bermudagrass (*Cynodon dactylon*) hay, and fed commercial grain 2 × /d in individual stalls. A modified frequent sampling i.v. glucose tolerance test (FSIGT) was performed on mares at 11 mo gestation and foals at 5 and 30 d of age. After a baseline plasma sample, a glucose bolus of 0.3 g/kg BW was administered, and then, an insulin bolus of 30 mU/kg BW after 20 min. 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. Glucose concentrations were analyzed using a colorimetric assay and insulin using a RIA kit. Data were analyzed using PROC MIXED of SAS with effects of plane of nutrition (Nutr), amino acid (AA), time, and their interactions. There was no influence of diet on mare glucose area under the curve (AUC) or peak glucose (PG) and peak insulin (PI) concentrations. Mare insulin AUC tended to be influenced by diet ($P \leq 0.06$) with HighCon mares having greater AUC than ModCon ($P \leq 0.05$), and HighCon having greater AUC than HighArg ($P \leq 0.05$). Foal glucose AUC, PG, insulin AUC, and PI were not influenced by maternal diet. Mare AA tended to influence foal PG with foals from Con having higher concentrations than Arg ($P \leq 0.09$). Foal age influenced glucose and insulin AUC with glucose greater at 5 d compared with 30 d ($P \leq 0.003$), and insulin tending to be greater at 30 d than 5 d ($P \leq 0.08$). Data suggest maternal nutrition and arginine supplementation can alter mare and foal glucose and insulin dynamics.

Key Words: glucose, insulin, arginine

501 Prevalence of internal parasites and anthelmintic efficacy in horses in relation to age, season and housing system. E. R. Share,* J. M. Reddish, C. Dyer, K. Koke, K. Barnhart, P. Sparks, and K. Cole, *The Ohio State University, Columbus.*

The effective control of internal parasites is important in maintaining horse health. The objective of this study was to determine the prevalence of internal parasites and anthelmintic efficacy in horses in relation to age, season and housing system. Fecal samples were collected from 65 horses, ranging in age from 1 to 22 years, on a farm in central Ohio between July 2011 and January 2012. Fecal egg count data were collected before treatment with pyrantel pamoate at the recommended dosage and 14 d post-treatment. Fecal samples were analyzed by the fecal float method, with the number of internal parasites recorded as eggs per gram (EPG) of feces. Fecal egg count (FEC) reduction was calculated as (pre-treatment EPG minus post-treatment EPG)/pre-treatment EPG. Data were analyzed using the PROC GLM procedure of SAS. A P value of ≤0.05 was considered statistically significant. Treatment with pyrantel pamoate was considered effective if FEC reduction was ≥90% by d 14 post-treatment. Strongyle, ascarid, hookworm, pinworm, whipworm and tapeworm eggs were identified in this study; however, strongyle, ascarid and tapeworm eggs were the most prevalent. Young horses (<3 yr) had greater FEC compared with mature horses (464.35 ± 239 EPG vs. 198.89 ± 234 EPG, $P < 0.05$). FEC were similar during summer months compared with winter months. Horses maintained on pastures had greater FEC than horses kept in stalls (280.4 ± 261 EPG vs. 72.6 ± 100 EPG; $P < 0.05$). Resistance to pyrantel pamoate was evident regardless of the age of the horses, season or housing system. In this study, treatment with pyrantel pamoate was more effective at reducing total FEC in mature horses (27.8%) compared with young horses (14.3%). Pyrantel pamoate was also found to be more effective at reducing total FEC in the summer months (15%) as compared with the winter months (0%). Horses maintained on pastures were less resistant (21.4%) to treatment with pyrantel pamoate compared with stalled horses (16.7%). Although pyrantel pamoate was not considered effective in reducing the total FEC of horses on this farm, it may still be a useful product if used in combination other anthelmintics.

Key Words: horse, internal parasites, pyrantel pamoate

502 Antibiotic therapy disrupts equine fecal microflora.

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Antibiotic associated diarrhea (AAD) is a side effect of antibiotic therapy in horses. AAD is attributed to the disruption of the normal microflora of the hindgut allowing colonization of pathogenic bacteria. However, there is little information on the effect of antibiotics on specific microflora. Therefore, we evaluated the effects of 2 common antibiotics on the equine hindgut microflora. Horses ranging from 2 to 14 y, were blocked by age and sex into 6 blocks of 3 horses. Within block, horses were randomly assigned to 1 of 3 treatments: CO (no antibiotic; $n = 6$), ST (trimethoprim-sulfadiazine, oral, 30 mg/kg; $n = 6$) and CF (ceftiofur sodium, IM, 2.2 mg/kg; $n = 6$). Each block consisted of a 21-d adaptation, a 7-d treatment and a 7-d withdrawal period. Fecal samples were collected during each block and were used to enumerate typical AAD pathogens (*Clostridium difficile*, *Clostridium perfringens* and *Salmonella* spp.) and selected normal microflora (lactobacilli and cellulolytics). Data were log-transformed, averaged within period, and analyzed by repeated measures ANOVA using the mixed procedure and the ttest procedure of SAS version 9.2. There were treatment x period interactions for cellulolytics ($P < 0.0001$) and lactobacilli ($P = 0.0504$) in that they decreased in response to CF and ST. No significant effects of period were found in the CO horses ($P > 0.05$). *C. difficile* was not detected during adaptation or in any CO horse throughout the study. However, there was a treatment by period interaction ($P < 0.0001$) where horses treated with antibiotics had an increase in *C. difficile* during the treatment and withdrawal periods. Antibiotics also increased *Salmonella* spp. prevalence ($P = 0.0024$). When comparing horses with and without detectable levels of *C. difficile*, horses with *C. difficile* had lower levels of lactobacilli ($P < 0.0001$) and cellulolytics ($P < 0.0001$). No effects of antibiotic treatment were observed for *C. perfringens* ($P > 0.05$). These results indicate that antibiotic therapy has negative effects on equine hindgut microflora, even when AAD does not occur.

Key Words: *Clostridia*, *Salmonella*, diarrhea

503 Influence of probiotics on microflora in the gastrointestinal and reproductive tracts of horses.

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Current scientific literature is limited on what microorganisms are present in the equine gastrointestinal and reproductive tracts. Microbial populations in these environments can be easily disrupted and probiotics have been utilized in other species to re-establish homeostasis and inhibit the growth of pathogenic bacteria. The objective of this study was to determine whether probiotics could influence the microflora in the gastrointestinal and reproductive tracts of mature horses. Eight Quarter Horse mares (10 ± 2 yrs of age) were randomly assigned to 1 of 2 treatment groups (probiotic or control) for a period of 56 d. All horses received 0.5% BW of a 12% CP pelleted concentrate, with water and mixed grass hay ad libitum. Horses in the probiotic treatment group were fed a supplement containing L. acidophilus at a target dose of 10^9 cfu/45 kg of BW per day. Fecal samples and vaginal swabs were collected weekly to measure pH and evaluate changes in microflora. Uterine swabs were collected when possible during periods of estrus. Mean pH values were analyzed using the PROC MIXED procedure of SAS. A P value of ≤ 0.05 was considered statistically significant. There were no changes in fecal, vaginal or uterine pH due to probiotic supplementation. Microbial diversity was investigated using PCR with universal primers specific to 16S rRNA gene sequences and subsequent denaturing gradient gel electrophoresis (DGGE) analyses. Images were captured and analyzed with Bionumerics software to compare microbial diversity. PCR using universal primers was successful in amplifying the 200 bp region of interest in all samples. DGGE analysis of fecal and vaginal samples revealed that the control horses had a more diverse microflora compared with the horses given the probiotic. However, DGGE analysis of uterine samples revealed no differences in microbial populations due to the probiotic. The ability of a probiotic to colonize the host may be species and/or environment specific. Further analysis with Lactobacillus specific primers is needed to determine the influence of the probiotic on microbial diversity within the gastrointestinal and reproductive tracts.

Key Words: horse, probiotic, reproductive tract

504 Effects of weight distribution on movement of mature riding horses.

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Several studies have shown that a rider's weight can affect the horse's movement. However, horses often carry riders with different skill levels who may or may not distribute their weight evenly. The objective of this study was to determine the effects of even and uneven weight distribution on the movement of mature riding horses ($n = 15$) at the walk and trot. Every 15 d for a period of 15 wk, each horse was fitted with a surcingle and increasing amounts of weight (13.6 kg evenly distributed, 27.2 kg evenly distributed, and 27.2 kg unevenly distributed), then videotaped in hand at the walk and trot tracking to the right and left on a flat surface. All horses carried each weight each time they were videotaped and the weight was always added in the same order. The camera was positioned at a height of 3.0 m and 8.6 m away from and perpendicular to the line of travel. Videos were analyzed using OnTrack Equine software for stride length, maximum knee angle and maximum hock angle at the walk and trot. The horses were unshod and their hooves were trimmed every 30 d to minimize changes in hoof shape due to normal hoof growth that may affect their movement. Data were analyzed using the PROC GLM procedure of SAS. A P value of ≤ 0.05 was considered statistically significant. Average stride length at the walk and trot for horses fitted with the surcingle only was 2.19 m and 2.21 m, respectively. There were no differences in average stride length at the walk for horses carrying 13.6 kg or 27.2 kg evenly distributed across their back compared with horses carrying no additional weight. However, a shorter stride length at the walk was observed for horses carrying 27.2 kg unevenly distributed across their back ($P < 0.01$). At the trot, average stride length and hock angle decreased in response to increasing amounts of additional weight and uneven distribution of that weight ($P < 0.01$). Average knee angle at the trot decreased in response to uneven weight distribution but not due to increasing amounts of weight. Overall, the results of this study indicate that additional weight placed on a horse's back and the distribution of that weight can influence the movement of the horse at both the walk and trot.

Key Words: horse, movement, weight distribution

Nonruminant Nutrition: Feed Ingredients

505 Energy, phosphorus, and amino acid digestibility in Lemna protein concentrate, fish meal, and soybean meal fed to weanling pigs. O. J. Rojas* and H. H. Stein, *University of Illinois, Urbana.*

Lemna protein concentrate (LPC; 68% CP) may be used in diets fed to pigs, but no data on the nutritional value to pigs of LPC have been published. Three experiments were, therefore, conducted to determine the concentration of ME, the standardized total tract digestibility (STTD) of P, and the standardized ileal digestibility (SID) of AA in LPC and to compare these values to values for fish meal (FM) and soybean meal (SBM). Experiment 1 was conducted to determine the ME of LPC, FM, and SBM. Thirty-two barrows (initial BW: 16.8 ± 2.8 kg) were placed in metabolism cages and allotted to a randomized complete block design with 4 diets and 8 replicate pigs per diet. A corn-based diet and 3 diets that contained corn and LPC, FM, or SBM were formulated. Feces and urine were collected for 5 d after a 5-d adaptation period and all samples were analyzed for GE. Results indicated that the concentration of ME was not different among the 3 ingredients. In Exp. 2, 24 barrows (initial BW: 10.5 ± 2.5 kg) were allotted to a randomized complete block design with 3 diets and 8 replicate pigs per diet and used to determine the STTD of LPC, FM, and SBM. Three diets that each contained 1 of the 3 test ingredients as the sole source of P were formulated. Pigs were placed in metabolism cages and feces were collected for 5 d after a 5-d adaptation period. The STTD of P in LPC (72.8%), FM (65.6%), and SBM (62.8%) was not different among ingredients. The SID of AA in LPC, FM, and SBM was determined in Exp. 3. Eight barrows (initial BW: 21.4 ± 4.0 kg) were equipped with a T-cannula in the distal ileum and randomly allotted to a replicated 4 × 4 Latin square design. An N-free diet and 3 cornstarch-based diets in which SBM or SBM and LPC or SBM and FM were the only sources of AA were formulated. The SID of most indispensable AA was greater ($P \leq 0.01$) in SBM than in LPC and FM. In conclusion, the concentration of ME and the STTD of P is not different among LPC, FM, and SBM, but SID of most indispensable AA is greater in SBM than in FM and LPC.

Key Words: Lemna protein concentrate, nutrient digestibility, pigs

506 Amino acid digestibility in camelina seeds and camelina expellers fed to growing pigs. F. N. Almeida*[1], J. K. Htoo[2], J. Thomson[3], and H. H. Stein[1], [1]*University of Illinois, Urbana,* [2]*Evonik Industries AG, Hanau, Germany,* [3]*Evonik Degussa Corporation, Kennesaw, GA.*

The nutritional value of camelina seeds (*Camelina sativa*) and camelina expellers fed to pigs has not been reported. Therefore, an experiment was conducted to determine the standardized ileal digestibility (SID) of CP and AA in camelina seeds and camelina expellers and to compare these values with SID values of CP and AA in canola meal fed to pigs. Two sources of camelina seeds (average of 27.9% CP, 39.4% acid hydrolyzed ether extract (AEE), and 27.6% NDF, as-fed basis), 3 sources of camelina expellers (average of 33.1% CP, 15.8% AEE, and 24.9% NDF, as-fed basis), and 1 source of canola meal (36.4% CP, 3.7% AEE, and 34.8% NDF, as-fed basis) were procured from companies located in the United States. Seven pigs (initial BW = 43.5 ± 3.5 kg) were allotted to a 7 × 7 Latin square design with 7 diets and 7 periods. Two diets contained camelina seeds (CS-1 and CS-2), 3 diets contained camelina expellers (CE-1, CE-2, and CE-3, respectively), and 1 diet contained canola meal as the sole source of CP and AA. Each test ingredient was included at 40% in the diets. A N-free diet was used to determine basal endogenous losses of CP and AA. Data were analyzed by the Mixed Procedure with diet as the main effect, and pig and period as random effects. Results indicate that the SID of AA in camelina seeds is less ($P < 0.05$) than in camelina expellers and canola meal (Table 1), which limits the use of camelina seeds in swine diets, but the SID of AA in camelina expellers is mostly comparable to that of canola meal. Camelina expellers may, therefore, be used as an alternative feed ingredient in diets fed to pigs.

Table 1. Standardized ileal digestibility (%) of AA in camelina seeds (CS), camelina expellers (CE), and canola meal

Item	CS-1	CS-2	CE-1	CE-2	CE-3	Canola meal	SEM	*P*-value
Ile	42^{c}	62^{b}	73^{a}	63^{b}	78^{a}	78^{a}	3	<0.01
Leu	49^{c}	66^{b}	77^{a}	67^{b}	80^{a}	81^{a}	3	<0.01
Lys	48^{c}	63^{b}	72^{ab}	68^{ab}	69^{ab}	75^{a}	3	<0.01
Met	54^{d}	72^{c}	84^{a}	76^{bc}	82^{ab}	85^{a}	2	<0.01
Phe	46^{d}	65^{c}	76^{ab}	68^{bc}	79^{a}	80^{a}	3	<0.01
Thr	38^{d}	56^{c}	64^{abc}	59^{bc}	67^{ab}	73^{a}	3	<0.01
Trp	45^{c}	57^{b}	67^{ab}	58^{b}	71^{a}	75^{a}	3	<0.01
Val	44^{c}	63^{b}	74^{a}	65^{b}	76^{a}	76^{a}	3	<0.01

$^{a\text{-}d}$Values within a row lacking a common superscript letter are different ($P < 0.05$).

Key Words: amino acid digestibility, camelina, pigs

507 Withdrawal patterns of DDGS on performance, belly firmness, and fatty acids in pigs—A cooperative study. G. L. Cromwell,* M. J. Azain, O. Adeola, S. K. Baidoo, S. D. Carter, T. D. Crenshaw, G. M. Hill, P. S. Miller, J. F. Patience, M. C. Shannon, and H. H. Stein, *NCCC-42 Committee on Swine Nutrition, University of Kentucky, Lexington.*

An experiment involving 580 pigs (20 reps of 4 to 8 pigs/pen) was conducted at 10 stations to assess the effect of various DDGS withdrawal patterns to pigs from 29 to 123 kg BW. Corn-soybean meal diets with 0 to 33.5% DDGS were fed in 3 phases. A single source of DDGS containing 8.8% fat, 26.4% CP, and 1.07% Lys was used at each station. Diets were formulated to contain 0.91, 0.73, and 0.58% SID Lys during the 3 phases with changes at 58 and 91 kg BW. Levels of DDGS in the 3 phases were Trt 1, 0–0–0%; Trt 2, 33.5–33.5–33.5%; Trt 3, 33.5–33.5–0%; Trt 4, 33.5–20–11%; and Trt 5, 20–20–20%. Levels of DDGS in Trt 3, 4, and 5 were such that total DDGS consumed during the experiment was nearly identical (55.3, 55.2, and 55.1 kg/pig, respectively). At each station, 2 pigs from each pen in 2 reps were killed and a backfat sample was obtained for fatty acid (FA) analysis and iodine value (IV). In most cases, there were differences among stations ($P < 0.05$), but station x treatment interactions were few. The ADG and ADFI of the 5 groups did not differ (957, 925, 922, 938, 927 g/d; 2.67, 2.73, 2.79, 2.76, 2.68 kg/d), but pigs fed the control diet with 0% DDGS were more efficient (0.360, 0.341, 0.331, 0.341, 0.348 G:F; $P < 0.05$). Hot carcass yield tended to be less (76.1, 75.4, 75.8, 75.9, 75.5%; $P = 0.06$), and calculated fat-free lean was greater for Trt 2 (52.4, 53.7, 52.5, 52.3, 52.9%; $P < 0.05$). Bellies were softer ($P < 0.01$) in pigs fed DDGS based on lateral (16.0, 11.6, 14.4, 14.9, 14.9 cm) and vertical flex scores (22.6, 27.2, 24.9, 24.4, 24.0 cm). Feeding the high level of DDGS throughout resulted in less saturated and monounsaturated FA in the backfat (39.3, 34.9, 37.9, 38.6, 37.2%, and 46.6, 41.6, 43.7, 43.8, 43.3% of total FA; $P < 0.001$)

and more polyunsaturated FA (13.5, 22.8, 17.8, 17.1, 19.0%; $P < 0.001$). The IV for outer fat layers were 67.9, 79.4, 73.2, 72.0, 74.3, and for inner fat layers were 60.4, 72.8, 65.0, 63.8, 67.2 ($P < 0.001$). Gilts had higher IV than barrows in outer (74.8 vs. 72.2) and inner (67.5 vs. 64.6) fat ($P < 0.001$). Withdrawal of DDGS in phase 3 or feeding less DDGS produced FA and IV levels that reverted toward those of control pigs.

Key Words: pigs, DDGS, fatty acids

508 Wheat-DDGS pig finishing diet reduces feed cost but does not improve net profit of production. G. A. Mastromano,* M. R. Ashby, R. C. Roberson, J. M. Scheffler, and J. Escobar, *Virginia Tech University, Blacksburg.*

Corn prices are increasing due, in part, to ethanol production, resulting in increased feed costs for swine producers. The objective of this experiment was to determine if a wheat-dried distiller's grains with solubles (DDGS) based diet (WD) would reduce cost efficiency of gain compared with a corn-SBM (CS) based diet. Fifty pigs (24 gilts and 26 barrows) were segregated by sex and housed 2–3 pigs/pen with free access to feed and water over a 53-d study. One-half of pigs were fed CS diet (85.92% corn, 12.50%SBM, 1.58% others) and the remainder were fed WD diet (50.50% wheat, 40% corn DDGS, 7.00% SBM, 2.5% others). Feed disappearance was monitored daily and pigs were weighed every 14 d. At the end of the study, pigs were transported about 6 h to a commercial slaughter facility. Initial BW was not different ($P = 0.83$) between CS (68.5 ± 1.7 kg) and WD (68.0 ± 1.7 kg) treatments. Overall ADG, ADFI, and G:F was not different ($P = 0.48$ to 0.67) between CS (1.17 ± 0.03 kg/d, 3.80 ± 0.09 kg/d, 0.32 ± 0.01, respectively) and WD (1.14 ± 0.03 kg/d, 3.85 ± 0.08 kg/d, 0.31 ± 0.01, respectively). Final BW was not different ($P = 0.23$) between CS (131.3 ± 1.8 kg) and WD (128.2 ± 1.7 kg) treatments, but hot carcass weight (HCW) was reduced ($P = 0.009$) 5.6% in WD compared with CS pigs. Dietary treatment had no effect on ham weight ($P = 0.41$); however, pigs eating WD had lower picnic ($P = 0.008$), boneless loin ($P = 0.03$), belly ($P = 0.06$), and butt ($P = 0.10$) weights compared with controls. Ultrasound measurements of last rib backfat (BF) and longissimus dorsi eye area (LEA) were recorded before transportation. BF was reduced ($P < 0.001$) in WD (1.30 ± 0.03 cm) compared with CS (1.52 ± 0.03 cm) pigs; however, treatment had no effect on LEA (42.1 ± 0.4 cm for CS vs. 41.5 ± 0.4 cm for WD). Feed cost (¢ per kg) was 9.45% lower ($P < 0.001$) in WD (37.97 ± 0.33) compared with CS (41.94 ± 0.33). Even though feed cost was reduced using the WD treatment, there was no difference in profit due to lower HCW in WD pigs. Further investigation in lengthening the trial period may be necessary to increase profit when feeding the WD diet.

Key Words: DDGS, swine growth, wheat

509 The effects of corn- or sorghum-based diets with or without sorghum dried distillers grains and solubles on lactating sow and litter performance. K. M. Sotak,* R. D. Goodband, M. D. Tokach, J. M. DeRouchey, S. S. Dritz, and J. L. Nelssen, *Kansas State University, Manhattan.*

A total of 140 sows (PIC 1050) and their litters were used to determine the effects of corn- or sorghum-based diets with or without 20% sorghum dried distiller's grains with solubles (DDGS; 31.1% CP and 9.2% crude fat) on lactating sow and litter performance. Sows were allotted to 1 of 4 dietary treatments 3 d before farrowing in a RCBD. There were 2 and 1 sows removed from the study for the sorghum and sorghum-DDGS treatments because of initial feed refusal with all others removed due to illness. Weaning age was 21 d. Treatments were arranged in a 2 × 2 factorial with main effects of grain source (corn vs. sorghum) and sorghum DDGS (0 vs. 20%). All diets were formulated to 0.97% standardized ileal digestible Lys but were not balanced for energy. Overall (d 0 to 21), ADFI increased in corn-based diets when DDGS were added, but decreased in sorghum-based diets resulting in a tendency ($P < 0.08$) for a DDGS × grain source interaction. Sows fed the sorghum-based diets had decreased ($P < 0.04$) lactation weight loss compared with those fed corn-based diets. Pig weights at weaning were lower ($P < 0.06$) for sows fed the diets containing DDGS compared with those fed the diets without DDGS. Overall, feeding sows corn- vs. sorghum-based (without DDGS) diets in lactation did not affect litter performance; however, the 4% decrease in litter weaning weight of sows fed sorghum with 20% sorghum DDGS needs to be taken into account in ingredient selection for lactating sows.

Table 1. Effects of corn- or sorghum-based diets with or without 20% sorghum dried distillers grains with solubles (DDGS)

	Corn DDGS		Sorghum DDGS			Probability, P <		
						DDGS × Grain source	Control vs. DDGS[1]	Corn vs. sorghum
Item	0%	20%	0%	20%	SED			
Sows, n	35	35	32	32				
ADFI, kg	5.76	5.93	6.30	5.88	0.24	0.08	0.46	0.15
Lact. wt change, kg	−14.3	−13.9	−11.0	−9.7	2.65	0.86	0.65	0.04
Lact. BF change, mm	−1.4	−1.3	−1.7	−2.2	0.62	0.39	0.65	0.15
Foster litter size	12.6	13.0	12.6	12.7	0.24	0.69	0.28	0.75
Wean litter size	11.8	12.1	11.8	11.8	0.29	0.38	0.48	0.58
Wean pig wt, kg	13.8	13.3	13.8	13.1	0.43	0.74	0.06	0.72
Wean litter wt, kg	73.6	73.0	73.4	70.2	2.90	0.53	0.34	0.46

[1] Basal diets vs. diets with 20% sorghum DDGS.

Key Words: sorghum, sorghum DDGS, sows

510 Amino acid digestibility in blood products fed to weanling pigs. F. N. Almeida*[1], J. K. Htoo[2], J. Thomson[3], and H. H. Stein[1], *[1]University of Illinois, Urbana, [2]Evonik Industries AG, Hanau, Germany, [3]Evonik Degussa Corp., Kennesaw, GA.*

Blood products are commonly used in diets for nursery pigs, but different processing techniques may result in differences in AA digestibility among these ingredients. Thus, the objective of this experiment was to compare values for the standardized ileal digestibility (SID) of AA in spray-dried animal blood (SDAB; 89.4% CP), spray-dried blood cells (SDBC; 92.6% CP), spray-dried plasma protein (SDPP; 77.7% CP), roller dried avian blood meal (ABM, 88.4% CP), and roller dried porcine blood meal (PBM, 94.6% CP), when fed to weanling pigs. Seven weanling barrows (initial BW: 11.5 ± 1.1 kg) were equipped with a T-cannula in the distal ileum and allotted to a 7 × 7 Latin square design with 7 diets and 7 periods in each square. One of the diets was based on casein, and 5 diets were based on a mixture of casein and each source of blood product. A N-free diet that was used to measure basal endogenous losses of AA and protein was also formulated. The SID of AA in each blood product was calculated by the difference procedure. The Mixed procedure of SAS was used to analyze the data. The model included diet as the main effect whereas pig and period were random effects. Results indicate that the SID of AA in SDAB, SDBC, and in SDPP is close to 100% and not different from casein. The SID of AA in ABM and PBM is less ($P < 0.05$) than those calculated for the 3 spray dried blood products, which indicates that the drying procedure used to prepare these products may have reduced the SID of AA.

Table 1. Standardized ileal digestibility (%) of AA

Item	SDAB	SDBC	SDPP	ABM	PBM	Casein	SEM	*P*-value
Ile	110^{a}	64^{cd}	99^{ab}	67^{bcd}	34^{d}	97^{abc}	13	<0.01
Leu	100^{a}	98^{a}	98^{a}	67^{c}	76^{b}	99^{a}	3	<0.01
Lys	100^{a}	98^{a}	98^{a}	74^{b}	79^{b}	97^{a}	2	<0.01
Met	102^{a}	98^{a}	98^{a}	^{b}	70^{b}	98^{a}	3	<0.01
Phe	100^{a}	98^{a}	98^{a}	67^{c}	76^{b}	99^{a}	3	<0.01
Thr	104^{a}	96^{a}	98^{a}	72^{b}	69^{b}	94^{a}	4	<0.01
Trp	99^{a}	94^{a}	97^{a}	69^{b}	77^{b}	96^{a}	3	<0.01
Val	100^{a}	98^{a}	98^{a}	67^{c}	76^{b}	97^{a}	3	<0.01

[a–c]Values within a row lacking a common superscript letter are different ($P < 0.05$).

Key Words: amino acid digestibility, blood products, pigs

511 Amino acid digestibility in hydrolyzed feather meal fed to pigs. F. N. Almeida*[1], L. I. Chiba[2], S. D. Brotzge[2], R. L. Payne[3], and H. H. Stein[1], *[1]University of Illinois, Urbana, [2]Auburn University, Auburn, AL, [3]Evonik-Degussa Corp., Kennesaw, GA.*

An experiment was conducted to determine the standardized ileal digestibility (SID) of AA in hydrolyzed feather meal (FM) products without or with blood addition when fed to pigs. Eight FM products were obtained from 4 sources with each source providing FM without and with added blood. Ten pigs (initial BW: 23.8 ± 1.3 kg) were allotted to a 10 × 10 Latin square design with 10 diets and 10 periods. One diet contained 36% soybean meal, and the 8 FM diets contained 12% soybean meal and 25% of 1 of the 8 FM products. Soybean meal and FM were the only ingredients contributing AA in these 9 diets. The 10th diet was a N-free diet that was used to determine the basal endogenous losses of AA. Pigs were fed experimental diets for 7 d with ileal digesta being collected during the last 2 d. Values for the SID of AA were calculated for each diet using the direct procedure, and the difference procedure was used to calculate the SID of AA in each FM product. Data were analyzed as a 2 × 4 factorial, with blood addition, FM source, and the interaction between blood addition and FM source as main effects. Differences ($P < 0.01$) in the SID of all indispensable AA were observed among the 4 sources of FM (Table 1). There were also effects ($P < 0.01$) of blood addition on the SID of Ile, Leu, Lys, Phe, and Val, but there was an interaction ($P < 0.05$) between FM source and blood addition, indicating that addition of blood did not have a consistent effect on the SID of AA in the 4 sources of FM. In conclusion, the SID of AA in FM varies among sources, and addition of blood to FM may affect the SID of AA.

Table 1. Standardized ileal digestibility (%) of AA in feather meal

Item	FM-1	FM-1	FM-2	FM-2	FM-3	FM-3	FM-4	FM-4	SEM
Blood addition:	No	Yes	No	Yes	No	Yes	No	Yes	-
Ile,[1,2,3]	76	66	86	96	82	83	80	72	2
Leu[1,2,3]	71	59	81	81	77	77	75	67	2
Lys[1,2,3]	48	56	59	79	59	71	59	55	3
Met[1,3]	65	58	72	77	63	72	70	63	2
Phe[1,2,3]	74	62	83	84	80	80	77	70	2
Thr[1]	65	56	72	76	70	70	66	60	2
Trp[1]	67	74	85	85	86	82	84	80	3
Val[1,2,3]	72	60	83	83	77	80	78	69	2

[1]Effect of FM source ($P < 0.01$).

[2]Effect of blood addition ($P < 0.01$).

[3]Interaction between FM source and blood addition ($P < 0.01$).

Key Words: amino acids, hydrolyzed feather meal, pigs

512 Nutritive value and relationship between nutrient content and protein quality of soybean meals according to origin. G. G. Mateos*[1], M. P. Serrano[1], M. González[2], S. Sueiro[2], M. Hermida[2], R. Lázaro[1], and P. G. Rebollar[1], *[1]Universidad Politécnica de Madrid, Madrid, Spain, [2]Laboratorio de Mouriscade, Pontevedra, Spain.*

Soybean meal (SBM) is the main protein source in pig and poultry feeds. United States (USA), Brazil (BRA), and Argentine (ARG) are the major SBM exporter countries. According to agronomic and processing conditions of the beans, the nutritive value of SBM varies among countries. This research studied the chemical composition and correlations between chemical analyses and protein quality of SBM by origin (USA, BRA, and ARG). Samples (n = 412) were collected during a 5-yr period and analyzed for major chemical components including amino acids (AA) and protein quality. On DM bases, USA meals (n = 164) had more CP (53.8 vs. 53.0 vs. 51.6%; $P < 0.001$) and sucrose (8.2 vs. 7.6 vs. 6.5%; $P < 0.001$) but less NDF (8.9 vs. 10.6 vs. 12.0%; $P < 0.001$) than ARG (n = 131) and BRA meals (n = 117). Stachyose content was higher and raffinose lower for USA than for ARG and BRA meals (6.47 vs. 5.56 vs. 5.29%; and 1.11 vs. 1.33 vs. 1.59%, respectively; $P < 0.001$). The USA meals had more P (0.79 vs. 0.69 vs. 0.75%; $P < 0.001$) than the BRA with ARG meals being intermediate. The CP content was negatively related with sucrose (−0.70, $P < 0.001$) for USA and with NDF (−0.64 and −0.46, $P < 0.001$) for ARG and BRA meals. The trypsin inhibitor activity (TIA) was higher (3.86 vs. 2.97 vs. 2.97 mg/g; $P < 0.001$) for USA meals than for ARG or BRA SBM. Protein dispersibility index and KOH were higher for USA than for ARG and BRA meals (19.7 vs. 16.8 vs. 15.3 and 86.8 vs. 82.1 vs. 83.3, $P < 0.001$), and were positively related with TIA of the meals (+0.70 and 0.73, $P < 0.001$ for USA; +0.62 and +0.65, $P < 0.001$ for ARG; +0.27 and +0.44, $P < 0.05$ for BRA, respectively). On CP bases, Lysine was higher (6.16 vs. 6.09 vs 6.05, $P < 0.001$) for USA than for ARG and BRA meals. The Lysine content was negatively related with CP content (−0.48, $P < 0.001$) for USA, but positively (+0.34, $P < 0.001$) for BRA SBM. Heat Damage Index (Aminored) was (−0.90, −0.87 and −0.90, $P < 0.001$) related with percentage of Lysine (%CP) for all origins. Nutrient values and the relationship between chemical composition and protein quality of the meal varied widely among origins. Thus, SBM origin should be considered in the evaluation of the nutritive value of the meal.

Key Words: chemical composition, origin, soybean meal

513 Influence of soybean meal source and micronization (fine grinding) of soybean meal on productive performance and digestive traits of Iberian pigs from 30 to 51 days of age. J. D. Berrocoso,* M. P. Serrano, L. Camara, P. G. Rebollar, A. Lopez, R. Abad, and G. G. Mateos, *Universidad Politecnica de Madrid, Madrid, Spain.*

In total, 216 Iberian piglets weaned at 30 d were used in a 21 d experiment to evaluate the effects of the inclusion of different sources of SBM on growth performance, nutrient digestibility (TTAD and AID), and morphological characteristics of the ileum. There was a positive control diet that included 10% soy protein concentrate (65% CP; SPC), a negative control diet with 14.8% regular SBM (44% CP; R-SBM), and 4 extra diets arranged factorially that included 13.3% of high protein SBM (USA vs. Argentina origin) with 49% CP (HP-SBM) at 2 different particle size (ground, 990 μm vs. micronized, 60 μm). Each of the 6 treatments was replicated 6 times (6 pigs per pen). The experiment design was completely randomized. The following orthogonal contrasts conducted: 1) SPC vs. all SBM diets, 2) micronized HP-SBM vs. ground HP-SBM, 3) HP-SBM of ARG origin vs. HP-SBM of USA origin, and 4) R-SBM vs. HP-SBM diets. Type of soy product had no effect on growth performance but the incidence of diarrhea (DI) was higher (*P*

≤ 0.01) for pigs fed R-SBM than for pigs fed HP-SBM. At 15 d of the experiment, the TTAD and AID of nutrients were higher ($P < 0.05$) for the HP-SBM than for the R-SBM diets. The inclusion of SPC in the diet had no effect on TTAD of nutrients except for CP that tended ($P = 0.06$) to be higher. The TTAD of DM ($P = 0.07$) and GE ($P = 0.05$) tended to be higher with micronized than with ground HP-SBM. Source of HP-SBM did not affect TTAD, except for GE that tended ($P = 0.05$) to be higher for the USA meal than for the Argentinean meal. At 15 d of experiment, pigs fed HP-SBM showed higher villi height:crypt depth ratio ($P < 0.05$) than pigs fed R-SBM. It is concluded that the inclusion of SPC in the diet improved TTAD of CP and reduced the DI but did not affect growth performance of the pigs. The inclusion in the diet of HP-SBM in substitution of R-SBM increased TTAD and AID of all nutrients, reduced the DI, and improved the morphological characteristics of the ileum but did not affect growth performance of the pigs.

Key Words: iberian pig, nutrient digestibility, soybean meal

514 Net portal absorption of amino acids in Iberian pigs fed with acorn.

J. M. Rodriguez-Lopez, M. Lachica, L. Gonzalez-Valero, and I. Fernandez-Figares,* *CSIC (Spanish National Research Council), Granada, Spain.*

Iberian pigs are reared indoors fed concentrate feeds until the final fattening period at the *dehesa* (Mediterranean woodland) where they are fed acorns and grass. The acorn is rich in carbohydrates and lipids but it has low protein content with unbalanced AA profile. This is a very abrupt nutritional challenge. There are no studies of how this nutritional challenge affect AA metabolism in the portal-drained viscera and consequently AA supply to peripheral tissues. For that reason, 6 pure Iberian pigs (26 kg BW) were fitted with chronic catheters, in carotid artery, portal vein and mesenteric vein and trained to consume 25 and 75% of their daily ration at 9.00 and 15.00, respectively. An equilibrated diet (140 g/kg CP and 14–14.5 MJ ME/kg DM) based on barley and soybean meal, at 85% ad libitum was consumed until surgery recovery (32 kg BW) in metabolic cages. The day before sampling, pigs were offered 2.4 kg of acorns (85% ad libitum: 1.405 kg DMI, 23.27 MJ MEI, 71.0 g CP intake) following the same feeding schedule. The first set of blood samples was taken the following day, after pigs were fed 600 g of acorns, every 30 min for 4 h and then hourly until 6 h after feeding,. Pigs were then fed acorns for 7 d and a second set of blood samples was taken following the same protocol as in the first set. Net portal AA absorption was calculated by multiplying porto-arterial plasma AA concentration difference by portal vein plasma flow rate, estimated by infusing p-aminohippuric acid into the mesenteric vein. Repeated measures analyses were carried out using the mixed procedure of SAS. Overall, net portal AAs absorption of sum of all AAs, sum of NEAA, Tyr, Ala, Asn, Pro, Hypro and His was greater when the pigs were adapted to acorn consumption. Furthermore, Phe, Leu and Gly also tended to increase. The peak of portal absorption of AAs in pigs fed acorns appeared at 0.5 h postprandial. In conclusion, after one week adaptation to acorns feeding, net portal absorption of AAs increased in Iberian pigs. Changes in microflora may be responsible of the improved utilization of AAs from acorn.

Key Words: pig, amino acids, portal drained viscera

515 Gas production, in vitro organic matter disappearance, volatile fatty acid concentrations and physicochemical characteristics of fibrous sources for pigs.

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Although dietary fiber enhances gut health, satiety and improves welfare of pigs, knowledge of physical and fermentation characteristics of bulky feeds is essential to understand the effects of dietary fiber on feed intake, digestibility and growth performance of pigs. The objective of the study was to characterize physicochemical properties and fermentation characteristics of common fibrous feed ingredients with a huge potential use formulating pig diets in Southern Africa. Crude fiber, neutral detergent fiber (NDF), acid detergent fiber (ADF), bulk density, water holding capacity (WHC), gas production parameters, in vitro organic matter disappearance (IVOMD) and volatile fatty acid (VFA) concentrations were assayed in groundnut haulms (GH), lucerne hay (LC), maize cobs (MC), maize stover (MS), rice bran (RB), saw dust (SD), sunflower husks (SH) and veld grass (VG). Fermentation was conducted over 24 h, using pig fecal inocula collected by rectal palpation from pigs (85.0 ± 5.49 BW) that had received a diet containing 12.6 MJ DE, 160 g CP/ kg DM and 80 g CF/ kg DM. Rice bran and maize cobs had the highest total VFA concentrations (6.5 ± 0.18 and 4.7 ± 0.18 μM, respectively). None of the fiber sources produced propionic acid, with acetic acid being the predominant acid. Surprisingly, maize cobs produced twice ($P < 0.01$) the amount of acetic acid (4.0 μM) than either groundnut haulms (2.2 ± 0.16 μM) or lucerne hay (2.0 ± 0.16 μM). Total gas production was 432, 485, 461, 428, 614, 210, 382 and 266 (s.e. = 12.2) ml g-1 OM for GH, LC, MC, MS, RB, SD, SH and VG, respectively. Total gas production and partitioning factor were reliable predictors of IVOMD and VFA concentrations ($P < 0.01$). Rice bran, maize cob, groundnut haulms were the most fermentable fibrous feed ingredients. The possibility of incorporating maize cob meal in pig diets, widely available in many countries where maize is a staple crop, should be explored. The influence of these physicochemical properties on voluntary feed intake is necessary to develop appropriate fiber-based feeding strategies for pigs.

Key Words: acetic acid, physical properties, rate of gas production

Physiology and Endocrinology: Pregnancy

516 Membrane progesterone receptors (α, β, and γ) in early pregnancy. R. L. Ashley,* S. M. Stanbrough, K. E. Quinn, J. D. Lindsey, and A. K. Ashley, *New Mexico State University, Las Cruces.*

Progesterone (P4) is required for maintenance of pregnancy and elicits physiological effects via binding to a nuclear receptor in various target tissues. Additionally, P4 can function through non-canonical membrane progesterone receptors (MPR) and numerous isoforms have been identified, including MPR α (MPRA), β (MPRB) and gamma (MPRG). P4 signaling through the MPRs has not been investigated in early pregnancy, and could effect initial maternal/fetal interactions. The objective of this study was to assess gene expression of MPRs in maternal and fetal ovine tissues during early pregnancy via real-time quantitative PCR (qPCR). Hypothalamus (HYP), pituitary (PIT), and caruncle (CAR) were collected from non-pregnant (NP) ewes on D10 of the estrous cycle, and from pregnant ewes on D20, 25, and 30 of gestation. Fetal placental tissue (FET) was also collected from pregnant ewes. RNA was isolated, cDNA synthesized and subjected to qPCR. Expression levels were normalized by standard methods, and subjected to ANOVA with Newman-Keuls post hoc test to determine significant differences ($P < 0.05$). Among the MPR isoforms in HYP, MPRA was highly expressed, while MPRG levels were the greatest in PIT. Both MPRA and MPRG were high in CAR, and MPRB were the most elevated in FET. In HYP, no gestation-induced alterations in any MPRs were observed. All 3 MPRs decreased with advancing pregnancy compared with NP in the PIT. MPRA decreased at early placentation (D20) and once attachment was established (D30) in CAR, whereas MPRG increased at early and mid-placentation (D25), but returned to basal levels by D30. MPRB decreased during mid-placentation in FET, with D20 and D30 expressing similar levels. MPRA and MPRG expression was similar across all times assessed in FET. During early gestation, P4 levels rise and are maintained in concert with critical fetal-maternal interactions for proper implantation and placentation. Our data indicate gestational status and stage effect MPR expression in numerous reproductive tissues, suggesting these proteins may be pivotal in P4-mediated establishment and maintenance of pregnancy. USDA-NIFA-AFRI 2009–65203–05717.

Key Words: implantation, placenta, membrane progesterone receptor

517 Expression of PRSS, the plasminogen activator system and its activity in the ovine placentome during stage 2 of parturition. A. K. McNeel,* R. A. Cushman, and J. L. Vallet, *USDA, ARS US Meat Animal Research Center, Clay Center, NE.*

The molecular mechanisms responsible for placenta separation are not completely understood. We know placentomes from cases of retained placenta possess limited matrix-metalloprotease (MMP) activity and retained placenta occurs at a greater incidence during induced parturition. The plasminogen activator (PA) system is a family of serine endoproteases capable of activating MMP. Two new serine proteases (PRSS) have been recently documented in multiple species, and in mice appear to be involved in follicular development and ovulation. We hypothesized that 1) the expression of PRSS and PA systems and PA activity increase as parturition approaches with maximal expression and activity during parturition, and 2) that both are reduced during induced parturition. To test these hypotheses, placentomes were collected at 17 and 10 d before projected parturition and during spontaneous and dexamethasone-induced parturition in ewes. Placentomes were separated into fetal and maternal tissues manually, snap frozen in liquid nitrogen, and stored at −80°C until protein and RNA extraction. Tissue replicates were homogenized and RNA and protein were extracted. Relative quantification for genes of interest was performed via RT-qPCR on purified RNA using the ΔΔCt method with GAPDH serving as the reference gene. Expression data were analyzed with the MIXED procedure of SAS with treatment as a fixed effect. Plasminogen-casein zymography was performed on protein isolates. There were no differences in expression of urokinase-type plasminogen activator (PLAU), SERPINB2, SERPINE1, or PRSS23 ($P \geq 0.05$). We were unable to detect expression of plasminogen, tissue-type plasminogen activator, or PRSS35. Plasminogen activator activity in placentomes was not detected using zymography. These data demonstrate that in the ewe, neither the PA nor PRSS systems change during Stage 2 of parturition compared with late gestation or induced parturition. USDA is an equal opportunity provider and employer.

Key Words: placental separation, proteolysis, ruminant

518 Physiological responses to repeated transportation of gestating Brahman cows. D. M. Price*[1], A. W. Lewis[1], D. A. Neuendorff[1], J. A. Carroll[2], T. H. Welsh Jr.[3], R. C. Vann[4], and R. D. Randel[1], *[1]Texas Agrilife Research, Texas A&M University System, Overton, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Texas Agrilife Research, Texas A&M System, College Station, [4]MAFES, Mississippi State University, Raymond.*

The transportation process acts as a stressor with adverse effects on animal health and performance. The purpose of this study was to examine physiological responses to repeated transportation of gestating Brahman cows; previously classified as mature cows into temperament groups of Calm, Intermediate, or Temperamental. Brahman cows (n = 48) were subjected to 2 h of transport (T) on d 60, 80, 100, 120, and 140 of gestation. Blood serum collected before and after each T was assayed for glucose and nonesterified fatty acid (NEFA) concentrations. Indwelling vaginal temperature (VT) monitoring devices were inserted before each T and VT were recorded before and every 5 min through 30 min after T. Statistical analysis of data used multivariate repeated measures and area under the curve methods. VT and serum glucose concentrations decreased in all temperaments ($P < 0.01$) with repeated T. Peak VT were greater ($P < 0.001$) in all cows regardless of temperament on d 60 of T, compared with all other T days. During T Temperamental cows tended ($P < 0.09$) to have higher peak VT (39.86 ± 0.15°C) compared with Calm (39.41 ± 0.16°C) and Intermediate cows (39.55 ± 0.08°C). Area under the VT curve decreased ($P < 0\ 0.003$) by d 140 as the cows habituated to T. On d 60 post T, Calm cows had numerically lower VT (39.18 ± 0.18°C), compared with Intermediate and Temperamental cows (39.39 ± 0.10°C and 39.53 ± 0.17°C, respectively). Pre-T glucose concentrations on d 60 were greater ($P < 0.03$) for Temperamental cows (68.13 ± 4.31μg/dl) compared with Intermediate (53.42 ± 2.78 μg/dl) and Calm cows (52.76 ± 4.60 μg/dl). All cows had numerically increased NEFA concentrations post T, with temperamental cows showing the least numerical change due to T. However, NEFA concentrations did not increase with repeated T ($P > 0.10$). Glucose concentrations were affected ($P < 0.02$) by a time by temperament interaction with Temperamental cows having greater changes in serum glucose concentrations. These results reflect the partial acclimation of cows to a stressor over time, and demonstrate that both temperament and the T process influence physiological responses to stress in gestating cows.

Key Words: metabolites, transportation, vaginal temperature

519 Reduced fertility in female progeny from beef heifers on dietary restriction during development. 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 does not affect fertility but may impart epigenetic effects on their progeny. Objective was to determine whether ovarian development or fertility is impeded in female progeny of replacement beef heifers developed on a lower energy diet. At 8 mo of age, Angus (n = 40) or composite MARC II (n = 40) heifers were assigned by BW and genetic line to be fed either a high (HE) or low (LE) energy diet for 180 d plus the first 22 d of the 47-d breeding period to achieve an ADG of either 0.45 or 0.9 kg/d or 55 vs. 65% of mature BW. Heifers within a line were mated to the same bulls. After breeding, treatment groups were combined and managed on pasture. Female progeny were developed on a standard heifer management protocol and bred at 14 mo of age. Total number of antral follicles (AFC), length and height of both ovaries, and uterine diameter were measured by transrectal ultrasonography in treated heifers (n = 72), and subsequently in female progeny (n = 32), at first breeding; pregnancy was diagnosed at about 75 d of gestation. Data were analyzed by ANOVA with diet and line as independent variables and their 2-way interaction. At 14 mo of age, LE heifers were lighter ($P < 0.01$) than HE heifers (344.8 vs. 429.4 ± 7.1 kg). Progeny birth weight (36.4 kg) was not affected by diet or line but Angus progeny were lighter ($P < 0.01$) at breeding (362.1 ± 7.2 vs. 387.2 ± 5.6 kg). Progeny of LE dams had fewer antral follicles than HE progeny (19.0 ± 1.9 vs. 26.0 ± 1.7; $P < 0.01$), whereas AFC (22.5 ± 2.8) did not differ between LE and HE dams. Ovarian size (length x height) was not affected by diet but was greater ($P < 0.05$) for MARC II vs. Angus heifers in both generations (dams, 301.3 vs. 351.9 ± 3.5 mm^2; progeny, 454.4 ± 31.8 vs. 586.3 ± 26.3 mm^2, respectively). Uterine diameter (12.1 mm) was not influenced by diet. Pregnancy rate was less ($P < 0.05$) for progeny from LE vs. HE dams (42.6 ± 15.3 vs. 80.3 ± 10.1%) and for Angus vs. MARC II progeny (39.3 ± 14.3 vs. 80.2 ± 12.1%). Results indicated that environmental effects imposed during early embryonic development in first-parity heifers may affect embryonic gametogenesis and fertility of progeny. USDA is an equal opportunity provider and employer.

Key Words: diet, progeny, fertility

520 The impact of cow nutrient status during the second and third trimester on development of the reproductive axis and fertility of daughters. R. A. Cushman,* A. K. McNeel, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Fluctuating feed resources to beef cows across the production cycle is a proven method for decreasing input costs; however, altering nutrients during gestation can decrease ovarian follicle numbers in female offspring. We hypothesized that limiting nutrients to mature (≥3 years) crossbred beef cows during the second and third trimester would result in daughters with decreased follicle numbers detectable by ultrasonography as yearlings. Over 4 breeding seasons, pregnant beef cows (n = 397) were assigned to Low (L), Moderate (M) or High (H) nutrient intake during the second and third trimesters to make 4 dietary treatment groups (L-H, L-L, M-H, and M-M). Heifers (n = 416) born to these cows were weighed at weaning and moved to a dry lot where they were monitored for behavioral estrus. Two weeks before their first breeding season, heifers were submitted for ultrasonographic examination of their ovaries to determine antral follicle numbers. Heifers were placed with bulls for 60 d and pregnancy status was determined 45 d after the bulls were removed. Growth and reproductive traits were analyzed using the MIXED Procedure of SAS with maternal diet, year, and the interaction as the independent variables and dam as a random effect. Maternal dietary intake did not affect heifer growth rates, age at puberty, or antral follicle counts ($P \geq 0.14$). However, heifers born to dams fed a high nutrient level during the third trimester (L-H or M-H) had a decreased number of days to calving ($P = 0.04$). From this we conclude that limiting nutrient intake during late gestation in mature (≥3 years) beef cows does not influence the ovarian reserve or maturation of the reproductive axis in daughters. However, high maternal nutrient levels during the third trimester improve the first service conception rates of their daughters when they go to their first breeding season. USDA is an equal opportunity provider and employer.

Key Words: beef heifers, puberty, antral follicle count

521 Feeding distillers grains as an energy source to gestating and lactating beef heifers: Impact on growth, puberty attainment and reproductive processes in female progeny. P. J. Gunn*[1], J. P. Schoonmaker[1], R. P. Lemenager[1], and G. A. Bridges[2], [1]*Department of Animal Sciences, Purdue University, West Lafayette, IN,* [2]*North Central Research and Outreach Center, University of Minnesota, Grand Rapids.*

Angus-cross beef heifers pregnant to a single sire (n = 80) 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 female progeny growth, puberty attainment and reproductive processes. From 192 d of gestation through 118 ± 0.2 d of lactation, dams were fed either a control diet of corn silage and haylage (CON; 10% CP prepartum; 11.8% CP postpartum) or corn stover and DDGS (DG; DDGS at 1.2% BW per d; 15.7% CP). Heifer progeny (n = 33) were weaned and commingled at 18 ± 0.4 d of age. Heifers were managed similarly for the remainder of the project. Heifer wt and blood samples for progesterone were collected weekly to assess wt and age at puberty. At 242 ± 0.4 d of age, 1 follicular wave was mapped via ultrasonography in 10 prepubertal heifers per treatment. Prepubertal antral follicle count and ovarian size were determined at 240 and 330 ± 0.4 d of age. Hip ht was recorded at 213, 297, and 436 ± 0.4 d of age. Estrous synchronization and AI was initiated at 447 ± 0.4 d of age. Categorical and continuous data were analyzed with the GLIMMIX and MIXED procedures of SAS, respectively. The DG progeny were heavier than CON ($P = 0.03$) at weaning (241 ± 5 kg vs. 223 ± 6 kg), but not at breeding (416 ± 7 vs. 401 ± 7 kg). Also, DG progeny had a greater ($P < 0.01$) frame score than CON throughout the developmental period. Ovarian size, antral follicle count, and follicular growth parameters did not differ between treatments. Age at puberty did not differ between CON (303 ± 10 d) and DG (320 ± 10 d) treatments; however, wt at puberty was heavier ($P = 0.01$) for DG (326 ± 7 kg) than CON (298 ± 8 kg) progeny. In addition, DG progeny (70.6%) had greater ($P = 0.05$) AI pregnancy rates than CON (33.3%). However, overall breeding season pregnancy rate did not differ. In summary, feeding DDGS at 1.2% of BW per d to first-parity heifers resulted in female progeny with greater skeletal growth that were heavier at onset of puberty, but had increased AI pregnancy rates.

Key Words: beef heifer, DDGS, developmental programming

522 Chronic uterine infusion of melatonin or melatonin receptor antagonist alters ovine placental efficiency and fetal blood flow during mid-gestation. C. O. Lemley,* L. E. Camacho, and K. A. Vonnahme, *North Dakota State University, Fargo.*

Objectives of the current experiment were to determine fetal descending aorta blood flow (BF), umbilical artery BF, and placental and fetal development following a 4 week uterine infusion of melatonin (MEL; n

= 5), melatonin receptor antagonist, luzindole (LUZ; n = 5), or vehicle (CON; n = 4). Multiparous singleton pregnant ewes were surgically implanted with mini osmotic pumps (2.5 µl/hr infusion of 1 mg/mL MEL or LUZ) on d 62 of gestation. Pumps and catheters were sutured under the perimetrium and catheters were advanced to the gravid uterine vascular network of the mesometrial region. On d 90 of gestation fetal BF was determined via Doppler ultrasonography followed by euthanasia. Data were analyzed using the mixed procedure of SAS. The model statement included infusion treatment and fetal sex. Placentome weight, cotyledon weight, and placentome number were not different ($P > 0.10$) among treatments. Caruncle weight was decreased ($P < 0.05$) in MEL and LUZ vs. CON treated ewes. Placental efficiency (fetal weight: placentome weight ratio) was increased ($P = 0.05$) in MEL vs. LUZ treated ewes with CON being intermediate. Fetal weight, biparietal distance, ponderal index, and crown rump length were not different ($P > 0.10$) among treatments, while thoracic girth was increased ($P < 0.02$) in MEL vs. LUZ treated ewes with CON being intermediate. Umbilical artery BF and umbilical artery BF relative to placentome weight were increased ($P < 0.05$) in MEL vs. CON and LUZ treated ewes. Fetal descending aorta BF was increased ($P < 0.05$) in MEL vs. LUZ treated ewes, while fetal descending aorta BF relative to fetal weight was increased ($P < 0.005$) in MEL vs. CON and LUZ treated ewes. The ratio of fetal descending aorta BF to umbilical artery BF was not different ($P > 0.95$) among treatment groups. The increase in umbilical artery BF due to chronic uterine melatonin infusion is potentiated by an increased fetal cardiac output through the descending aorta. Moreover, melatonin receptor antagonism did not alter umbilical artery blood flow compared with CON ewes. Therefore, mechanisms apart from melatonin receptor activation may mediate the observed increase in fetal BF following melatonin treatment.

Key Words: fetal blood flow, melatonin, placental efficiency

523 Influence of metabolizable protein supplementation during late gestation on vasoreactivity of maternal placental arteries in sheep. L. A. Lekatz*[1], A. Reyaz[1], M. S. Sane[2], F. Yao[2], S. T. O'Rourke[2], C. Schwartz[1], M. L. Van Emon[3], C. S. Schauer[3], K. M. Carlin[1], C. O. Lemley[1], and K. A. Vonnahme[1], *[1]Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University, Fargo, [2]Department of Pharmaceutical Sciences, North Dakota State University, Fargo, [3]Hettinger Research Extension Center, North Dakota State University, Hettinger.*

To examine the effects of metabolizable protein (MP) intake during late gestation on the vasoreactivity of placental arteries, 18 pregnant ewes received isocaloric diets containing 60% (MP60), 100% (MP100), or 140% (MP140) of MP requirements from d 100 to 130 of gestation. On d 130, several caruncular (CAR) arteries from placentomes of similar size and in close proximity to the umbilicus were selected for vasoreactivity studies using wire myography. Arterial rings (n = 4/ewe) were suspended in organ chambers with a wire myograph filled with 5 mL of physiological salt solution aerated with a mixture of 95% O_2 and 5% CO_2 and kept at 38.6°C. Optimal tension was found by progressively stretching the rings until the contractile response to KCl (20 mM) was maximal. The presence or absence of endothelium was verified by testing the ability of bradykinin (BK; 10^{-7} M) to produce endothelium-dependent relaxation during contraction evoked by norepinephrine (10^{-6} M). Each ring underwent a dose response curve (DRC) to BK in the presence or absence of an inhibitor. Rings were contracted with either U46619 (10^{-6} M) or 5-HT (10^{-6} M), and the DRC to BK in the absence of an inhibitor was obtained. In addition, BK DRC were obtained for rings which were incubated for 30 min with one of the following inhibitors: iberiotoxin (IBTx; an inhibitor of Ca^{2+}-activated K^+ channels; 10^{-7} M), indomethacin (INDO; a cyclooxygenase inhibitor; 10^{-5} M), or *N*(omega)-L-arginine methyl ester (NLA; a nitric oxide synthase inhibitor; 10^{-5} M) before the BK DRC was obtained. There was no difference ($P = 0.97$) in the response to BK among the 3 groups. While there was no difference ($P = 0.67$) in relaxation due to BK in the presence of IBTX, there was a treatment by dose interaction ($P = 0.02$) when arteries were incubated with NLA where pattern of relaxation differing slightly among treatments. The response to BK is inhibited similarly by IBTx and NLA in across all treatments indicating vasorelaxation being partially dependent on NO and BKCa channels. In MP140, inhibition of cyclooxygenase by INDO enhances the response to BK ($P = 0.09$) compared with MP100 and MP60. This could suggest that contractile arachidonic acid metabolites are produced in MP140 CAR arteries.

Key Words: bradykinin, placental vasoreactivity, sheep

524 Transgenerational effects of n-3 and n-6 supplementation under the control of transcription factors related to lipid metabolism. C. B. Jacometo[1], S. Halfen[1], F. T. da Rosa[1], A. Schneider[1], C. C. Brauner[1], F. A. B. Del Pino[1], J. J. Loor[2], N. J. L. Dionello[1], L. F. M. Pfeifer[3], E. Schmitt*[1], and M. N. Corrêa[1], *[1]Federal University of Pelotas, Pelotas, Rio Grande do Sul, Brazil, [2]University of Illinois, Urbana, [3]Embrapa Rondônia, Porto Velho, RO, Brazil.*

Our objective was to determinate the influence of omega-3 and omega-6 consumption throughout generations under transcription factors expression related to lipid metabolism. Wistar rats females, 8 week old, (G0, n = 18/group) were divided in: diet containing flaxseed oil (G3) and diet containing soybean oil (G6). The diets were elaborated in accordance with AIN-93G recommendations (AIN-93G). After 30 d of acclimatizing the rats were mated for 3 d in 1:3 male:female ratio. The Males received only the control diet. The F1 female were selected at weaning (n = 16/group) and was divided into 3 groups: females from G3 group that continued receiving diet containing flaxseed oil (G3–3); females from G3 group that began to receive diet containing soybean oil (G3–6); and females from G6 group that continued to receive diet containing soybean oil (G6–6). These animals were mated with 60 d old as described above (G0). The F2 (n = 16/group) was selected like F1 and the diet groups were maintained: G3–3-3; G3–6-6 and; G6–6-6. The F2 was mated like the F1. Prepartum euthanasia (19 ± 1 d) was conducted in each generation (n = 4/group) to collect liver samples. The Real-Time quantitative PCR was performed to evaluate the peroxisome proliferator-activated receptor α (PPARα), retinoid X receptor α (RXRα), liver X receptor α (LXRα), sterol regulatory element binding protein 1c (SREBP-1c), carbohydrate regulatory element binding protein (ChREBP) and nuclear corepressor receptor 1 (NCoR1) expression. Actin β (ACTB), Glyceraldehyde-3-phosphate (GAPDH) and 18S subunit ribosomal RNA (18S) were used as internal control. NCor1 and ChREBP did not differ between groups and so throughout generations, indicating a PUFA independent control. Differences between groups were not observed in G0 generation. In the F1, the PPARα were higher expressed in the G6–6 group than the G3–6 group ($P = 0.03$) and LXRα were lower in the G3–6 group than the G3–3 group ($P < 0.01$) and G6–6 group ($P < 0.05$). In the F2 generation LXRα had a lower expression in the G3–3-3 group compared with the G3–6-6 ($P < 0.01$) and G6–6-6 ($P < 0.01$). There were cumulative effects throughout generations in all groups with crescent RXRα (G0-F2:$P < 0.01$ and F1-F2:$P < 0.02$) and LXRα expression (G0-F2: $P < 0.01$ and F1-F2:$P < 0.01$) along generations. In the F2 generation the G3–3-3 group had a higher PPARα expression and a lower LXRα expression indicating lipolytic and anti-lipogenic effect. Our results indicate that the PUFAs effect on the control of lipolysis and lipogenesis is cumulative throughout generations.

Key Words: lipid metabolism, epigenetic, nutriphysiogenomics

Production, Management and the Environment: Dairy

525 Use of electrical conductivity for the detection of subclinical mastitis in dairy cows in Saudi Arabia. A. Alyemni[1,2], R. Aljummah[2], M. Ayadi[2], M. Hussein[2], and M. Alshaikh*[2], [1]*Arasco, Riyadh, Saudi Arabia,* [2]*King Saud University, Riyadh, Saudi Arabia.*

The objective of this study was to evaluate the use of milk electrical conductivity (EC) for predicting subclinical mastitis in high-producing dairy cows under Saudi Arabian conditions. Three hundred and 60 lactating Holstein cows were randomly selected and divided into 2 herds of 180 cows each, based on parity and days in milk (DIM). A total of 11350 quarter milk samples were collected weekly from the animals during the morning milking. Both EC and somatic cell count (SCC) were used as indirect measures of udder health. Milk fat, protein, lactose, and solids non-fat (SNF) were measured weekly. The effect of seasonal variation during summer and winter months was taken into account. Data were analyzed using a mixed model. The average milk EC and SCC values of cows were 4.68 mS/cm and 181,900 cells/ml, respectively. The highest EC value for healthy quarters was 5.27 mS/cm. Milk EC values were lower ($P < 0.01$) in summer (4.62 mS/cm) than winter (4.73 mS/cm) months. Using inter-quarter ratio (IQR), 232 cases were diagnosed as subclinical mastitis at different periods of time. Our results indicated that low or high basic levels affect the sensitivity and specificity of EC test, while using (IQR) improved the results. There was a significant correlation between milk EC, SNF and lactose content. A significant positive correlation ($r = 0.36$; $P < 0.01$) between EC and SCC was also observed, which increased the percent sensitivity and specificity of the results and the certainty of the diagnosis for cows with subclinical mastitis. The significant effects of stage of lactation on milk EC and milk components varied significantly with different stages of milking. Hence, it was not possible to conclude that milk EC can be used as an effective means for detecting early signs of subclinical mastitis and predicting clinical cases before symptoms arise, unless it is used in combination with other methods.

Key Words: milk electrical conductivity, dairy cows, mastitis

526 Effect of feeding duration on growth, health, and economics of group-fed dairy calves in an organic production system. B. J. Heins* and E. A. Bjorklund, *University of Minnesota, West Central Research and Outreach Center, Morris.*

Heifer calves (n = 67) were used to evaluate the effect of early life feeding duration in an organic group management system on growth, health, and economics of organic dairy calves. Calves were assigned to replicate 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 2011. Breed groups of calves were: Holsteins (n = 11) selected for high production (HO), Holsteins (n = 10) maintained at 1964 breed average level (H64), crossbreds (n = 28) including combinations HO, Montbéliarde, and Swedish Red selected for high production (HMS), and crossbreds (n = 18) including combinations of HO, Jersey, and Swedish Red selected for durability (HJS). Calves were weaned at 30 (EW), 60 (MW), or 90 (LW) days of age, and groups were fed 1.5% of birth weight of 13% total solids organic milk once daily and then weaned when the group consumption averaged 0.91 kg starter/calf/day. Body weight and hip height were recorded at birth, once per week, and at weaning. Analysis was with PROC GLM of SAS, and independent variables for statistical analysis were the fixed effects of weaning group and breed group. Weaning group performance was weaning age (days), EW (44.2), MW (61.3). LW (91.5) ($P < 0.01$); gain per day (kg), EW (0.52), MW (0.68), LW (0.75) ($P < 0.01$); weaning weight (kg), EW (61.7), MW (79.6) LW (106.8), ($P < 0.01$); and weaning hip height (cm), EW (88.3), MW (91.4), LW (97.0) ($P < 0.01$). The HO (0.72; 89.0), H64 (0.61; 80.5), HMS (0.67; 84.5), and HJS (0.60; 76.6) calves were not significantly different for gain per day (kg) or weaning weight (kg), respectively. Total costs (grain and organic milk) to weaning per calf were $108.81 for EW, $167.68 for MW, and $275.79 for LW groups; however, the cost per pound of gain was significantly higher ($P < 0.01$) for the EW ($4.83) group than the MW ($4.18) or LW ($4.06) groups. In summary, late weaned calves had higher daily gains than early weaned calves; however, the optimum time for weaning of organic dairy calves may be between 30 and 90 d.

Key Words: organic, calf growth, crossbreeding

527 Survey of lameness, body condition score, hygiene, and hock lesions of Colorado dairy cows housed in outdoor dirt lots or free stalls with outdoor access. R. Woiwode,* T. Grandin, and I. Roman-Muniz, *Colorado State University, Fort Collins.*

The objective of this study was to conduct a survey of the conditions of dairy cattle in Colorado. Dairies were visited between July and December 2011. Data were collected on locomotion score, body condition score (BCS), hygiene, and hock lesions. Cattle were observed on 10 dairies ranging in size from 400 to 3800 cows. An average of 12% of the lactating herd was scored on each dairy for lameness and hock lesions. Lactating cows observed were housed either in free stalls with outdoor access available (80%) or in dirt lots (20%). Lactating cows were gait scored using the Zinpro Locomotion Score, a 5 point numerical rating system, with 1 and 2 classified as non-lame and ≥ 3 classified as lame. An average of 3.2% (±2.5) of all cattle observed were classified as lame. Severe hock lesions were negligible, with only 0.1% (±0.04) of lactating cows exhibiting hock swelling ≥ baseball size. Lameness was much lower than the estimated national average of 20–25% (Cook, 2003; Espejo et al., 2006), possibly due to a combination of factors, including cows housed in free stalls having access to outdoor dirt lots, and other management practices. Body condition was scored on all lactating cows using a 5 point numerical rating system, with ≤ 2 classified as too low. The average BCS of lactating cows classified as too low was 2.4% (±1.7). Hygiene was scored using a 4 point numerical rating system, with 4 classified as unacceptable. Lactating and nonlactating cow hygiene was observed to be very good with an average of 2.4% (±3.2) cows classified as having unacceptable hygiene. Cow hygiene was observed to be better than calf hygiene, as an average of 7.8% of calves were observed to have unacceptable hygiene. Additional dairies and data will be included at the time of presentation.

Key Words: dairy, lameness, hygiene

528 Economics of using sheath protectors at the time of AI in dairy cows. S. Bas*[1], K. N. Galvão[2], and G. M. Schuenemann[1], [1]*Department of Veterinary Preventive Medicine, The Ohio State University, Columbus,* [2]*Department of Large Animal Clinical Sciences, University of Florida, Gainesville.*

The use of disposable sheath protectors (SP) to minimize contamination of the AI catheter at the time of AI improved conception risk (CR; 5

percentage points) of lactating dairy cows. The objective was to assess the effect of 5 percentage points increase in CR (from 32% to 37%) on dairy herd economics using an individual cow-based stochastic model. For the simulation, lactating dairy cows were enrolled in a Presynch-Ovsynch for first AI followed by estrus detection (ED) and resynchronization of cows diagnosed open 32 d after AI using Ovsynch. Herd size was maintained at 1,000 cows. Mortality was set at 6% and abortions at 13%. Cows not AI after 365 DIM and open cows were culled after 450 DIM. Culled cows were immediately replaced. The dry and VWP were set to 60 d. Compliance to each injection of the synchronization program was 95% and estrus detection (ED) was set to 60% with an accuracy of 95%. Simulation was performed at 32% for 3,000 d until steady-state was reached, then the model was set at 37% CR for the subsequent 2000 d to calculate the new economic values ($/cow/d). Average values from 10 runs were used. Net daily value was calculated by subtracting the costs of replacements ($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 PF2α ; $3.0/dose GnRH; $0.17/injection administration, and other costs ($3.5/d) from the daily income [milk sales ($0.31/kg milk), cow sales ($0.75/kg live weight), and calf sales ($200/calf)]. According to the model, the use of SP provided an additional $4.8 cow/yr (or $4,800/yr for a 1,000-cow herd) for each point increase in CR (from 32% to 37%). Use of SP can increase farm profitability by increasing CR at a minimal cost.

Key Words: sheath protector, pregnancy, economics

529 Effect of AI technicians on reproductive performance and economics of lactating dairy cows.

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It is common to observe large within-herd variation in AI technician conception risk (CR). The objective was to assess the effect of AI technicians on reproductive performance and economics using a stochastic dynamic model. CR from 3 distinct AI technicians (A = 38%, B = 32%, and C = 26%) were assessed. For the simulation, lactating dairy cows were enrolled in a Presynch-Ovsynch for first AI followed by estrus detection (ED) and resynchronization of cows diagnosed open 32 d after AI 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). CR from AI technician A (38%), B (32%), and C (26%) was compared. 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. ED was set to 60%. Accuracy of ED and compliance with each injection were set at 95%. 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%. The breeding costs/cow/yr for AI technician A, B, and C were $88, $96, $106, respectively. The profit/cow/yr for AI technician A, B, and C were $179, $139, and $82, respectively. Assuming that the herd remains constant, each point increases in CR (from 26% to 38%) represented $6 per cow/yr or $6,000/yr for a 1000-cow dairy. Compliance with the AI procedure (semen handling, accuracy of ED, hygiene, site of semen deposition) affects the bottom line of dairy herds and should not be compromised for convenience. Investing in educational training for professional AI technicians should be a top priority.

Key Words: AI technician, economics, dairy cow

530 The effect of reproductive performance on the herd value assessed by integrating a daily dynamic programming with a daily Markov chain model.

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The objective of this study was to determine the effect of reproductive performance on the herd value. The herd value was defined as the herd's average retention payoff (RPO) which is the expected profit from keeping the cow compared with immediate replacement. First, a daily dynamic programming model was developed to calculate the RPO of all cow states in a herd. Second, a daily Markov chain model was applied to estimate the herd demographics. Then, herd value was calculated by aggregating the RPO of all cows in the herd. Cow states were described by 5 milk classes (MC1 = lowest to MC5 = highest), 9 lactations, 750 d in milk (DIM) and 282 d in pregnancy. Five different reproductive programs were studied (RP1 to RP5). The RP1 used 100% timed artificial insemination (TAI) (42% conception rate (CR) for 1st TAI and 30% for 2nd and later services) and the other programs combined TAI with estrous detection (ED). The proportion of cows receiving AI after ED ranged from 30 to 80%, with CR of 25, 30, and 35%. These 5 reproductive programs were categorized according to their 21 d pregnancy rate (21 d PR), which is an indication of the rate the eligible cows become pregnant every 21 d. The 21 d PR was 17% for RP1, 14% for RP2, 16% for RP3, 18% for RP4, and 20% for RP5. Results showed a positive relationship between 21 d PR and the herd value. The most extreme herd value difference ($/cow per year) between 2 RP was $77 for MC3 (RP5 – RP2); $13 for MC1 (RP5 – RP1); and $160 for MC5 (RP5 – RP2). Reproductive programs were ranked based on their calculated herd value. With exception of the best reproductive program (RP5), all other programs showed some level of ranking change with MC. The most dramatic ranking change was observed in RP1, which moved from being the worst ranked for MC1 to the second best ranked for MC5. Supported by AFRI Competitive Grant no. 2010–85122–20612

Key Words: retention pay-off, economics, dairy cattle

531 Regression meta-models to predict the value of pregnancy in dairy cows.

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The value of a new pregnancy can be calculated with a complex dynamic programming model (DairyVIP) for a variety of input parameters, but the model needs to be installed on a computer and each calculation takes time. The objective of this study was to predict the values of pregnancy for 9 important input parameters using a regression meta-model. Meta-models provide instant predictions of the value of pregnancy for the fitted inputs and can be used in web-based dashboard tools for easy access by interested users. Nine input parameters were randomly varied over reasonable ranges using 265 design points. The value of pregnancy and profit per cow per year were calculated for each design point with DairyVIP. Mean ± SD of the 265 values of pregnancy was $246 ± $131. Values of pregnancy increased with greater replacement costs and lower pregnancy rates. The procedure Glmselect in SAS was used to fit the meta-model. The Glmselect procedure included learning (n = 150 design points), validation (n = 50) and testing (n = 65). The 9 main effects included the prices of replacement heifers, milk, feed, cull cows, and calves, as well as the probabilities of insemination, conception, culling, and the level of milk yield. The main effects, logs of the main effects, and all 2-way interactions were fitted. At most 10 effects were selected for the regression model. Stepwise selection with the Press criteria was used to select the best fitting meta-model. Statistics for the final meta-model were $R^2 = 0.987$ and AIC = 990. Mean ± SD of the prediction error was \$0 ± \$15 (range -\$30 to \$41). Prediction errors were independent of the profit per cow per year. In conclusion, regression meta-models were able to accurately predict the value of pregnancy in most cases. Meta-modeling may be a useful approach to make results from complex computer models widely available.

Key Words: regression, meta-model, value of pregnancy

532 Effect of heat stress during the dry period on immune function and growth performance of the offspring fed standardized pooled colostrum.

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Calves born and fed with colostrum from dairy cows exposed to heat stress during the dry period have compromised passive immunity and cell-mediated immune function compared with calves born to cows under cooling. However, it is unknown if this compromised immune response is caused by calf or colostrum intrinsic factors. Our objective was to evaluate the effect of maternal heat stress during the dry period on calf specific factors related to immune response and growth performance of the offspring. Cows were dried off 46 d before expected calving and randomly assigned to a cooling (CL, n = 18) or heat stress (HT, n = 18) environment. Cows of the CL group were housed with sprinklers, fans and shade, whereas cows of HT group had only shade. Colostrum from cows exposed to neutral environmental conditions during the dry period was pooled and stored frozen (−20°C). Within the first 4 h of birth, 3.78 L of pooled colostrum was fed to calves from both treatment groups. All the calves were exposed to the same management and were weaned at 50 d of age. The day of birth was considered study d 0. Blood samples were collected before colostrum feeding, 24 h after birth and twice weekly up to d 32. Total plasma protein and IgG concentrations were determined. Body weight was recorded at birth and at d 15, 30, 45 and 60. HT calves were lighter ($P < 0.01$) at birth than CL calves (38.3 vs. 43.1 kg), and no differences ($P = 0.36$) in weight gain were observed up to d 60 (31.9 vs. 34.2 kg gain). Additionally, HT calves had lower ($P < 0.05$) apparent efficiency of IgG absorption (26.04 vs. 30.24%), but no differences were observed for total plasma protein (5.42 vs. 5.50 g/dL; $P = 0.34$) and serum IgG concentration (2.09 vs. 2.15 g/dL; $P = 0.57$). Calves born from cows exposed to heat stress during the dry period had lower birth weight and lower apparent efficiency of IgG absorption. Thus, heat stress during the last 6 wks of gestation negatively affects the ability of the calf to acquire passive immunity regardless of colostrum source.

Key Words: calves, dry period, heat stress

533 Accuracy of the AfiLab real time milk analyzer to predict DHIA fat, DHIA protein and lactose.

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Objective of this study was to quantify the agreement between the AfiLab real time milk analyzer based on light scattering and test day DHIA fat, DHIA protein and lactose, all based on the Bentley 2000 analyzer (BA). AfiLab data were collected twice daily at 12h intervals from the double 12 parlor at the University of Florida Dairy Unit in Hague, FL, from January 2010 to December 2011. Alternating AM/PM BA data for the 24 test days in 2010 and 2011 were also obtained. Approximately 450 cows were tested each month. AfiLab data were matched with DHIA fat and protein (n = 10,273; 23 test days) and lactose (n = 6,741; 16 test days). Means and SD of BA fat, protein and lactose were 3.76 ± 0.80%, 3.08 ± 0.37% and 4.72 ± 0.30% respectively. Mean and SD of average AfiLab minus BA observations of the test day milking were −0.077 ± 0.116% for fat (n = 23), 0.024 ± 0.107% for protein (n = 23) and −0.024 ± 0.083% for lactose (n = 16). Mean and SD of within test day SD of AfiLab minus BA observations of the test day milking were 0.659 ± 0.110% for fat, 0.274 ± 0.031% for protein and 0.262 ± 0.025% for lactose. Mean and SD of the corresponding correlations were 0.59 ± 0.09 for fat, 0.74 ± 0.03 for protein and 0.46 ± 0.08 for lactose. The accuracy of various combinations of AfiLab observations from up to 6 milkings before and after the test day milking was also evaluated. The accuracy of fat predictions was not improved. The average of the 13 protein observations improved the average difference to 0.011 ± 0.095% and SD of the difference to 0.227 ± 0.029%. The correlation increased to 0.78 ± 0.04. The average of 13 lactose observations improved the SD of the difference to 0.229 ± 0.021% but the mean of the difference was −0.031 ± 0.089%. The correlation increased to 0.55 ± 0.05. In conclusion, the accuracy of protein prediction was better than the accuracy of lactose and fat prediction. Combination of AfiLab observations from various milkings may improve the accuracy of prediction.

Key Words: accuracy, agreement, fat, protein, lactose

534 Potential utility of a parlor-based individual quarter milking system.

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Overmilking may lead to teat end hyperkeratosis (HK). The objective of this study, conducted at the University of Kentucky Coldstream Dairy, was to examine changes in teat end HK in a herd transitioning from a standard pulsation system to an individual quarter pulsation milking system. Teat end HK was evaluated immediately after cluster removal using the scoring system outlined by Mein et al. (2001) where N signifies no ring; S signifies a smooth, raised ring; R signifies a rough ring; and VR signifies a very rough ring. Scorings were classified for 69 cows (48 Holstein, 12 Crossbred, and 9 Jersey) relative to installation (April 28, 2011) of the Milpro P4CTM (Milkline, Gariga di Podenzano, Italy) system as follows: PRE1-April 7; PRE2-April 21; POST1-May 12; POST2-May 26; POST3-June 9. The Milpro P4CTM system stops milking individual quarters using a unique individual quarter pulsation system with 4 pulsation channels instead of 2. Hyperkeratosis scores were converted to numerical values as follows: n = 1; S = 2; R = 3; VR = 4. The MIXED Procedure of SAS® (Cary, NC) was used to evaluate fixed effects of age, breed, parity, and teat position and their interactions with variables repeated by scoring with cow within breed as subject. The effects of position and scoring × breed were significant ($P < 0.01$ and $P = 0.02$, respectively). Hyperkeratosis scores improved for Holsteins from PRE1 to POST3 (1.75 ± 0.09 and 1.41 ± 0.10, respectively, $P < 0.01$), PRE1 to POST2 (1.75 ± 0.09 and 1.54 ± 0.09, respectively, $P < 0.01$), PRE2 to POST3 (1.64 ± 0.09 and 1.41 ± 0.10, respectively, $P < 0.01$) and POST1 to POST3 (1.62 ± 0.10 and 1.41 ± 0.10, respectively, $P < 0.01$) whereas Jersey and crossbred scores did not change among scorings ($P > 0.05$). Right front HK scores varied significantly from right rear and left rear scores (1.58 ± 0.09, 1.37 ± 0.09, and 1.36 ± 0.09, respectively, $P < 0.01$) and left front teat end HK scores varied significantly from right rear and left rear scores (1.62 ± 0.09, 1.37 ± 0.09, and 1.36 ± 0.09, respectively, $P < 0.01$). Teat end HK scores improved for Holsteins after installation of the individual quarter pulsation milking system.

Key Words: hyperkeratosis, teat end, individual quarter pulsation

535 Reducing dietary protein decreased the ammonia-emitting potential of manure from commercial dairy farms. A. N. Hristov,* K. Heyler, E. Schurman, K. Griswold, P. Topper, M. Hile, V. Ishler, E. Wheeler, and S. Dinh, *The Pennsylvania State University, University Park.*

The objective of this project was to decrease manure NH_3 emissions through reducing dietary crude protein (CP) concentration on commercial dairy farms. Twelve Pennsylvania dairies (169 ± 50 cows) with scrape, gravity-flow, or flush manure management systems participated in the project. Background data on barn floor and laboratory manure emissions (i.e., emitting potential, EP) of NH_3, N_2O, CH_4, and CO_2 were collected during 4 sampling events (2 in the spring and 2 in the fall) in Yr 1 of the project. In Yr 2, dietary CP concentration was reduced ($P < 0.001$) from an average across all farms of 16.5 (in Yr 1; HighCP period) to 15.4% (LowCP period) and data collection was repeated. Diets were sampled throughout the project to verify CP levels. Milk yield and milk composition data were also collected throughout the project. Data were analyzed with farm as random effect using the MIXED procedure of SAS. Barn floor NH_3 emissions were drastically lower during the LowCP compared with the HighCP periods (186 vs. 445 mg/m^2/h; $P < 0.001$). These results, however, were confounded by lower ambient temperature during the LowCP period (6.3 vs. 13.6°C, respectively). The NH_3 EP, which was based on evaluation of reconstituted (urine and feces) manure at the same temperature, was on average 23% lower ($P < 0.001$) for LowCP vs. HighCP manure (292 vs. 378 mg/m^2/h). Emissions of CH_4, and CO_2 were not affected by dietary CP and emissions of N_2O were negligible. Barn floor NH_3 emissions were lower ($P = 0.02$) for flush vs. scrape and gravity-flow manure management systems. The greatest ($P < 0.001$) CH_4 emissions were observed for the gravity-flow manure system (1,215 vs. 486 and 37 mg/m^2/h, gravity-flow, scrape, and flush, respectively). Milk yield (32.2 vs. 32.5 kg/d; $P = 0.81$) and milk composition were not different between the HighCP and LowCP periods. MUN tended to be lower during the LowCP period (13.2 vs. 14.5 mg/dL; $P = 0.06$). This on-farm project demonstrated that manure NH_3 emissions can be significantly reduced by moderately decreasing dietary CP content without affecting milk yield and composition in dairy cows.

Key Words: dairy farm, ammonia emission, dietary protein

536 Dose effects of monensin on methane emissions from lactating Holstein dairy cattle. S. E. Place*[1], Y. Pan[1], Y. Zhao[1], C. E. Moore[2], J. K. Wittman[2], and F. M. Mitloehner[1], [1]*Department of Animal Science, University of California-Davis, Davis,* [2]*Elanco Animal Health, Greenfield, IN.*

Monensin is a feed additive used in dairy cattle diets that may reduce methane emissions; however, past results have been variable, which could be due to the dose of monensin fed to cattle. To test the dose effects of monensin, 20 lactating Holstein cows were stratified by days in milk and randomly assigned to one of 4 treatments provided in a pelleted top dress (CON, LOW, MED, HIGH containing 0, 175, 368, and 518 mg cow^{-1} d^{-1} of monensin, respectively). All cows were fed the same basal TMR throughout the trial and CON top dress for 19 d (PRE period), then their respective treatment top dress for 21 d (MON period), then returned to the CON top dress for 21 d (POST period). Milk production and feed intake (DMI) were monitored daily, milk composition once during each period, and gas emissions were collected on the last day of each period for each cow. Gas emissions were sampled with a ventilated hood system. All statistical analysis was conducted using Proc Mixed procedures in SAS version 9.3 (SAS Institute Inc., Cary, NC). Methane emissions, milk production, DMI, and milk composition were similar across treatments in the MON period. There were no carryover effects of monensin in the POST period. The change in methane emissions from the PRE to MON period across treatments varied (6.4, 6.1, 1.6 and 3.9 g cow^{-1} h^{-1} for the CON, LOW, MED, and HIGH treatments, respectively), with MED having a lower ($P < 0.05$) change in methane emissions per cow, per kg of DMI, and per kg of milk compared with CON. Changes from the PRE to MON period in milk yield (3.5, 2.8, 1.3, and 2.4 kg cow^{-1} d^{-1} for CON, LOW, MED, and HIGH, respectively) and DMI (1.6, 0.63, 0.15, and 0.92 kg cow^{-1} d^{-1}, for CON, LOW, MED, and HIGH, respectively) were lower for the MED treatment cows compared with those in CON ($P < 0.05$). All treatments had similar emissions and animal performance measures within the MON period, but the MED treatment did have lower changes over time in methane emissions, DMI, and milk yield from the PRE to MON periods. Over time, monensin had dose effects on methane emissions, DMI, and milk yield, but the effects do not seem to be linear in nature.

Key Words: monensin, methane, dairy cows

537 Characterization of Shanghai dairy cattle lactation performance in 2008. C. G. Zhang[1], G. L. Liu*[1,2], L. M. Huang[1], Z. G. Wang[1], and G. Yang[1], [1]*State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co. Ltd., Shanghai, China,* [2]*Shanghai Dairy Breeding Center Co., Ltd., Shanghai, China.*

Accurate knowledge of a lactation performance has an important relevance to management and research of dairy cattle production systems. The purpose of the study presented was to determine the characterization of Shanghai dairy cattle lactation performance in 2008. Milk production data for 157 dairy farms (31,800 cows and 357,600 data points) were obtained from Dairy Herd Improvement (DHI) project of Shanghai Dairy Breeding Center, the data of 305-d milk yield was collected and calculated by each farm′s records. Daily and 305-d milk yields were summarized and evaluated by parity using ANOVA procedure of SAS. We also compared 2008 milk yield with previous milk data from 2003 and 1998. The results indicated that average daily milk yield for parity 1, parity 2 and parity 3 or greater was 17.2 ± 2.9 kg, 23.5 ± 3.3 kg and 22.2 ± 3.9 kg, average peak milk yield was 29.5 ± 4.6 kg, 34.5 ± 6.2 kg and 33.4 ± 5.7 kg, and average days to peak milk were 65 ± 9 d, 47 ± 8 d and 54 ± 9 d, respectively. Parity 2 cows had greater ($P = 0.04$) average 305-d milk yield (8,300 ± 973 kg) than parity 1 (7,789 ± 845 kg) cows and tended ($P = 0.11$) to have greater yield than parity 3 or greater cows (7,956 ± 899 kg). In contrast, the highest average 305-d milk yield was found for parity 4 cows (7,569 ± 813 kg) in 1998 and parity 3 cows (8,361 ± 937 kg) in 2003. These results are valid to suggest that a better understanding of lactation curves would allow producers to evaluate their production compared with averages in Shanghai region.

Key Words: lactation curve, dairy cattle, Shanghai (China)

Ruminant Nutrition: Beef Production III

538 Effect of the forage-to-concentrate ratio on DMI and ruminal fermentation based on timing of feeding relative to feed restriction. R. I. Albornoz*[1], J. R. Aschenbach[2], D. R. Barreda[3], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Free University of Berlin, Berlin, Germany, [3]University of Alberta, Edmonton, AB, Canada.*

The objective of this study was to evaluate the interaction between the forage-to-concentrate ratio (F:C) of diets fed before (baseline) and during short-term feed restriction (FR; collectively denoted as PRE) and those fed post-feed restriction (POST) on DMI and rumen fermentation. Twenty ruminally cannulated heifers (477 ± 38 kg BW) were exposed to 14 d for adaptation followed by 5 experimental periods; 5-d baseline, 5-d FR, and 3 wk of recovery (R1, R2, and R3). Heifers were fed, ad libitum, a high forage diet (HF; F:C = 92:8) or a moderate forage diet (MF; F:C = 60:40) during baseline, and FR was imposed at 25% of ad libitum DMI. During recovery, one half of the HF and MF heifers remained on the same diet, and the other half were exposed to an abrupt switch (e.g., HF/HF, HF/MF, MF/HF, and MF/MF). PRE × period ($P = 0.02$) and POST × period ($P = 0.04$) interactions were detected for DMI. Although DMI, within periods, was not different for HF and MF, heifers fed HF PRE increased DMI from R1 to R3. Heifers fed HF POST had higher intake during R1 than heifers fed MF with no differences observed between diets within other periods. A PRE × POST × period interaction was detected for butyrate concentration ($P = 0.01$). Butyrate was higher for cows fed MF PRE than HF PRE. Butyrate concentration decreased from baseline to FR and returned to baseline values by R3; although the extent of the increase was greater for heifers fed HF PRE than MF PRE. PRE × period ($P = 0.02$) and POST × period ($P < 0.01$) interactions were detected for mean pH. For the PRE × period interaction, heifers fed HF had higher pH than those fed MF during baseline, but pH did not differ between diets during FR. Despite this, pH was higher during FR than baseline and decreased for all heifers during R1 with mean pH returning to baseline values by R2 for HF heifers. For the POST × period interaction, mean pH during R1 was lower for MF than HF, but no other differences were detected among treatments. This study indicates that feeding MF before, and HF after FR reduces risk for ruminal acidosis following FR.

Key Words: beef cattle, feed restriction, rumen fermentation

539 Rumen and cecum methane emissions between steers that are either negative or positive for residual gain. H. Freetly*, K. Hales, and J. Wells, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Cattle produce CH_4 in the rumen and the cecum, and it represents a loss of feed energy. A possible cause of variation in feed efficiency may be differences in capacity to produce CH_4. We hypothesized that cattle with a higher residual gain (RG) would have a decreased capacity to produce CH_4. Individual DMI and BW gain were determined on crossbred steers (n = 132, initial age = 348 ± 1 d and BW 444 ± 4 kg) for 56 d. Steers were offered feed ad libitum and intake was measured using an Insentec RIC Feeding System (Insentec B.V., Marknesse, The Netherlands). The diet consisted of 82.75% rolled corn, 12.75% corn silage, and 4.5% Biegerts supplement (Bradshaw, NE; contains 0.066% monensin, 51% CP). On d 0, 1, 21, 42, 56, 62, and 63 BW was measured, and BW gain was calculated using the regression coefficient. Residual gain was calculated from the regression of BW on DMI; $f(x) = (0.1262 \pm 0.0128)x + (25.7 \pm 9.9)$, $R^2 = 0.43$. The 7 animals with the most extreme positive and negative RG that were within 32% of the STD of the mean DMI (772 ± 90 kg) were sampled. Steers received the diet until they were slaughtered. One positive and negative RG steer were slaughtered at 12, 13, 14, 15, 19, 20, and 21 d after the end of the feeding period. At slaughter, rumen fluid was filtered and placed in a flask in a 39°C waterbath and allowed to settle. Samples were taken from the center layer. Cecum contents were placed directly into an incubation flask. For each sample site, 10 g of sample was anaerobically transferred to incubation bottles (110 mL) that contained 70 mL of buffer (4 replicates/steer). Bottles received 40 mL of hydrogen gas and were incubated in a 39°C shaking waterbath. Gas volume and CH_4 concentrations were determined at 2, 4, 6, and 8 h. Rate of CH_4 production was the average of replicate bottles within steer. Data were analyzed as a 2 × 2 factorial with sample site and RG as fixed effects. Methane production per unit DM ($\text{mmol}\cdot\text{g}^{-1}\cdot\text{min}^{-1}$) was greater in rumen 0.000510 ± 0.000051 than cecum 0.000036 ± 0.000051 samples ($P < 0.001$). Methane production did not differ between high and low RG ($P = 0.98$). Partially funded by NIFA Grant 2011-68004-30214 National Program for Genetic Improvement of Feed Efficiency in Beef Cattle. USDA is an equal opportunity provider and employer.

Key Words: cattle, methane

540 Evaluation of a complete-feed (RAMP) receiving diet. C. J. Schneider*[1], B. L. Nuttelman[1], W. A. Griffin[1], D. B. Burken[1], R. A. Stock[2], T. J. Klopfenstein[1], and G. E. Erickson[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]Cargill Inc., Blair, NE.*

Two receiving trials were conducted in 2010 and 2011 to evaluate effects of feeding RAMP on cattle performance during the receiving period. Crossbred steers (yr 1: n = 642; BW = 264 ± 12.3 kg, yr 2: n = 758; BW = 257 ± 15.3 kg) were received over 2 consecutive d in 2010 and 2 d, one wk apart in 2011. Steers were blocked by arrival date and location within the feedlot yielding 2 blocks in yr 1 and 3 blocks in yr 2. Cattle were randomly allocated based on processing order to 34 pens in yr 1 and 44 pens in yr 2, within block, resulting in 15 to 20 cattle per pen. Treatments included a control receiving diet (CON;35% alfalfa hay, 30% sweet bran, 30% dry rolled corn, and 5% supplement, DM basis; 16.7% CP, 36.7% NDF) and RAMP (21.9% CP, 41.9% NDF), a complete feed (formulated and provided by Cargill Inc., Blair, NE) that contained a high level of sweet bran with a minimal amount of forage. 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 in yr 1 and 21, 24, or 28 d in yr 2. Following the feeding period, cattle were limit-fed a common diet (47.5% sweet bran, 23.75% grass hay, 23.75 alfalfa hay, and 5% supplement, DM basis) for 5 d before to collecting final BW to minimize variation in gut fill. Final BW were averages of 2-d weights. There was a year × treatment interaction for ADG ($P = 0.05$) and DMI ($P < 0.01$). RAMP increased ADG ($P < 0.01$) compared with CON in yr 1 (1.63 and 1.47 kg, respectively), but in yr 2 ADG was not different ($P = 0.93$) at 1.59 kg for CON and 1.60 kg for RAMP. In yr 1 DMI were not different ($P = 0.11$) with 7.11 and 7.34 kg/d for CON and RAMP, respectively. However, in yr 2, DMI was different ($P < 0.01$) with 6.37 and 5.82 kg/d for CON and RAMP, respectively. Across both yr, RAMP increased ($P < 0.01$) G:F compared with CON (0.250 and 0.230, respectively). Incidence of BRD was not different ($P = 0.27$) for CON and RAMP across both years. Feeding RAMP improved G:F compared with feeding a traditional receiving diet.

Key Words: beef cattle, feedlot, receiving

541 Effects of RAMP on feed intake and ruminal pH during adaptation to finishing diets. C. J. Schneider*[1], A. L. Shreck[1], R. A. Stock[2], T. J. Klopfenstein[1], and Galen Erickson[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]Cargill Inc., Blair, NE.*

A metabolism trial was conducted using 6 ruminally fistulated steer calves (BW = 255 ± 30 kg) to evaluate using RAMP, a complete feed provided by Cargill containing Sweet Bran and minimal forage, to adapt cattle to finishing diets. Steers were gradually adapted to finishing diets using 4 adaption diets followed by 7 d feeding a common finishing diet for a total of 5 periods consisting of 7 d each. Treatments were imposed during grain adaption using 2 programs. One treatment used RAMP by decreasing RAMP (100 to 0%) while increasing inclusion of the finishing diet (0 to 100%). For this treatment RAMP was mixed with the finishing ration and fed as a single diet. The control adaptation treatment (CON) contained (DM basis) 25% sweet bran, 5% supplement, with alfalfa hay inclusion decreasing from 45 to 7.5% while increasing a 60:40 blend of high-moisture corn and dry-rolled corn from 25 to 62.5%. All diets contained 27.6 mg/kg monensin and 26.5 mg/kg thiamine. Steers were offered ad libitum access to feed and water and fed once daily at 0800 h. Ruminal pH was recorded every min continuously for all 5 periods using wireless pH probes. Adapting cattle with RAMP increased DMI ($P < 0.01$) by 45% relative to CON in period 1 and by 25% in period 3 ($P = 0.04$). Intakes were not different during periods 2 and 4 ($P = 0.14$ and $P = 0.12$, respectively). RAMP adaptation tended to increase DMI ($P = 0.09$) compared with CON when cattle were fed the common finishing diet (6.05 and 7.35 kg for CON and RAMP, respectively). Maximum pH tended ($P = 0.07$) to be higher for CON compared with RAMP in period 2, but maximum pH was not different ($P > 0.28$) between treatments for other periods. Average ruminal pH, minimum pH, time below pH 5.6 and area below 5.6 were not affected ($P > 0.23$) by adaption method in any period. Adapting cattle with RAMP had no effect ($P > 0.11$) on magnitude of pH change or ruminal pH variance in any period. Adapting cattle to high-grain finishing diets using RAMP increased DMI but did not affect ruminal pH.

Key Words: beef cattle, grain adaptation, metabolism

542 Effect of maturity on the yield and in situ digestibility of whole-crop cereals. C. L. Rosser*[1], A. Beattie[1], H. C. Block[2], J. J. McKinnon[1], H. A. Lardner[1,3], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Agriculture and Agri-Food Canada, Brandon, MB, Canada, [3]Western Beef Development Centre, Humbolt, SK, Canada.*

The objective of this study was to determine the optimal maturity at harvest for common whole-crop cereals used in swathgrazing systems in western Canada. Four replicate plots of barley (*Hordeum vulgare* L. 'CDC Cowboy'), millet (*Panicum milliaceum* 'Red Proso'), oat (*Avena* spp. 'CDC Weaver'), and wheat (*Triticum aestivum* L. '07FOR21') were grown. Subsections in each replicate were randomly assigned to 1 of 4 harvest maturities (cut at a 5-cm stubble height); head elongation, late milk to early dough, hard dough, and fully mature. At each stage of maturity, the wet and DM yields and chemical composition (DM, OM, NDF, crude fat, and NFC) were determined. Whole-crop samples were ground to pass through a 2-mm screen, weighed into nylon bags, and exposed to rumen incubation for 0, 2, 4, 8, 16, 24, 48 and 72 h. Rates of degradation were determined using a first-order kinetic model. Data were analyzed with stage of maturity as a fixed effect and plot as a random effect. For all crops evaluated, DM yield increased ($P < 0.001$) with advancing maturity. The concentration of CP, and NDF decreased ($P \leq 0.012$) while the concentrations of OM and NFC increased ($P < 0.001$) with advancing maturity for all crops investigated. Despite the large increase for DM yield, the yield of CP was not affected by advancing maturity for all crops except that it increased for wheat ($P < 0.001$), whereas, the yields of OM, NDF, NFC, and crude fat increased ($P < 0.023$) for all crop types. The DM degradation rate (%/h) was not affected by maturity, but the rate for NDF degradation decreased for millet and oat as plants matured ($P \leq 0.031$). However, the stage of maturity did not affect NDF degradation rate for barley or wheat. The yield of effectively degradable DM for barley ($P = 0.196$) was not affected by maturity, but increased for millet ($P = 0.016$), oat ($P = 0.004$), and wheat ($P < 0.001$) with advancing maturity. These findings suggest that harvesting whole-crop annual cereals at a mature stage may maximize the yield of effectively degradable DM.

Key Words: harvest maturity, in situ, swathgrazing

543 Rumen bacterial population responses to inclusion of wet distillers grains plus solubles in finishing diets of feedlot cattle. G. M. Shipp*[1], W. E. Pinchak[2], D. W. Pitta[3], B. Milligan[4], S. L. Ivey[4], and J. C. MacDonald[1], *[1]Texas AgriLife Research, Amarillo, [2]Texas AgriLife Research, Vernon, [3]Department of Clinical Studies, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, [4]New Mexico State University, Las Cruces.*

A 6 × 6 Latin square with repeated measures design with dry rolled (DRC), steam flaked corn (SFC), and SFC with levels of wet distillers' grains plus solubles (WDGS) at 15%, 30%, 45% and 60%. Rumen samples collected at 0 and 4 h post feeding on d 21 of each period were strained into fluid and solid fractions (FRAC) and archived. Genomic DNA was extracted for amplification of V4 region of 16S rDNA gene and sequenced utilizing a Roche 454 FLX platform. Phylogenetic distribution of taxa, multivariate non-metric multidimensional scaling (NMDS) to compare community populations and Proc MIXED models were used to determine the influence of diet, time, FRAC and their interactions on rumen bacterial communities. Total sequences (1,747,630) were assigned to taxa. Different rumen bacterial communities developed in response to diet ($P < 0.05$) and FRAC within diet ($P < 0.01$) but not time ($P > 0.05$) and were readily differentiated utilizing NMDS at respective taxa level. The phyla *Firmicutes* dominated solid FRAC (up to 85%) while *Firmicutes* and *Proteobacteria* co-dominated (up to 95%) fluid FRAC. In contrast, *Bacteriodetes* constituted < 5% of all communities. Quantitative differences ($P < 0.05$) in *Firmicutes*, *Proteobacteria*, *Cyanobacteria*, and *Tenericutes* existed among diets. The family *Lachnospiracea* dominated the solid FRAC and decreased with WDGS inclusion. In contrast, *Rumincocacceae*, increased with all levels of WDGS. *Veillonellaceae*, exhibited a quadratic ($P < 0.05$) response by decreasing above 30% WSDGS. Genera *Eubacterium*, *Schwartzia*, and *Acidaminococcus* were dominant at ≥30% WDGS compared with DRC, SFC and 15% WDGS diets. *Paralactobacillus*, *Slackia*, and *Desulfovermiculus* were unique to WDGS diets and associate to specific functions. In summary, decreased animal performance observed with increasing WDGS inclusion in SFC diets supports our tenant that the rumen microbiome plays a key role in production efficiency of feedlot cattle.

Key Words: cattle, microbial ecology, rumen microbiology

544 Effect of sugarcane fiber digestibility and mode of conservation on intake and rumen pH of growing Nellore steers. D. O. Souza, B. S. Mesquita, J. Diniz-Magalhães, F. D. Rodriguez, B. S. Marques, and L. F. P. Silva,* *Universidade de São Paulo, Pirassununga, SP, Brazil.*

Sugarcane attains maturity and is available for daily harvest during the dry season; however, ensiling is an effective option for reducing labor costs. The objective of this study was to evaluate the effects of sugarcane stalk fiber digestibility (NDFD), and of mode of conservation on intake and rumen pH. Eight ruminally cannulated Nellore steers (275 ± 20 kg BW) were used in a replicated 4 × 4 Latin square design. Two sugarcane genotypes with differing NDFD were used: IAC2480 with higher NDFD (15% 30-h NDF digestibility), and IAC2094 with lower NDFD (6.5% 30h-NDF digestibility). Treatment diets contained 40% sugarcane, of total DM, as sole roughage source given as freshly chopped, or as silage, to evaluate the possible interaction between NDFD and mode of conservation on DM intake. Diets were formulated to provide daily gain of 1.2 kg/d. Animals were housed individually in a tie-stall with free access to water and fed ad libitum with 10% orts. Periods lasted for 14d, being 10d for adaptation, and 4d for sample collection. DM intake was determined on d 10, 11 and 12, and rumen pH on d 14 at 6 time points: 0, 1, 3, 6, 9 and 12h after the morning feeding. Main effects of sugarcane genotypes (CANE), of mode of conservation (CONS), and their interaction were tested by ANOVA. Feeding sugarcane with higher NDFD increased DM intake (5.7 vs. 5.1 ± 0.5 kg/d, $P < 0.01$), however the interaction CANE x CONS was significant ($P = 0.04$). The effect of greater NDFD on DM intake was only significant when feeding sugarcane as silage ($P < 0.01$), having no effect on DM intake when sugarcane was offered and freshly cut ($P = 0.53$). The mode of conservation did not affect DM intake ($P > 0.05$). Regarding rumen pH, there was no effect of CANE, nor there was a CANE × CONS interaction ($P > 0.30$). Feeding sugarcane as silage, as opposed to freshly cut, increased mean rumen pH (6.69 vs. 6.37 ± 0.08, $P < 0.01$). There was a clear reduction of pH during the day ($P < 0.01$), but there was no effect of TIME x CONS on rumen pH ($P = 0.23$). We conclude that sugarcane silage with higher NDFD increased DM intake, and feeding silage as opposed to freshly cut increased rumen pH.

Key Words: cattle, NDF digestibility, sugarcane silage

545 Impact of diet on the abundance and diversity of fecal *Escherichia coli* shed from cattle in overwintering environments.

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The objective of this study was to determine the effect of diet and overwintering strategy on *E. coli* populations in beef cattle during 2, 21-d periods. Sixty beef cows were assigned to 3, replicated feeding strategies, each with 10 cows. Four groups of cows were fed using a bale-grazing strategy while the other 4 groups of cows were fed in dry lot pens. During period 1, 2 pens in the bale graze system received grass hay supplemented with DDGS (dried distiller's grains with solubles; 2.5 kg/cow every third day) while the remaining 4 pens received grass hay only. During period 2, the DDGS supplemented cows remained on the same diet while the other 4 pens received 1 kg/cow/day of barley. Three cows in each pen were randomly selected and individual fecal samples were collected and cultured on selective media (Eosin Methylene Blue Agar). Colonies of *E. coli* were counted and 3 isolates were selected for DNA extraction. Isolates were subjected to PCR in search of 18 selected genes encoding for a range of virulence factors, including adhesins, aggregation factors, toxins, pathogenicity islands, autotransporters, and capsule synthesis. There were no significant differences in *E. coli* numbers between the treatments ($\alpha = 0.05$;P-value = 0.06) but the highest number of *E. coli* were isolated from bale grazed cows receiving barley (6.71 log cfu/g) and the lowest number were from bale grazed DDGS cows (5.78 log cfu/g). Comparison of the virulence genes present in the *E. coli* isolates resulted in a significant difference in *cnf* (cytotoxic necrotizing factor; induces prominent stress fiber formation and increase adherence to epithelia) between treatments ($\alpha = 0.05$;P-value < 0.001). Contrast analysis of the virulence data by diet resulted in significant differences in the presence of *aidA* (adhesion involved in diffuse adherence), *fliC* (flagellan structural gene), and *cnf*. The data suggests that diet may affect the abundance of *E. coli* shed in the feces and increase the presence of *E. coli* harbouring particular virulence genes that mediates adhesion of the bacterium to the epithelial surfaces.

Key Words: *Escherichia coli*, dried distillers grains with solubles, virulence genes

546 Comparison of different supplemental cobalt forms on fiber digestion and cobalamin levels.

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Cobalt (Co) is essential for rumen microbial metabolism to synthesize methane, acetate and methionine. It also serves as a structural component of vitamin B_{12}, which functions as a coenzyme in energy metabolism. A study was conducted to determine if Co form (cobalt carbonate vs. cobalt glucoheptonate) supplemented above NRC requirements would improve fermentability of a low quality forage diet and change serum cobalamin concentrations. Twenty ruminally-cannulated cows (577 ± 13 kg) were individually fed in a completely randomized experimental design. Cows were fed a grass hay diet (7.9% CP, 56% TDN, 63% NDF, 87% DM) at 2.25% of BW for a 62 d study, which consisted of 3 periods: acclimation (AC), treatment (TR), and residual (RE). Cows were stratified by age (5 ± 0.37 yr) and lactational history, and assigned to receive 12.5 mg supplemental Co in 1 of 2 forms: (1) 27.2 mg of cobalt carbonate (CC, n =11 cows) or (2) 50 mg of cobalt glucoheptonate (CGH, n = 9 cows). Supplementation was administered daily via a gelatin capsule placed directly into the rumen 2 h after daily feeding. During the last 96 h of each period, forage fermentability was measured using an in situ nylon bag technique. Serum samples were collected 4 and 6 h following feeding, 24 h before the end of each period. Measurements taken in the AC period were used as covariates for analysis in the TR and RE periods. A treatment × period interaction ($P = 0.03$) was exhibited for in situ OM fermentability at 96 h; (TR period, 68.44 and 70.83 ± 0.81%, and RE period, 67.61 and 66.82 ± 0.75%, for CC and CGH; respectively). Once inclusion of Co in the CGH group was removed, fermentability was reduced by 4.01% compared with 0.82% in the CC cows. The NDF disappearance (OM basis) was lower for the TR period compared to the RE period at 48 h ($P < 0.001$; 62.95 and 65.18 ± 0.39%; respectively). However, by 96 h the NDF disappearance was higher for TR period than the RE period ($P = 0.02$; 70.44 and 68.89 ± 0.44%; respectively). No differences were detected for cobalamin serum levels or rate of fiber fermentation. The outcomes of this research signify that while there are no residual effects of Co supplementation on fermentation, there is an indication that Co glucoheptonate supplementation does enhance the overall extent of fermentation. The extent of fiber disappearance is also improved with Co supplementation regardless of form.

Key Words: beef cattle, cobalt, vitamin B12

547 Comparison of animal and dietary effects on ruminal methanogens and their association with protozoa in beef cattle.

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This study investigated the effects of animal (host) and diet on the variation in ruminal methanogenic communities of 4 beef heifers sequentially adapted to corn- (CDDGS), wheat-based (WDDGS) dried distillers grain with solubles (DDGS), and WDDGS plus pure corn oil. The methanogenic diversity was examined using PCR-denaturing gradient gel electrophoresis (PCR-DGGE) and methanogen abundance was measured quantitative real-time PCR (qRT-PCR). The methanogen DGGE profiles were analyzed using BioNumerics software and Global R statistics. Methanogen abundance was compared host-wise and diet-wise using Analysis of Variation (ANOVA) and the correlation between methanogens and protozoa was analyzed using PROC CORR within SAS. Observed DGGE patterns of methanogens were similar among the 4 diets but distinctive within each individual animal (Global R = 0.87, $P < 0.01$). Methanogenic phylotypes displayed unique responses to the different sources of DDGS, and the ecological shifts were host-specific. Populations of methanogens and protozoa varied among animals and diets, while densities of *Methanobrevibacter* sp. AbM4 and *Methanosphaera stadtmanae* only differed among animals. The diversity and abundance of methanogenic community adapted to different diets uniquely within individuals. In addition, *Mbb.* sp. AbM4 and total number of protozoa ($P < 0.01$) were positively correlated within animal. In conclusion, the response of ruminal methanogenic community to different diets was host dependent, suggesting that the host biology should not be ignored if dietary strategies are used to manipulate ruminal methanogens.

Key Words: diet effect, host effect, methanogenic ecology

548 Withdrawn by author

549 Assessing how RFI classification in the growing phase predicts RFI classification in the finishing phase. D. Johns,* G. Vander Voort, C. Campbell, M. Quinton, and I. Mandell, *Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Residual feed intake (RFI) is being used to replace feed efficiency due to its accuracy in determining production efficiency. The objective of this study was to examine whether assessment of production efficiency via RFI in the growing phase (GP) accurately predicts production efficiency in the finishing phase (FP). RFI was calculated at the end of an 84 d GP for 204 crossbred steers. Steers were then allocated to one of 5 finishing management regimens (based on an 87% concentrate diet) designed to produce a wide range in growth performance (average daily gain (ADG), feed:gain (F:G), RFI) and carcass traits. Management regimens included a nonimplanted control (CON), Synovex implant (SYN), Revalor implant (REV), REV plus the β agonist (βA), Optaflexx (OPT), and REV plus the βA, Zilmax (ZIL). The allocation evenly distributed Low (RFI^-) and High (RFI^+) cattle from the GP across all finishing management regimens. Post-slaughter, RFI was calculated for the FP and the overall trial to examine how GP RFI classification predicted performance in the FP. FP ADG ranged from 1.60 (CON) to 2.23 (REV/ZIL) kg/d; F:G ranged from 7.17 (CON) to 5.61 (REV/ZIL). Over the entire trial ADG ranged from 1.72 (CON) to 1.94 (REV/ZIL) kg/d; F:G ranged from 6.37 (CON) to 5.68 (REV/ZIL). RFI ranged from −0.61 to 1.60 in the GP, −2.20 to 2.49 in the FP and −3.15 to 3.61 for the trial overall. The lowest overall and FP RFI was found in ZIL (−0.14 and −0.25 respectively), indicating the most efficient conversion of feed to gain. Overall RFI was improved in all management regimens using REV, with increased efficiency vs. GP RFI. There was limited improvement in efficiency for CON and SYN cattle between GP and FP RFI. For 14.4% of steers, RFI ranking changed from RFI^+ rank in the GP to RFI^- in the FP, becoming more efficient; 19.4% of steers became less efficient while 66.3% kept the same RFI ranking. RFI classification in the GP did not accurately predict RFI classification in the FP for all cattle. More work is needed to examine when RFI should be determined for predicting finishing performance.

Key Words: beef cattle, RFI, growth performance

Ruminant Nutrition: Dairy: Feed Additives

550 Effects of trace mineral source on oxidative metabolism, subclinical endometritis, and performance of transition dairy cows. T. Yasui*[1], C. M. Ryan[1], R. O. Gilbert[1], K. Perryman[2], and T. R. Overton[1], [1]*Cornell University, Ithaca, NY,* [2]*Micronutrients Inc., Indianapolis, IN.*

Multiparous Holstein cows (n = 60) were used to determine effects of trace mineral source on oxidative metabolism, subclinical endometritis, and performance of transition cows. After a 1-wk preliminary period, cows were assigned randomly to one of 3 topdress treatments from 21 d before expected calving through 84 d post calving: 1) Inorganic sources based upon sulfates of Zn, Cu, and Mn (ITM); 2) a blend (75:25) of sulfates and chelated sources of Zn, Cu, and Mn (ITM/OTM); and 3) Hydroxy Trace Minerals (HTM) of Zn, Cu, and Mn (IntelliBond; Micronutrients, Inc., Indianapolis, IN). Final concentrations of Zn, Cu, and Mn were similar among treatments and averaged 40, 10, and 27 ppm before calving and 59, 15, and 40 ppm after calving. An interaction of treatment and week existed ($P = 0.02$) for milk yield such that cows fed HTM increased milk yield faster than cows fed the other 2 treatments; a similar interaction was also present for yields of fat-corrected milk ($P = 0.03$) and lactose ($P = 0.05$). Cows fed HTM during the prepartum period tended ($P = 0.08$) to have higher body weight and had higher body weight during the postpartum period ($P = 0.04$) than those fed the other 2 treatments. Plasma antioxidant capacity was lower in cows fed HTM than ITM during both prepartum (1.84 vs. 2.09 mM; $P = 0.03$) and postpartum (1.95 vs. 2.16 mM; $P = 0.04$) periods; cows fed ITM/OTM had intermediate values. Cows fed HTM tended to have lower concentrations of plasma thiobarbituric acid reactive substances than those fed ITM during whole study period (1.95 vs. 2.11 µM; $P = 0.07$). Endometrial cytology as characterized by low volume uterine lavage at 7 d postcalving and on one day between 40 and 60 d post calving was not affected by treatment. In conclusion, supplementation with HTM sources of Zn, Cu, and Mn resulted in evidence of improved productive performance during early lactation along with modulation of plasma variables related to oxidative metabolism.

Key Words: trace minerals, oxidative status, subclinical endometritis

551 Effects of essential oils on methane production, fermentation, abundance and diversity of rumen microbial populations. A. Patra[1,2] and Z. Yu*[1], [1]*The Ohio State University, Columbus,* [2]*West Bengal University of Animal and Fishery Sciences, Kolkata, India.*

Five essential oils (EO), namely, clove oil (CLO), eucalyptus oil (EUO), garlic oil (GAO), origanum oil (ORO) and peppermint oil (PEO) were tested in vitro using 3 replicates at 3 different doses (0.25, 0.50 and 1.0 g/L) for their effect on methane production, fermentation, and select groups of ruminal microbes, including total bacteria, cellulolytic bacteria, archaea and protozoa. All the data were analyzed using the mixed model procedure of SAS. All the EO significantly ($P < 0.01$) reduced methane production with increasing doses, with a reduction by 34.4%, 17.6%, 42.3%, 87% and 25.7% for CLO, EUO, GAO, ORO and PEO, respectively, at 1.0 g/L compared with the control. However, apparent degradability of dry matter (DM) and neutral detergent fiber (NDF) also decreased linearly ($P < 0.01$) with increasing doses by all EO except GAO. The concentration of total volatile fatty acids (VFA) was not affected ($P > 0.05$) by GAO, EUO or PEO, but altered linearly and quadratically ($P < 0.01$) by CLO and ORO. All the EO also differed in altering the molar proportion of acetate, propionate, and butyrate. As determined by qPCR, all the EO decreased the abundance of archaea, protozoa, *Fibrobacter succinogenes*), *Ruminococcus flavefaciens* and *Ruminococcus albus*) linearly ($P < 0.01$) with increasing EO doses. Based on DGGE analysis, different EO changed the composition of both archaeal and bacterial communities to different extents. The Shannon-Wiener diversity index (*H'*) was decreased for archaea by all EO in a dose-dependent manner, but increased for bacteria at low and medium doses (0.25 and 0.50 g/L) for all EO except ORO. Due to the adverse effects on feed digestion and fermentation, a single EO may not effectively mitigate methane emission from ruminants unless used in combinations.

Key Words: essential oils, methane, microbes

552 Effect of dietary fat and Rumensin on ruminal bacteriome revisited using metagenomic analysis. M. Kim[1], M. Morrison[2,1], M. Eastridge[1], and Z. Yu*[1], [1]*The Ohio State University, Columbus,* [2]*CSIRO Livestock Industries, St Lucia, QLD, Australia.*

Monensin and dietary fats have been used to improve feed efficiency and to reduce methane production. However, the effect of these dietary manipulations on ruminal bacterial community (bacteriome) has not been examined in detail. The objective of this study was to examine and compare the effects of dietary addition of monensin alone (as Rumensin, 12 g/ton TMR) or monensin plus fat (4% supplemental) on ruminal bacteriome in lactating dairy cattle. Ruminal bacteriomes in the liquid and adherent fractions were analyzed using 454 pyrosequencing analysis. In total, 56,160 non-chimeric 16S rRNA gene (rrs) sequences were obtained. Most of the sequences were assigned to phyla *Firmicutes* and *Bacteroidetes*, irrespective of fractions. *Firmicutes* was more abundant in the adherent fraction than in the liquid fraction, while *Bacteroidetes* was less abundant in the adherent fraction than in the liquid fraction. Gram-positive *Firmicutes* was not affected by monensin. Two minor phyla, TM7 and SR1, were highly sensitive to monensin. In total, 13,041 species-level OTUs were identified from the 56,160 sequences across all the fractions. However, only 65 of them were represented by more than 30 sequences. Only 5 *Firmicutes* OTUs among the predominant OTUs were sensitive to monensin. On the other hand, 12 *Firmicutes* OTUs, most assigned to the family *Ruminococcaceae*, were stimulated by the combination of monensin and fat. These OTUs may be involved in lipolysis or biohydrogenation. These results suggest that some gram-positive rumen bacteria are not inhibited by monensin and that the interaction between monensin and fat can have an effect on rumen bacteriome.

Key Words: fat, monensin, rumen bacteriome

553 Effect of dietary potassium on water intake and rumen dynamics. S. E. Fraley*[1], M. B. Hall[2], and T. D. Nennich[1], [1]*Purdue University, West Lafayette, IN,* [2]*USDA-ARS, Madison, WI.*

Water is a critical nutrient for dairy cows, though little work has looked at the effects of water intake on rumen parameters. The objective of this study was to evaluate the effect of water intake on rumen parameters and determine effects of increased dietary K on water intake in dairy cows. Potassium carbonate was added to the diets of 9 ruminally cannulated, late lactation Holstein cows (207 ± 12 DIM) that were randomly assigned to 1 of 3 treatments in a replicated 3 × 3 Latin square design with 18-d periods. Dietary treatments (on a DM basis) were baseline dietary K levels of 0.94% dietary K (Control), 0.75% added dietary K (LowK), and 1.5% added dietary K (HighK). Cows were fed treatment diets for a 14-d adaption period followed by a 4-d collection period. Total rumen evacuations were conducted on d 4 of the collection period. Weights of rumen contents were recorded and subsamples were dried. Rumen fluid samples were collected to determine volatile fatty acids (VFA) and NH_3 concentrations. Milk samples were collected twice daily during the collection period. Data were analyzed using PROC MIXED of SAS with linear and quadratic contrasts. Milk, milk fat and protein yields showed quadratic responses ($P = 0.001$, 0.01 and 0.001, respectively) with greatest yields for LowK. Dry matter intake had a quadratic response ($P < 0.001$) with 21.8 kg/d for LowK and 20.4 and 20.5 kg/d for Control and HighK, respectively. Water intake showed a linear relationship with HighK being the greatest (102.4, 118.4 and 129.3 L/d, $P = 0.001$). Total and wet weight of rumen contents declined linearly ($P = 0.01$ and 0.01, respectively) and dry weight tended ($P = 0.09$) to decline linearly for LowK and HighK. There was a negative linear relationship for rumen NH_3 concentrations for LowK and HighK ($P = 0.004$). Concentrations of acetate as a percentage of total VFA linearly increased for LowK and HighK ($P = 0.002$), while concentrations of propionate declined ($P = 0.003$) as percentage of total VFA. Increasing dietary K in the diets of lactating dairy cows increased water consumption and rumen ammonia concentrations, while decreasing total water weight in the rumen.

Key Words: dairy cow, potassium, water intake

554 Effects of rumensin in lactating dairy cow diets with differing starch levels.

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The objective of this study was to determine the effects of Rumensin on lactation performance in either reduced (RS) or normal (NS) starch diets. One hundred and 28 Holstein and Holstein × Jersey cows (90 ± 33 DIM) were stratified by breed and parity and randomized to 1 of 16 pens, each with 8 cows. Pens were then randomly assigned to 1 of 4 treatments in a 2 × 2 factorial arrangement of treatments. The RS and NS diets contained 20.4 and 26.9% starch (DM basis), respectively. A 4 wk covariate adjustment period preceded the treatment period with all pens receiving the NS diet with 18 g/ton Rumensin (NSR). Following the 4 wk covariate adjustment period, study animals were fed their assigned treatment diets of either NSR, NS with 0 g/ton Rumensin (NSC), RS with 18 g/ton Rumensin (RSR), or RS with 0 g/ton Rumensin (RSC) for 12 wk. Mean DMI (27.0 kg/d) was not affected by Rumensin, starch or their interaction. Inclusion of Rumensin, as well as feeding the NS diet, increased ($P = 0.01$) milk yield by 1.3 and 1.5 kg/d per cow, respectively. Feeding the NS diet compared with the RS diet increased ($P < 0.02$) milk protein percent and yield and lactose and SNF yields while decreasing ($P < 0.01$) MUN. Rumensin increased ($P < 0.05$) all measures of milk production efficiency (MPE; milk yield/DMI) as well as lactose yield and tended ($P = 0.06$) to increase SNF yield and MUN. Rumensin decreased ($P = 0.02$) milk protein percent, but did not affect protein yield, milk fat percent or yield, and lactose or SNF percentages. There was a tendency ($P = 0.08$) for a starch by Rumensin interaction for MPE such that Rumensin inclusion tended to increase MPE more for NS versus RS diets. Feeding RS diets reduced milk and protein yields, but had similar component-corrected milk yields and efficiencies when compared with NS diets. Rumensin improved MPE and lactation performance when added to both RS and NS diets.

Key Words: lactating cow, rumensin, starch

555 Feeding blood meal or two rumen-protected lysine sources in early lactation dairy cows and the effect of withdrawal on production parameters.

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Seventy-two multiparous cows were used to examine the effects of feeding rumen-protected lysine (RPL) sources or blood meal from wk 4 through 7 postpartum and then withdrawing them. All cows entered the individual tie stalls on d 14 ± 3 postpartum and received the Control diet through d 21 ± 3. Cows were balanced across treatments based on wk 3 postpartum milk production. In addition the information obtained during wk 3 was used as a covariate in the statistical analysis. Cows were assigned to one of 4 subsequent treatments: C: Control, BM: C with blood meal, AP: C with AjiPro-L (Ajinomoto Co., Inc.), and AS: C with AminoShure-L (Balchem Corporation). Manufacturer suggested bioavailabilities were used for RPL sources. Metabolizable Lys supply calculated by CPM Dairy was 153.1, 166.1, 166.8, and 166.8 g/d, for C, BM, AP, and AS, respectively. Cows remained on their treatment for 4 weeks (4–7 wk postpartum, phase 1). From wk 8 through 11 postpartum (Withdrawal, phase 2) all cows again received the Control ration. Individual dry matter intake (DMI) and milk yield was measured daily, and milk components were measured weekly. Body weights and BCS were recorded on d 21, 49 and 77 postpartum. During phase 1, AP showed higher ($P < 0.01$) milk yield compared with C, BM and AS. FCM was increased ($P < 0.01$) in AP compared with C and AS. Milk/DMI efficiency was higher for AP than AS. Milk fat yield was higher ($P < 0.01$) for AP than AS or C, whereas protein yield was highest ($P < 0.01$) for AP compared with other treatments. Milk fat percentage was highest ($P < 0.01$) for BM compared with C, with AP and AS being intermediate. Milk protein percentage was not affected by lysine supplementation. During phase 2, ECM yield was higher ($P < 0.01$) for AP compared with C, BM and AS. However, cows in AP treatment demonstrated the most dramatic drop in milk post withdrawal (1 kg from wk 5–6 on trial) compared with BM or AS. There was no effect of treatment on body weights or BCS. These results demonstrate that not all RPL sources perform in a similar fashion in early lactation cows.

Key Words: rumen-protected lysine, milk production, early lactation

556 Evaluation of dietary betaine (BET) in heat-stressed Holstein cows in lactation.

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Betaine, a natural, organic osmolyte may reduce cellular work and improve efficiency and act as a chaperone, refolding denatured proteins. To test if dietary BET reduced the effect of heat stress, multiparous, lactating Holstein cows (n = 23) were blocked (n = 101.4 ± 8.6 DIM) and randomly assigned to one of 3 diets of BET; control (CON) group no BET, mid dose (MID) cows (57 mg of BET / kg BW), and high dose (HIGH) was (114 mg of BET / kg BW). Cows were fed twice daily and treatments were top-dressed at each feeding. Cows were milked 2 times/ d and milk samples and were taken daily for analysis. Milk components, yield, feed intake, and water intake records were taken daily. Temperature and respiration rates were taken 3 times/ d at 0600, 1400, and 1800. Cows were housed in environmentally controlled rooms and following acclimation for 7 d the cows were subjected to cyclic thermal neutral (TN mean THI of 56.6) for 7 d and heat stress, represented by the Thermal Humidity Index (THI) (HS mean THI of 71.5) for 10 d. Temperature data loggers were inserted vaginally to read the last day of TN and the first 2 d of HS to follow body temperature changes. Dietary BET increased milk yield and protein % during the TN period ($P < 0.01$). There were no differences between treatments in total milk production or % protein during HS. Feed and water intake decreased during HS with betaine treated (CON vs. MID, and CON vs. HIGH) cows ($P < 0.01$) with no difference in TN. The Con diets had higher pm HS respiration rates than both MID and HIGH treatments ($P = 0.04$, $P = 0.001$), but lower HS body temperature compared with BET treatments ($P < 0.05$). Vaginal temperatures were higher in BET treated cows and were highest in MID. We conclude that BET increased milk and protein production in TN conditions and was associated with reduced feed and water intake and slightly increased body temperatures during HS at the doses tested.

Key Words: betaine, dairy cow lactation, heat stress

557 Effect of dietary phytate on phosphorus digestibility in dairy cows.

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The objective was to evaluate the effect of dietary phytate P (Pp) supply on ruminal and post-ruminal Pp digestion and net disappearance of P from lower digestive tract of lactating cows. Six ruminally and ileally cannulated crossbred lactating cows were used in 2 incomplete Latin squares with 4 21-d periods (17 d of diet adaptation, 4 d of total collection). Dietary treatments were low Pp, medium Pp, and high Pp, and a high inorganic P (Pi) diet with the same total P content as the highest phytate diet but with P mostly from inorganic sources. The diets contained 0.10, 0.18, 0.29 and 0.11% Pp and 0.43, 0.48, 0.54 and 0.52% total P on dry matter (DM) basis, with cottonseed meal used to increase Pp content. Ytterbium-labeled corn silage and Co-EDTA were used as particulate and liquid phase markers to measure omasal and ileal digesta flow. Omasal and ileal digesta were collected every 6 h on d 20 and 21 and rumen contents were collected on d 21. Samples were analyzed for total P (molybdovanadate yellow method), Pi (blue method), and Pp (high performance ion chromatography). Data were analyzed using PROC GLIMMIX in SAS. Polynomial contrasts were used to test the effect of increasing dietary Pp on intake, small and large intestinal disappearance, and fecal excretion, and to compare these measures in the high Pp and high Pi diets. Phytate P intake increased ($P < 0.05$) with increasing dietary Pp but dietary Pp did not influence ruminal Pp digestibility. Small intestinal total P disappearance decreased ($P < 0.05$) with increasing dietary Pp, but large intestinal disappearance of total P, Pi, and Pp were not affected by dietary Pp. Fecal DM increased linearly ($P = 0.002$) with increasing dietary Pp, as did fecal P excretion ($P < 0.05$). Dry matter digestibility was higher for high Pi than for high Pp ($P < 0.05$; 68.9 vs. 64.5%) but fecal DM was not affected by form of P. Fecal P excretion decreased ($P < 0.05$) when a portion of Pp was replaced with Pi (high Pi vs. high Pp) despite equal total P intake. In lactating cows phytate digestibility was not affected by phytate content but fecal P increased when P was from phytate rather than from inorganic sources.

Key Words: phytate, digestibility, dairy cow

558 Application of rumen-protected lysine to lower crude protein diets for lactating dairy cows.

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The study objective was to evaluate the application of supplemental rumen-protected Lys (RP-Lys) to maintain milk production when reducing crude protein levels in diets of lactating dairy cows. Twelve lactating multiparous Holstein cows, averaging 129 DIM, 50.2 kg milk yield, 3.6% fat and 2.9% true protein were randomly assigned to one of 4 3x3 Latin squares. Each 14-d period had 11-d for adaptation followed by 3-d of data collection. Cows were offered one of 3 experimental treatment rations formulated with CPM Dairy (v3.0); Positive control (PC) — formulated to meet all nutrient requirements; Test diet (Test) — negative control diet formulated to meet nutrient requirements, except deficient in MP (approximately 200 g/d) and first limiting in Lys (approximately 10 g/d); and Test+RPL — same basal diet as negative control + RP-Lys to provide 14.5 g/d of MP-Lys. For Test+RPL, 45g of RP-Lys (AminoShure-L; containing 23.4g Lys) was top-dressed on the TMR once daily. The PC diet resulted in lower intake ($P = 0.03$) as compared with either the Test or Test+RPL diet. PC, Test, and Test+RPL cows averaged 42.6, 42.9, 43.6 kg/d of milk and 27.3, 28.4, 28.8 kg/d of DMI, respectively. Crude protein intake for the PC, Test, and Test+RPL diets were 4.83, 4.67, and 4.74 kg/d respectively. MUN decreased ($P < 0.01$) for cows on Test and Test+RPL diets as compared with PC diet (12.5, 12.5 and 14.9 mg/dL, respectively). Milk yield, milk components, milk component yields, FCM, ECM, SCM and production efficiencies (milk, ECM, SCM and FCM) did not differ ($P > 0.05$) among treatments. A post-study CPM evaluation using final chemical composition analyses of the feedstuffs and average production data from the animals predicted that diets supported more than 47 kg of milk and Lys was not limiting. Cows on the study produced slightly less milk; however, DMI was 5–8% more than predicted by initial formulations. Formulation accuracy of the MP and Lys deficient diet may have been improved if data had been available from an initial adjustment period measuring DMI, body weight, milk yield and milk composition.

Key Words: amino acids, dairy cattle, rumen-protected lysine

559 A meta-analysis of the effects of feeding yeast culture produced by anaerobic fermentation of *Saccharomyces cerevisiae*, on milk production of lactating dairy cows.

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The purpose of this study was to estimate the average impact of a commercially available yeast culture product on milk production and other production measures in lactating dairy cows through the use of a meta-analysis of random controlled trials. A total of 61 research publications (published journal articles, published abstracts, and technical reports) were identified through a review of literature provided by the manufacturer and search of published literature using 6 computer search engines. Thirty-six separate studies with a total of 67 comparisons met the criteria for inclusion in the meta-analysis. The fixed effect meta-analysis showed substantial heterogeneity for milk yield, ECM, 3.5% FCM, butterfat yield, protein yield and DMI. Sub-group analysis of the data set showed much less heterogeneity in peer reviewed studies versus, non-peer-reviewed abstracts and technical reports, and tended to show higher treatment effects. A random-effects meta-analysis showed an estimated weighted mean difference between treated and untreated cattle reported in peer-reviewed publications to be 1.18 kg/d (95% CI, 0.55 to 1.81), 1.61 kg/d (95% CI, 0.92 to 2.29), and 1.65 kg/d (95% CI, 0.97 to 2.34) for milk yield, 3.5% FCM and ECM respectively. Butterfat yield and protein yield for peer-reviewed studies increased 0.06 kg/d (95% CI, 0.01 to 0.10) and 0.03 kg/d (95% CI, 0.00 to 0.05). Dry matter intake was analyzed by the sub-groups early lactation (<70 DIM) and not-early lactation. The studies reported in peer-reviewed journals showed an increase in DMI between the treated and untreated cattle of 0.62 kg/d (95% CI, 0.21 to 1.02) for early lactation and a decrease DMI of 0.78 kg/d (95% CI, −1.36 to −0.21) for later lactation studies. These findings provide strong evidence that this commercially available yeast culture product provides significant improvement in several important milk production parameters as evaluated in production settings typical for commercial dairies in North America.

Key Words: yeast culture, meta-analysis, lactating

560 Impact of feeding yeast culture under normal and SARA conditions in lactating dairy cows. S. Li*[1], E. Tesfaye[1], H. Khazanehei[1], M. Scott[2], I. Yoon[2], E. Khafipour[1], and J. C. Plaizier[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Diamond V, Cedar Rapids, IA.*

Eight rumen- and cecum-fistulated cows (42–90 DIM, 605 ± 60 kg BW) were used in a crossover design to examine the effects of a *Saccharomyces cerevisiae* fermentation product (SCFP) on production performance and rumen and hindgut fermentation during normal and sub-acute ruminal acidosis (SARA) conditions in lactating dairy cows. Each experimental period consisted of 4 wk of normal feeding followed by 1 wk of SARA challenge. During normal feeding, cows received a diet containing 42% concentrate, 28% corn silage and 30% alfalfa baleage (DM basis). A grain-based SARA challenge was conducted by replacing 22% corn silage in the diet with the same amount of pellets that contained 50% ground wheat and 50% ground barley. Treatment cows were supplemented with 14 g/d of SCFP (Original XPC, Diamond V) mixed with 140 g/d ground corn, and control cows received ground corn only. During wk 4 and 5 of each period, DMI and milk production were determined daily and milk samples were collected from 4 subsequent milkings; rumen pH was monitored continuously by indwelling rumen pH data loggers; rumen fluid, cecal digesta, feces, urine and blood samples were collected on Tuesdays and Thursdays. SARA challenge increased ($P < 0.01$) time that rumen pH stayed below 5.6 (11.1 vs. 311.1 min/d), decreased ($P < 0.01$) average rumen pH (6.33 vs. 5.94), DMI (21.9 vs. 20.1 kg/d) and 4% FCM (29.6 vs. 26.2 kg/d). SCFP did not affect measures of ruminal pH, DMI or FCM. An interaction between SCFP and SARA challenge was observed ($P < 0.09$) for milk fat concentration; 3.25, 2.71, 3.24, and 2.92% for Normal-Control, SARA-Control, Normal-SCFP and SARA-SCFP, respectively. The SARA challenge increased ($P < 0.05$) free LPS in rumen fluid (18,858 vs. 101,158 EU/mL), in feces (15,367 vs. 29,978 EU/mL), and tended to increase ($P = 0.08$) LPS in the cecum (18,235 vs. 30,549 EU/mL). SCFP tended to decrease ($P = 0.13$) ruminal LPS (54,438 vs. 35,043 EU/mL). The LPS-binding protein concentration in blood plasma was increased, (9.9 vs. 38.0 μg/mL, $P < 0.01$) by the SARA challenge, but was not affected by the SCFP. Results indicate that SCFP can alleviate milk fat depression and may reduce the production of ruminal LPS during grain-induced SARA.

Key Words: cow, SARA, yeast culture

561 Effects of chromium propionate supplementation during the periparturient period and early lactation on metabolism, performance, and subclinical endometritis in dairy cows. T. Yasui*[1], J. A. A. McArt[1], C. M. Ryan[1], R. O. Gilbert[1], D. V. Nydam[1], F. Valdez[2], and T. R. Overton[1], *[1]Cornell University, Ithaca, NY, [2]Kemin Industries, Des Moines, IA.*

Multiparous Holstein cows (n = 61) were used to determine effects of chromium propionate supplementation during the periparturient period and early lactation on metabolism, performance, and subclinical endometritis. After a 1-wk preliminary period, cows were assigned randomly to one of 2 treatments from 21 d before expected calving through 63 d post calving: 1) control (n = 31) and 2) chromium propionate (n = 30; Cr-Pro, KemTRACE Chromium Propionate, Kemin Industries, Des Moines, IA) administered by daily topdress at a rate of 8 mg/d of chromium. Evaluation of endometrial cytology by low volume lavage was determined on all cows at 7 d postcalving (1st lavage) and on one day between 40 and 60 d (2nd lavage) post calving. There was a tendency for increased DMI during the prepartum period in cows fed Cr-Pro (16.5 vs. 15.8 kg/d; $P = 0.07$). Cows fed Cr-Pro tended to have lower plasma NEFA during the prepartum period (184 vs. 211 μEq/l; $P = 0.08$). Effects of Cr-Pro supplementation on postpartum DMI and milk yield were not significant; however, cows fed Cr-Pro had higher somatic cell counts (275 vs. 160 × 1000/ml; $P = 0.04$) and tended to have higher urea nitrogen concentrations in milk (11.2 vs. 10.6 mg/d; $P = 0.08$) than controls. An interaction ($P = 0.05$) of treatment and day existed during the postpartum period such that cows fed Cr-Pro had lower plasma glucose concentrations immediately postpartum than controls. Cows fed Cr-Pro had lower incidence of subclinical endometritis for between 40 and 60 d using a cut-point of 10% neutrophils (30% vs. 57% of cows; $P = 0.04$). In conclusion, supplementation with chromium propionate resulted in trends for increased DMI and lower NEFA prepartum. Postpartum milk yield and DMI were not affected by treatment; however, Cr-Pro supplementation decreased the incidence of subclinical endometritis between d 40 and 60 postcalving, suggesting the potential for effects on subsequent reproductive performance.

Key Words: chromium, subclinical endometritis, transition cow

Ruminant Nutrition II

562 Study of effects of conjugated linoleic acid (CLA) on milk production and composition, and milk fatty acid profile of Holstein dairy cows. A. Mahdavi,* K. Rezayazdi, A. Z. Shahneh, and M. Dehghan-Banadaky, *Department of Animal Science, College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The aim of this experiment was to determine the effects of conjugated linoleic acid (CLA) on milk production and composition, and milk fatty acid profile of dairy Holstein cows. Three lactating Holstein cows (203 ± 9 DIM; mean ± SD) fitted with rumen fistula were used in a 3 × 3 Latin square experiment with 21-d periods, including a 14-d adaptation period followed by a 7-d sampling period. Treatments were: 1) control (115 g/d calcium salts of palm fatty acids), 2) rumen protected CLA (120 g/d of lipid-encapsulated CLA), and 3) unprotected CLA (40 g/d unprotected CLA that replacing and balancing by Ca salts of palm fatty acids). Each dose provided 96 g/d fatty acids. Both of CLA supplements provided 12 g/d of trans-10, cis-12 CLA. Supplements were administered intraruminally once per day immediately before morning feeding. Individual milk yield and dry matter intake were recorded daily and milk composition was determined every day. Data were analyzed by MIXED procedure of SAS. Dry matter intake and milk yield were not affected by CLA supplements. The CLA supplements reduced milk fat content compared with control ($P < 0.01$), which were 2.58, 3.51, and 3.77 for rumen protected CLA, rumen unprotected CLA and control, respectively. In contrast, there were no significant differences in content of Milk protein and lactose between treatments. The milk fatty acid profile was significantly affected by rumen protected CLA. The proportion of short- and medium-chain fatty acids decreased in rumen protected CLA compared with control whereas the proportion of long-chain fatty acids increased in rumen protected CLA. The milk fat content of trans-10, cis-12 CLA was increased by CLA supplements compared with control ($P < 0.01$) especially by rumen protected CLA. The Δ^9-desaturase index was not affected by CLA supplements. The results of this experiment indicated that rumen protected CLA could decrease milk fat content and yield, and alter milk fatty acid profile, but has no effect on dry matter intake and milk yield during late lactation in Holstein dairy cows.

Key Words: conjugated linoleic acid, Holstein cow, milk fat

563 Measurement and regression models of methane emissions from sheep. Y.-G. Zhao, C.-G. Jiang, J. Liu, Y. Tu, K.-D. Deng, X.-H. Gao, and Q.-Y. Diao,* *Feed Research Institute of Chinese Academy of Agricultural Sciences, Beijing, China.*

This trial was designed to study the effects of dietary composition, nutrients intake, digestible nutrients, ruminal fermentable nutrients and volatile fatty acid (VFA) on rumen methane(CH_4) emissions from sheep and develop regression models. Eight rumen-fistulated adult crossbreed rams [Dorper (male) × Small Tail Han sheep (female)] with the body weight of (50.37 ± 1.13) kg, were used in an 8 × 4 incomplete Latin square with 8 different diets and 4 21-d periods. Eight total mixed rations (TMR) with different neutral detergent fiber (NDF) content of 51.83, 50.47, 44.58, 42.34, 38.20, 35.43, 30.10, and 27.03%, were offered to 8 sheep correspondingly and exchanged sequentially in 4 periods. The experimental duration consisted of a preliminary 8-d adaptation period followed by an 8-d period to conduct digestive trials in metabolism cages by total feces collection method and CH_4 was measured using open-circuit respiration calorimetry system with 3 sheep every 2 d, simultaneously. Nylon bags technique was used for the evaluation of ruminal fermentable nutrients with 6 different incubation times (0, 6, 12, 24, 48 and 72 h, respectively) from d 17 to d 19. Ruminal contents were taken through rumen cannulas of each sheep at 08.00 h, 14.00 h and 20.00 h on d 20 and at 02.00 h, 05.00 h, 11.00 h, 17.00 h and 23.00 h on d 21. The concentrations of VFA were measured after the liquor was strained through 4 layers of gauze. Prediction equations for CH_4 emissions were developed as linear or multiple regression models using the PROC REG of SAS software. Correlations were declared significant at $P < 0.05$. CH_4 per kg fermentable organic matter (L/kg FOM) of 8 diets was 81.64, 87.22, 77.42, 61.87, 52.19, 54.90, 57.07 and 58.72, respectively. In linear relationships, CH_4 (L/kg FOM) was negatively related to organic matter intake (OMI), gross energy intake (GEI), crude protein intake (CPI), digestible organic matter (DOM), digestible energy (DE), digestible crude protein (DCP), digestible ether extract (DEE), FOM, Butyrate/total VFA (TVFA) and Valerate/TVFA ($P < 0.05$) and positively related to NDF intake (NDFI), ADF intake (ADFI), digestible NDF (DNDF), digestible ADF (DADF), fermentable ADF (FADF), fermentable NDF (FNDF)/FOM, FADF/FOM, and Acetate/TVFA ($P < 0.05$). The relationship between methane energy (CH_4-E)/DE and DADF/DOM was CH_4-E/DE(%) = 0.17984 (±0.02178)DADF/DOM(%)+5.25136 (±0.43411) which obtained the highest R^2 (0.9191) and lowest P (0.0002) in all linear models. The multiple relationship between CH_4 and nutrients intake was CH_4 (L/kg FOM) = 0.18188 (±0.07433)OMI -0.54702(±0.09244)CPI-1.17661(±0.12692)NDFI+1.57775(±0.14902)ADFI-3.39557(±0.38786)EEI+154.94964(±40.25930) (all nutrients in kg) which increased R^2 to 0.9992 with a low P (0.0021). Multiple analysis of CH_4 and VFA resulted in CH_4 (L/kg FOM) = 0.82530(±0.10455)Acetate+4.57099(±0.30178) Propionate-7.15948(±0.30917)Butyrate-20.30966 (±1.04868)Valerate+10.49258 (±0.98749) Isovalerate+9.02963 (±5.09327) (all VFA in mmol/L) with a high R^2 (0.9989) and low P (0.0028). The results indicated that CH_4 (L/kg FOM), CH_4-E/GE and CH_4-E/DE were affected by the ratio of forage to concentrate (F:C) or dietary roughage content. In the linear regression models, NDF and ADF were more reliable than other nutrients to estimate methane emissions with higher precision. Compared with the linear regression models, the multiple regression models clearly provided a higher accuracy. Therefore, they may be useful to improve the prediction of methane emissions from sheep.

Key Words: methane, regression models, sheep

564 Response of postpartum dairy cows to contrasting feeding strategies: Grazing plus supplements versus confinement on milk and solids production. M. Sprunck[1,2], D. A. Mattiauda[1], G. Motta[1], M. Fajardo[1], and P. Chilibroste*[1], [1]*Facultad de Agronomía, Paysandú, Paysandú, Uruguay,* [2]*Agencia Nacional de Investigación e Innovación, Montevideo, Montevideo, Uruguay.*

The effect of feeding strategies involving grazing plus supplements (GS) versus confinement (TMR) on performance of early lactation Holstein dairy cows was under research. The experiment was carried out in autumn 2010 in Uruguay (30° S). Dairy cows (n=48, LW= 593 ± 94 kg and BCS = 3 ± 0.6) were randomly assigned to one of the following treatments: TMR (ad libitum; CP = 171 ± 10 g/kg of DM, NDF = 400 ± 20 g/kg of DM) and G+S with a herbage allowance of approximately 10 kg of DM/d per 100 kg of BW. Herbage chemical composition was: CP = 173 ± 31 g/kg of DM, NDF = 465 ± 65 g/kg of DM. Grazing took place on a 2nd year mix pasture (30% legumes and

70% grasses) between am and pm milking. After pm milking G+S cows were supplemented with 8.5 kg DM of TMR. The differential treatment duration was 8 weeks (2-10 postpartum) and residual measurement was until the end of lactation (week 11-30 postpartum). Cows in TMR had higher daily production of fat and protein during the first 8 weeks than cows on G+S treatments: +209 g/d and +266 g/d, respectively. G+S cows had a higher percentage of fat and a tendency to lower percentage of protein in milk. TMR cows had higher LW during the experimental period. Cows in TMR treatment results in greater solids production (kg of solids/d of fat and protein) and LW during treatment application, but differences disappear during the post-experimental period.

Table 1. Experimental period (E) and residual effects (R)

Treatment	G+S (E)	TMR (E)	P-value	G+S (R)	TMR (R)	*P*-value
L/cow per day	26.2	34.36	< 0.001	25.7	27.02	0.144
% fat	3.71	3.49	0.034	3.64	3.49	0.519
% protein	3.11	3.25	0.093	3.20	3.25	0.424
Fat (kg/d)	0.960	1.169	< 0.001	0.960	0.98	0.565
Protein (kg/d)	0.819	1.2	< 0.001	0.85	0.87	0.579
LW (kg)	558	606	0.004	572	587	0.219
Pasture intake (kg/DM)	15.6	-	-	-	-	-

Key Words: confining cows, early lactation, grazing cows

565 Effects of rumen-protected γ-aminobutyric acid on feed intake, performance and antioxidant status in transition cows. D. M. Wang*[1], C. Wang[1,2], H. Y. Liu[1], and J. X. Liu[1], [1]*Institute of Dairy Science, MoE Key laboratory of Molecular Animal Nutrition, College of Animal Sciences, Zhejiang University, Hangzhou, China,* [2]*College of Forestry and Biotechnology, Zhejiang A & F University, Lin'an, Hangzhou, China.*

The objective of this study was to investigate the effects of unprotected and rumen-protected γ-aminobutyric acid (GABA) addition on dry matter intake, energy balance, milk performance, and serum metabolites in transition cows. Forty cows were blocked based on previous milk production, parity, estimated calving date and body weight, and randomly assigned to one of 4 treatments: added with unprotected GABA (0 or 0.6 g/d) or rumen-protected GABA (1.2 or 2.4 g/d), respectively. The rumen-protected product was 50% GABA. The experiment lasted from 2nd week before calving to 4th week after calving. Milk yield and milk composition were recorded weekly. Serum concentrations of GABA, neuropeptide Y, cholecystokinin, leptin and biochemical and antioxidant metabolites were analyzed weekly. All the data were analyzed using the PROC MIXED of SAS with cow as the repeated subject using the covariance type AR (1). The model included week, treatment, and interaction of treatment × week. In 3rd and 4th weeks after calving, dry matter intake was higher ($P < 0.05$) in the cows fed 2.4 rumen-protected GABA, compared with that of the control. In 4th week after calving, milk protein yield was higher ($P < 0.05$) in the cows fed 2.4 g/d rumen-protected GABA than that of the control. No significances were observed in the serum concentrations of GABA, neuropeptide Y and leptin among all the treatments, while cholecystokinin concentrations decreased ($P < 0.05$) in cows fed 2.4 g/d rumen-protected GABA in 3rd and 4th weeks after calving. Serum concentrations of total antioxidant capacity, glutathione peroxidase and superoxide dismutase were not different among cows fed rumen-protected GABA. In conclusion, addition of rumen-protected GABA at 2.4 g/d could increase feed intake, improve milk protein yield, and be beneficial to postpartum dairy cows′ health.

Key Words: γ-aminobutyric acid, dry matter intake, transition cows

566 Productive performance by lactating cows fed with different levels of Palm kernel cake. R. L. Oliveira*[1], R. L. N. Vaz Silva[2], A. C. Ferreira[1], A. G. Leão[1], M. C. A. Santana[1], A. A. Pinheiro[1], O. L. Ribeiro[1], and L. F. B. Pinto[1], [1]*Universidade Federal da Bahia, Salvador, BA, Brazil,* [2]*Instituto Federal Baiano, Catu, BA, Brazil.*

With the objective of verifying the most appropriate level of inclusion of palm kernel cake in a dietary supplement for lactating cows on pasture, 16 multiparous dairy cows of the Holstein x Gir crossbreed, with an average weight of 436.6 kg (±59.7), were used. The experiment was conducted at the Experimental Farm of the Federal University of Bahia, Brazil, during August to October 2009. A Latin square design was utilizes, with the cows distributed in 4 Latin squares, 4 × 4 simultaneous (4 treatments × 4 periods × 4 animals in each treatment), data were analyzed using the GLM (General Linear Models) and REG (Regression). The growth performance was evaluated for the cows at pasture that were provided with a dietary supplement that contained levels of 0%, 25%, 50% and 75% of palm kernel cake. The available forage was *Panicum maximum* ‘Massai’. A decrease in the intake of the supplement was observed (R2 = 0.84, $P < 0.05$), however, the milk production and the body condition of the cows were not influenced by the levels of palm kernel cake within the supplement. The milk production and the milk production corrected for 3.5% fat (9.96 and 9.56 kg/day, respectively) can be considered normal for crossbred dairy herds in north-eastern Brazil, these values are associated with a lower degree of specialization of the experimental herd due to their low genetic potential. The body condition of the cows was not altered with the inclusion of palm kernel cake at increasing levels, as the intake of dry matter and total digestible nutrients was not suppressed and the observed body condition score mean (2.88) was close to that which would be expected (3.0 to 3.5), because the dairy farming techniques are demanding on the animals. This indicates that the nutritional requirements were met and that there was a significant mobilization of body energy reserves to produce milk. The low cost of the ingredient and the absence of the restrictive effects on the milk production and the body condition of the cows suggest that palm kernel cake is a suitable co-product for supplements designed for lactating cows at pasture, especially in scenarios of low income per kilogram of milk produced.

Key Words: co-product, milk, pasture

567 Effect of ruminal adaptation on short-chain fatty acid absorption and risk for ruminal acidosis. T. Schwaiger*[1,2], K. A. Beauchemin[2], and G. B. Penner[1], [1]*University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Lethbridge Research Center, Lethbridge, AB, Canada.*

This study was conducted to determine if the duration of time that cattle are fed a high-grain diet affects short-chain fatty acid (SCFA) absorption and susceptibility to ruminal acidosis. Sixteen Angus heifers (BW ± SEM, 261 ± 6.1 kg) were assigned to 4 blocks, and fed a backgrounding diet consisting of 60% barley silage, 30% barley grain and 10% supplement (DM basis). Cattle were then adapted, over 20 d, to a high-grain diet containing 9% barley silage, 81% barley grain and 10% supplement (DM basis). Within block, cattle were randomly assigned to 1 of 2 treatments differing in the number of days they were fed the high-grain diet before an acidosis challenge: 34 d for long adapted (LA) and 8 d for short adapted (SA). Ruminal acidosis was induced by withholding feed to 50% of DMI for 24 h followed by an intraruminal infusion of ground barley at 0.33% BW on a DM basis. Cows were then given their regular diet allocation 1 h after the intraruminal infusion. Data were collected during the baseline period, following the acidosis challenge and after 1 wk of recovery. Absorption of SCFA was measured using the isolated washed reticulo-rumen technique. LA animals had greater fractional absorption rates of propionate (41.6 vs. 33.8%/h; $P = 0.032$) and butyrate (44.9 vs. 35.2%/h; $P = 0.012$) compared with SA animals. In addition, LA animals also had greater absolute butyrate absorption (94.9 vs. 76.9 m*M*/h; $P = 0.048$). Absolute and fractional absorption of all individual SCFA increased during the recovery period ($P \leq 0.050$) relative to the challenge, except for fractional acetate absorption, which only tended to increase ($P = 0.089$). Mean and minimum pH both increased during the recovery period ($P < 0.001$) while daily duration and area that pH <5.5 both decreased during the same time period ($P < 0.001$). There were no treatment differences for pH, DMI, or ruminal fluid SCFA concentrations. This study suggests that increasing the duration that cattle are fed a high-grain diet increases SCFA absorption, without affecting susceptibility to ruminal acidosis.

Key Words: diet adaptation, ruminal acidosis, short-chain fatty acid

568 Effect of simultaneous reduction of ruminally degradable protein and ruminally undegradable protein in dairy cattle. M. Aguilar* and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg.*

Previous studies have shown that RDP and RUP (Cyriac et al., 2008; Rius et al., 2010) can be reduced independently below NRC requirements, with no effect on milk production or animal health, suggesting requirements may exceed true needs. However, because some RDP requirement is met by urea recycling which is dependent on overall protein supply, reducing both RDP and RUP simultaneously could induce an RDP deficiency. We hypothesized that dairy cattle may be able to maintain performance when fed a combination of sub-NRC requirement levels of RUP and RDP. Thirty-six mid-lactation dairy cows (24 Holstein and 12 Jersey × Holstein cross-breds) were fed diets containing sufficient or deficient amounts of RDP and RUP in a 2 × 2 factorial arrangement within a 4 × 4 Latin Square design with 3-wk periods. Diets were formulated to contain 16.5, 15.75, or 15.0% CP (DM basis) with RUP and RDP balances of +57 and +58 g/d (High-RUP/High-RDP, 16.5% CP); +42 and −209 g/d (High-RUP/Low-RDP, 15.75% CP); −133 and +61 g/d (Low-RUP/High-RDP, 15.75% CP); or −182 and −186 g/d (Low-RUP/Low-RDP, 15.0% CP), respectively. All diets contained 46.8% forage and 53.2% concentrate on a DM basis. Milk yield and composition were measured and urinary purine output was calculated from urinary concentrations of allantoin and uric acid. Treatment had no effect on DMI, milk production, milk protein, lactose, or fat yield. Diets containing low levels of RUP had significantly reduced MUN and urinary urea N levels as compared with diets with higher RUP levels. Urinary N excretion was significantly reduced in the Low-RUP/Low-RDP diet. Microbial N flow, calculated from urinary purine derivatives, was not significantly affected by treatment. Reduced levels of dietary RUP and RDP reduced N excretion and improved N efficiency without altering microbial outflow.

Key Words: ruminally degradable protein, ruminally undegradable protein, nitrogen requirement

569 Effects of dietary forage-to-concentrate ratio and sulfur concentration on ruminal fermentation and sulfur metabolism in feedlot heifers. S. Amat,* J. J. McKinnon, G. B. Penner, E. Simko, and S. Hendrick, *University of Saskatchewan, Saskatoon, SK, Canada.*

This study was conducted to evaluate the effects of the dietary forage-to-concentrate ratio (F:C) and S concentration on ruminal fermentation, S metabolism, short chain fatty acid (SCFA) absorption, and histopathological changes suggestive of polioencephalomalacia (PEM) in the brain. Sixteen ruminally cannulated heifers (initial BW 628 ± 48 kg) were used in a randomized complete block with a 2 × 2 factorial treatment arrangement. Main factors included the F:C ratio (4% forage vs. 51% forage, DM basis), and the S concentration which was modified using differing sources of wheat dried distillers grains with solubles (DDGS) to achieve low and high S diets (LS = 0.30 vs. HS = 0.67% S DM basis, respectively). Elemental S was also added to increase the S content for the HS diets. Blood, rumen gas cap and urine samples were collected for serum sulfate, H_2S, and urinary sulfate analysis, respectively. Continuous rumen pH and SCFA (acetate, butyrate and propionate) absorption were measured. At the end of the study, heifers were euthanized and brain tissue was subjected to histopathological analysis. There were no interactions between the F:C and S concentration. The F:C did not ($P = 0.871$) affect DMI or ($P > 0.05$) S metabolism but ruminal pH was reduced ($P < 0.01$) and SCFA was greater ($P < 0.01$) for low-forage diets. Cows fed HS diets had reduced DMI ($P < 0.01$), greater rumen pH ($P < 0.01$) and greater concentrations of ruminal H_2S ($P < 0.01$), serum sulfate ($P < 0.01$), and urinary sulfate ($P < 0.01$) relative to low S diets. Ruminal H_2S was positively correlated with serum sulfate (r = 0.89; $P < 0.01$). Feeding HS diets reduced SCFA absorption ($P \leq 0.05$). No macroscopic or microscopic changes were detected in the brains of the heifers. In summary, S metabolism in feedlot heifers was not influenced by different F:C, but HS reduced DMI and inhibited SCFA absorption.

Key Words: DDGS, short chain fatty acids, sulfur metabolism

570 Intake, digestibility and microbial protein synthesis in heifers fed pasture, total mixed ration or both. A. Santana*[1], A. Perez-Ruchel[2], C. Cajarville[2], and J. L. Repetto[1], [1]*Facultad de Veterinaria, UdelaR, Depto. Bovinos, Montevideo, Uruguay,* [2]*Facultad de Veterinaria, UdelaR, Depto. Nutrición, Montevideo, Uruguay.*

We evaluated the intake and digestibility of dry matter (DM), organic matter (OM) and nitrogen (N), microbial protein synthesis (MPS), efficiency of microbial protein synthesis (EMPS) and nitrogen efficiency for MPS (NEMPS), in heifers. Nine individually housed cross-breed heifers (214 ± 18kg BW) were ad libitum fed total mixed ration based on sorghum plant silage, soybean meal, corn high moisture silage and dry corn, (TMR), fresh forage, cut daily from a temperate pasture (*Trifolium repens* and *Lolium multiflorum*) (PA) or TMR for 18h plus 6h pasture (TMR-PA) in a latin square design of 3 × 3 triplicate. Each experimental period consisted in 10d of adaptation and 8d for sampling. Intake was individually determined during 8d as the difference between offered and rejected food. Total feces and urine excretion were measured during 5d. The results are shown in the Table below. The TMR- PA presented similar intake, MPS, EMPS and NEMPS than TMR, being the intake of DM and OM and MPS of PA the lowest. There were no differences in DM and OM digestibility between treatments. Pasture addition for 6h allowed to maintain nutrient ingestion and did not affect microbial protein synthesis regarding to TMR.

Table 1.

	TMR	TMR-PA	PA	SEM	*P*-value
Intake, kg/d					
DM	5.99^{ab}	7.36^{a}	5.49^{b}	0.56	0.042
OM	5.84^{ab}	7.02^{a}	5.13^{b}	0.55	0.040
N	0.58	0.77	0.73	0.06	0.144
Digestibility, %					
DM	66.5	71.1	73.2	2.35	0.166
OM	71.6	74.2	75.4	1.70	0.329
N	61.1^{b}	69.8^{ab}	77.3a	2.38	0.003
MPS and efficiency[1]					
MPS, gmN/d	100.6^{a}	105.6^{a}	64.9b	8.9	0.018
EMPS, gmN/kg DOMI	39.8^{a}	24.7^{ab}	20.9b	5.2	0.053
NEMPS, gmN/gN intake	0.24^{a}	0.16^{ab}	0.10b	0.03	0.052

[1] MPS = microbial protein synthesis; gmN = g of microbial N/d; DOMI = digestible OM intake; EMPS = efficiency of MPS; NEMPS = N efficiency for MPS.

Key Words: feeding systems, fresh forage, ruminant

571 A technology that enhances the utilization of low quality forages in ruminant animals.

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Effects of various levels (0, 1, 2 and 3 g/L) of *Saccharomyces cerevisiae* fermentation product (YC; Diamond V XP) on ruminal fermentation of major forage sources of China (rice straw, corn stover, corn silage with grain and corn silage without grain) were examined in an in vitro study with a 4 × 4 factorial arrangement of treatments. Rumen fluid was collected from 3 rumen cannulated Hu sheep fed a diet consisting of lucerne hay and concentrate mixture (50:50) twice daily. Gas pressure measurements were recorded at 3, 6, 9, 12, 24 and 48 h of incubation and then converted to gas volume. Ammonia N, pH, volatile fatty acids (VFA), and microbial crude protein (MCP) were determined at 12, 24 and 48 h. Microbial population was examined at 24 h incubation. Data were analyzed using the GLM procedure of SAS. Terminal pH varied within normal range (6.53 to 6.96) regardless of treatment or substrate. The YC showed inconsistent effect on ammonia N (8.0 to 23.1 mg/dL) with different substrates. Gas production reached peak at 2 g/L YC for rice straw and corn silage without grain, while reached peak at 1 g/L YC for corn stover and corn silage with grain. Total VFA concentration (mmol/L) at 24 h tended to increase with 1 and 2 g/L YC for rice straw, while increased ($P < 0.05$) with 1 g/L YC for corn silage with grain, 1 and 2 g/L YC for corn silage without grain, and 3 g/L YC for corn stover. Acetate, propionate and butyrate concentrations followed similar trend as total VFA. The MCP (mg/mL) increased ($P < 0.05$) with increasing level of YC at 24 h for rice straw. For corn silage without grain, MCP increased ($P < 0.05$) with 1 and 2 g/L YC at 12 h, became insignificant at 24 h, then increased ($P < 0.05$) again with all additional levels at 48 h. For corn silage with grain, 2 g/L YC increased ($P < 0.05$) MCP at 12 h, while 1 g/L YC showed the highest ($P < 0.05$) response at 24 h. Fungi population was increased ($P < 0.05$) with 1 g/L YC for all forages but corn silage without grain. Addition of YC also increased ($P < 0.05$) the percentages of protozoa, *Fibrobacter succinogenes*, *Ruminococcus albus* and *R. flavefaciens*. Although the optimum level of YC for different parameters varies depends on forage substrate and incubation time, rumen fungi was enhanced and VFA and MCP were increased with a stable rumen pH when the YC was added at a level of 1 or 2 g/L. It is suggested that addition of YC can improve the ruminal microbial utilization of low quality forages.

Key Words: forage, rumen fermentation, yeast culture

572 In vitro manipulation of Jersey cow rumen ecology with microbes from the wildebeest, horse and zebra.

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Ruminal microbes have the ability to convert low quality feeds into high quality protein and to utilize feeds (roughage) from land not suitable to grow crops for human consumption. Only 10–35% of energy intake is captured as net energy while 20–70% of cellulose may not be digested by herbivores. There is need to increase the amount of energy harvested by ruminant systems without necessarily increasing intake. The objective of the study was to compare fiber breakdown by microbes from the cow (CW) system (A) to its composite systems with the horse (H), wildebeest (WB) and Zebra (ZB). Four in vitro composite enzyme systems B (CW and H), C (CW and WB), D (CW and ZB) and E (CW, H, WB and ZB) were created. Exocellulase, endocellulase, xylanase and cellobiase specific activities of these systems upon incubation with cellulose, carboxymethyl cellulose (CM), xylan and cellobiose, respectively were determined by measuring the amount of reducing sugars released. The catalytic efficiency (Kcat) of the enzymes was also determined. In vitro microbial fermentation and degradability of maize stover (MS) and NDF with inocula from the 4 systems over 72 h at 39°C were determined by measuring the amount of gas released and true degradability (TD). Systems E (Kcat = 17.1 ± 1.28) and B (Kcat = 8.5 ± 1.28) were the most active ($P < 0.05$) enzyme systems upon incubation with cellulose with specific activity 9.6 ± 0.05 and 4.5 ± 0.05 µg glucose/mg/min, respectively. Upon incubation with CM, system B (Kcat = 15.4 ± 0.40) was more active ($P < 0.05$) than E (Kcat = 9.5 ± 0.40). Xylan hydrolysis was highest ($P < 0.05$) in E and D while B and C were intermediate. Gas released during MS fermentation was highest ($P < 0.05$) in system C (141 ± 9.9 mL) and intermediate in systems B, D and E(135 ± 0.4, 133 ± 0.4 and 134 ± 0.4 mL, respectively). MS fermentation was higher in B(694 ± 38.4 kg) and E(695 ± 38.4 kg) with gas volumes of 128 ± 58.1 and 118.62 ± 58.1 mL, respectively. TD of NDF showed that system D(709 ± 32.1 kg) and E(700 ± 0.4032.1 kg) were the most active ($P < 0.05$). These results suggest that mixing microbes from horses, wildebeest and zebras can improve the fibrolytic potential and digestion of roughages in cattle.

Key Words: exocellulase, in vitro fermentation, roughage digestibility

573 Growth curve analysis of Sahiwal calves up to six-month age given milk or milk replacer up to weaning.

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Data of 2 feeding trials were used to understand the growth patterns of Sahiwal calves fed different dietary treatments up to weaning and then a single treatment during post-weaning period. The objective of this study was to predict body weight changes of Sahiwal calves up to 6-mo of age. The 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 given following dietary treatments up to weaning: A) whole cow milk + starter ration (SR; CP = 20%, TDN = 72%) + Berseem clover hay (H; *Trifolium alexandrinum*; CP = 21% TDN = 63%); B) whole cow' milk + H; C)

Milk replacer (MR) + SR + H and D) MR + H. Milk or MR was offered at 10% of the body weight until d 56 and then gradually withdrawn until calves were weaned completely by d 84. The SR and H continued until d 84. During post-weaning period the calves were fed ad libitum a single mixed ration containing 16% CP and 70% TDN, from wk 13 to 24. Body weights were recorded weekly. Gompertz, Exponential, 3-degree Polynomial, Logistic and Sinusoidal models, using CurveExpert software, were tested to predict body weight during the experimental period. All the models explained variation in growth of Sahiwal calves reasonably well; R^2 ranged from 91.9 to 97.9% for individual treatments and 89.4 to 89.5% on overall basis. Female calves, on average, had 3% better fit than male calves (92 vs 89%). Growth curves of milk-fed and MR-fed calves had R^2 93.1 and 89.4%, respectively. Any of the 5 tested models may be used to predict first 6-mo growth pattern in Sahiwal calves with almost equal efficiency.

Key Words: computational models, growth curve, Sahiwal calves

Small Ruminant Symposium: Novel Uses of Natural Bioactive Compounds in Small Ruminant Production and Future Directions

574 Bioactive compounds and their mode of action in forage-fed ruminants. T. N. Barry,* *Massey University, Palmerston North, New Zealand.*

Bioactive compounds are generally secondary compounds and include lignin (all forages), condensed tannins (lotus, sulla and sainfoin), sesquiterpene lactones (chicory), endophyte alkaloids (perennial ryegrass and fescue), S-methyl cysteine sulphoxide (SMCO) and glucosinolates (brassica plants). They have all evolved as part of the plant's defense mechanism, to protect against microbial attack and being eaten by insects and herbivores. Hence high concentrations of all these compounds are associated with reduced voluntary feed intake (VFI) by ruminants and with animal health effects for SMCO (anemia) and endophyte alkaloids (staggers). Condensed tannins (CT) react reversibly with forage proteins, reducing protein degradation in the rumen and for some forages increasing the absorption of essential amino acids (EAA) from the small intestine, depending on the concentration and structure of the CT. For CT such as *Lotus corniculatus* beneficial effects are seen at 20–40 g/kg DM with no depression in VFI. For CT in this range that increase EAA absorption beneficial effects are reduced bloat in cattle, increased wool growth, ovulation rate, lactation performance, reduced parasite problems in sheep and reduced methane production. Methodology has just been published to induce CT production in legumes containing only traces of CT (white clover). Chicory is a herb that disintegrates rapidly in the rumen, has rapid rumen clearance, high VFI and promotes good growth in grazing ruminants. Young sheep and deer grazing chicory have reduced need for oral anthelmintics and part of this anthelmintic effect is due to its content of sesquiterpene lactones and to low levels of CT. Forages containing bioactive compounds can be used in sustainable grazing systems.

Key Words: bioactive plant secondary compounds, chicory, condensed tannins

575 Consequences of plant secondary compounds on ruminant nutrition. B. R. Min* and S. Solaiman, *Department of Agricultural and Environmental Sciences, Tuskegee University, Tuskegee, AL.*

Plant secondary compounds are varied in nature but are characterized by hydroxylated aromatic rings (e.g., flavan-3-ols). They are considered as secondary metabolites, and their nutritional aspects in ruminants are often poorly understood. This paper mainly considers 2 classes of plant secondary compounds in this context, i.e., proanthocyanidins (condensed tannins; CT) and hydrolysable tannins (HT) and their effect on rumen environment and animal nutrition. The CT are prevalent in browse materials and are expressed in the foliage of some legumes, but rarely in grasses. The HT are present in oak (*Quercus* spp.), Acacia, Eucalyptus and a range of browse and tree leaves. Nutritionists and researchers continue to define dietary CT and HT in terms of concentration, as well as either beneficial or detrimental effects on ruminant animals. Beneficial effects are dependent on the chemical and physical structure, and concentration of the CT and HT in the diet. The HT may be toxic because products of their metabolism can cause liver damage and other metabolic disorders. However, the CT, when present in diet at a proper level (2 to 4% DM) can exert beneficial effects on protein, and minerals metabolism; blood parameters; rumen fermentation (VFA and ammonia production); rumen and fecal microbial populations; feed efficiency; and overall animal performance. Dietary CT may also contribute to animal health by preventing the risk of frothy bloat in cattle. In contrast, high dietary CT concentrations (>5% DM) depress feed intake, digestive efficiency, and animal productivity. From the biochemical standpoint, CT have a wide range of biological activities and enormous potential for uses in livestock industry which requires in-depth investigation and evaluation in the perspective ruminant production systems. Future research should identify optimum level and chemical structures for expression in the high-quality diets to be offered as extract or mixed with grasses or with legumes. Animal feeding systems will be empowered by the choice of variety and concentration of CT in the diet. The potential of novel secondary compound plant sources for use in animal production warrants further investigation.

Key Words: plant secondary compounds, ruminants, tannins

576 Bioactive compounds for control of internal parasites. T. H. Terrill,* *Fort Valley State University, Fort Valley, GA.*

Livestock producers have used nutraceutical plants to improve health and productivity of their animals for several millennia. A large number of bioactive secondary plant metabolites with activity against gastrointestinal nematodes (GIN) of livestock have been identified, including alkaloids, terpenes, and various phenolics, although relatively few plants have been validated scientifically as anti-parasitic. A class of phenolic bioactive compounds for which there is a growing body of evidence for anti-parasitic properties in the diet of ruminants is condensed tannins (CT). Recent work with tropical and temperate CT-containing forages and CT extracts in a series of in vitro and in vivo studies have greatly expanded the scientific knowledge base on use of these compounds to control GIN of livestock. Evidence for these effects has been both direct and indirect. Direct effects of CT on all phases of the GIN life cycle (eggs, larvae, adults) have been reported, although for the most part, determining the exact mechanism of action has remained an elusive target. There have also been reports of indirect effects of certain types and concentrations of CT in the diet improving host resilience and resistance to GIN infection by improving the animal′s nutritional status and immune function. The anti-parasitic efficacy of CT-containing forage/browse in animal diets is likely due to a combination of direct and indirect effects and can vary greatly, depending upon the form of feed (fresh versus dried), CT astringency and concentration in extractable and bound forms, previous exposure to CT-containing plants, seasonal effects, animal age, and the parasite and host species involved. Nevertheless, there appears to be great potential for increased use of bioactive compounds as anti-parasitic agents in livestock production systems in the future.

Key Words: bioactive compounds, condensed tannins, gastrointestinal nematodes

577 Emerging opportunities and challenges on exploitation of bioactive plant secondary compounds to mitigate environmental impacts by ruminants. J.-S. Eun*[1] and B. R. Min[2], [1]*Utah State University, Logan,* [2]*Tuskegee University, Tuskegee, AL.*

Greenhouse gas (GHG) emissions from livestock and their impacts on climate changes are a major concern worldwide. It has been reported that enteric methane is the most important GHG emitted (50 to 60%), at the farm scale, in ruminant production systems. Methane represents also a significant energy loss to the animal ranging from 2 to 12% of gross energy intake. Therefore, mitigating the production of enteric methane from ruminants without altering animal production is desirable both as a strategy to reduce global GHG emissions and as a means of improving feed efficiency. Some of plant secondary compounds (PSC) such as tannins and polyphenols play key roles in animal health, quality of animal products, mitigation of GHG emissions, and efficiency of N use by ruminants. However, the beneficial effects on methane production and N utilization efficiency have not been consistently observed. The discrepancies among different studies in response to feeding PSC-containing forages or supplementing PSC extracts are attributed to the different chemical structures and concentrations of PSC and type of diets. For example, reliable and distinguishable effects of tannins on methane reduction can be expected only from levels >20 g/kg DM, a threshold often not exceeded in current commercial feed supplementation with tannins. Hence, the challenge is to identify PSC sources that can be feasibly added to the diet in a cost effective manner that also result in a net reduction in GHG emissions. Measurements with in vitro culture systems could provide an inexpensive starting point for screening of potential PSC, whereas individual promising PSC need to be investigated in detail in vivo. Different PSC exert their characteristic effects on ruminal fermentation in association with the inhibition of methanogenesis; however, their ultimate impacts on environmental performance by ruminants should be assessed on the amount of emissions/kg of livestock product.

Key Words: greenhouse gas emissions, methane, bioactive plant secondary compounds

578 Bioactive plant compounds and food safety. R. C. Anderson,* *Southern Plains Agricultural Research Center, United States Department of Agriculture/Agricultural Research Service, College Station, TX.*

The gut of food-producing animals is a reservoir for human pathogens such as *Salmonella*, *Campylobacter*, *Clostridium*, *Listeria*, enterohemorrhagic *Escherichia coli* as well as other commensal and pathogenic bacteria expressing important antimicrobial resistance traits. Food producers recognize a need to continuously develop new technologies that effectively minimize contamination of foods and may be used as alternatives to antibiotics at risk from regulatory restrictions. In the search for new interventions, the use of functionally bioactive plant compounds may be viewed favorably as many of these are generally recognized as safe (GRAS). Essential oils extracted from several different plant species have been shown to exhibit broad spectrum bactericidal activity against gram-negative and gram-positive foodborne pathogens, purportedly by disrupting bacterial cell wall integrity. The antimicrobial activity of tannin-derived compounds against a variety of bacteria has also been demonstrated. In the case of hydrolysable tannins such as tannic acid, bacterial growth is inhibited by chelation of iron thus reducing its availability. The mechanisms by which condensed tannins inhibit bacterial growth are less clear and have been proposed to be due to cell wall disruption or binding of proteins, enzymes or amino acids. The antimicrobial activity of hop extracts rich in lupulones has also been demonstrated against certain amino acid-fermenting bacteria such as *Campylobacter*, presumably by exhibiting an ionophore-like effect. While most commonly associated with yeast cell wall products, oligosaccharides produced in certain forestry products are now being explored for their ability to prevent gut colonization mediated by mannose-specific binding by *Salmonella* and *E. coli*. Whereas results from in vitro studies have shown good efficacy, often yielding several log-fold reductions in bacterial numbers, results from animal studies have been less conclusive, possibly because of their absorption or degradation in the stomach or proximal small intestine. Clearly, more research is needed to better understand how to fully harness the biological activity of these compounds.

Key Words: antimicrobial resistance, bioactive plant compounds, foodborne pathogens

Swine Species

579 Industry productivity analysis: Grow-finish traits. C. E. Hostetler*[1] and M. T. Knauer[2], *[1]National Pork Board, Des Moines, IA, [2]North Carolina State University, Raleigh*

The objective of this study was to quantify US swine production benchmarks and trends for nursery and finishing traits from a representative database. Data were provided by a data management company representing approximately 1.8 million sows in North America. Production records were available from 2005 to 2010. Nursery and finishing traits included entry age, entry weight, exit age, exit weight, ADG, G:F, caloric efficiency (kcal:kg) and mortality. Nursery and finishing kcal:kg were standardized from 5.4 to 22.7 kg and 22.7 to 118 kg, respectively. Data were analyzed in SAS using PROC MIXED. Models included year and month as fixed effects. Standard errors for nursery entry age, entry weight, exit age, exit weight, ADG, G:F, kcal:kg and mortality were 0.11, 0.026, 0.22, 0.09, 0.0041, 0.0031, 38.6 and 0.19, respectively. Standard errors for finishing exit age, exit weight, ADG, G:F, kcal:kg and mortality were 0.5, 0.41, 0.007, 0.0015, 79.4, 0.34, respectively. Nursery entry age and weight increased ($P < 0.05$) from 2005 to 2010 (19.2 to 20.5 d and 5.53 to 5.85 kg, respectively). Nursery exit age decreased ($P < 0.05$) from 68.3 to 67.1 d and exit weight increased ($P < 0.05$) from 22.7 to 23.4 kg. Finishing exit age decreased ($P < 0.05$) from 191 to 190 d and exit weight increased ($P < 0.05$) from 117.7 to 119.9 kg. Means for ADG, G:F, kcal:kg and mortality are shown by year in Table 1. Finishing ADG increased ($P < 0.05$) and mortality decreased ($P < 0.05$) indicating more weight sold in a fixed amount of time. However, finishing kcal:kg did not differ ($P > 0.05$) between 2005 and 2010. Both producers and scientists can use these grow-finish benchmarks to better understand swine industry trends.

Table 1. Grow-finish means for ADG, G:F, kcal:kg, and mortality

	Year					
Trait	2005	2006	2007	2008	2009	2010
Nursery						
ADG, kg	0.367^{ab}	0.362^{a}	0.359^{a}	0.364^{a}	0.374^{b}	0.382^{c}
G:F	0.637^{c}	0.645^{b}	0.644^{b}	0.632^{c}	0.652^{a}	0.655^{a}
Kcal:kg	5183^{c}	5267^{d}	5218^{cd}	5227^{cd}	5042^{b}	4903^{a}
Mortality, %	4.6^{a}	4.4^{a}	4.4^{a}	5.9^{c}	5.2^{b}	5.0^{b}
Finishing						
ADG, kg	0.73^{a}	0.76^{b}	0.80^{c}	0.79^{c}	0.80^{c}	0.80^{c}
G:F	0.354^{d}	0.361^{b}	0.361^{ab}	0.357^{c}	0.364^{a}	0.364^{ab}
Kcal:kg	9399^{bc}	9358^{abc}	9231^{a}	9216^{a}	9257^{ab}	9464^{c}
Mortality, %	6.7^{de}	6.3^{cd}	7.1^{e}	5.9^{bc}	5.4^{ab}	5.2^{a}

$^{a–e}$Means within a row with different subscripts differ ($P < 0.05$).

Key Words: benchmark, finishing, nursery

580 Periweaning failure to thrive syndrome in nursery pigs is associated with gastrointestinal lesions, but not enteric pathogens. C. K. Jones,* D. M. Madson, R. G. Main, N. K. Gabler, and J. F. Patience, *Iowa State University, Ames.*

Periweaning failure to thrive syndrome (PFTS) has challenged both the profitability and welfare of the US pork industry in recent years. However, it is unknown if PFTS is associated with increased disease incidence. Our objective was to determine if light birth weight (BRW) pigs or those from the bottom 10th percentile of transition ADG (tADG) have a higher incidence of gastrointestinal lesions and enteric pathogen presence compared with their heavier or faster-growing contemporaries. A total of 1,500 pigs were weighed at birth and divided into 5 BRW categories: <1 kg, 1–1.25 kg, 1.25–1.5 kg, 1.5–1.75 kg, >1.75 kg. At weaning, 1,054 randomly selected pigs were moved to a commercial wean-to-finish barn. Pigs were weighed individually at 0, 3, 6, and 22-weeks post-weaning. Gain from 0 to 3 weeks post-weaning was calculated and termed tADG. Pigs from 3 tADG percentiles were of interest: 10th, 30th, and 70th. Forty pigs from each of the 3 tADG percentiles were matched for sex, litter size, and sow parity, but not BRW to create 20 matched sets of 60 total pigs. This allowed for the main effects of BRW and tADG to be studied as a 5 × 3 factorial design. At 3-weeks post-weaning, pigs were necropsied and lesions on the gastrointestinal tract and other organ systems were characterized. Lung, lymph node, and fecal samples were analyzed for presence of various pathogens by PCR. Colon samples were cultured for *E. coli* and *Salmonella* spp. Data were analyzed using PROC GLIMMIX, where pig served as the experimental unit. The fixed effects were BRW and tADG; and the random effect was matched set. There were no BRW × tADG interactions ($P > 0.16$). Presence of lesions decreased linearly with increasing tADG in the large intestine ($P = 0.03$; 62, 55, 26% for 10th, 30th, and 70th percentiles, respectively) and total gastrointestinal tract ($P = 0.05$). However, tADG was not associated with increased incidence of pathogens ($P > 0.44$). Increasing birth weight was associated with a linear decrease in stomach lesion presence ($P = 0.05$; 29, 10, 15, 0, 0% for <1 kg, 1–1.25 kg, 1.25–1.5 kg, 1.5–1.75 kg, >1.75 kg, respectively), and was quadratically associated with the presence of *Salmonella* spp. ($P = 0.02$; 43, 10, 15, 40, 63% for <1 kg, 1–1.25 kg, 1.25–1.5 kg, 1.5–1.75 kg, >1.75 kg, respectively). In summary, PFTS appears to be associated with increased gastrointestinal lesions, but not with the presence of enteric pathogens.

Key Words: enteric disease, pig, periweaning failure to thrive

581 Umbilical vein blood-oxygen relationship with pre-weaning growth in piglets. E. A. Hale*[1], T. J. Safranski[1], M. C. Lucy[1], J. N. Rhoades[1], J. W. Ross[2], N. K. Gabler[2], R. P. Rhoads[3], and L. H. Baumgard[2], *[1]University of Missouri, Columbia, [2]Iowa State University, Ames, [3]Virginia Tech, Blacksburg.*

Management techniques to improve piglets′ chances of surviving are common, but North American farms still lose nearly 20% of piglets as stillborns plus pre-weaning mortalities. This project was to characterize the range in blood-oxygen levels in neonatal piglets and its effects on viability and growth. A group of 23 parity-one Large White × Landrace sows were monitored for 24h daily over one week beginning at the time the first sow was due and ending when the last sow farrowed. Each piglet was caught at birth and dried. A 3mL blood sample was taken from the umbilical vein and the sample ran through an IRMA blood analyzer. At birth piglet weight and rectal, rump, and back temperatures were recorded. After approximately 5 min under a heat lamp the piglets were placed at the udder to nurse. Piglets were weighed again at 2 h and 24h post birth and at weaning around 21d. All piglet processing was one day after farrowing. Of the total 264 piglets born alive, blood samples were obtained from 137 piglets (52%). Of the 264 piglets, 12 pre-wean mortalities were recorded, only 3 of which were successfully blood sampled. Birth order of all piglets in their respective litter was recorded. For analyses piglets with a 2 h weight change exceeding 400 g were excluded as were arterial samples resulting in 126 records. Weight changes at 2 h and 24 h as well as pre-weaning ADG were fitted to a least squares regression model including rectal temperature and weight at birth and birth order with dam fitted as a random effect. Two-hour weight change was affected by birth order; piglets born later in the litter gained less weight. No model effects affected 24hr weight change. Pre-weaning average daily gain was increased in piglets having higher blood oxygen or rectal temperatures at birth and unaffected by birth order. The low pre-weaning mortality precludes meaningful analyses of the effect of blood gas on this variable. While surprising that neonatal growth was affected by birth order and not blood oxygen at birth, the effect of the latter on subsequent growth is intriguing and implies a long-term impact on the physiology of the pig. Supported by USDA NIFA #2011–67003–30007

Key Words: neonatal growth, blood oxygen, piglet viability

582 Breed difference of porcine sirtuin 1 and its regulation by insulin. Y. Ren,* T. Z. Shan, L. N. Zhu, J. Huang, and Y. Z. Wang, *Institute of Animal Science, Zhejiang University, Key Laboratory of Molecular Animal Nutrition, Ministry of Education, Key Laboratory of Feed and Animal Nutrition of Zhejiang Province, Hangzhou, Zhejiang Province, China.*

Sirtuin 1 (*Sirt1*) plays an important role in insulin signaling pathway especially insulin sensitive organs. However, there were few data about the differences of *Sirt1* expression between fatty breed and lean breed of pigs. Furthermore, whether insulin could feedback or regulate the expression of *Sirt1* is unclear. Therefore, in the current study, the breed difference and the expression pattern of *Sirt1*, as well as key lipid metabolism enzyme adipose triglyceride lipase (*ATGL*) and hormone sensitive lipase (*HSL*), in adipose tissue, liver and pancreas between Jinhua pigs (a local fatty breed of China) and Landrace (a leaner breed) were investigated. In addition, the effect of insulin on gene expression of *Sirt1*, *ATGL* and *HSL* in fat metabolism was also studied in vitro. Results showed that at the age of 180 d, the body fat content of Jinhua pigs were significantly higher ($P < 0.01$). Serum triglyceride (TG), total cholesterol (TCHO) ($P < 0.01$) and glycerol ($P < 0.01$) of Jinhua pigs were lower comparatively. Higher serum insulin and leptin concentrations were consistent with higher fat percentage in Jinhua pigs. When compared with Landrace, *Sirt1* protein abundance and mRNA levels of Jinhua pigs were lower ($P < 0.01$) in adipose tissue. Likewise, in liver and pancreas, protein abundance and mRNA level of *Sirt1* were also lower ($P < 0.01$) in Jinhua pigs. Consistent with *Sirt1* gene, the mRNA expression of *ATGL* and *HSL* in Jinhua pigs were lower ($P < 0.01$) than Landrace in the 3 tissues. In vitro treatment with different doses of insulin (10, 50 and 100 nM) significantly decreased ($P < 0.01$) glycerol release and *Sirt1*, *ATGL* and *HSL* mRNA levels in porcine adipocytes. These results indicated that porcine *Sirt1* and key fat metabolic enzymes (*ATGL* and *HSL*) expressions are different between fatty breed and lean breed and insulin can decrease gene expression of *Sirt1*, *ATGL* and *HSL* in adipocytes. This will provide some information for further study of porcine *Sirt1* gene function and regulating fat metabolism in pigs and for dietary manipulation of expression of these genes.

Key Words: sirtuin 1, insulin, pig

583 Growth response and blood profile of weaner pigs fed additive-enhanced agro-industrial by-product based diet. A. O. K. Adesehinwa*[1], O. O. Mgbere[2], O. O. Obi[1], B. A. Makanjuola[1], and I. A. Okere[1], [1]*Institute of Agricultural Research & Training, Obafemi Awolowo University, Ibadan, Oyo State, Nigeria,* [2]*Hatfield International Biometrical Service Centre, Houston, TX.*

Ninety (90) weaner pigs (average initial weight 9.78 ± 0.36kg) were randomly assigned to 3 dietary treatment groups in a completely randomized design to evaluate the growth response and blood profile of weaner pigs fed additive-enhanced [directly-fed microbial (DFM) or Hemicell] agro-industrial by-product based diets. The 19.85% crude protein basal diet was formulated to contain 35, 20, 20, 12, 3 and 5% of yellow maize, brewers dried grain, palm kernel cake, groundnut cake, 72% fish meal and micro-nutrients respectively. The additive-enhanced diets contained either 1.5 L of direct-fed microbial, a source of live (viable), naturally occurring microorganism, also known as Rumen Enhancer 3 (RE-3)/tonne of basal diet, or 200 g Hemicell (a mannanase)/tonne of the basal diet. There were 6 pen replicates per treatment, with each pen containing 5 pigs. The pigs were allowed ad libitum access to the diets and water throughout the 35-d study period. Weekly weight and feed intake were recorded and used to determine the weight gain, average daily gain (ADG), average daily feed intake (ADFI) and gain:feed ratio (G:F). At the end of the study, blood samples were collected from 2 pigs/replicate to evaluate the hematological and biochemical profile. Data were analyzed as a completely randomized design using ANOVA procedures as described by Steel and Torrie (1997). The addition of DFM resulted in a higher ($P < 0.05$) ADFI compared with the results obtained with the basal-control and Hemicell-enhanced diets. However, pigs fed the DFM-enhanced diet consequently had a superior ADG (0.40kg) compared with the basal-control (0.35kg) but not the Hemicell-enhanced diet, as the gains were comparable ($P > 0.05$). The efficiency of feed conversion (G:F), hematological and biochemical indices were not significantly ($P > 0.05$) influenced by either of the additives but for a higher serum glucose obtained with Hemicell-enhanced diet. Arising from the comparable results obtained with direct-fed microbial and Hemicell-enhanced diets, it could be inferred that both diets could be used as animal feed additives to enhance the utilization of agro-industrial by-products in diets of this class of pigs.

Key Words: weaner pigs, feed additives, agro-industrial by-product

584 An evaluation of the effects of a blend of essential oil compounds (Crina Piglets AF), a feed-grade antibiotic program, and their combination in nursery diets on the growth and economic performance of pigs in a commercial research facility. J. Bergstrom*[1], D. Campbell[1], C. Paulus[2], and M. DeBeer[1], [1]*DSM Nutritional Products, Parsippany, NJ,* [2]*DSM Nutritional Products, Kaiseraugst, Switzerland.*

A total of 880 pigs (initially 6.8 kg) were used in a 42-d experiment to evaluate the effects of dietary supplementation with a blend of essential oil compounds (Crina Piglets AF, EO), a feed-grade antibiotic program (AB), and their combination on the performance of pigs in a commercial research facility. After weaning (d 0), pigs were randomly placed into 44 pens of 20 pigs each and allotted to one of 4 dietary treatments to provide 11 replicate pens per treatment. Treatments were arranged in a 2 × 2 factorial to evaluate possible EO and AB interactions. Dietary treatments consisted of 1) a control diet without EO and AB, 2) EO added, 3) AB added, and 4) both EO and AB added. Supplementation occurred at the expense of corn in the control diets and all pigs were fed the same 4-phase program of commercial starter diets. Diet phases were d 0 to 7, 7 to 14, 14 to 28, and 28 to 42. Pigs fed EO were supplemented with 100 mg/kg throughout the study. Pigs fed AB were supplemented with 39 mg/kg Denagard + 441 mg/kg Aureomycin from d 0 to 14 and 55 mg/kg Mecadox from d 14 to 42. Economic performance was also determined using costs of \$0.94, \$0.46, \$0.29, and \$0.28/kg for the phase 1 thru 4 control diets, respectively. Added costs for treated diets were \$0.029/kg for Denagard + Aureomycin, \$0.026/kg for Mecadox, and \$0.004/kg for EO. Value of BW gain was determined using \$1.33/kg. Growth performance, diet costs, and value of gain were used to determine feed cost per kg of gain (fd$/kg) and income-over-feed-cost (IOFC). Overall (d 0 to 42), there were EO × AB interactions for ADG ($P \leq 0.07$) and final BW ($P \leq 0.03$). No interactions occurred for other response criteria. Although EO and AB each improved ($P \leq 0.01$) ADG (490, 499, 513, and 562 g/d; treatment 1 thru 4, respectively) and final BW (27.6, 27.8, 28.4, and 30.8 kg), these improvements were considerably greater when EO and AB were used in combination. Pigs fed AB had greater ($P \leq 0.01$) ADFI (726, 708, 758, and 798 g/d) and pigs fed EO had improved ($P \leq 0.01$) G:F (0.67, 0.71, 0.67, and 0.70 g/g). Pigs fed AB had greater ($P \leq 0.01$) fd$/kg ($0.66, $0.64, $0.71, and $0.68), but fd$/kg was reduced ($P \leq 0.01$) for pigs fed EO; however, IOFC ($15.07, $15.89, $14.70, and $16.79) was only improved ($P \leq 0.01$) for pigs fed EO.

Key Words: essential oils, feed-grade antibiotics, pigs

585 Dietary antioxidant (Agrado Plus) sparing vitamin E in nursery pigs fed distillers dried grains with solubles (DDGS). J. Zhao*[1], T. Engle[2], T. Wineman[1], M. Vazquez-Anon[1], and R.J. Harrell[1], *[1]Novus International Inc., St. Charles, MO, [2]Colorado State University, Fort Collins.*

Synthetic dietary antioxidants have been shown to improve liver and plasma vitamin E levels in broilers regardless of dietary vitamin E levels. The objective of this trial was to test whether synthetic antioxidants spare vitamin E in nursery pigs fed distiller dried grains with soluble (DDGS). A total of 924 weanling pigs (PIC, 28 d of age, 7.0 ± 0.07 kg) were randomly assigned to 6 treatments blocked by sex and body weight, with 7 replicates per treatment and 22 pigs per pen. The trial was a 3 × 2 factorial arrangement with 3 levels of dietary vitamin E (0, 22, and 44 IU/kg) with or without synthetic antioxidant (Agrado Plus liquid, at 0.025%). Agrado Plus is a blend of synthetic antioxidants containing ethoxyquin and propyl gallate (Novus International Inc., St. Charles, MO). All pigs were fed a common nursery diet for 7 d post-weaning, and started the experimental diets on d 8. After 7 d, pigs were fed 2-phase commercial diets (d 0–14, d 14–35) with 20% and 30% DDGS, respectively. At the end of the study, one pig per pen was harvested for tissue vitamin E (liver and plasma) and oxidation status measurement. Growth performance (ADG, ADFI, G:F) was not affected by vitamin E, AOX, or their interaction ($P > 0.24$). Dietary AOX increased plasma (33%, $P < 0.01$) and liver vitamin E concentration (30%, $P = 0.04$) regardless of dietary vitamin E level (interaction, $P > 0.17$). Vitamin E concentration in the liver ($P < 0.01$) but not in plasma was linearly increased with dietary vitamin E supplementation. The non-responsive plasma vitamin E might due to transportation stress immediately before harvest. The result suggests that liver vitamin E is a better indicator of vitamin E status than blood vitamin E levels No statistical differences were observed on loin drip loss ($P > 0.26$), plasma free carbonyl ($P > 0.16$), plasma 4-hydroxynonenal (HNE, $P > 0.22$). In summary, AOX spared vitamin E in vivo based on liver and plasma vitamin E concentration, and can be used to spare dietary vitamin E in swine diets fed high DDGS diets.

Key Words: antioxidant, vitamin E, swine

Teaching/Undergraduate and Graduate Education: Graduate and Undergraduate Teaching

586 Gender has a substantial impact on student success in introductory animal science courses. C. G. Jackson*[1], B. J. Williams[2], and E. P. Berg[1], [1]*North Dakota State University, Fargo,* [2]*Hutchinson Community College, Hutchinson, KS.*

The demographic populations of animal science courses at land-grant institutions have changed in the last 20 years. More female and urban students are filling the chairs of agricultural classrooms. The objective of this study was to determine the effect of agricultural background and gender on determining student success in introductory animal science courses. Students enrolled in Introduction to Animal Science 114 (n = 150) and Livestock Production 220 (n = 69) from the spring and fall semesters of 2011 were included in the study. There were more females (n = 134) compared with males (n = 85) and as expected, freshman (n = 93) represented the majority followed by sophomores, juniors, and seniors (n = 56; n = 35; and n = 34; respectively). Each participant completed a survey consisting of 22 questions. Questions pertained to demographic information and their exposure to agriculture during their youth; whether it was participation in 4-H or FFA, showing livestock, or if they grew up on a farm/ranch. More than half of the students grew up on a farm/ranch (n = 127) and were involved in either 4-H or FFA (n = 113). Less than half of the students (n = 75) grew up showing livestock. Females finished the courses with greater semester percentage scores (final grade = 86%) compared with their male counterparts (80%). Female freshman received grades that were greater ($P \leq 0.02$) than both freshman and sophomore males. Additionally, females who participated in 4-H and FFA as well as those who did not performed better ($P \leq 0.05$) than males who were involved in both 4-H and FFA. Furthermore, females who did not show livestock had increased ($P \leq 0.04$) performance compared with males with showing and non-showing experience. Females not from a farm/ranch had greater ($P \leq 0.04$) success than males who grew up on a farm/ranch. Also, non-farm/ranch students had increased ($P \leq 0.03$) performance compared with those who grew up on a farm/ranch. Student gender was the largest factor influencing student success in introductory courses to animal science, for females performed greater than males regardless of agricultural background.

Key Words: animal science, gender, teaching

587 Meeting the changing needs of animal science majors. G. M. Hill* and J. E. Link, *Michigan State University, East Lansing.*

The composition of animal science classes has changed over time. Utilizing response clicker technology, we determined that our introductory animal science course has over 70% freshmen with 55 to 60% of students pursuing an emphasis in pre-veterinary medicine. However, the shift toward veterinary medicine is accompanied by fewer students being raised on farms. Our response technology found that 40% of today's students are from a small town, 20 to 25% are from a large city, and only 15 to 20% are from a farm of over 20 ha. Over 50% of the students reported that the animals they have the greatest contact with are dogs and cats. Hence, large agricultural enterprises are no longer the source of our animal science students. Additionally, we observed that the favorite lab for the past 5 yr was our sheep lab in which students had hands-on experience with the animals. This lab dropped out as the favorite when it was modified to an observation only lab in the spring semester of 2011. To meet the educational needs of this current population, we renovated the course curriculum in the fall semester of 2011 to increase access to livestock and begin early development of basic livestock skills. All labs now involve visits to the university farms and handling either animals or their products (eggs, carcasses, reproductive tracts). Students worked directly with livestock in 71% of the laboratories compared with 7% the previous spring semester. Numerous photos were taken of students' activities to share with family and friends and to serve as study material. Data from one semester of the new curriculum indicated that laboratories with hands-on livestock experience were consistently rated higher than laboratories that were facility tours with limited hand-on experience. Students rated the following lab sessions good or very good for tour vs. hands-on with animals, respectively: dairy: 89 vs. 93, poultry: 66 vs. 86, beef: 81 vs. 94, sheep: 83 vs. 90, swine: 77 vs. 84%. While this type of course takes accessible farms and dedicated managers, it appears that the needs of today's students are being met.

Key Words: undergraduate, livestock, teaching

588 Addressing agricultural and societal issues using a variety of teaching methods. E. L. Walker,* *Missouri State University, Springfield.*

To address societal issues related to agriculture a AGR 399 Animal Welfare Course was designed as a traditional 16 wk lecture type 3 credit hour course at Missouri State University (MSU). However, due to increased demand by place-bound students for quality courses, alternative teaching methods have been implemented. In the fall, 2011, AGR 399 was taught as a combined on-line and traditional 2 1/2 h live lecture course that was broadcast to an additional 5 locations via interactive television. Time was allocated during the lecture portion for invited speakers and discussions directed by student interest. Other than outside speakers, only short, non-formal discussions were planned by the instructor with most discussions being initiated by the students and moderated by the instructor allowing for student directed learning. As part of the online component, 9 PowerPoint lectures along with l notes were posted online using Blackboard 9.1. *Compassion by the Pound* by F. B. Norwood and J. L. Lusk (2011) was used as the text for the course. In addition, students were required to read and discuss assigned articles in 16 graded on-line discussions. One anonymous discussion was initiated so students could voice opinions they felt might not be popular. In total, there were over 1,100 posts from 25 students in a 16 wk period. The 2 reading assignments that generated the most discussion (over 80 each) covered ethics and morality. One was by S. L. Davis (Poult. Sci. 2008) *What Would the World Be Like Without Animals for Food, Fiber and Labor? Are We Morally Obligated To Do Without Them* and the other by J. Hodges (J. Anim. Sci. 2003) titled *Livestock, Ethics, and Quality of Life*. By using a variety of delivery methods, on campus as well as place-bound students have access to the class. In addition, the on-line portion of the class allows for all lectures, quizzes, exams, and homework to be done outside of a regular class period, thus allowing time for invited speakers, discussions over the readings, perusal over current event news headlines, and any topic that the students were deemed important that was related to animal welfare.

Key Words: teaching, distance education, animal welfare

589 Assessing the land-grant mission through undergraduate demographic data: A quantitative approach.

S. Archibeque-Engle* and K. Pond, *Colorado State University, Fort Collins.*

Part of the mission for land grant universities is to serve and represent the state of its location. This analysis was conducted to assess the representation of the state of Colorado by its land grant university and to identify potential talent pools for educated agriculturalists within Colorado. Colorado State University's (CSU) 2010 (n = 696) and 2011 (n = 696) annual fall census data for the Department of Animal Sciences are used and presented here as a model to examine the current situation of the intersection higher education and animal sciences. First, demographics of the undergraduate populations within CSU's Department of Animal Sciences are investigated to determine the current sex and ethnic representation. Second, the current demographics of the department are compared statistically and visually with those of the state of Colorado as a measure of meeting the land grant mission to represent the state. To explore differences statistically, expected frequencies were calculated and a Chi Square Goodness of Fit test was employed to compare the ethnic percentages observed in both 2010 and 2011 for the Department of Animal Sciences undergraduate students to what is expected if the Department of Animal Sciences is representative of the state of Colorado's ethnic demographics. For both 2010 and 2011 the Department of Animal Sciences Latina/o undergraduate representation is significantly lower than expected, $X^2 = 76.6$, $\Phi = 0.33$ and $X^2 = 69.8$, $\Phi = 0.33$; the African American undergraduate representation is significantly lower than expected, $X^2 = 17.1$, $\Phi = 0.16$ and $X^2 = 9.0$, $\Phi = 0.12$; no statistical difference for the Asian/Pacific Islander group was found; for 2010 no statistical difference for the Native American group was found and in 2011, the Native American undergraduate representation is significantly higher than expected, $X^2 = 17.1$, $\Phi = 0.16$. The effect sizes found in this comparison are small to very small and are due to the small numbers of ethnic minority students in CSU's Department of Animal Sciences. In summary, CSU's Department of Animal Sciences is not representative of the ethnic demographics of the state of Colorado.

Key Words: undergraduate education, demographics, land grant

590 Student perceptions of ethics and animal intelligence influenced by introductory animal science course.

A. L. Adams,* G. A. Holub, W. S. Ramsey, and T. H. Friend, *Texas A&M University, College Station.*

Instructors of introductory animal science classes are faced with a wide range of student experiences and perceptions of livestock production practices. This study examined whether these perceptions change as students acquire more knowledge and experience with different species. Students in an introductory animal science course participated in a 26-question pre-course (Pre, n = 310) and post-course (Post, n = 282) survey. Pearson correlation coefficients were used to determine if any associations occurred between responses. Pre and Post responses were analyzed using either the pooled or Satterthwaite *t*-test. Fifty-four percent of participants were first-year undergraduates, 70% were female, and 60% had not been involved in 4-H or FFA. Majority of participants were enrolled in the College of Veterinary Medicine and Biomedical Science (56%) and the College of Agriculture and Life Sciences (30%). Sixty-five percent of participants were interested in pursuing a career in veterinary medicine. Participants had the most experience handling horses (33%), but 30% of the participants had no experience handling livestock. All students considered horses (Pre = 64%, Post = 51%) and swine (Pre = 24%, Post = 44%) to be the most intelligent livestock species ($P = 0.001$). Pre and Post, participants agreed that animals have feelings (94%, $P = 0.76$) and deserve respect from humans (99%, $P = 0.49$). Pre, only 33% of the participants stated that the news media negatively portrays agriculture, whereas, 77% of the participants shared this view Post ($P < 0.0001$). Pre, only 51% of the participants agreed that it is ethical to clone animals, but 77% of the participants agreed with this statement Post ($P < 0.0001$). These results suggest that exposure to livestock production issues and multiple livestock species may influence student perceptions of different livestock species, along with the societal and ethical issues of livestock production.

Key Words: livestock, perceptions, teaching

591 Background experience affects student perceptions of the livestock industry.

A. L. Adams,* G. A. Holub, W. S. Ramsey, and T. H. Friend, *Texas A&M University, College Station.*

Demographic information of students in introductory animal science courses allows instructors to tailor content to student needs and interests. This study compared student demographics with student perceptions of livestock production practices. Students in 2 introductory animal science sections (A: n = 310, B: n = 328) participated in a 26-question pre-course and post-course survey. Pearson correlation coefficients were used to determine if any associations occurred between student responses. Pre-course and post-course survey responses were analyzed using either the pooled or Satterthwaite *t*-test. Both sections were comprised primarily of first-year undergraduate students; a majority was female with either horse experience or no livestock experience. Thirty percent of section A and 58% of section B was enrolled in the College of Agriculture. Sixty percent of section A and 40% of section B had no involvement in 4-H or FFA. Sixty-four percent of all participants were interested in pursuing a career in veterinary medicine. Pre-course, 61% of section A considered horses to be pets, 63% of section B considered horses to be livestock ($P < 0.0001$), 55% of section A stated media portrays agriculture without bias, and 56% of section B stated media negatively portrays agriculture ($P = 0.0004$). Both sections agreed that weather has the greatest influence on producer success ($P = 0.0003$) and genetically-modified foods are safe for consumption ($P = 0.003$), with more variation occurring in section B. Fifty-three percent of section A and 44% of section B believed slaughterhouse practices are inhumane ($P = 0.02$). Post-course, more of section A than section B considered horses as livestock ($P = 0.005$), and both sections agreed that media negatively portrays agriculture, weather has the greatest influence on producer success, genetically-modified foods are safe for consumption, and slaughterhouse practices are humane (all $P > 0.05$). These results suggest that students with no livestock experience may view agriculture differently than students with experience, but more exposure to livestock production issues may challenge students to evaluate their views of agriculture.

Key Words: experience, livestock, student

592 Beef production student instructional video project.

C. L. Pickworth*[1,3] and S. Boyles[2], [1]*The Ohio State University, Wooster,* [2]*The Ohio State University, Columbus,* [3]*North Carolina State University, Raleigh.*

Changes in information technology directly affects today′s beef producers. Developing means to provide fast, accurate information to these producers is a challenge that many extension educators face. To help address this need, students enrolled in the Beef Production II class at The Ohio State University Agricultural Technical Institute were challenged to develop and produce educational videos about basic beef management techniques. Students were randomly assigned to 6 groups and each group selected a topic from a list provided by the Ohio Beef Team extension educators. Students then were responsible for developing a script, filming and editing, the cattle management video. Extension educators worked with students to ensure accuracy of information and the educational value of materials. Student-developed videos were filmed using Flip Cam video cameras and edited with the associated software. Videos were evaluated for value of content, accuracy of information, and quality of visual attributes by the course instructor, extension educators, and peers within the course. Upon completion of the assignment, students were asked to evaluate the effectiveness of the video project. On a scale of 1 to 6 (1 = improved understanding or agree, 6 = detrimental to understanding or disagree), students favorably evaluated the educational value of this team video project. This project helped enhance teamwork (1.54 ± 0.78), knowledge of beef industry (1.62 ± 0.87), understand the difficulty of communicating beef management tasks (1.38 ± 0.51), and was valuable to the course (1.38 ± 0.65). Greatest limitations of the project included access to video cameras, inability to merge separate video and audio files, and having ample time for extension educators to review video clips before final video was developed. Copyright of the videos were provided to The Ohio State University by the students to allow extension educators the ability to use the movies they created in part or whole for extension education. Engaging students in video production on beef cattle management techniques can connect students with extension educators and enhance extension education resources.

Key Words: beef production, extension education, video

593 Integrated program for reducing bovine respiratory disease complex (BRDC) in beef and dairy cattle, coordinated agricultural project (CAP): overview of the teaching program. M. G. Thomas*[1], G. R. Hagevoort[2], T. T. Ross[2], R. M. Enns[1], H. Van Campen[1], A. L. Van Eenennaam[3], H. L. Neibergs[4], C. Chase[5], S. V. Dindot[6], N. D. Cohen[6], and J. E. Womack[6], *[1]Colorado State University, Fort Collins, [2]New Mexico State University, Las Cruces, [3]University of California, Davis, [4]Washington State University, Pullman, [5]South Dakota State University, Brookings, [6]Texas A&M University, College Station.*

Bovine respiratory disease complex is a common cause of morbidity and mortality in cattle, especially young animals exposed to stress. This disease is considered a complex because of numerous involved pathogens. The research objective of this CAP is to use genomic approaches to identify host chromosome regions associated with susceptibility to BRDC and then translate results to beef and dairy industries via selective breeding tools and increased awareness of the need for disease prevention and management (http://www.brdcomplex.org/). The translational effort is supported by teaching and extension efforts. Objectives of the teaching effort include: 1) develop 2 nationally accessible distance-learning courses on the integration of animal health management with genomic and animal breeding approaches (i.e., Improvement of BRDC Resistance and Animal Health and Genetic Approaches to Disease), 2) develop an undergraduate summer research internship program, 3) develop a veterinary feedlot and dairy internship program, 4), sponsor graduate and undergraduate students to attend the Southern Great Plains Dairy Consortium-Teaching (SGPDC-T), where research components of the project are ongoing, and 5) develop 4-H curriculum to expose and train youth on animal disease using BRD as an example application. The educational component of this CAP is greatly assisted because its activities are organized with infrastructure of established and collaborating programs, SGPDC-T; (http://sgpdct.tamu.edu/) and Breeding and Genetics Graduate Education Online (http://bggeo.iddl.vt.edu/). The internship programs are integrated with the research program as students are involved in animal and tissue sampling and data collection. This CAP is in the second year of a 5-year effort and welcomes additional student participation, especially students from under-represented minorities. In summary, the education component of the BRDC-CAP (USDA-AFRI 2011–68004–30367) is developing and offering distance and experimental multi-disciplinary learning approaches for undergraduate, graduate, and veterinary students studying BRDC.

Key Words: cattle, disease, genomics

594 Why your school should host a Block and Bridle National Convention. M. W. Orth,* *Michigan State University, East Lansing.*

Good communication, leadership, and problem solving skills are qualities we desire to see mature in our students. In the classroom, mastering disciplinary content is the primary objective. However, extracurricular activities such as clubs can facilitate the development of soft skills. In animal science departments, Block and Bridle (at some schools Saddle and Sirloin) is the club that includes students with interests in several livestock species. Besides participating in many local activities, each year a school or group of schools will host a National Convention that is open to all clubs across the country. Getting schools to commit to the undertaking has been difficult in the past few years. Michigan State University hosted the National Convention in the fall of 2010 for the first time in its history. Hosting a convention requires a tremendous amount of energy over several months. They are expensive to fund and require a lot of coordination with a very diverse group of people. However, the benefits for the students are well worth the effort. Organizing a convention requires a wide range of activities to make it successful. Students at Michigan State had to develop written materials, such as a sponsorship brochure and convention program, organize bus tours all around the state, stock buses with food and drinks before 6 a.m., and resolve conflicts quickly to name a few. Two unexpected benefits were the greater involvement of members in the club throughout the entire year and the initiation of the Sparty Farm Fresh Tour, a one-day bus tour designed to expose new students to animal agriculture in Michigan. With employers putting a greater emphasis on soft skills in hiring decisions, animal science departments must encourage activities to develop those skills. Hosting a Block and Bridle National Convention is one extremely effective activity that will help prepare a large number of students for their future professions. Additionally, it will showcase agriculture in your state and provide a lot of lasting memories.

Key Words: soft skills, block and bridle, student development

595 Enhancing the student learning experience through an undergraduate research program. E. L. Karcher* and N. L. Trottier, *Department of Animal Science, Michigan State University, East Lansing.*

Between fall 2009 and 2011, enrollment in the Department of Animal Science at Michigan State University (MSU) increased by 11.6%. This increase was accompanied by curricular change including a requirement for undergraduate students in Animal Science to participate in an experiential learning activity. Based on a perceived growing interest in undergraduate research, the Animal Science Undergraduate Research Student Association (ASURSA) was established in fall 2009. Three main learning outcomes were identified: 1) to engage students in annual group undergraduate research projects, 2) to increase general understanding and proficiency of the scientific method, and 3) to provide a forum for professional and social interaction. In spring and fall 2011, club members were identified to work with advisors to formulate a proposal and serve as project managers. Students submitted multiple grant applications and were successfully awarded $10,950 in funding.

During this process, bi-weekly club meetings were used as a forum to discuss the rationale for the project, steps of the scientific method, and discussions on the importance of animal care and use forms. In spring 2011, 18 ASURSA members conducted the first research project at the MSU Poultry Teaching and Research Center. In January 2012 a second study involving 29 members was initiated at the MSU Dairy Teaching and Research Center. Project managers were responsible for leading discussions at club meetings. Discussion topics included nutrition and diet formulation, rationale behind key laboratory techniques, and project updates. Communication of results included presentations by students at MSU and scientific meetings and submission of an article to *Poultry Science*. In addition to research, members host the MSU Animal Science Undergraduate Research Forum. This forum, initiated in 2009 by club members, offers students conducting research in animal science an opportunity to present their work to both students and faculty. In conclusion, the development of an undergraduate animal science club focused on research has offered a unique opportunity to engage a large number of students in research. This coincides with a time of increased student enrollment and increased desire by students to participate in undergraduate research.

Key Words: education, undergraduate research, experiential learning

596 Implementation of a capstone experience requirement in animal and poultry sciences. C. M. Wood,* D. M. Denbow, E. A. Dunnington, and R. K. Splan, *Virginia Tech, Blacksburg.*

Beginning with the graduating class of 2011, undergraduates in the Department of Animal and Poultry Sciences at Virginia Tech must complete a 2-credit capstone experience within 45 credits (3 semesters) of graduation. Each capstone experience is unique to the student who designs it in consultation with faculty. Specific learning objectives include: 1) using critical thinking skills to acquire, analyze, interpret, and integrate information from a variety of sources; 2) solving problems in authentic or realistic situations; 3) planning and completing a project pertaining to each student's discipline and field; 4) demonstrating verbal, visual, and written communication skills; 5) contributing to a team effort; 6) assessing and describing potential contributions to society; and 7) effectively competing for career and/or post-baccalaureate opportunities. An outline of the approval process was presented by Wood et al. (2008). The first proposals were approved in fall 2009. To date, 211 proposals have been approved; 55 of those are in progress and scheduled to be completed by May 2012. Internships (35% of the total) are more popular in the summer whereas formal courses (27%) are chosen most often in the spring semester. Independent studies (13%), undergraduate research (14%), and study abroad (7%) make up most of the rest. Some students (n = 7) fulfill the requirement through a semester spent in the equine program at the Middleburg Agricultural and Research Center in northern Virginia. Almost half the students participate in a poster symposium, held on campus fall and spring semesters, that highlights their accomplishments. Grades assigned by on-site supervisors are mostly A's but a few have assigned C's and D's. Analysis of student perceptions (n = 66 students) indicated that 97% of those completing an internship achieved at least 5 of the 7 learning objectives; 49% achieved all but one and 30% achieved all 7. With more than 450 APSC majors, the challenges presented by this new requirement are many but are outweighed by the tremendous opportunities for student growth.

Key Words: undergraduate education, experiential learning, capstone experience

597 The Graduate Experience Program: An opportunity for undergraduates to explore graduate study. E. L. Berg*[1], A. M. Meyer[2], and L. A. Lekatz[1], *[1]North Dakota State University, Fargo, [2]University of Wyoming, Laramie.*

The objective of the Graduate Experience Program (GEP) at North Dakota State University (NDSU) is to give undergraduate students the opportunity to explore graduate study in the animal sciences and provide mentorship opportunities for graduate students. This class is modeled after a course developed at the University of Missouri in 2006. Admittance into the class is dependent on an application and recommended GPA $\geq$3.0 and junior standing. Class discussion topics include research areas in animal sciences, the land-grant mission, searching for graduate programs, graduate program structure, professionalism, scientific reading and writing, and career options with an advanced degree. Undergraduates are paired with a graduate student mentor for one-on-one dialog and participation in their research. In addition, undergraduates are required to attend departmental seminars, complete a graduate school application, discuss a journal article, and present their future plans as a final project. Graduate student mentors are expected to explain research methods and lab techniques, keep mentees informed of research opportunities and be accessible to their mentees. Since inception of the course in 2009, 19 undergraduate and 13 graduate students have participated during 4 semesters. When asked to rate the overall quality of the course from very good (5) to very poor (1), the average response from undergraduates (n = 18) over 4 semesters was 4.1. When asked if they would recommend this course, the average response was 4.4 (strongly agree = 5; strongly disagree = 1). All students agreed that GEP was helpful in their decision to pursue or not pursue graduate study. Of the 19 undergraduates who participated, 37% (n = 7) are still completing their B.S., 26% (n = 5) are currently enrolled in animal science graduate programs, 26% (n = 5) are working in animal science-related industry jobs, 5% (n = 1) are working in non-animal science jobs and 5% (n = 1) are in veterinary school. In conclusion, the GEP helped NDSU students in the decision making process regarding pursuit of graduate school, as well as encouraged them to consider graduate study in the animal sciences.

Key Words: undergraduate, graduate

WSASAS Symposium: Growing Beef Cattle: The future of stocker/backgrounding systems in beef production

598 Improving the production, environmental, and economic efficiency of the stocker cattle industry in the Southeastern United States. P. Beck*[1], M. Anders[2], B. Watkins[2], S. Gunter[3], D. Hubbell[4], and S. Gadberry[5], *[1]University of Arkansas, Southwest Research & Extension Center, Hope, [2]University of Arkansas Rice Research & Extension Center, Stuttgart, [3]USDA-ARS Southern Plains Range Research Station, Woodward, OK, [4]University of Arkansas Livestock & Forestry Research Station, Batesville, [5]University of Arkansas Cooperative Extension Service, Little Rock.*

Grazing small-grain forage can be a profitable "2nd crop" for grain producers and an opportunity for retained ownership for cow-calf producers. The costs of conventional tillage and movement of soil nutrients into streams and water ways creates a need for sustainable production practices. Systems research at the Livestock and Forestry Research Station near Batesville, AR and the Southwest Research and Extension Center near Hope, AR has been conducted over a 9-yr span to characterize the effects of pasture systems on forage production, animal performance, soil quality, water runoff, and economics of stocker cattle enterprises. Compared with both bermudagrass or toxic endophyte-infected tall fescue, gains of growing cattle are increased by 80% with non-toxic endophyte-infected tall fescue and 150% with small-grain forages. Producers with spring-calving cowherds can utilize these improved forages to accelerate stocker programs with retained calves. Economic analysis indicates a 99% improvement in net returns for producers retaining ownership of calves with these production systems. Rainfall simulation indicates that runoff volume and nutrient load does not differ between conventionally tilled fields and no-till fields in the spring before tillage when surface cover is similar. In the fall following tillage operations conventionally tilled fields had 4-times greater runoff, 1.9-times greater N, and 3.2-times greater P leaving the field in runoff compared with no-till. Total natural rainfall runoff from conventionally tilled wheat fields were 2-times greater than that from no-till fields with 2.5 cm rainfall events yet were 4-times greater with 6.25 cm rainfall events. Soil analysis shows that soil aggregate content was greater in no-till compared with conventional till, indicating greater soil porosity, improved water infiltration rate, and reduced erositivity of soil. Carbon content of no-till soils was 50% greater than conventional tillage indicating increased C sequestration. Together these studies show that production systems can be designed that provide improved production economics, increase soil quality and C sequestration, and reduced nutrient loads of streams and water ways that also do not decrease productivity of pastures.

599 Growth, development, and the expression of genes in marketable tissues. P. A. Lancaster*[1], E. D. Sharman[1], M. A. Vaughn[2], C. R. Krehbiel[1], G. W. Horn[1], J. D. Starkey[2], and U. DeSilva[1], *[1]Oklahoma State University, Stillwater, [2]Texas Tech University, Lubbock.*

Increasing adipose tissue development during the stocker phase of production could increase value and efficiency of beef cattle production. Our objective was to evaluate rate of gain on growth and development of adipose tissue, and skeletal muscle characteristics in growing cattle. Two experiments were conducted where Angus cross-bred steers were grown on winter wheat pasture or dormant native range to achieve divergent rates of gain. A subset of steers was harvested at similar age (Exp. 1) or BW (Exp. 2) at the end of the stocker phase. During the stocker phase, ADG ranged from 0.19 to 1.37 kg/d in Exp. 1 and 0.49 to 1.41 kg/d in Exp. 2. At the end of the stocker phase, steers were fed a common finishing diet to a rib fat thickness of 1.27 cm. In Exp. 1, marbling score at intermediate harvest increased linearly with ADG, whereas rib fat thickness increased at an increasing rate. In Exp. 2, there was not a strong relationship between ADG and marbling score or rib fat thickness. In Exp. 1, there was no treatment × adipose tissue interaction for lipogenic gene expression indicating that each adipose tissue responded similarly to the treatments. Lipogenic gene expression increased with increasing ADG. There was a significant ($P < 0.05$) treatment × adipose tissue interaction for adipogenic gene expression, with no difference in subcutaneous adipose tissue (SC), but in intramuscular adipose tissue (IM) PPARγ mRNA expression increased and DLK1 mRNA expression decreased with increasing ADG. In contrast to Exp. 1, there was a treatment x adipose tissue interaction for both lipogenic and adipogenic gene expression in Exp. 2, where expression of FASN and PPARγ mRNA expression increased with increasing ADG in SC, but not IM. In Exp. 2, low rates of gain tended to increase satellite cell differentiation, Type 1 (oxidative) muscle fibers, and capillary density, as well as final marbling scores. These data indicate that rate of gain to similar BW affects metabolic pathways in SC and IM differently than rate of gain to similar age, and that low rates of gain result in skeletal muscle characteristics that are more favorable for marbling deposition.

Key Words: adipose tissue, growth rate, stocker cattle

600 Opportunities for grazing cattle systems. J. C. MacDonald*[1,2] and F. T. McCollum[3], *[1]Texas AgriLife Research, Amarillo, [2]West Texas A&M University, Canyon, [3]Texas AgriLife Extension, Amarillo.*

Yearling production systems serve several purposes in the beef cattle industry. Utilizing grazed forage resources to grow stocker cattle spreads the feeder calf supply across the calendar year from a national calf crop that is largely fall-weaned. Grazed forage resources have historically reduced the cost of gain over the lifetime of a feeder calf. Yearling production systems allow producers to fully utilize forage resources while providing flexibility to stock and manage grazed forages. Finally, yearling systems have increased beef supply by increasing carcass weights relative to feeder cattle entering the feedlot at lighter BW. Dynamics of agricultural enterprises have changed over the past decade and present new challenges and opportunities for yearling production systems. The size of the national cow herd has declined which increases competition for feeder calves. Volatility of commodity prices has increased which exposes producers to greater risk and often narrower margins. Increasing societal awareness of agricultural production practices will cause more scrutiny of the industry. However, the functional role of yearling operations in the US beef industry has not changed. The supply of byproduct and alternative feeds provides opportunities to increase production while cattle are grazing. The reduction in cow inventory may result in increased forage resources available for yearling systems, as well as the need for feeding entities to capture future supplies of feeder calves. Increased cooperation between the stocker and finishing segments may be the result. New information will be required to ensure the future success of these production systems. The upper BW limit of stocker cattle entering the feedlot has been discussed, but not clearly defined. Residual effects of stocker management on feedlot performance and beef quality will increase in importance. The age old issue of compensatory gain and body composition at feedlot entry will need to be clearly defined.

Despite reduced inventories relative to feeding capacity, higher feed commodity costs, relatively lower costs for grazing, and the continued need to spread the harvest of finished cattle across the year will ensure the role of stocker production in the future.

Key Words: grazing cattle, yearlings, beef production systems

601 Opportunities for drylot backgrounding systems in the beef industry. B. P. Holland,* *Department of Animal Science, South Dakota State University, Brookings.*

Traditional feedstuff prices, with roughages costing a premium to grains on an energy basis, resulted in the proliferation of cattle feeding and reduced the placement weight of cattle in feedlots. However, recent increases in the cost, and price volatility, of feedstuffs, inputs, and feeder cattle have put a strain on commercial feeders. Although roughage-based backgrounding and grazing programs often result in decreased G:F in subsequent finishing, increasing the weight of feeder cattle through backgrounding results in decreased days on feed and a potentially more economical system. In some scenarios, cattle can be grown on higher-roughage, lower-energy diets at a cost-competitive advantage to high-concentrate feeding. This is especially true in situations where a significant portion of feed is produced on-site and does not require outside purchase. Improvements in plant varieties allow the production of higher yield and quality forages for lower costs, and some available by-product feeds seem to have positive associative effects with roughages. These factors, combined with cattle that have superior growth potential, allow for high rates of gain on relatively low quality feeds. Traditional wisdom may have suggested purchasing feeder cattle with less condition, hoping to achieve compensatory growth in the feedlot. Because of this, there is a perceived upper gain limit for backgrounding cattle. However, in recent studies, fatter steers entering feedlots have been more efficient during finishing. This may be be indicative of backgrounding diet and intake having more impact on feedlot performance than empty body fat. As a result, the acceptable ADG range for backgrounding programs is increased. Viability of feedlots will depend on a steady supply of feeder cattle, and a greater flexibility by backgrounders to produce feeder cattle will reduce inefficiencies and risk associated with keeping lots full. This paper will highlight potential scenarios in which drylot-based backgrounding programs can fit into the beef industry.

Key Words: backgrounding, cattle, feedlot

Wednesday, July 18, 2012

POSTER PRESENTATIONS
Animal Behavior and Well-Being: Behavior Emphasis

W1 Ruminal fermentation and behavior in Simmental heifers fed TMR with non-forage fiber sources in feedlots. S. P. Iraira,* J. L. Ruíz de la Torre, M. Rodríguez-Prado, X. Manteca, S. Calsamiglia, and A. Ferret, *Universitat Autònoma Barcelona, Bellaterra, Spain.*

The objective of this experiment was to determine the effects of non forage fiber sources on rumen fermentation and behavior of heifers fed TMR. Eight rumen cannulated Simmental heifers (initial BW 313 ± 13.2 kg) were randomly assigned to 1 of 4 treatments in a 4 × 4 double Latin Square design. The experiment was performed in 4 28-d periods. Treatments were barley straw (BS), soybean hulls (SH), beet pulp in pellets (BP) and whole cottonseed (WCS). Fiber ingredients were incorporated at 10, 16, 17 and 17% (DM basis) in BS, WCS, SH and BP, respectively. Diets were isoenergetic and isonitrogenous and were offered ad-libitum as TMR. Each heifer was individually housed in a roofed pen. Feed offered and refusal samples of each heifer were collected over 7 d in the last week of each experimental period to determine DM intake, chemical composition and particle size. Particle size separation was performed using the Penn State Particle Separator. On d 28 of each period, rumen samples were taken immediately before feeding and at 4, 8, 12, 16, and 24 h after feeding. Behavior was video-recorded for 24-h on d 2 and d 6 of each experimental period. NDF intake and ruminal pH were statistically analyzed using the MIXED procedure and behavior activity using the GLIMMIX procedure, both in SAS. NDF intake was higher in WCS than in BS (1.4 vs 1.3 kg/d; $P = 0.001$). Proportions of offered particles that were greater than 8 mm were 15.3, 6.1, 23.0 and 36.9% for BS, SH, WCS and BP, respectively. Average rumen pH was 5.87 in SH and 6.32, on average, in BS and BP ($P = 0.006$), but there were no differences between SH and WCS (6.20, on average).Time spent chewing was higher ($P = 0.001$) in BS and WCS (355 min/d, on average) than in SH and BP (252 min/d, on average). Time spent doing tongue-rolling in BP (16.8 min/d) tended to be higher than in the other 3 treatments (3.4 min/d, on average; $P = 0.069$) and no differences were found for licking or biting the fixtures. In conclusion, SH affected ruminal fermentation and BP tended to increase stereotypies when used as fiber sources in feedlot diets.

Key Words: cattle behavior, non-forage fiber, ruminal pH

W2 Foraging behavior of beef cows grazing native grassland: Effect of herbage allowance on temporal and spatial grazing patterns. S. Scarlato*[1], M. Carriquiry[1], M. Do Carmo[1], A. Faber[1], C. Genro[3], E. Laca[2], and P. Soca[1], *[1]Unviersidad de la República, Paysandu Uruguay, [2]University of California, Davis, [3]Embrapa, Bage, Bage, RS, Brazil.*

A 2-year study was conducted on a native grassland located in South America, to quantify grazing and ruminating times and patterns of spatial use in beef cows grazing at 2 herbage allowances (HA; 4 and 2.5 kg DM kg-1 BW, for high and low, respectively) in a completely randomized block design (Block 1: Hereford and Angus purebred cows and Block 2: their F1 crossbred cows). Sixteen cows (n = 4 for HA and block) were assigned to 4 plots, remaining there in a continuous grazing system. The Put-and-take method was used monthly to adjust HA. Grazing and ruminating times were recorded over 24-h period using IGER recorders for 3 consecutive days. Location (bottom, toe slope and shoulder slope zones) of cows within the plot during grazing activity was recorded by direct observation during daylight hours, and a relative preference index (RPI) was used to quantify preference for each zone. Recording periods were: spring 2007, 2008, and 2009, autumn 2008, and winter 2008 and 2009. Mean daily grazing and ruminating times were 738 ± 27 and 453 ± 26 min, respectively. Grazing activity was largely diurnal with 2 main sessions, one in the morning and another in the afternoon. Daily grazing time was greater ($P \leq 0.047$) for low than high HA cows in spring and autumn, which could indicate a compensatory mechanism for reduced HA but also for the less forage mass and height. Daily ruminating time decreased ($P \leq 0.044$) for low than high HA cows in spring, autumn and winter, suggesting a reduced DM intake, and showing constraints to compensate for limitations imposed by pasture in low HA. In general, the RPI for plot zones were not affected by HA ($P > 0.05$) but were affected by session ($P \leq 0.005$). During the afternoon grazing session, cows grazed in the shoulder slope zone ($P \leq 0.002$), with greater forage mass availability, while during morning grazing session, the bottom zone, close to the water source, was preferred ($P \leq 0.005$). This spatio-temporal behavior pattern may indicate an attempt to maximize intake before dusk, through increasing intake rate, minimizing the risk of predation. Quantifying spatio-temporal behavior of grazing ruminants in heterogeneous environments may help to improve livestock systems by integrating behavioral principles and processes into management practices.

Key Words: beef cow, grazing behavior, native pasture

W3 Feeding behavior of grazing buffalo calves fed different types of supplement in tropical conditions. R. M. Patiño,* L. G. Altahona, and L. M. Botero, *University of Sucre, Sincelejo, Colombia.*

The objective of this study was to evaluate the effect of different types of supplementation on feeding behavior of buffalo calves grazing in tropical conditions. Thirty Murrah calves, with average initial BW of 65 ± 1.97 kg, were assigned to 3 treatments, in a completely randomized design. One group received mineral supplementation, another group mineral and concentrate (0.5% BW) supplementation, and the third group remained as control, without supplementation. The animals grazed a pasture of Canutillo grass (*Hymenachne amplexicaulis*). After the adaptation period, animals were individually identified and their feeding behavior (idling, ruminating and grazing) was observed using visual method from 0800 to 1700 h, every 5 min, during 12 d, in a period of 60 d. Watering, consuming supplement and suckling times were measured using stopwatch. The animals were weighted every 15 d. The daily time spent in each behavior was analyzed considering the effect of the type of supplement (Table 1). The animals supplemented with mineral mixture and concentrate had a greater ($P < 0.05$) average of daily gain (0.547 kg) compared with mineral mixture treatment (0.388 kg) and the control group (0.320 kg). Drinking water time was not affected ($P > 0.05$) by the type of supplementation. The other activities were affected ($P < 0.05$). The animals supplemented with mineral mixture and concentrate spent more time ($P < 0.005$) to feed intake (grazing, suckling and consuming mineral mixture), that explained the best weight gain.

Table 1. Means of behavior (min/d) of buffalo calves under grazing and supplementation

Behavior	Nonsupplement	Mineral mixture	Mineral mixture and concentrate	SEM	P-value
Grazing	299.3^a	336.3^b	356.0^b	5.656	<0.0001
Ruminating	312.8^a	261.8^a	253.8^b	8.286	0.005
Idling	640.3^{ab}	663.5^a	597.5^b	9.749	0.017
Suckling	7.0^a	3.5^a	15.3^b	1.345	0.001
Watering	6.3^a	3.5^a	7.3^a	0.784	0.129
Consuming mineral mixture		8.3	13.8	1.005	<0.0001

^{a,b}Means within a row followed by the same letter do not differ ($P > 0.05$) by Tukey test.

Key Words: behavior, buffalo calves, supplementation

W4 Effects of housing systems on behavioral responses of newborn Holstein calves.

S. V. Matarazzo*[1], T. T. Fonseca[1], J. R. P. Arcaro[2], F. P. Campos[2], and S. A. de A. Fernandes[3], *[1]Universidade Estadual de Santa Cruz, UESC, Ilhéus, BA, Brazil, [2]Instituto de Zootecnia de Nova Odessa, Nova Odessa, SP, Brazil, [3]Universidade Estadual do Sudoeste da Bahia, Itapetinga, BA, Brazil.*

The objective of this research was to evaluate the effects of housing systems on behavioral responses of newborn Holstein calves. The experiment was carried out from October to December 2006. Twenty female Holstein calves, 1-mo old and 46.2 ± 7.0 kg of body weight were randomly assigned to the treatment groups. Treatments were: individual shelter with 0.9 m wide, 1.2 m tall and 1.1 m long covered with recycled tiles maintained in pasture or individual hutch with located at 0.5 m above the floor with 0.9 m wide, 0.9 m and 1.1 m long maintained inside the barn. Calves received 4 L of milk a day, divided into 2 meals (8am and 3pm). Shelters were provided with individual enclosures for provision of concentrated and hay, which were offered ad libitum. The behavioral patterns activities (standing or lying down, rumination, resting, drinking, eating) were evaluated once a week from 8:00am to 8:00pm. Time spent standing up was higher (41%) in calves of individual shelter in relation to individual hutch (22%). Due to space limitation, animals probably chose to spend more time laying down (78%) for overcoming the uncomfortable situation and even to avoid traumas and other physical damages. On the other hand, animals kept in pasture were tightened to a chain, which allowed them to move around, either searching for shadow, exploratory behavior or grazing. There was no difference among calves from the different treatments in terms of time spent in rumination (23%), eating (8%) or drinking (3%). Resting time of calves in individual cage was higher (51%) than those of individual shelter (43%). Probably, the reason this time lasted longer for animals inside barns was because space and environmental restriction. Once time consumed with other activities is concerned, this was more intense (24%) for animals in individual shelters in pasture than for animals in hutches (14%). These activities were related to elimination activities, exploratory behavior, such as grazing around the shelter, which could only be observed for the last group of animals, besides stereotypical behaviors, such as biting, grabbing, hit the head, typical of animals in hutches.

Key Words: newborn, welfare, housing systems

W5 A preliminary study on the behavior of rodeo animals just prior to bucking events.

E. A. Pajor*[1], T. Grandin[2], G. B. Bond[1], and C. Goldhawk[1], *[1]University of Calgary, Calgary, Alberta, Canada, [2]Colorado State University, Fort Collins.*

Animals are used in numerous types of competitions. Many animal owners describe their animals as enjoying and anticipating these competitions. Despite these assurances, many criticize such animal use and claim that animals experience fear and mistreatment. In fact, there is very little empirical evidence to support either claim. One of the most criticized competitive events is rodeo. The purpose of this preliminary study was to describe the behavior of animals before bucking events at a rodeo. Direct observations were carried out by 5 trained observers at a national rodeo between July 11 and July 17, 2011. Animals were observed over 3 bucking events, bareback (n = 48 horses), saddle bronc (n = 57 horses), and bull riding (n = 48 bulls). Behaviors quantified were those associated with frustration and arousal (eye white, tail swishing, defecation) and escape behaviors (kick, paw at ground, move back and forth in chute). The period immediately before performance was divided into 3 separate time periods, loading the chute, tacking up, and mounting the animal. Only descriptive results are presented. Bareback horses and saddle bronc horses responded in a similar fashion and are grouped as horses. Horses tended to kick more than bulls (45% compared with 15%), while bulls tended to show more eye white than horses (45% vs. 40%). Horses performed more behaviors associated with arousal and escape while being loaded in the chute and during tacking up than when being mounted, 45% vs. 20% of the animals. Bulls were more aroused when being mounted than when loading (40% vs. 15%). Mounting animals involves not just the cowboy but numerous individuals in close proximity to the bull. It is not clear if animals are responding to the upcoming performance or the presence of large groups of people to which they are unaccustomed. This preliminary study suggests that although some animals were aroused and demonstrated escape behaviors, the majority of animals were calm and showed little arousal before leaving the chutes. Additional results will be presented at the meeting. This study is one of the first to describe the behavior of rodeo animals before the event.

Key Words: behavior, welfare, rodeo

W6 Determining the effects of castration with or without analgesia on growth performance, hematology, and behavior in neonatal beef cattle.

A. C. Brown*[1], J. G. Powell[1], M. S. Gadberry[2], E. B. Kegley[1], J. T. Richeson[3], J. L. Reynolds[1], and Y. V. Thaxton[1], *[1]University of Arkansas Division of Agriculture, Fayetteville, [2]University of Arkansas Division of Agriculture, Little Rock, [3]West Texas A&M University, Canyon.*

Angus-cross bull calves (n = 61) were weighed within 72 h of birth and assigned randomly to 1 of 3 treatments. Treatments were surgical castration, oral administration of meloxicam (1 mg/kg of BW) followed by surgical castration, or bulls remained intact (control). Subsets of 7 calves/treatment for castrates and 15 calves that remained intact were selected randomly and calf standing and lying activity was monitored by recording x and y-axis positions of a datalogging accelerometer attached to a leg for 7 d, in addition blood was collected on d 0, 1, 3, and 7. Calves were weighed every 28 d through d 112. Body weight did not differ between treatments ($P \geq 0.74$). Castrated calves receiving meloxicam tended ($P = 0.06$) to have greater % neutrophils and lower % lymphocytes on d 7 compared with castrates that had not received meloxicam (treatment × day, $P < 0.02$). Hematocrit was greater ($P = 0.02$) in bulls on d 1 than in calves castrated without analgesic (treatment × day, $P = 0.03$). The XY plots from accelerometers revealed 3 distinct clusters of data and cluster analysis within calf was used to categorize observations into 3 clusters. Clusters (C) were determined to represent lying flat on side (C1), standing (C2) and lying (C3). Proportion of time expressed in C1, C2, and C3 was 0.36, 0.23, and 0.41, respectively. Proportion of daily activity expressed as C1 differed among treatments over time ($P = 0.05$); however, test of simple effects by day indicated no treatment differences on most days with the exception of d 5 where castration at birth with analgesia differed from castration without analgesia and non-castrated calves ($P < 0.01$). Proportion of time expressed as C3 was 0.38, 0.40, and 0.42 (SE 0.01) for castrated with analgesia, castrated without analgesia, and non-castrated, respectively; and differed for castrated compared with non-castrated ($P < 0.01$) and tended to differ for castrated calves given analgesia vs. those without analgesia ($P = 0.08$). Over the 7 d period following neonatal castration, use of pain control at the time of surgery had minimal effects on time spent standing and lying.

Key Words: castration, meloxicam, analgesia

W7 Pain and pessimism: Dairy calves show negative bias in judgment tasks following hot-iron disbudding. H. W. Neave,* M. A. G. von Keyserlingk, and D. M. Weary, *University of British Columbia, Vancouver, BC, Canada.*

Cognitive bias tasks involve interpretation of ambiguous stimuli. Depressed or anxious humans are known to judge ambiguous events negatively, and recent work on animals suggests that judgment bias can also provide a method of assessing emotions in non-human animals. No previous work has applied cognitive bias testing in cattle, and none has used judgment bias as a method of pain assessment. We assessed cognitive bias in dairy calves before and after hot-iron disbudding. Previous work has shown that calves experience pain for at least 24 h after this procedure. Holstein dairy calves (n = 8) were trained using a go/no-go task to expect positive (a milk reward) or negative (a time-out with no opportunity to access milk) outcomes following nose contact with a video screen that was either white or red; calves were alternatively assigned white or red as the positive training stimulus, and the opposite color as the negative training stimulus. Once calves had learned to discriminate between these 2 training stimuli (at least 90% correct over 3 consecutive training sessions), they were tested with unreinforced probes (screen colors at 25%, 50%, and 75% red) introduced randomly within training sessions. Probes were presented in sessions 1 d before and 1 d after disbudding. Calves approached the ambiguous probe screens less frequently after disbudding (78.1 ± 9.8, 31.3 ± 11.8, 2.5 ± 2.5% for the probe most similar to the positive screen, the mid-way probe, and the probe most similar to the negative screen, respectively) compared with before disbudding (84.6 ± 6.1, 48.7 ± 9.9, 18.5 ± 4.4%), a difference that was most pronounced for the probe closest to the negative screen. These results illustrate that calves experiencing pain during the hours after hot-iron disbudding interpret ambiguous stimuli negatively compared with before disbudding. This “pessimistic” bias supports the use of a cognitive bias task as a measure of emotional state, including pain, in dairy calves.

Key Words: animal welfare, cognitive bias, animal emotion

W8 The effect of previous experience on the adaptation to headlocks by Holstein dairy cows. P. D. Krawczel* and J. M. Hale, *Department of Animal Science, University of Tennessee, Knoxville.*

Moving dairy cows into new facilities requires an adaptation to novel environments. The objective of this study was to determine differences in behavior following the delivery of TMR between lactating cows with or without previous experience using headlocks. Forty-four Holstein dairy cows, from 3 different facilities, were assigned to 4 pens (n = 11 per pen) within a new facility using headlocks as the only feed barrier. Two pens comprised naïve cows (originating from facilities using only post-and-rail feed barriers; parity = 1.0 ± 0.0; body weight = 525.2 ± 13.5 kg; DIM = 234 ± 8; milk production = 25.8 ± 0.2 kg per d) and 2 pens comprised of experienced cows (originating from a facility with only headlock feed barriers; parity = 1.4 ± 0.1; body weight = 661.2 ± 22.1 kg; DIM = 328 ± 11; milk production = 18.6 ± 0.2 kg per d). Their response was assessed from the mean percentage feeding, lying, standing in the feed alley, or other using 10-min scan samples collected via direct observation. Data were collected during 2 h after the morning and afternoon delivery of feed for 7 d. Data were log-transformed (back transformed means reported) due to lack of normality and analyzed with the mixed procedure of SAS using repeated measures. More naïve cows engaged in feeding (47.3 ± 1.0%) than experienced cows (29.4 ± 1.0%; $P < 0.001$). However, a greater percentage of experienced cows engaged were lying (48.3 ± 1.0) and standing in the alley (15.4 ± 1.0%) relative to the naïve cows (lying = 20.9 ± 1.0% ($P < 0.001$) and standing = 13.7 ± 1.0% ($P = 0.02$)). Experience level had no effect on other behavior ($P = 0.71$). The initial hypothesis, previous experience would benefit cows (indicated by a greater percentage of cows feeding and a lower percentage standing in the feed alley following the delivery of TMR), was rejected. Experienced cows and naïve cows behaved differently following introduction to headlocks, but there was no indication of a benefit from previous experience. This suggests other factors may be more important during adaptation to novel environments.

Key Words: dairy cow, behavior, adaptation

W9 Lying behavior of lactating dairy cows is influenced by lameness especially around feeding time. C. Yunta*[1], I. Guasch[2], and A. Bach[1,3], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Barcelona, Spain, [2]La Pirenaica, La Seu d’Urgell, Lleida, Spain, [3]ICREA, Barcelona, Spain.*

Lameness is considered one of the most common welfare and productive problem in dairy cattle. The objective of this study was to evaluate differences in lying behavior between lame and non-lame lactating cows under commercial conditions. Data were collected from 10 different free-stall commercial herds, which were feeding exactly the same ration once daily. All lactating cows were scored for lameness according to a 1–5 locomotion scoring system. Only cows with a lameness score between 1 and 4 were considered in the study. In each herd between 10 and 15 lame cows (scored as 3 or 4) were chosen for the study and for each lame cow, a non-lame cow (scored as 1) with same parity number and similar DIM was chosen within each herd. Pendant data loggers were then placed in the hind leg of each cow during 10 d to record lying behavior at 1-min intervals. In addition, the time of feed delivery was recorded in each herd on a daily basis. Total daily lying time, daily number of lying bouts, lying bout duration, laterality (side of recumbence), and lying behavior around feed delivery were evaluated using a mixed-effects model that accounted for the fixed effects of lameness score, DIM, parity, and the interaction between parity and lameness score, plus the random effects of herd and cow. Total daily lying time (721 ± 24.2 min/d) tended ($P = 0.07$) to increase with DIM, but it was not affected by lameness or parity. Likewise, no differences were found in the number of lying bouts (9.6 ± 0.49 d-1) or laterality (47 ± 2.6% of time lying on the right side). However, the mean bout duration was longer ($P < 0.05$) in lame compared with non-lame cows (89.3 ± 3.89 vs. 80.7 ± 3.90 min, respectively). Interestingly, lame cows stood up 13 min later ($P < 0.05$) than non-lame cows relative to the time when the ration was delivered. In addition, lame cows lied down 19 min earlier ($P < 0.05$) than non-lame ones after the feed was delivered, which implies that non-lame cows spent more time standing and probably eating than lame cows. It is concluded that lame cows have longer lying bouts than non-lame animals, and that lying behavior around feed delivery time may be an effective proxy to identify moderately lame cows.

Key Words: feeding time, lameness, lying behavior

W10 Effect of grouping calves post-weaning according to pre-grouping feed intake on eating behavior. C. M. Matuk*[1], M. Chahine[1], A. Bach[2,3], B. Ozer[1], M. E. de Haro Marti[4], J. B. Glaze Jr.[1], T. Fife[1], and M. Nelson[1], *[1]University of Idaho, Twin Falls, [2]IRTA, Caldes de Montbui, Spain, [3]ICREA, Barcelona, Spain, [4]University of Idaho, Gooding.*

The effect of grouping calves post-weaning according to pre-grouping feed intake on eating behavior was evaluated using 755 replacement Holstein calves raised on a large operation in southern Idaho. In 4 different periods, individual feed intake was recorded 4 times a week during the last 3 wk that calves were individually hutched (60 d of age). Calves were classified as high eaters (highest feeding level quartile) and low eaters (lowest feeding level quartile). When leaving the individual hutches in each period, calves were assigned to 6 treatments: 20 animals randomly chosen without considering their level of feed intake (CTRL), 20 calves within the highest quartile of feed intake during the 3 wk prior leaving the hutches (HH), 20 within the lowest quartile (LL), 10 from the highest and 10 from lowest feeding level (HL), 5 from the highest and 15 from lowest feeding level (HLL), and 15 from the highest and 5 from lowest feeding level (HHL). Thus, out of 755 tracked heifers, 480 were chosen to form the 20 groups (6 groups per period) that were studied. After grouping, calves received a TMR composed of 95% starter and 5% alfalfa. Pen eating behavior was video recorded twice a week after grouping for 4 wks. Heifers in the highest feeding quartile in the HL, HLL and HHL were differentiated from the lowest quartile in their groups with a red plastic collar and reflective tape. A total of 192 d of recordings were collected and analyzed. Heifers were recorded as eating after 5 s of eating at the feedbunk. Data were analyzed using a mixed-effects model accounting for the random effect of period and pen and the fixed effects of treatment and intake level class and their 2-way interaction. CTRL and HL Heifers spent more time ($P < 0.05$) eating than HHL and HLL heifers (6.9 ± 0.6 min/hr vs. 5.8 ± 0.6 min/hr respectively). There was no significant effect of intake level class in HHL, HL and HLL ($P > 0.05$) with high eaters spending 6.0 ± 0.4 min/hr eating and low eaters spending 6.3 ± 0.4 min/eating. In this study, grouping calves according to their individual feed intake had no effect on time spent eating post-grouping.

Key Words: calves, heifers, eating behavior

W11 Association between behavioral patterns and risk of elevated somatic cell count in lactating dairy cows. M. E. A. Watters[1], K. Meijer[1], H. W. Barkema[2], K. E. Leslie[3], M. A. G. von Keyserlingk[4], and T. J. DeVries*[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. of Production Animal Health, University of Calgary, Calgary, Alberta, Canada, [3]Dept. of Population Medicine, University of Guelph, Guelph, Ontario, Canada, [4]Animal Welfare Program, University of British Columbia, Vancouver, British Columbia, Canada.*

The objective of this study was to determine the association between dairy cow standing and lying behavior patterns and risk of experiencing a newly elevated somatic cell count (SCC). Five commercial free-stall dairy herds, milking 3x/d, were enrolled in a longitudinal study. Forty Holstein-Friesian cows/herd were selected as focal animals based on DIM (<200 d) and SCC (<100,000 cells/mL). The study consisted of four 5-wk periods. Cow-level composite SCC was recorded at the beginning of each period and the end of the final period. Elevated SCC (eSCC) was used as an indicator of subclinical mastitis. Incidence of a newly eSCC was defined as having a SCC > 200,000 cells/mL at the end of each period, when SCC was < 100,000 cells/ml at the beginning of the period. Standing and lying behavior of the cows, as well as the times of milking and fresh feed delivery, were collected for 5 d after each SCC sampling using data loggers. A multivariable logistic regression model was used to assess the relationship between post-milking standing time and occurrence of a newly eSCC. There was no effect of the time of feed delivery on post-milking standing time, which averaged 97.4 ± 15.5min. Over the study period 48 newly eSCC were detected, resulting in an incidence rate of 0.97 eSCC/cow-year at risk. A non-linear relationship between post-milking standing time and eSCC incidence was found ($P = 0.01$). Those cows that lie down >90 min after milking were found to have a lower risk (OR = 0.38, 95% CI = 0.18, 0.80) of an eSCC compared with cows that lie down for the first time < 90 min after milking. Further, the risk of experiencing an eSCC was increased ($P < 0.01$) in multiparous cows (OR = 3.72. 95% CI = 1.37, 10.14), and in cows with a higher SCC at the beginning of the study (OR = 1.92, 95% CI = 1.44, 2.55; for one standard deviation [23,071 cells/ml] increase in initial SCC). These results indicate that management practices that promote longer post-milking standing time may be recommended to reduce the risk of free-stall housed cows experiencing newly eSCC. This should, in the longer term, reduce the overall prevalence of eSCC.

Key Words: free-stall, somatic cell count, behavior

W12 Association of social rank during the prepartum period with health, reproduction, and milk production of dairy cows. K. M. Lobeck,* M. I. Endres, P. R. B. Silva, and R. Chebel, *University of Minnesota, St. Paul.*

The objective of this study was to examine social rank during the close up prepartum period and its association with health, reproduction, and milk production during early lactation. The study was conducted in a freestall sand-bedded dairy farm in south-central Minnesota from June to August 2011. One hundred and 90 Jersey cows were enrolled in the study 5 weeks before expected calving date. Cows were balanced for body condition score and those cows with locomotion score >2 were not included in the study. Displacements from the feed bunk were measured during 3 h on the day of move-in (d0) at 13:00 ± 1:00 and following fresh feed delivery (05:00 ± 1:00) on d 1, 2, 3 and 7 of each wk. A displacement index was calculated as the number of displacements initiated by a cow divided by the number of displacements initiated plus number of displacements received by a cow. Cows with a displacement index of <0.4 were categorized as low-ranking, 0.4 to 0.6 middle-ranking, and >0.6 were considered high-ranking. Health events for the first 100 DIM, milk production and composition for the first 3 DHIA tests, and first breeding pregnancy rate were recorded for each cow. The Logistic procedure was used to evaluate health and reproductive events. The Mixed procedure was used to analyze milk and milk composition. There was no association of social rank with retained placenta, metritis, death, displaced abomasum, and mastitis events. Displacement index was associated with first breeding pregnancy rate ($P < 0.01$). Middle rank cows were 3 times more likely to become pregnant after first AI than low ranking cows with no differences between low ranking and high ranking cows. There was no association between milk production and social rank. Percent milk fat from the second test was associated with social rank ($P = 0.04$). Milk fat percentage was greater in low ranking cows than high-ranking cows (4.1 ± 0.13 vs 3.7 ± 0.16%). Middle-ranking cows, however, had similar milk fat percentage to low and high-ranking cows. In summary, social rank in the prepartum period was associated with pregnancy status and 2nd test milk fat percentage in early lactation dairy cows. However, pregnancy status may be more complex than simply being associated with social rank.

Key Words: social rank, displacements, dry cow

W13 To move or not to move: When should dairy cows be moved to maternity pens? K. L. Proudfoot*[1], M. B. Jensen[2], and M. A. G. von Keyserlingk[1], *[1]University of British Columbia, Vancouver, British Columbia, Canada, [2]Aarhus University, Tjele, Denmark.*

Cows are often moved from a group to an individual maternity pen just before calving. However, moving cows too soon before calving may alter their behavior and delay labor. The aim of this study was assess if moving cows to a maternity pen at different time periods before calving would influence labor or cow behavior. Thirty-six multiparous Holstein dairy cows were moved from a group to 1 of 10 maternity pens adjacent to the group pen. Cows were moved either 3d before calving, or when signs of calving were present. The time of moving relative to calving was determined retrospectively and cows were assigned to 1 of 3 treatments: "very late" (2.5 ± 1.2 h (mean ± SD) range 1.5 to 5 h; n = 12), "late" (12.9 ± 4.0 h, range 8 to 20 h; n = 12) or "early" (83 ± 23 h, range 37 to 122 h; n = 12). Calves were weighed within 12 h of birth. Using video, behavioral data collected 4 h before calving was used to approximate the length of the second stage of labor (the time between first 'expulsive' contractions, recorded when the cow's abdomen engaged in rhythmic movements, to the delivery the calf). During the 1h before calving we recorded the total time of contractions, lying time and number of position changes made by the dam. The effect of treatment on these variables was tested with ANOVAs (Proc GLM in SAS); treatment was a fixed effect and calf BW and cow parity were covariates. There was an effect of treatment and calf BW on the length of the second stage of labor; cows with heavier calves ($P = 0.01$) and those moved very late took longer to expel the calf (very late = 76.6 ± 6.9, late = 56.9 ± 5.6, early = 58.3 ± 6.6 min; $P = 0.02$). Cows with heavier calves spent more time having contractions 1 h before calving ($P = 0.03$), but there was no effect of treatment ($P = 0.42$). Cows moved very late spent twice as much time standing 1h before calving (very late = 25.5 ± 4.5, late = 12.4 ± 3.6, early = 11.6 ± 4.3 min; $P = 0.01$), but there was no effect of treatment on the number of position changes ($P = 0.85$). Results suggest that moving cows within 5h of calving from a group to a maternity pen prolongs the second stage of labor, and this may partly be driven by a longer time spent standing during the final hour before calving.

Key Words: transition, labor, calving

W14 Web forums as a method for engagement on contentious issues in dairying: Should cows have access to pasture? M. A. G. von Keyserlingk,* C. A. Schuppli, and D. M. Weary, *University of British Columbia, Vancouver, BC, Canada.*

Animal welfare is emerging as one of the key social concerns regarding animal agriculture. Key welfare concerns include poor biological functioning (such as ill health), negative affective states (such as pain and distress), and inability to engage in important natural behaviors (such as the ability to walk and turn around in tethered cattle). Some concerns are shared broadly by the public and within the dairy industry. In other cases, practices within the dairy industry may fall out of step with public expectations in part because the industry lacks mechanisms to discuss these issues. For example, many producers no longer provide access to pasture for dairy cattle, but people outside the industry may view pasture and grazing behavior as important elements of cattle welfare. We used web-based virtual "town hall" meetings to provide opportunities for people to comment on the question "Should dairy cows be provided access to pasture"? A total of 178 people participated in 5 web forums. Across all groups the majority of participants (73%) chose "Yes," 24% chose "Neutral" and 3% chose "No." Responses varied with participant demographics, but the large majority of both producers (89%) and people not associated with the industry (91%) felt that cows should be provided access to pasture. Veterinarians, other dairy industry professionals and students, often chose "Neutral" (43%); the reasons participants used to explain their neutral votes included that they considered pasture access desirable but difficult to achieve on some farms because of a lack of available land, and concern about reduced milk production. That the majority of respondents indicated that cows should have pasture access suggests that common practice in the dairy industry (i.e., a high usage of zero grazing systems) does not correspond with widely held values of participants both within and outside of the dairy industry.

Key Words: animal welfare, attitudes, grazing

W15 Social learning of feeding behavior in weaned pigs: Effects of the familiarity with conspecific model on flavor preferences. J. Figueroa,* D. Solà-Oriol, J. F. Pérez, and X. Manteca, *Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

It has been observed in other species that feed cues can be transferred from one animal (demonstrator) to another (observer) due to a social learning process. The aim of this experiment was to evaluate if preferences for a flavor can be modified by previous interactions with conspecifics in pigs and if acquired preferences are affected by the familiarity of the demonstrator. A total of 256 piglets (49-d-old) were used. Animals were separated in 2 groups depending on the familiarity of the demonstrator/model. Sixteen pens (8 pigs/pen) were used for the familiar demonstrator condition (G1). Four animals per pen were randomly selected to act as observers and 4 as demonstrators. Demonstrator animals were temporary moved to an empty pen where a flavored feed (anis (A) or garlic (G); 0.075%) were offered for 30 min. After that, demonstrator piglets were mixed again with the observer animals for 30 min. In the unfamiliar demonstrator condition (G2), the same procedure was performed but unfamiliar next-door pen demonstrators were used. Flavors were counterbalanced across pens to act as the social or control flavor. After interaction time, a double choice test (DCHT) between A and G flavored feeds was performed in each observer group. Feed intake was measured after 30 min. Data was analyzed by using the GLM procedure of SAS. Intake was higher in observer pigs when the flavors had been previously eaten by familiar rather than by unfamiliar demonstrators (264g vs. 167g; $P < 0.01$). Animals that learned from a familiar conspecific showed higher intakes of the social learned flavored feed over the control flavored feed (264g vs. 154g $P < 0.005$). On the other hand, animals that interacted with unfamiliar conspecifics did not show different intakes during the DCHT between both feeds. It is concluded that piglets, like other mammals, are able to prefer flavors previously learned by social interactions, and that the familiarity of a conspecific demonstrators play a key role in learning probably due to less aggressive behaviors that allows them to get a close mouth to mouth contact.

Key Words: social, learning, pigs

W16 Effect of feeding DDGS diets on behaviors of gestating sows in different housing systems.

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The high fiber content of DDGS (distillers dried grain with solubles) may affect behaviors and welfare of limited-fed gestating sows both in stalls and group-housed systems. A study was conducted to investigate the effect of feeding diets containing DDGS on stereotypic behaviors of gestating sows housed in individual stalls (n = 27, wt = 176.8 ± 16.5 kg) and aggression in group-housed system (n = 40, wt = 174.3 ± 14.1 kg). All focal sows (parity 1 and 2) were fed either control or treatment diets during their previous gestation and lactation. Control diets (CON) were corn-soybean meal based formulated according to NRC (1998) recommendations for gestating or lactating sows. Treatment diets (DDGS) were nutritionally identical to CON but included 40% DDGS during gestation and 20% during lactation. Behaviors of focal sows were video-recorded for 24 h during 4 to 8 d after breeding. For group-housed sows, video-recording was conducted immediately after mixing, and was analyzed by continuous observation of aggressive interactions involving focal sows during the entire 24 h. For stalled sows, video-recording occurred 10 d after sows were moved into stalls, and analyzed by instantaneous scan sampling of behaviors of interest (resting, eating, stereotypies, and others) at 5-min intervals for 24 h. Data were analyzed using Proc Glimmix of SAS. In the group-housed system, sows fed DDGS were more aggressive, fought for longer periods (16.49 vs. 3.98 s/sow/h; $P = 0.05$) and tended to fight more frequently (0.82 vs. 0.37 fights/sow/h; $P = 0.06$) compared with CON sows. In gestation stalls, sows fed DDGS spent more time resting (73.1% vs. 66.4%; $P = 0.02$) and less time performing stereotypic behaviors (23.3% vs. 28.5%; $P = 0.05$) compared with CON sows. Eating behavior was not affected (2.3% vs. 2.9% for treatment and CON, respectively) by dietary treatment. These results indicate that the effect of feeding DDGS diets on behavior and welfare of gestating sows depended on housing system. In the group-housed system, dietary DDGS increased aggression among sows at mixing, and consequently, may compromise welfare of sows. However, in gestation stalls, sows fed DDGS spent more time resting and less time performing stereotypic behaviors, indicating improved satiety and welfare of sows.

Key Words: behavior, DDGS, sow housing

W17 Piglet behavior as a measure of viability.

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The aim of the study was to develop a vitality scoring method based on piglet behavior which may be related to piglet growth and mortality during lactation. Two hundred sixty-six piglets, from 21 multiparous sows, were used. Within 3 h after the end of the farrowing (d 0), piglets were weighed and individually tested for 2 parameters (Table 1) in a circular enclosure (55cm diameter) receiving a U and N score and a total UN score (sum of U and N: 0–3). All the sows that needed intervention during farrowing were excluded, and piglets were not removed from the dam. Piglets were weighed again on d 1 and d 20 (weaning). Piglet rectal temperature (RT) was recorded on d 0, 1, 2 and 3. Sow farrowing information was also recorded. Regression analyses were performed using GLIMMIX procedure of SAS for survival, and GLM procedure of SAS for body weight (BW) gain and RT. Piglet BW gain at weaning was influenced by BW at birth ($P < 0.001$), sow parity ($P < 0.05$), total number of piglets born per sow ($P < 0.001$) and UN score ($P < 0.05$). Piglet rectal temperature on d 3 was influenced by BW at birth ($P < 0.001$), litter weight ($P < 0.001$), and UN score ($P < 0.05$). Piglet survival during lactation was influenced by BW at birth ($P < 0.05$), N score ($P < 0.05$) and RT on d 3 ($P < 0.10$). Furthermore, N score is highly related with piglet survival and may be a good criterion to identify piglets with a low viability. UN score, in combination with BW at birth and information of the sow might be useful to predict piglet performance during lactation, thus becoming a useful tool to improve piglet management during the first days of lactation. In conclusion, UN score seems to be an easy way to assess piglet vitality for both scientific and commercial purposes.

Table 1. Description of the two different parameters evaluated to establish the vitality of the piglets

Udder searching (U)
- 0: No searching or udder stimulation behavior within 30s.
- 1: Searching or udder stimulation behavior within 30s.

Number of rounds (N)
- 0: Not able to turn 360° nor walk along the limits of the enclosure
- 1: Able to turn 360° or walk along the limits of the enclosure within 30s.
- 2: Able to turn 360° or walk along the limits of the enclosure at least twice within 30s.

Key Words: pig, viability, behavior

W18 Habitat selection and ranging patterns of the African elephant (*Loxodanta africana*) in the Pongola game reserve, South Africa.

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African elephants (*Loxodanta africana*) were reintroduced to the Pongola Game Reserve (PGR), South Africa, in 1997 via translocation. Fourteen elephants established the original population in the 73.6 km^2 reserve and it has since grown to over 50 individuals. Elephant conservation and management has continued to increase in importance throughout the southern African countries, and along with efforts of Space for Elephants, the PGR currently monitors herd health and behavior, as well as habitat use of the elephants. The purpose of this research was to establish the unique dry season ranging patterns of the main herd of female elephants and bull elephants to help determine how they were utilizing the area within the reserve and what habitats they are selecting. Selection ratios were calculated using Jacob's Index to determine the degree of selection in each habitat. A total of 412 GPS location were collected between May and August, ranging patterns showed that the main herd has expanded to the western side of the reserve, increasing possible ranging area by 40 km^2. Selection ratios for both the main herd and bulls showed a positive selection of 0.59 and 0.54 respectively for Floodplain Grasslands (6.0% of total area of the reserve) and ratios of 0.48 and 0.40 for *Euclea* and *Acacia* thickets (4.2% total reserve area), areas that should have comparatively high moisture levels due to the presence of the Jozini Dam. Negative selection indices were calculated, −0.23 for the herd and −0.14 for bulls, for River line thickets (3.3% total reserve area), and −0.69 and −0.62 for *Acacia* and *Marula* Woodland (38.9% total reserve area). Results of this study indicate that the elephants are expanding their home ranges due to population increases and that dry season ranging patterns are mostly driven by the presence of water and vegetation quality. Further population control methods or herd size reduction may be required to sustain the population and avoid detrimental environmental damage.

Key Words: African elephant, ranging, selection conservation

Animal Health III

W19 Impaired vitamin E status in post-partum dairy cows as a complication of left displaced abomasum. G. Bobe,* K. Lytle, and M. Traber, *Oregon State University, Corvallis.*

Left displaced abomasum (LDA), a costly disease in early lactation dairy cows, is associated with hepatic lipidosis, inflammation, and increased hepatic lipid peroxidation. Alpha tocopherol (ATOC) is an antioxidant that can limit lipid peroxidation and potentially inflammation. The objective of this study was to evaluate the serum ATOC status in multiparous dairy cows with and without LDA. We hypothesized that the oxidative damage postulated to be associated with LDA depletes Vitamin E reserves and results in serum ATOC concentrations that are indicative of deficiency (<7.4 μM). Blood samples were taken at approximate prepartum d −28 (−34 to −27), −21 (−26 to −18), −14 (−17 to −11), −7 (−10 to −5), −3 (−4 or −3), −1 (−2 or −1); and d 0, 1, 3, 7, 14, 21, 28, 35, 42, and 49 postpartum. Serum concentrations of ATOC, cholesterol, haptoglobin, nonesterified fatty acids, and β hydroxybutyrate were determined in samples from cows that were visually healthy ($n = 9$) and those that developed LDA ($n = 7$). Serum ATOC concentrations decreased in healthy cows during the first wk postpartum to a nadir of 7.7 ± 0.9 μM and increased back to prepartal concentrations (~13 μM) by 28 d postpartum. By contrast, LDA cows′ serum ATOC concentrations between d 14 and 49 postpartum remained depressed compared with those in healthy cows (all $P < 0.01$). On average, LDA cows had serum ATOC concentrations <7.4 μM between d 3 and 21 postpartum. At d 14 postpartum, all LDA cows had ATOC concentrations <7.4 μM, which remained <10 μM until d 49 postpartum. Concentrations of ATOC concentrations were inversely associated with serum concentrations of haptoglobin ($r = -0.35$), nonesterified fatty acids ($r = -0.54$), and β hydroxybutyrate ($r = -0.50$) and positively associated with cholesterol concentrations ($r = 0.54$; all $P < 0.001$). These results demonstrate that LDA cows have an inadequate serum ATOC status, which may be caused by increased oxidative stress, or a result of liver damage and impaired lipoprotein secretion, a complication of hepatic lipidosis. Pre- or postoperative vitamin E alimentation may improve the recovery of cows with LDA.

Key Words: dairy cows, left displaced abomasum, serum alpha tocopherol

W20 Validation of three sampling strategies for estimating lameness prevalence in dairy herds. A. Hoffman[1], D. A. Moore*[1], J. R. Wenz[1], and J. Vanegas[2], [1]*Washington State University,* [2]*Oregon State University.*

Lameness is an important problem in dairy herds because it decreases production and reproductive performance, increases culling, and has a negative impact on animal welfare and longevity. Monitoring farm lameness prevalence has utility for dairy producers and veterinarians in their efforts to reduce lameness, animal welfare assessment programs, and researchers. Locomotion scoring is a method used to quantify lameness and calculate prevalence. Due to the time necessary to locomotion score each cow, a herd sampling strategy that allows one to score less cows would be useful. Such a sampling strategy must be validated for accuracy in comparison to true lameness prevalence. The purpose of this study was to assess the accuracy of 3 previously suggested methods of estimating lameness by strategic sampling of a dairy herd. Sampling strategies tested include: (1) sampling a calculated number of cows in the middle third of the milking parlor exit order, (2) sampling a calculated number of cows weighted across pens and distributed evenly within each pen, and (3) sampling all cows in a high production pen, a low production pen, and the hospital pen. All cows on 5 dairy farms in Washington and Oregon ($n = 4,550$) were locomotion scored to determine true herd level lameness prevalence. Additionally, milking order and order observed in pen was recorded for each cow. Individual cow data on days in milk and parity was collected from farm computer records. Information on pen grouping strategy was collected by interview with farm management. Sampling strategies were then tested using the locomotion score data set. Estimated prevalence using sampling strategy 1 and 2 were not statistically different than true herd level prevalence ($P < 0.05$), as true lameness prevalence fell within the 95% confidence interval of the sample proportions. Strategy 3 accurately estimated the lameness prevalence on one farm, but overestimated prevalence on 3 others. These data show that the sampling strategies using the middle of milking parlor exit order and a calculated sample distributed across the herd may be used to accurately estimate herd lameness prevalence.

Key Words: dairy, lameness, prevalence

W21 Effects of feeding endophyte-infected fescue seed to Holstein cows during the dry period on plasma nitric oxide (NO), xanthine oxidase (XO), and haptoglobin (Hp) status in newborn calves. S. Kahl*[1], T. H. Elsasser[1], R. L. Baldwin VI[1], A. V. Capuco[1], P. Grossi[2], and K. R. McLoad[3], [1]*USDA, Agricultural Research Service, Beltsville, MD,* [2]*Istituto di Zootecnica, Università Cattolica, Piacenza, Italy,* [3]*University of Kentucky, Lexington.*

Fescue toxicosis in cattle, caused by ingestion of endophyte-infected fescue (EIF), is associated with decreased feed intake, growth, milk production and reproductive efficiency as well as decreased resistance to heat, transportation and immune stress. Increased inflammatory response to immune challenge was also reported in steers grazing EIF. The purpose of this study was to evaluate whether in utero exposure to ergot alkaloids from EIF seed fed to cows during the dry period would affect the developmental pattern of plasma indicators of birth stress in newborn calves. Starting at 90-d prepartum, multiparous Holstein cows were fed endophyte-free fescue seed (CON; $n = 9$) or EIF seed as 10% of the as-fed diet (INF; $n = 8$). Newborn calves were separated from their dams after birth. Blood samples were collected from calves within 12 h of birth (d 0) and then at d 4, 7, 14, 21, 28, 35, and 42. No differences ($P > 0.05$) were found between CON and INF calves on d 0 in BW (41 ± 1 kg) and in plasma concentrations of urea nitrogen (PUN; 7.1 ± 0.4 mg/dL) and the acute phase protein, Hp (0.20 ± 0.04 mg/mL). However, on d 0, plasma concentrations of nitrate+nitrite (NO_x; an estimate of NO production and neonatal vascular adaptation) were lower (155 vs. 223 μmol/L; $P < 0.01$), whereas XO activities (generation of oxygen-derived free radicals) were greater (9.07 vs. 3.27 mU/mL; $P < 0.01$) in INF than in CON calves. Plasma Hp concentrations were greater ($P < 0.05$) at d 4 (0.44 vs. 0.29 mg/mL) and 7 (0.55 vs. 0.38 mg/mL) in INF than in CON calves although no differences were found thereafter. Between d 4 and 42, time related developmental changes in calf plasma PUN, NO_x and XO levels were observed ($P < 0.01$) but they were not affected by the dam's dietary treatment. These results indicate that feeding toxin-associated components of EIF seed to dairy cows altered selected plasma indicators of birth stress in newborn calves during the first week of life but had no long-term effect on the developmental pattern of these mediators.

Key Words: fescue, Holstein calves, neonatal stress

W22 Leukocyte profiles of cows with claw horn disorders. K. K. M. O'Driscoll* and B. Earley, *Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath, Ireland.*

Claw horn disruption (CHD) in dairy cows weakens the integrity of the hoof, results in lesions ranging in severity from mild hemorrhages to ulcers, and can cause lameness and pain. These 2 studies examined the hematology profiles of cows with sole ulcers (the most severe pathology associated with CHD), and of cows with moderate and severe hemorrhaging, with sound cows. Study 1: 12 cows clinically lame due to solar ulceration were identified using locomotion and hoof scoring. These were paired with cows (sound) of similar lactation number, DIM, BCS and liveweight, that had healthy feet. Study 2: Cows (n = 41) were locomotion and hoof scored at 111 ± 23 DIM, then assigned to 3 categories on the basis of hemorrhage score; 1 = no/minimal hemorrhage, 2 = moderate hemorrhage; 3 = severe hemorrhage. Blood samples for both studies were taken via jugular venipuncture on the morning of hoof scoring. Total leukocyte, neutrophil (N), lymphocyte (L), monocyte, eosinophil and basophil counts were determined within 3 h of blood collection from K3EDTA anti-coagulated blood (6 mL) using an automated hematology analyzer (ADVIA 2120, Bayer Healthcare, Siemens, UK). All data were analyzed using PROC MIXED in SAS v9.1. Study 1: Cows with ulcers had higher locomotion scores than sound cows (13.5 ± 0.54 vs. 6.7 ± 0.54; $P < 0.001$). There was no difference in total leukocyte counts, neutrophil, lymphocyte, or monocyte count, or of eosinophil or basophil count and percentage. However cows with ulcers had higher neutrophil % ($P < 0.05$) and tended to have a lower lymphocyte % ($P = 0.1$) than sound cows. Ulcer cows had a higher N:L ratio (1.04 ± 0.1) than sound cows (0.76 ± 0.1; $P = 0.05$). Study 2: There was no effect of hemorrhage category on locomotion score or on any hematology variable. Cows that were clinically lame with sole ulcers had a leukocyte profile indicative of systemic inflammation and stress. A similar pattern was not evident in study 2. It is possible that only CHD severe enough to cause clinical lameness, and thus a sickness response, affects leukocyte profiles.

Key Words: dairy cow, lameness, leukocyte

W23 Investigation on a bio-hygienizing additive for oral use in dairy cows: Effect on milk somatic cell count. P. Luparia*[1], M. Poggianella[1], and V. Bronzo[2], *[1]SOP srl, Busto Arsizio, VA, Italy, [2]Universita di Milano, Milan, Italy.*

The aim of the present study was to assess the efficacy of a technological feeding additive, put into the mixing wagon, on the somatic cell count in milk from a commercial farm situated in Northern Italy, housing 140 lactating cows on straw which were bedding packs renewed every 60–90 d. The commercial bio-hygienizing product (SOP GOLD COW), based on an inert material (verxite) treated with the frequential blend SQC 233, was monitored from April 2011 until September 2011, a period chosen for its critical somatic cell levels due to the seasonal increase in temperature. The most striking characteristic of this product is that it can be mixed directly with the feed in the mixer wagon, at a dosage of 2g /head (0.07 oz), once a day. The data gathered, resulted from official DHI controls (Dairy Herd Improvement test date) carried out, cow by cow, on a monthly basis and regarded the SCC level, fat %, protein % and average daily milk production. The data was elaborated using the statistical software SPSS 19.0 (IBM, SPSS, New York, U.S.A.) and compared the average SCC values with the linear score (LS) via analyses of the variance in the generalized linear model. The decrease in the SCC levels in the treated animals' milk was significant at 99% ($P < 0.01$). On monitoring the data regarding the qualitative component of the milk, the index used to evaluate the correct functioning of the rumen during this study did not show any statistically significant difference, as neither the data regarding milk production. Further investigations are planned to explore any beneficial influence of the product on the cellulosolytic ruminal bacteria populations.

Key Words: SCC, hygiene, cow

W24 Oral administration of lipopolysaccharide and lipoteichoic acid modulated innate and humoral immunity in periparturient dairy cows. S. Iqbal,* Q. Zebeli, D. A. Mansmann, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, Alberta, Canada.*

Various investigators have indicated that cell-mediated and humoral immune functions are suppressed in dairy cows around parturition. As a result, dairy cows are affected by different infectious diseases immediately after calving including infection of the mammary gland (mastitis), and uterus (metritis). The cause of infectious diseases are the presence of pathogenic gram-negative and gram-positive bacteria in the infected tissues. The objective of this study was to investigate immune responses 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 a flat dose of LTA from *Bacillus subtilis* (i.e., 120 μg/animal). Blood samples were collected on wk -4, -1, $+1$, and $+4$ around parturition and analyzed for plasma anti-LPS immunoglobulin-(Ig)A, IgG, and IgM, serum amyloid A (SAA), lipopolysaccharide binding protein (LBP), tumor necrosis factor-α (TNF-α), and Interleukin-1 (IL-1). Results indicated that cows treated with oral LPS-LTA had lower concentrations of plasma anti-LPS IgA, IgG, and IgM antibodies compared with the control group ($P < 0.01$). Furthermore, results showed a tendency for the concentration of plasma LBP to be lower in the treatment group ($P < 0.10$). Additionally, no differences were found in the concentration of plasma SAA between the control and the treated cows ($P > 0.05$). Also, cows treated with oral LPS and LTA had lower concentrations of TNF-α in the plasma ($P = 0.02$); whereas IL-1 was numerically lower, particularly during the week following parturition, although the value did not reach significance ($P = 0.60$). Altogether, results of this study indicated that repeated oral administration of LPS from *E. coli* 0111:B4 and LTA from *Bacillus subtilis* modulated systemic innate and humoral immune responses in periparturient dairy cows around parturition.

Key Words: lipopolysaccharide, lipoteichoic, innate and humoral immunity

W25 Repeated oronasal administration of lipopolysaccharide modulated selected markers of innate and humoral immune responses in periparturient dairy cows. S. Iqbal,* Q. Zebeli, D. A. Mansmann, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, Alberta, Canada.*

Dairy cows go through a decrease in their immune response around calving. This is associated with increased incidence of infectious diseases. There is a scarcity of research regarding strengthening of immune responses against common bacterial agents. In this study, we investigated the innate and humoral immune responses to repeated oronasal application of lipopolysaccharide (LPS) during the transition period in periparturient dairy cows. One hundred primiparous (P) and multiparous (M) Holstein dairy cows with average BW of 620 and 720 kg, respectively, were randomly assigned into control (CTR; $P = 18$; $M = 32$) and treatment (TRT; $P = 19$; $M = 31$) groups. Treatment cows were administered increasing doses (0.01, 0.05, and 0.1 μg/kg BW) of LPS from *Escherichia coli* 0111:B4 oronasally (1 mL nasally and 2 mL orally) or carrier alone (3 mL of 0.85% saline) twice a week on wk −4, −3, and −2 before the expected day of parturition. Blood samples were collected from the tail vein on wk −4, −1, +1, and +4 around parturition and analyzed for plasma anti-LPS immunoglobulin-(Ig)A, IgG, and IgM antibodies, serum amyloid A (SAA), lipopolysaccharide binding protein (LBP), tumor necrosis factor-alfa (TNF-α), and interleukin-1 (IL-1). Overall, results indicated that the treatment cows had numerically greater concentrations of plasma anti-LPS IgM ($P = 0.32$) and IgG antibodies, particularly during the wk following parturition with a sharp increase in the plasma anti-LPS IgG antibodies, although the value did not reach significance ($P = 0.40$). Additionally, plasma anti-LPS IgA antibodies were slightly lowered in the treated cows compared with the control group ($P = 0.32$), and this effect was more pronounced on wk 4 following parturition ($P < 0.01$). Moreover, there was a treatment by time interaction for plasma SAA, which was lower in the treated cows ($P < 0.01$) after parturition. There was no effect of oronasal LPS on plasma TNF-α and IL-1 ($P > 0.05$). In conclusion, oronasal treatment of prepartum dairy cows with LPS modulated selected plasma markers of the innate and humoral immune responses suggesting that oronasal treatment of periparturient dairy cows with bacterial LPS might modulate their immune status.

Key Words: lipopolysaccharide, Innate immunity, humoral response

W26 Effect of polyunsaturated fatty acids (PUFA) on the infection of bovine epithelial cells with *Chlamydia psittaci*.

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In cattle, several clinical syndromes but also subclinical infections compromising performance caused by *Chlamydia* (*C.*) infection are known around the world. The prevalence is high, the benefit of therapeutic antibiosis is limited, vaccines for cattle are not consistently available, and most efforts to control the infection thus focus on hygiene management. PUFA are known for their immune modulating effects; moreover, when considering the response of epithelial cells to infection with the obligate intracellular *C.* bacteria, PUFA are promising candidates to mitigate *C.* infection. We thus aimed to test various PUFA in a bovine epithelial cell line for their potential of reducing *C.* infection rates. Epithelial cells from embryonic bovine lung (EBL, DSMZ ACC192 provided by BgVV, Jena, Germany) were seeded at 1,5 x10^5 cells/mL and preincubated for 24 h in presence or absence of the individual PUFA (C18:3n-3, C18:3n-6, C18:2n-6, C18:1n-9, C20:4n-6, C20:5n-3, *cis*-9,*trans*-11-conjugated linoleic acid (*c*9,*t*11-CLA), and *t*10,*c*12-CLA) at 33 or 100 μM. Cells were then infected with *C. psittaci* DC15 at 4 cfu/cell in presence of PUFA. After 48 h incubation, cells immunofluorescence stained for *C.* were subjected to flow cytometric quantification (Grün et al. 2009. J Microbiol Methods 78:360–2). Prior to the experiments, culture and infection conditions were optimized; the uptake of PUFA into the cells as well as undisturbed viability of the cells in the presence of PUFA was confirmed. The portion of *C.* positive cells in the presence of PUFA was compared with the solvent (DMSO) control using 5 replicates per combination. From all PUFA tested, *c*9,*t*11-CLA and C20:4n-6 were able to reduce the infection rates. The effect of C20:4n-6 was dose-dependent and significant at 100 μM (by 42% reduced infection rate, $P < 0.01$, as determined by Student's *t*-test), whereas *c*9,*t*11-CLA caused a reduction by 29% already at 33 μM ($P < 0.05$,). At 100 μM, no further effect was observed for *c*9,*t*11-CLA. Based on our results, the spectrum of beneficial effects of C20:4n-6 and *c*9,*t*11-CLA might be extended to antichlamydial effects at least in vitro.

Key Words: chlamydia, polyunsaturated fatty acids, bovine cell line

W27 Immune status of dairy calves in the northern plains of Costa Rica: Year 1.

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The objective of this study was to characterize the immune status of dairy calves in the Northern Plains of Costa Rica. The data correspond to total serum protein (TSP) measurements obtained during the period of August and November 2010 on 57 dairy farms. Of 506 animals sampled, 267 suckled colostrum from their dams and 239 received colostrum by bottle. Dam breeds were classified into Holstein, Jersey, Holstein × Jersey crosses, and other. For the purpose of this study, failure of passive immunity was considered when TSP concentration was <5.5 g/dL. Concentration of TSP ranged from 2.8 to 11.0 with an overall mean of 6.2 g/dL. Failure of passive transfer was observed in 31.8% of calves. A higher proportion of male than female calves failed to obtain adequate immunity (35.3 vs. 31.4%, respectively), and male calves had on average lower ($P < 0.05$) TSP than females (5.9 vs. 6.2 g/dL). Calves born to Holstein x Jersey crosses had higher ($P < 0.05$) TSP concentrations than calves born to Holstein dams. Offspring born to first-calf heifers had TSP concentrations of 6.3 g/dL and, compared with other parity groups, fewer of these calves had inadequate transfer of immunity. Method of colostrum feeding did not affect TSP; however, a higher proportion of calves that suckled colostrum showed inadequate passive transfer when compared with calves that received colostrum by bottle (34.1 vs. 29.3%). The findings of this study suggest that colostrum management practices should be improved to minimize the risk of failure of passive transfer in dairy herds in the Northern Plains of Costa Rica.

Key Words: passive immunity, immunoglobulin, total serum protein

W28 Effects of Calibrin-Z on weanling pigs fed diets with naturally occurring deoxynivalenol.

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One-hundred eighty weanling pigs were used to evaluate the effects of Calibrin-Z in diets containing naturally occurring deoxynivalenol (DON) and zearalenone in a 3 × 2 factorial arrangement of treatments (TRT). Pigs were fed a common diet from d 0 to 7. Treatment diets were fed from d 7 to 35 post-weaning (average wt d 7 = 6.76 kg). There were 6 TRT with 6 pens of 5 pigs each, pen was the experimental unit. Data was analyzed for main effects of anticipated mycotoxin effect (MXE) and Calibrin-Z concentration. Single degree of freedom contrasts were used to determine the effect of Calibrin-Z within each MXE. Defusion, (Akey, DEF) had previously been shown to decrease the effects of DON contaminated diets, so the 3 levels of MXE were: 1) low mycotoxins with DEF (LDEF); 2) high mycotoxins with DEF (HDEF); and 3) high mycotoxins without DEF (HIGH). These MXE levels were each fed with Calibrin-Z at 0 or 0.5%. Pigs were allowed to access feed and water ad libitum. The high DON TRT were manufactured with corn and DDGS with 3.3 and 13 ppm, of DON respectively. Zearalenone was found at <1 ppm in the low DON corn and >50 ppm in the high DON corn source. There was no effect of TRT for feed intake or for gain. From d 7 to 35 gain: feed (G:F) showed no difference ($P = 0.14$) between the LDEF, HDEF, and HIGH TRT, with values of 721, 692, and 696 g /kg, respectively. Analyzing the main effect of Calibrin-Z inclusion showed that G:F was not significantly improved ($P = 0.10$) when Calibrin-Z was added at 0.5%, with values of 692 vs. 714 g/kg, without and with Calibrin-Z. There was a MXE x Calibrin-Z interaction as G:F improved most when Calibrin-Z was added to the LDEF diet. When diets within MXE with and without Calibrin-Z were compared the LDEF diet had significantly improved ($P < 0.05$) G:F from d 7–35 with Calibrin-Z addition, with values of 693 g/kg and 749 g/kg for 0 or 5% Calibrin-Z, respectively. These results show that Calibrin-Z can improve feed efficiency in pigs, even under low mycotoxin challenge.

Key Words: mycotoxin, feed efficiency, pigs

W29 Reproductive toxicity of liquid dishwashing detergent on male Swiss albino mice. A. Ata, M. S. Gulay,* S. Gungor, O. Yildiz Gulay, and A. Demirtas, *Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Burdur, Turkiye.*

The aim of this study was to investigate the possible effects of liquid dishwashing detergent on some spermatologic parameters of male Swiss albino mice. Forty healthy male Swiss albino mice (60 d old) were randomly assigned to 5 groups of 8 animals each. Animals in TR1 served as control and received tap water while TR2, TR3, TR4 and TR5 received 0.1, 0.5, 1 and 5% v/v of the liquid detergent in tab water, respectively as the only source of water. The treatments lasted for 35 d (1 spermatogenesis duration). Mice were kept in plastic cages, under standard laboratory conditions. Food and water provided ad libitum. At the end of the experiment, mice were sacrificed under Sevorane anesthesia. For spermatological examinations, right cauda epididymis was excised and placed in a pre-warmed Petri dish containing Dulbecco Phosphate Buffered solution at 37°C for 30 min. Epididymal spermatozoa were used to evaluate spermatozoon concentration, progressive motility, viable spermatozoon rates, intact spermatozoon rates and hypo osmotic swelling positive (HOS+) test. Data were analyzed by one way ANOVA. At the end of the experimental period no differences due to detergent treatment were observed in spermatozoon concentration($P > 0.1$). However, significant differences were detected among the treatment groups for progressive motility (TR1 = 80.87 ± 2.01, TR2 = 75.37 ± 1.30, TR3 = 62.50 ± 3.60, TR4 = 52.12 ± 4.54 and TR5 = 56.00 ± 2.73%; $P < 0.01$), viable spermatozoon rates (TR1 = 84.25 ± 1.88, TR2 = 79.50 ± 1.75, TR3 = 70.50 ± 2.32, TR4 = 59.62 ± 1.77 and TR5 = 60.87 ± 1.48%; $P < 0.01$), and intact spermatozoon rates (TR = 86.12 ± 0.78, TR2 = 85.50 ± 1.16, TR3 = 83.37 ± 1.86, TR4 = 80.12 ± 1.60 and TR5 = 75.12 ± 1.05%;$P < 0.01$), and HOS+ (TR1 = 78.75 ± 1.03, TR2 = 75.37 ± 1.26, TR3 = 63.12 ± 3.99, TR4 = 44.00 ± 6.12 and TR5 = 43.62 ± 2.11%; $P < 0.01$). Therefore, the results of the current study suggested that daily oral consumption of liquid detergent exerted significant adverse effects on spermatologic parameters in swiss albino males.

Key Words: detergent, Swiss albino mouse, reproduction

W30 Valuation of antimicrobial activities of 29 kinds of Chinese herbs against *E. coli*. L. C. Xiao[1,2], X. F. Kong[1], M. Q. Huang[1,2], X. Q. Guo[2], and Y. L. Yin*[1], *[1]Research Center for Healthy Breeding of Livestock and Poultry and Key Laboratory for Agro-ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, Hunan, China, [2]College of Animal Science and Technology, Jiangxi Agricultural University, Nanchang, Jiangxi, China.*

Chinese herbs, which contain many antimicrobial ingredients, are widely used to prevent and treat bacteriosis, especially infectious disease caused by antibiotic-resistant bacterium. To develop effective Chinese herbal extracts as feed additives with antimicrobial activity, the present study was conducted to determine the antimicrobial activity of Chinese herbs against E. Coli isolated from swine production. The aqueous and ethanol extracts (1 g/mL) of 29 kinds of Chinese herbs were prepared, respectively, and then their antimicrobial activities against 10 isolated strains of antibiotic-resistant E. Coli (including SEC023, SEC206, SEC298, SEC470, SEC616, SEC817, SEC911, SEC1284, C193 and C197) and 3 type strains of *E. coli* (including K88, K99 and K101) were evaluated by determining diameter of inhibition zone (IZD, mm). The data showed that the IZD of ethanol extracts from Chinese nut-gall were higher than 20 mm and of its aqueous extracts varied from 9.5 to 13.0 mm against all of the tested *E. coli* strains, as well as of extracts from Thea viridis and Thea nigra; the IZD of both ethanol and aqueous extracts from Weeping forsythia capsule varied from 10.0 to 14.0 mm, as well as from garden burnet root against SEC023, and from Cortex fraxini against SEC1284; the IZD of ethanol extracts from hawthorn fruit were higher than 10.0 mm against SEC470 (11.0), SEC817 (10.3), K101 (10.0) and SEC1284 (10.0), as well as from Granati cortex against SEC470 (13.3), SEC023 (10.3), SEC1284 (10.3), K99 (10.0) and C193 (10.0), and from Coptis root against SEC1284 (16.0), SEC470 (15.0) and SEC206 (10.0), and from Cortex fraxini against K101 (11.5), K88 (10.8), SEC206 (10.8), SEC616 (10.5), C197 (10.5) and SEC470 (10.0). These findings provided some theoretical basis for further study and application of Chinese herbal resources in animal feed.

Key Words: pigs, Chinese herbs, health

W31 Putrescine stimulates the mammalian target of rapamycin signaling pathway and protein synthesis in porcine trophectoderm cells. X. F. Kong[1,2], B. E. Tan[1,2], Y. L. Yin*[1], L. A. Jaeger[3], F. W. Bazer[2,3], and G. Y. Wu[1,2], *[1]Research Center for Healthy Breeding of Livestock and Poultry and Key Laboratory for Agro-ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, Hunan, China, [2]Faculty of Nutrition and Department of Animal Science, Texas A&M University, College Station, [3]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station.*

Impairment of placental growth is a major factor contributing to intrauterine growth retardation in domestic animal production. Growing evidence shows that the polyamines (including putrescine, spermine and spermidine) produced from arginine (Arg) or proline via catalysis of ornithine decarboxylase are key regulators of angiogenesis and embryogenesis as well as placental and fetal growth. However, the underlying mechanisms are largely unknown. The present study was conducted to test the hypothesis that putrescine (Put) stimulates the mammalian target of rapamycin (mTOR) signaling pathway and protein synthesis in porcine conceptus trophectoderm (pTr2) cells. The cells were cultured for 4 d in Arg-free DMEM containing 0, 10, 25, or 50 micromole Put and 100 micromole Arg. Cell count, protein synthesis and degradation, as well as the total and phosphorylated amounts of mTOR, ribosomal protein S6 kinase 1 (p70S6K), and eukaryotic initiation factor 4E-binding protein-1 (4EBP1) were determined. The pTr2 cells exhibited time (0 to 6 d)- and Put concentration (0 to 25 micromole)-dependent increases in the cell count. Addition of 25 micromole Put to culture medium increased the protein synthesis, amounts of total and phosphorylated mTOR and 4EBP1 proteins, as well as the phosphorylated p70S6K. The cell growth were only modestly affected when Put synthesis was inhibited by addition of 1 to 5 mM difluoromethylornithine. Collectively, these findings indicate a novel and important role for Put in promoting growth of porcine placental cells largely via an mTOR signaling pathway, which help to explain beneficial effects of Put supplementation on improving survival and growth of embryos/fetuses in mammals.

Key Words: pigs, growth, nutrition

W32 Dietary arginine supplementation confers immunostimulatory effects on inactivated *Pasteurella multocida* vaccines immunized mice. W. K. Ren[1], Y. L. Yin*[1], L. X. Zhou[2], Y. Wang[2], and Y. Peng[2], *[1]Institute of Subtropical Agriculture, the Chinese Academy of Sciences, Changsha, Hunan, China., [2]Chongqing Key Laboratory of Forage & Herbivorce, College of Animal Science and Technology, Southwest University, Chongqing, China.*

This study was conducted to test the adjuvant effect of arginine on inactivated vaccines immunized mice. Mice immunized with inactivated *Pasteurella multocida* (*P. multocida*) vaccines alone and with dietary 0.2% or 0.5% arginine supplementation showed 100% protection after challenge with *P. multocida* serotype A (CQ2) at dose of 4.4Ã—105 cfu (2LD50). However, the antibody titers in vaccine-0.2% arginine group were much higher than those in vaccine-oil adjuvant group before challenge, meanwhile immunization with inactivated vaccines and dietary 0.2% arginine supplementation significantly increased the antibody titers at 36 h post infection, compared with the mice immunized with inactivated vaccines alone or with oil adjuvant. Furthermore, immunization with inactivated vaccines and dietary 0.2% arginine supplementation significantly increased the serum Interleukin-1 β and glutathione peroxidase levels in comparison with the vaccine and vaccine-adjuvant groups of mice. Collectively, dietary arginine supplementation performs a significant immunostimulatory effects in inactivated *P. multocida* vaccines immunized mice, and dietary 0.2–0.5% arginine supplementation was the optimal supplementation dose in mouse model.

Key Words: amino acids, mice, nutrition

W33 Prevalence of clinical and subclinical ketosis at 8 and 30 days in milk and its relationships with parity, dry period length, peak milk yield and change in body condition score in a Jersey herd in the highlands of Costa Rica. J. M. l. Sánchez* and A. Saborío, *Centro de Investigaciones en Nutrición Animal. Universidad de Costa Rica, San José, Costa Rica.*

The prevalence and grade of ketosis at 8 and 30 d in milk (DIM), as well as its relationships with parity, dry period length, peak milk yield and change in body condition score (BCS) were measured in a 203 cows Jersey herd in Oreamuno, Cartago, Costa Rica (9° 55′ North Latitude, 83° 51′ West Longitude, 2350 m of altitude).The aim was to investigate management and feeding risk factors associated with this metabolic disease. Pre and post calving feeding practices were based on intensive grazing of 30 d regrowth kikuyu (*Kikuyuocloa clandestina*) and on average cows were supplemented with 4 kg of a concentrate mix (14% CP, 1.7 Mcal of NE_L/kg, 35% starch, 0.2% Ca) per day during the close up period, and 4 to 6 kg (20% CP, 1.9 Mcal NE_L/ kg, 48% starch, 1% Ca) in the fresh period. Average BCS at calving was 3.9 (1 to 5 scale). Prevalence of ketosis was determined by measuring blood concentration of β-hydroxybutyric acid (βHBA) at 8 ± 3 DIM in 117 animals and at 30 ± 3 DIM in 114 animals. No clinical ketosis was detected at 8 DIM, and 4.27% of the cows had subclinical ketosis (1.4 to 2.9 mmol/L) during this period. Percentages of cows with clinical (>2.9 mmol/L) and subclinical ketosis at 30 DIM were 3.51 and 9.65, respectively. Incidence of clinical and subclinical ketosis in this herd is under the average prevalence of 15% reported for confinement herds in literature. Cows developing ketosis at 30 DIM lost more body condition during the last week of gestation, than cows that did not develop this disease. During this week, body condition loss for healthy and ketotic cows was 0.09 and 0.31 points ($P < 0.05$), respectively. Cows with ketosis at 30 DIM were of greater ($P < 0.01$) parity, longer ($P < 0.05$) dry period length and greater ($P < 0.01$) peak milk yield. A logistic regression analysis showed that increments of one, 2 or 3 weeks over the 60 d dry period increases the risk of developing ketosis at 30 DIM 1.21, 1.47 and 1.79 times, respectively. Results suggest that scoring body condition during the last week of gestation could be useful to predict the risk of the animals developing ketosis at 30 DIM. Based on these results, management to avoid dry periods in excess of 60 d will help reduce the incidence of ketosis. Furthermore, feeding and management of older cows and higher producing cows to reduce the loss of body condition post calving could also reduce the incidence of ketosis.

Key Words: ketosis, β-hydroxybutyric acid, grazing cows

W34 Effects of soy isoflavones on the male reproductive regulation in Huanjiang male pigs. X. Yuan[1], L. Li[1], J. Fan[1,2], B. Zhang*[2], C. Xiao[3], and Y. Yin[1], *[1]Institute of Subtropical Agriculture, the Chinese Academy of Science, Changsha, Hunan, China, [2]College of Animal Sciences, Hunan Agricultural University, Changsha, Hunan, China, [3]Nutrition Research Division, Food Directorate, Health Products and Food Branch, Health Canada, Ottawa, Canada.*

To evaluate the effects of soy isoflavones on male reproductive regulation in Huanjiang male pigs. Fifty male black small-eared pigs were randomly divided into control group (fed a test diet), low, medium and high doses of soy isoflavones group and diethylstilbestrol group. Three different doses of soy isoflavones (125 mg/kg, 250 mg/kg, and 500 mg/kg) and 0.5 mg/kg diethylstilbestrol were evenly mixed in the feed and fed to pigs for 60 d (The purity of soy isoflavones is 80%). Analysis levels of GnRH, LH, FSH, Tes and E2 by radioimmunoassay; weigh testis and epididymis; the mRNA expression of P450scc, 3Î^2 -HSD and StAR in testicular tissue, which associated with testosterone synthesis, was measured by RT-PCR. In 250 mg/kg soy isoflavones group, testicular index increased by 44.76% than the control group, the difference was significant ($P < 0.05$); serum testosterone level increased by 51.49% than the control group, the difference was significant ($P < 0.05$); mRNA expression of StAR was up to 1.43%, a significant difference with control group ($P < 0.05$). In 500 mg/kg soy isoflavones group, testicular index decreased by 39.92% than the control group, the difference was significant ($P < 0.05$); serum testosterone level decreased by 53.69% than the control group, the difference was significant ($P < 0.05$); mRNA expression of StAR 0.49%, a significant difference with 250 mg/kg soy isoflavones group ($P < 0.05$). Soy isoflavones can affect the male reproductive hormone secretion, the growth and development of testis and epididymis, enzyme activity of testosterone synthesis, and expression of reproductive hormone genes in the brain, and in dosage-dependent ways.

Key Words: soy isoflavones, reproductive hormone, Huanjiang male pigs

W35 Estimate of serum IgG concentration using refractometry with or without caprylic acid fractionation. K. M. Morrill*[1], A. Lago[3], J. Polo[3], J. D. Quigley[3], and H. D. Tyler[2], *[1]Cornell Cooperative Extension, Westport, NY, [2]Iowa State University, Ames, [3]APC Inc., Ankeny, IA.*

The objective of this study was to develop a rapid, calf-side test to determine serum IgG concentration using a refractometer and caprylic acid (CA) fractionation. Serum samples (n = 200) were obtained from 1 d old calves on a single California dairy, frozen and shipped to Iowa State University. Samples were allowed to thaw at room temperature (1 h). Fractionation with CA was conducted by adding 1 mL of serum to a tube containing 45, 60 or 75 µL CA and 0.5, 1.0 or 1.5 mL 0.06 M acetic acid (AcO). The tube was shaken (10 s), allowed to react for 1 min and centrifuged (3,000 × *g*) for 0, 10 or 20 min. Refractive index (nD) of fractionated and whole serum was determined using a digital refractometer (SPER Scientific model 300034). Serum IgG concentration was determined by radial immunodiffusion (RID). The nD of whole and fractionated serum were compared with IgG concentration. Mean serum IgG concentration was 19.0 mg/ml (SD = 9.7) with a range of 3.5 to 47.0 mg/mL. Whole serum nD correlated with IgG concentration (r = 0.86, n = 185). Serum treated with 1 mL 0.6 M AcO and 60 µL CA and not centrifuged before analysis resulted in the strongest relationship between fractionated serum nD and IgG (r = 0.80, n = 45). Regression equations were used to determine cut-points that would be indicative of 10, 12 and 14 mg/mL to determine the sensitivity and specificity of refractometry to identify failure of passive transfer (FPT) calves. Fractionated samples were evaluated by cut-points 1.33895, 1.3392, and 1.3395 nD. The cut-point of 1.3395 resulted in the greatest specificity (100%) and positive predictive value (100%) for fractionated samples; however, 11.1% of samples with adequate IgG were incorrectly classified as inadequate. Whole samples were evaluated by nD cut-points 1.34414, 1.34448 and 1.3448. The cut-points of 1.34448 and 1.3448 resulted in identical specificities (86.67%), while the lower cut-point had a specificity of 60.0%. These results suggest that refractometry of whole or fractionated calf serum provides a strong estimate of IgG concentration and can be used to identify FPT calves before 24 h of age.

Key Words: passive transfer, IgG, refractometer

W36 Haptoglobin is a potential early indicator of postpartal diseases. D. Sabedra[1], E. Ramsing[1], C. Shriver-Munsch[1], J. Males[1], W. Sanchez[2], I. Yoon[2], and G. Bobe*[1], *[1]Oregon State University, Corvallis, [2]Diamond V, Cedar Rapids, IA.*

Haptoglobin is an acute phase protein that is elevated in response to tissue damage and infections in dairy cows. The objective of this study was to evaluate whether serum concentrations of haptoglobin are elevated before clinical signs of diseases can be observed. Blood samples were taken from 161 Holstein cows (2 to 7 parities) at d −28 (−34 to −27), −21 (−26 to −18), −14 (−17 to −11), −7 (−10 to −5), −3 (−4 or −3), −1 (−2 or −1), 0, 1, 3, 7, 14, 21, 28, 35, 42, and 49 postpartum during spring and summer 2010 and analyzed for serum haptoglobin concentrations. Between d −28 and 100 postpartum, cows were monitored daily for signs of diseases and treated according to standard treatment protocols. Based on the severity of the observed symptoms, cows were grouped into 4 health categories: visually healthy (n = 20), mild or subclinical disease (n = 41), severe disease requiring antibiotics, glucose precursors, or both (n = 70), and died or sold within the first 100 d postpartum (n = 30). In healthy cows, serum haptoglobin concentrations were increased in the first week after calving and peaked at d 1 postpartum. Compared with healthy cows, peak concentrations were greater and duration of elevated haptoglobin concentrations was longer in sick cows ($P < 0.001$). Cows that died or were sold had the highest peak concentrations and the longest duration of elevated haptoglobin concentrations ($P < 0.001$). The increase in haptoglobin concentrations in the first wk postpartum was observed in cows with various types of diseases (metritis, ketosis, laminitis, mastitis; all $P < 0.01$). These results suggest that prolonged elevated haptoglobin concentrations in the first week postpartum precede the clinical onset of various diseases and may assist in early detection and treatment of subclinically sick cows during the first phase of lactation.

Key Words: dairy cows, disease, haptoglobin

W37 Bovine hepatic retinol binding protein gene expression and its relationship with tumor necrosis factor-α. P. Rezamand[1], K. M. Hunt[1], J. S. Watts[1], J. D. Blickenstaff*[1], B. J. Bradford[2], and L. K. Mamedova[2], *[1]University of Idaho, Moscow, [2]Kansas State University, Manhattan.*

Circulating retinol binding protein (RBP) transports retinol from the liver to target tissues, has one binding site for retinol in the *all-trans* form, and is bound to transthyretin (TTR). The objectives were to determine the temporal pattern of bovine hepatic mRNA expression of RBP during the periparturient period and whether its expression is influenced by tumor necrosis factor (TNF)-α. In experiment I, hepatic mRNA expression of RBP during the periparturient period was assessed. Liver tissues were sampled from periparturient dairy cows (n = 9) at −21, −4, +1, +7 and +21 relative to parturition. Total RNA was extracted and cDNA was generated. Transcript abundance of RBP and β-actin, as a housekeeping gene, were measured in relative quantity using rt-PCR. Data were analyzed using delta Ct values and significance was determined at $P \leq 0.05$. Cows had variable hepatic RBP expression over the transition period ($P = 0.037$), with a decline around parturition and a rebound toward prepartum levels later in lactation, resembling abundance of plasma retinol. In experiment II, Holstein dairy cows were blocked by parity and feed intake, and randomly assigned to control, recombinant bovine (rb)TNF-challenge or pair-fed control (n = 5/treatment). Cows were either injected with rbTNF (SQ injection of 2 µg/kg BW in saline) or sterile saline (control and pair-fed control) once daily for 7 d. Liver biopsy was performed on d 7 and samples were processed for mRNA expression of RBP, TNF-α and GAPDH. Although TNF challenge caused an upregulation of hepatic TNF-α expression ($P < 0.01$), it did not cause an alteration in hepatic RBP expression ($P = 0.32$). Overall, temporal pattern of hepatic RBP gene expression during periparturient period followed that of plasma retinol. Although a strong positive correlation was previously detected between bovine hepatic RBP and TNF-α transcripts, rbTNF challenge did not cause an alteration in RBP expression. These observations collectively imply that regulation of RBP at the transcription level is influenced by physiological state but may be independent from that of TTR, which is altered by pro-inflammatory stimuli (e.g., TNF-α) via induction of transcription factor nuclear factor-interleukin 6.

Key Words: gene expression, retinol binding protein, TNF-α

W38 Dried citrus pulp modulates the physiological and acute phase responses of crossbred heifers to an endotoxin challenge. N. C. Burdick*[1], J. T. Cribbs[2], J. A. Carroll[1], T. R. Callaway[3], T. B. Schmidt[4], B. J. Johnson[2], and R. J. Rathmann[2], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]Texas Tech University, Department of Animal and Food Sciences, Lubbock, [3]USDA-ARS, Food and Feed Safety Research Unit, College Station, TX, [4]Mississippi State University, Department of Animal and Dairy Science, Mississippi State.*

This study examined the effect of feeding dried citrus pulp (CP) pellets on the physiological and acute phase responses (APR) of newly received crossbred heifers to an endotoxin (lipopolysaccharide; LPS) challenge. Heifers (n = 24; 218.3 ± 2.4 kg) were obtained from commercial sale barns and transported to the Texas Tech Univ. Beef Center. Heifers were separated into treatment groups receiving a Control Diet (C; n = 8), CP10 (10% CP DM basis; n = 8) or CP20 (20% CP DM basis; n

= 8) and were fed for 65 d while being systematically stepped up to a finishing ration. On d 63, heifers were fitted with indwelling vaginal temperature (VT) recording devices and jugular catheters and moved into a barn with individual stalls. On d 64, heifers were challenged i.v. with LPS (0.5 µg/kg BW) and blood samples were collected every 0.5 h from −2 to 8 and again at 24 h relative to LPS challenge (0 h). Sickness behavior scores (SBS) were also assigned following collection of each blood sample. Serum was isolated and stored at −80°C until analyzed for cortisol, interleukin-6 (IL6), interferon-γ (IFNγ), and tumor necrosis factor-α (TNFα) concentrations. Pre-LPS VT were lower in CP10 (38.44 ± 0.02°C) than C (38.74 ± 0.02°C) and CP20 treatments (38.68 ± 0.02°C; $P < 0.01$). There was an increase in VT in all treatments post-LPS ($P < 0.001$), with CP10 (38.69 ± 0.02°C) maintaining lower VT post-LPS than C (38.98 ± 0.02°C) and CP20 treatments (38.97 ± 0.02°C; $P < 0.01$). Post-LPS SBS increased ($P < 0.01$) and were greater in CP10 (1.14 ± 0.02) than CP20 (1.09 ± 0.02) and C (1.03 ± 0.02; $P < 0.01$). Post-LPS cortisol concentrations were greatest in CP10 (68.1 ± 2.1 ng/mL) heifers than C (60.9 ± 2.0 ng/mL) or CP20 treatments (59.5 ± 1.9 ng/mL; $P < 0.01$). Concentrations of IFNγ, TNFα, and IL6 increased post-LPS ($P < 0.01$) and were greater in CP20 (24.6 ± 1.1, 123.03 ± 11.1, and 2370 ± 123 pg/mL, respectively) than CP10 (16.9 ± 1.0, 91.3 ± 11.1, and 1981 ± 124 pg/mL, respectively) and C treatments (12.2 ± 0.9, 19.1 ± 10.2, and 1175 ± 104 pg/mL, respectively; $P < 0.01$). These data indicate that CP inclusion in the diet can modulate both the physiological and APR of newly received heifers to an endotoxin challenge.

Key Words: acute phase response, cattle, citrus pulp

Beef Species

W39 Survey of beef quality assurance on California dairies. S. Aly[1], H. Rossow[1], G. Acetoze*[2], T. Lehenbauer[1], M. Payne[3], D. Meyer[2], J. Maas[4], and B. Hoar[3], *[1]Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California-Davis, Tulare, [2]Department of Animal Science, University of California-Davis, Davis, [3]Western Institute of Food Safety and Security, University of California-Davis, Davis, [4]Veterinary Medicine Extension, School of Veterinary Medicine, University of California-Davis, Davis.*

In October 2010 a mail and internet survey of California's dairy industry was implemented to assess the Dairy Animal Care and Quality Assurance (DACQA) program. The DACQA program, which involves cattle of all ages, benchmarks practices on the dairy that affect the use of dairy cattle for beef. The survey was mailed to a random sample of 1071 California dairies (65%) stratified by county with allocation proportional to density of dairies in each of the state's 32 counties with dairies. Data from the 173 (16%) responses from 19 counties received which represented 10% of the state's milking herd, showed that 90% of culled cows on California dairies were sold for beef. Survey results also showed that personnel from 45% of California's dairies preferred injecting drugs subcutaneously if possible, 97% kept track of withdrawal periods and 49% maintained a form of drug inventory. Personnel who maintained a drug inventory were 3 times more likely to test for drug residues compared with those who didn't (P value 0.02). Furthermore, 44% of personnel of California's dairies reported knowledge of their culled cows' hot carcass weight or USDA carcass grade. In addition to the estimated 34% of California dairies that supported a beef quality assurance certification program, approximately 45% would specifically request more information on such a program. Although few dairies were familiar with the DACQA website, approximately half requested more information on the program. The likelihood that the DACQA certification program would be applied on California dairies is favorable given the interest support for it.

Key Words: beef quality, DACQA, survey

W40 Effects of stabilizing oxidative balance through dietary means on growth performance, antioxidant metabolites and fertility factors in bulls. T. J. Wistuba,* M. Becker, S. Court, and G. I. Zanton, *Novus International Inc., St. Charles, MO.*

One of the most important factors of farm profitability in Australian beef herds is fertility. Numerous factors can influence oxidative balance in livestock (environmental, dietary, health, etc.) and thus fertility, especially in young bulls. Nutritionally Cu, Mn and Zn have been shown to affect superoxide dismutase activity (SOD), Se has an important role in glutathione peroxidase activity (GPX), and dietary antioxidants have been shown to improve overall immune status. The objective of this study was to improve oxidative balance in young bulls through nutrition and measure the response in antioxidant metabolites, semen quality and morphology and animal performance. Two hundred-one Droughtmaster bulls (614.6 ± 35.61 kg) were tested for semen morphology 19 d pre-treatment. Animals were then blocked into pen groups by age, average sperm morphology and BW for apparent maturity and physiological status. The control ration was balanced to meet or exceed NRC (1996) requirements, the treatment diet was the control ration plus 2-hydroxyl-4-methyl-thio butanoic acid (MHA), Agrado Plus dietary antioxidant, Mintrex-Cu, -Mn and -Zn as well as Zorien SeY (Novus International) and was fed for 59 d. The ANOVA was generated utilizing the GLM procedure of STATA version 11 (College Station, TX); model included treatment, date and the interaction between treatment and date. Results indicated no benefit to sperm morphology or performance when compared with control. However, SOD/g Hemoglobin was reduced in both treatment and control. Semen concentrations of GPX increased significantly for treatment when compared with the control ($P = 0.025$). Rectal temperature increased to a greater degree ($P = 0.001$) for control compared with treatment ($P = 0.014$). Additionally, radiant temperature at the testicular surface increased significantly in control during the trial ($P = 0.008$). This study indicates feeding dietary antioxidants, hydroxy methyl analog, chelated trace minerals, and organic selenium can encourage maintenance of antioxidant metabolites.

Key Words: bull development, oxidative balance, semen quality

W41 Phenotypic correlations of the residual intake and gain with ultrasound carcass traits and other feed efficiency measures in Nellore cattle. R. C. Gomes*[1], S. L. Silva[2], M. H. A. Santana[2], J. B. S. Ferraz[2], P. Rossi Jr.[3], and P. R. Leme[2], *[1]Department of Animal Science, State University of Londrina, Londrina, Parana, Brazil, [2]College of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, Sao Paulo, Brazil, [3]Federal University of Parana, Curitiba, Parana, Brazil.*

The residual feed and gain (RI&G) was recently reported as an alternative feed efficiency trait in beef cattle; however, associations of RI&G with carcass traits have not been described. The aim was to evaluate the phenotypic correlations of RI&G with ultrasound carcass traits in Nellore bulls and steers. Individual dry matter intake (DMI) and average daily gain (ADG) were computed in Nellore steers (n = 267, 20-mo old; 346 ± 30 kg initial BW) and bulls (n = 277, 22-mo old; 391 ± 40 kg initial BW) in performance tests that were carried out from 2005 to 2011. Ultrasound backfat thickness (UBFT), rump fat thickness (URFT) and rib eye area (UREA) were measured at the beginning and at the end of each test and the daily gain of each trait was calculated. Residual feed intake (RFI), residual gain (RG) and RI&G were computed using test as a contemporary group effect in the model. Pearson correlation analyses were carried out separately for steers or bulls. Coefficients of correlation of RI&G with feed conversion ratio (FCR), RFI and RG were respectively −0.79; −0.86 and 0.86 for steers and −0.70; −0.87 and 0.87 for bulls ($P < 0.0001$). RI&G, RFI and RG were not correlated with mid-test body weight ($P > 0.05$). For steers, RI&G was not correlated with final UBFT (0.00, $P > 0.05$), final URFT (−0.03, $P > 0.05$) and with the daily gain of both traits (−0.03 and 0.01, respectively, $P > 0.05$). Positive low correlations were observed between RI&G and final UREA (0.13, $P < 0.05$) and with UREA gain (0.14, $P < 0.05$). In bulls, RI&G was not correlated with UREA gain (0.00, $P > 0.05$), final UBFT (−0.06, $P > 0.05$), final URFT (−0.04, $P > 0.05$) and with the gain of both traits (0.08 and 0.02, respectively, $P > 0.05$). A low positive correlation was observed between RI&G and final UREA (0.17, $P < 0.05$). In the same data set, RFI and RG were correlated with UBFT and URFT gains in steers, whereas RG was also correlated with final UREA in both genders. Residual intake and gain is highly correlated with other feed efficiency traits and seems independent of subcutaneous fat deposition, but not rib eye area.

Key Words: beef, *Bos indicus*, gain to feed

W42 Estimation of genetic parameters for carcass and image analysis traits of Japanese Black (Wagyu) in Australia.

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Japanese Black (JB) is the major breed of beef cattle in Japan and is known for high marbling (intramuscular fat). JB were introduced into Australia in the 1990′s with importation of embryos and live JB from USA. Similar to Japan, improvement in marbling is rewarded in some domestic and export beef markets in Australia. The AUS-MEAT marbling score (MS) grading system was designed for rating relatively lean meat. The AUS-MEAT MS system has problems in adequately describing the relatively higher marbling that occurs in JB. The objectives of this study were to estimate genetic parameters for carcass and image analysis traits and to investigate an effective indicator of improving marbling of JB in Australia. Australian bred and raised JB (n = 414) were used for this study. All animals were fed in Australian feedlots and shipped to an Australian abattoir and processed from August 2010 to July 2011. Image analysis traits were collected with a Mirror Type camera taking digital images at the 5th-6th rib cross section. The mathematical model for genetic analysis included sex and month of kill data as fixed effects and slaughter age as covariate. Heritabilities and genetic correlations were estimated by the AIREMLF90 program. The peak of frequency distribution of AUS-MEAT Marbling Score with the range from 1 to 9 was 9. Estimated heritabilities for grading and image analysis traits were 0.23 for MS, 0.59 for HCW, 0.44 for rib eye area, 0.54 for marbling percent (intramuscular fat) (MP), 0.37 for coarseness index of marbling (CIM), 0.55 for fineness index of marbling, 0.32 for minor-major axes ratio of rib eye, 0.08 for complexity of rib eye shape, 0.57 for average luminance of lean, respectively ($P < 0.05$). Heritability of MS was less than MP. These results show that MS is an unsuitable evaluation value for JB, when compared with Image analysis traits for the effective genetic improvement of marbling in Australian JB. However, genetic correlation between MP and CIM was positive (0.33). Thus, marbling improvement using selection for MP may also increase the negative attribute of CIM.

Key Words: Australian Japanese Black (Wagyu), heritability, image analysis

W43 Effect of different feeding system on the fatty acid and lipid oxidation of raw and cooked meat of Sarda-Bruna young bulls.

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Fatty acid composition, nutritional quality and oxidative stability was determined in raw (RW) and cooked (CK) samples of Longissimus dorsi (LD) of 10 Sardo-Bruna young bulls from 2 different feeding systems. After weaning (mean = 8.5 mo of age) bulls were divided into 2 groups: 5 animal reared on pasture during the daylight (5 - 6 h/d) and supplemented with a mixture of concentrate and of meadow hay (P), and 5 confined in stable (NP). Young bulls were slaughtered at about 500–550 kg live weight. Five days after slaughtering, the LD, between 5th and 7th rib, were remove and split into 2 pieces: 50 g of each sample was RW and 50 g was CK in a microwave at 650 W for 45 s to a final internal temperature of 75°C. Lipid oxidation was measured as mg of malondialdehyde (MDA) per kg of meat. Data were analyzed using a model including feeding systyem, cooking and their interaction. Fat content did not differ between P (1.42%) and NP (1.50%) groups in RW samples ($P = 0.68$), whereas it tended to be greater in CK samples ($P = 0.07$) of both groups (2.86% and 2.06 in P and NP, respectively). The RW samples of P group showed a lower content of PUFA n6 (12.7 vs 15.1; $P = 0.07$), and a greater proportion of PUFA n3 (1.7 vs 1.1; $P = 0.08$), with a more favorable n6/n3 ratio (7.6 vs. 14.5; $P < 0.01$) compared with NP group. In particular, the RW samples of P group had higher content of C18:3n3, C18:1t11, CLA c9t11 isomer and odd-branched fatty acids and a lower content of C20:2n6, C20:4n6 and C22:4n6 fatty acids than NP group ($P < 0.05$). The microwave cooking did not change the relative proportion of fatty acid in both feeding system treatment ($P = 0.23$). Lipid oxidation was not influenced by feeding, but was markedly increased by cooking ($P < 0.01$) in P (from 0.07 to 0.52) and NP (from 0.23 to 0.56). The results showed that grazing for few hours per day influenced positively the fatty acid profile of meat from young bulls. Research funded by Associazione Melina, Sardinia, Italy.

Key Words: beef meat, feeding system, fatty acid

W44 Analysis of twin births, calf stillbirth, abortion and calf death before 28 days of age in Irish Charolais and Limousin populations.

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Twinning in beef cattle provides an opportunity for improvements in production efficiency. However, twinning may also have adverse effects on animal welfare and management. A greater understanding of factors associated with twinning will help us to formulate management strategies that will increase twinning while minimizing adverse affects. The objective of this study was to analyze the incidence of twin births in Irish Charolais (CH) and Limousin (LM) herds and potentially associated factors of calf stillbirth, abortion, and calf death before 28 d. Incidence of stillbirth, abortion and calf death before 28 d was analyzed through a comparison between single and twin births. Calving records of CH (n = 110,401) and LM (n = 138,416) herds from 2004 to 2009 were used for the analysis. The mean twinning, calf stillbirth, abortion, and calf death before 28 d was 4.5%,1.84%,0.32%, and 1.73% for CH and 1.5%, 1.35%,0.25%, and 1.45% for LM respectively. Twinning increased as the parity increased (Odds Ratio (OR) = 1.77 for CH parity 5 vs. parity 1; OR = 1.80 for LM parity 5 vs. parity 1). The greatest odds of twinning occurred for calves born in summer for each of the breeds. Calf stillbirth was higher for twin births than for single births in CH (OR = 3.78 twin vs. single birth) and LM (OR = 2.38 twin vs. single birth). Calving difficulty greatly influenced the odds of stillbirth occurring, particularly in twin births, where CH (OR = 16.30 calving score 4 vs. calving score 1) and LM (OR = 33.74 calving score 4 vs. calving score 1). Abortion is also more likely for twin pregnancies than single pregnancies in LM animals (OR = 4.14 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 parity, season, sex of calf and year of calving. This research shows that twinning rate may be affected by breed and age of the dam, and can affect calving difficulty and mortality. Twinning rates are affected by breed and age of the cow and management strategies are therefore required to reduce calving difficulty and mortality where cows are pregnant with twins.

Key Words: twinning, abortion, stillbirth

W45 The effect of limiting feed intake on visceral organ mass and performance in the pregnant beef cow.

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Twenty-two multiparous pregnant beef cows were used to investigate the effect of dietary restriction on the visceral organ mass and cow performance. Cows were fed a haylage-based total mixed ration containing 20% wheat straw at either 85% ($n = 35$; LOW) or 140% ($n = 34$; HIGH) of NEm. Cows were blocked by date of parturition and were slaughtered at approximately 250 d of gestation, after 83 d on dietary treatment and every wk thereafter for 6 wks. Visceral organs were removed of digesta, trimmed of fat and weighed. Statistical analysis was conducted using Proc Mixed in SAS and included the fixed effect of dietary treatment, cow age, block and the random effect of pen. Cows fed HIGH consumed 10.9 kg DM per d and LOW consumed 6.8 kg DM per d ($P < 0.001$). Cows fed HIGH had a greater ($P = 0.003$) ADG than LOW. Cows fed HIGH had a greater final BW than LOW ($P = 0.04$), even though initial BW did not differ ($P = 0.9$). There were no differences ($P \geq 0.32$) between treatments for grade fat, ribeye area or marbling score, while HCW tended to be greater ($P = 0.07$) in HIGH. Rumen weight was greater ($P = 0.02$) in HIGH and liver weight tended to be greater ($P = 0.07$) in HIGH, however these variables expressed relative to HCW were not ($P \geq 0.40$) different. Weights (actual or relative to HCW) of kidney, lungs, heart, pancreas, spleen and lower GI (large + small intestine + cecum) did not differ ($P \geq 0.14$) between treatments. Total visceral fat was numerically greater in HIGH ($P = 0.2$) however large variation was observed. This data indicates that restricted dietary intake impacted the performance of the cow during late gestation, but did not affect visceral organ mass. This data will further the understanding of feed efficiency and maintenance energy requirements in the pregnant beef cow.

Key Words: beef cows, visceral organ mass, feed intake

W46 Whole cottonseed can promote as much rumination activity as barley straw when incorporated in TMR fed beef heifers at finishing period. S. P. Iraira,* J. L. Ruíz de la Torre, M. Rodríguez-Prado, X. Manteca, S. Calsamiglia, and A. Ferret, *Universitat Autònoma Barcelona, Bellaterra, Spain.*

Eight Simmental heifers (initial BW 313 ± 13.2 kg) were randomly assigned to one of 4 experimental treatments in a 4 × 4 double Latin square design. The experiment was performed in 4 28-d periods. Treatments tested were a control diet in which barley straw was used as a fiber source (BS), and 3 diets where the main difference was the non-forage fiber source used: soybean hulls (SH), beet pulp in pellets (BP) and whole cottonseed (WCS). Fiber ingredients were incorporated at 10, 17, 17 and 16% (on DM basis) in BS, SH, BP and WCS, respectively. All diets were offered ad-libitum as TMR and designed according to NRC (1996) to be isoenergetic (2.95 Mcal/kg DM) and isonitrogenous (15% on DM). Animals were individually housed in roofed pens. Intake was recorded over 7 d in the last week of each experimental period. Behavior was recorded for 24-h on d 2 and d 6 of each experimental week using a digital video-recording device. A digital color camera was set up in front of each pen. Recorded activities were registered together with their beginning and ending times. Data for each activity is presented as the total time, expressed in minutes per day, in which the animal showed the specific activity. An observation was defined as eating when the animal had its muzzle in the feedbunk or was chewing or swallowing food with its head over it. Ruminating included regurgitation, mastication and swallowing of the bolus. Intake of DM was statistically analyzed using the MIXED procedure of SAS. To test treatment effect for each behavioral activity, analysis was performed by using the GLIMMIX procedure of SAS. DM intake was higher in WCS than in the remaining treatments (7.9 vs 7.3 kg/d; $P = 0.05$). Time spent eating tended ($P = 0.10$) to be higher in WCS and BP (93 min/d) than in BS and SH (76 min/d). Time spent ruminating was not different between BS and WCS (294 and 249 min/d) but was lower ($P = 0.001$) in SH and BP (168 and 166 min/d). In conclusion, WCS can promote ruminating behavior as much as BS.

Key Words: cattle behavior, concentrate diet, whole cottonseed

W47 Protein supplementation of low-quality forage: Effects of amount and frequency on cow performance and intake and nutrient digestibility by steers. D. W. Bohnert[1], R. F. Cooke[1], B. I. Cappellozza[1], D. L. McGuire*[1], and S. J. Falck[2], *[1]Eastern Oregon Agricultural Research Center, Oregon State University, Burns, [2]Eastern Oregon Agricultural Research Center, USDA-ARS, Burns.*

Two experiments were conducted to determine the effects of supplement amount and supplementation frequency (SF) on performance, DMI, and nutrient digestibility by cattle consuming low-quality forage. Treatments were arranged in a 2 × 3 factorial design (2 levels of CP and 3 SF; CON = unsupplemented; D = supplemented daily; 5D = supplemented once every 5 d; 10D = supplemented once every 10 d; 1/2 D = supplemented at 50% of D; 1/2 5D = supplemented at 50% of 5D; 1/2 10D = supplemented at 50% of 10D). In Experiment 1, 84 cows in the last third of gestation were used in a randomized complete block design to evaluate treatment effects on BW and BCS change while in Experiment 2, 7 steers were used in a 7 × 4 incomplete Latin square to evaluate nutrient intake and digestibility. Soybean meal (SBM) was used as the source of supplemental CP. Full CP refers to D, 5D, and 10D (each full CP treatment received the same amount of CP over a 10 d period) and half CP refers to 1/2 D, 1/2 5D, and 1/2 10D dietary treatments. In Exp. 1, precalving BCS change was more positive ($P = 0.03$) for supplemented treatments. We did note a linear effect of SF × amount of CP for precalving BCS ($P = 0.06$), with full CP treatments decreasing more as SF decreased from D to 10D compared with half CP (0.1 to −0.3 and −0.2 to −0.3, respectively). Straw and total DMI were increased with supplementation ($P < 0.03$) in Experiment 2; however, we observed a linear effect of SF × amount of CP for both variables ($P = 0.02$); DMI with full CP decreased a greater amount as SF decreased compared with minimal change for half CP. Apparent total tract DM, OM, and NDF digestibility was not affected by supplementation ($P > 0.10$), while DM and OM digestibility responded quadratically to SF with lower digestibility occurring on 5D treatments ($P < 0.05$). Plasma urea was greater with supplementation ($P < 0.001$) and for full compared with half CP ($P < 0.001$). Reducing the amount of supplemental CP provided to ruminants consuming low-quality forages, when supplementation intervals are greater than 5 or 6 d, can be a management tool to maintain acceptable levels of DMI, digestibility, and performance while reducing supplement cost.

Key Words: cattle, frequency, supplementation

W48 Using corn stover and DDGS to conserve stockpiled forages and improve reproductive performance and progeny growth in fall-calving beef cows. P. J. Gunn*[1], R. P. Lemenager[1], and G. A. Bridges[2], *[1]Department of Animal Sciences, Purdue University, West Lafayette, IN, [2]North Central Research and Outreach Center, University of Minnesota, Grand Rapids.*

Angus-cross, fall-calving beef cows ($n = 153$; $BCS = 5.4 \pm 0.5$) were used to determine if incorporating a period of corn stover and dried distillers grains with solubles (DDGS) feeding into a preexisting nutritional program that included grazing stockpiled fescue affects reproductive performance and progeny growth. Calving began on Julian d 243. On Julian d 267, cows were stratified and allotted by BW, BCS, and calving date (if calved) to receive 1 of 2 isocaloric dietary treatments through timed-AI (TAI): stockpiled fescue (CON) or corn stover and DDGS (DG; DDGS at 0.7% BW per d). Following TAI, CON cows were fed grass hay, and DG cows were placed on stockpiled fescue until grass was exhausted (Julian d 20) and then fed grass hay. Cow BW and BCS were assessed every 28 d during supplementation. Estrous cycling status was determined by evaluation of progesterone in 2 blood samples taken at and 10 d before estrous synchronization, and on Julian d 336, TAI was conducted. Pregnancy determination was done by transrectal ultrasonography 35 d after TAI and the end of the breeding season. Calf weights were recorded at 62 ± 16 and 146 ± 16 d of age and again at weaning (steers and heifers were weaned at 144 ± 16 and 208 ± 18 d of age, respectively). Categorical and continuous data were analyzed with the GLIMMIX and MIXED procedures of SAS, respectively. Cow BW and BCS did not differ during the supplementation period. The proportion of cows cycling at breeding season initiation tended ($P = 0.06$) to be greater in CON (92.2%) than DG (80.6%) treated cows. TAI pregnancy rates did not differ between the CON (42.4%) and DG (50.0%) treatment. However, breeding season pregnancy rates were greater ($P = 0.03$) in the DG (89.6%) than CON (74.2%) treatment. DG progeny were heavier at 62 d of age and at weaning and had a greater 205 d adjusted weaning wt ($P \leq 0.03$) than CON progeny. In summary, including a dietary period of corn stover and DDGS to a traditional management practice of grazing stockpiled fescue and feeding hay resulted in greater breeding season pregnancy rates and heavier progeny.

Key Words: beef cow, DDGS, fertility

W49 Meta-analysis on the effects of supplementing distiller′s grains to beef cows during early lactation on reproductive efficiency and pre-weaning progeny growth.

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Three independent studies using Angus-cross beef cows (n = 284) at Purdue University assessed the effects of feeding dried distiller′s grains with solubles (DDGS) as a primary dietary energy source during various phases of production on performance, reproduction, and progeny development. The purpose of this meta-analysis was to determine the effects of DDGS supplementation during early lactation on reproductive performance and progeny growth. In all studies, cows were stratified and allotted by BW and BCS to 1 of 2 isocaloric dietary treatments initiated either at 192 d of pregnancy or during calving. Diets were: 1) corn silage and haylage, or stockpiled forage (CON); or 2) low quality forage with DDGS (DG) supplementation. DG supplementation concluded at either timed-AI or at ultrasonography pregnancy diagnosis approximately 30 d after timed-AI. All cows were synchronized for estrus using the 5 d CO-Synch + CIDR protocol. BW and BCS were assessed throughout the supplementation periods. Categorical and continuous data were analyzed with the GLIMMIX and MIXED procedures of SAS, respectively. Meta-analysis demonstrated that days postpartum, BW, and BCS at estrous synchronization, as well as the proportion of male offspring born did not differ ($P \geq 0.53$) between treatments. However, the meta-analysis revealed that timed-AI pregnancy rates were greater (64.1 vs. 50.0%; $P = 0.02$), and overall breeding season pregnancy rates tended to be greater (91.5 vs. 84.9%; $P = 0.10$) in DG than CON treatments. Although DG progeny were heavier than CON at birth (36.2 ± 0.5 vs. 34.4 ± 0.5 kg; $P = 0.01$), DG progeny had greater pre-weaning ADG (0.99 ± 0.01 vs. 0.95 ± 0.01 kg; $P = 0.009$), weaning weights (236 ± 3.1 vs. 228 ± 3.0 kg; $P = 0.04$), and 205 d adjusted weaning weights (230 ± 2.5 vs. 222 ± 2.4 kg; $P = 0.009$) than CON progeny. In conclusion, using a meta-analysis to combine 3 independent studies demonstrated that utilization of DDGS as a primary dietary energy source during early lactation appears to result in improved fertility and accelerated progeny growth.

Key Words: DDGS, developmental programming, fertility

W50 Effects of water stress and plant population on corn plant yields and composition.

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Higher plant densities and adequate irrigation typically increase corn silage yield, but their effect on quality remains uncertain. Four elite commercial Pioneer corn hybrids (109–116 d CRM) planted in 4 rows 76 cm apart and 4.6 m long were thinned to 59, 89, and 119 thousand plants per hectare in quadruplicate subplots. In addition to 17 cm rain, sub-subplots received 65 cm (full), 34 cm (moderate), or 18 cm (limited) of subsurface irrigation water by irrigating at each, alternate, or every third cycle during the growing season. Whole plants were chopper harvested when kernels were fully dented (one-third milk line); hybrids averaged 30.4 to 33% DM. Harvest weight was measured and chemical components were determined for the 144 sub-subplots. Main effects are described only when interactions were not significant ($P > 0.05$). Although DM yield and calculated milk per acre were least ($P < 0.05$) with the lowest plant population, milk per ton of DM (Milk 2006) was reduced ($P < 0.05$) at the highest plant population. Limiting the water supply linearly reduced ($P < 0.05$) plant height, DM yield, and milk per acre. However, NDF digestibility increased linearly ($P < 0.05$; from 50 to 55%) as water supply was restricted; severe water restriction reduced milk per ton. NDF digestibility was greater ($P < 0.05$) for Pioneer BMR hybrid P1376XR than for the other 3 hybrids (55 vs. 50 to 52%). Averaged across hybrids, limiting the water supply decreased yield and concentration of starch but increased plant protein, sugar, and NDF; in vitro DM digestion and milk per ton was greatest when water supply was moderate. As plant population increased, DM yield increased but starch content and NDF digestibility decreased; in vitro DM digestion and milk per ton was greatest with the lowest plant population. Although hybrid rankings generally remain similar, local and yearly differences in both yield and quality of corn silage can be ascribed partially to differences in water availability and plant population.

Key Words: corn silage, irrigation, plant population

W51 Prediction of preweaning ADG in beef calves from milk fatty acid methyl esters.

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Research has shown milk yield (MWT) has an important influence on calf preweaning ADG (PRWADG), but MWT accounts for only a moderate amount of variation in PRWADG. The objective of this study was to determine if milk fatty acid methyl esters (FAME), alone and in combination with MWT, could improve accuracy of prediction of PRWADG. Forty-five beef cows sired by Bonsmara, Brangus, Charolais, Gelbvieh, Hereford and Romosinuano bulls were used in a 2 yr study. Spring-calving cows were milked 6 times per year every 28 d beginning late May, and milk samples were analyzed for milk fat and protein. Milk samples collected in May, July and September each year were analyzed for FAME. Percentages of 42 FAME in each milk sample were acquired using a gas chromatograph flame ion detector. Milk weights, quality data, and FAME were averaged over collection dates before analyses. Stepwise regression was used to identify linear models to predict PRWADG using MWT, age of dam (AOD), and percent FAME. The R^2 and associated condition index (CI, an indicator of collinearity) were used in model evaluation. Condition indexes less than or close to 30 were considered to have low collinearity. Regression of PRWADG on MWT resulted in an R^2 of 0.35 with a CI of 9.4 while inclusion of AOD gave an R^2 of 0.4 and a CI of 21.6. A regression equation using 8 FAME accounted 54% of the variation in calf ADG with a CI of 33. When MWT and AOD were included with FAME as predictors, a prediction equation with 8 FAME, MWT, and AOD accounted for 69% of the variation in PRWADG with a CI of 29. Partial least squares regression (PLS) was also used to predict PRWADG from FAME, MWT, and AOD. Results from PLS analyses yielded a dependent variable R^2 of 0.61 using all 42 FAME with 7 extracted factors and a dependent variable R^2 of 0.78 when MWT and AOD were included with the 42 FAME with 7 extracted factors. Results from these preliminary analyses suggest that FAME composition of milk influences calf ADG and that data on percent FAME in combination with MWT and AOD can improve the accuracy of prediction of calf PRWADG compared with MWT and AOD alone.

Key Words: beef cattle, milk fatty acids, preweaning ADG

W52 Correlation of IGF-1, growth hormone, and leptin to breeding beef heifer productivity.

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The use of metabolic parameters associated with growth and tissue development may aid in predicting productivity of beef heifers, thus reducing potential production inefficiencies. Dam and offspring production variables were collected on 84 Angus-based crossbred heifers retained from the 2006 (n = 40 heifers; 3.42 parities/heifer) and 2007 (n = 44 heifers; 2.64 parities/heifer) calf crops. Blood samples were obtained at approximately 1 yr of age and analyzed for IGF-1, GH, and Leptin concentrations. Data within each hormone category were grouped (GROUP) into upper 25% (HIGH), middle 50% (MID), and lower 25% (LOW) of hormone concentrations using univariate analysis. Production variables within hormone category were analyzed as a one-way ANOVA with GROUP as the main effects and heifer birth year as a covariate. Experimental unit was heifer and the error term was residual error. Pearson correlation coefficients were determined between production variables and hormone concentrations. Pregnancy interval was correlated ($r = -0.273$; $P = 0.020$) with IGF-1, with higher concentrations associated with shorter intervals (−5 d/yr). Pregnancy interval was 5.9 d less ($P = 0.045$) for HIGH vs. MID IGF-1, 9.9 d less ($P = 0.013$) for HIGH vs. LOW GH, and tended ($P = 0.082$) to be 4.2 d greater for MID vs. LOW leptin. Number of parity was not associated ($P > 0.10$) with hormone concentrations or GROUP within hormone categories. Percentage of calves weaned/born tended ($P = 0.086$) to be less for HIGH (94.7%) vs. MID leptin (99.4%). No correlations ($P > 0.10$) between hormone concentrations and percent calves weaned/born were observed. Offspring carcass weights (HCW), ratio of ribeye area-to-HCW, and marbling scores were not affected ($P > 0.10$) by heifer hormone concentrations within any hormone category. Yield grade (YG) of offspring was correlated ($r = 0.256$, $P = 0.057$) with heifer IGF-1 concentrations; with MID (2.74) tending ($P = 0.073$) to have lower YG vs. HIGH (3.01). These data indicate that concentrations of IGF-1, GH, and Leptin at time of replacement heifer selection have limited value as prediction tools of female productivity.

Key Words: hormones, beef heifers, productivity

W53 Exposure of prepubertal beef bulls to cycling females does not enhance sexual development.

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The objectives of the study were to determine if continuous, long-term, fenceline exposure of prepubertal beef bulls to cycling beef females affects bull age at puberty and ability to pass their first breeding soundness examination (BSE). Angus, Simmental, and Hereford bulls (n = 77) within breed were stratified by age and assigned to treatment (average age of 196 ± 22 d). Exposed bulls (EXP) had continuous fenceline contact with cycling females for the duration of the study while control (CON) bulls were penned a minimum of 42 m from cycling females without visual or physical contact. Estrous cycles were synchronized, such that 2 to 5 females were in estrus each week. Body weights (BW) and scrotal circumference (SC) were measured every 28 d. When bulls achieved a ≥ 26 cm SC, semen samples were obtained monthly via electroejaculation until puberty was reached. Bulls were considered pubertal when sperm concentration was $\geq 50 \times 10^6$/mL and motility was ≥ 10 percent. Homosexual mounting behavior (MB) of bulls was assessed twice/mo during diestrus (D) and estrus (E) stages of females. BSEs were conducted when bulls averaged 364 ± 22 d of age. Normal sperm morphology of $\geq 70\%$ and sperm motility of $\geq 30\%$ were considered passing. Age and SC at puberty and MB were analyzed using PROC MIXED in SAS, with fixed effect of treatment and random effect of pen; mo and stage of estrous were included as fixed effects for MB. BSE data were analyzed using PROC GLIMMIX in SAS with fixed effect of treatment. Age and SC at puberty were similar for EXP and CON ($P > 0.10$; 323 d and 311 d, respectively; 34.6 cm and 34.9 cm, respectively). Treatment and female estrous stage interacted to affect bull MB ($P < 0.01$). EXP bulls had more MB when females were in E as compared with D ($P < 0.01$). Similar MB were observed for EXP bulls when females were in E compared with CON bulls during both E and D ($P > 0.10$). A similar percentage of bulls passed their first BSE ($P > 0.10$; EXP = 87.8% and CON = 74.4%). In conclusion, continuous, fenceline exposure of developing bulls to cycling beef females does not reduce age at puberty nor influence ability to pass first BSE.

Key Words: bulls, puberty, breeding soundness examinations

Breeding and Genetics: Molecular Biology and Genomics

W54 Protection and stabilization of whole blood at room temperature does not influence DNA yield, purity, and integrity. R. Flores*[1], M. Udtha[1], J. E. Sanner[1], E. A. Backes[2], L. S. Wilbers[2], and J. D. Caldwell[2], *[1]The University of Texas Health Science Center at Houston, Houston, [2]Lincoln University, Jefferson City, MO.*

Preservation of bio-specimens for molecular biological applications traditionally involves freezing which increases laboratory and research project costs. Protection and stabilization of DNA at room temperature (RT) may eliminate the costs associated with freezer storage. However, there is a paucity of information describing the yield, purity, and integrity of DNA stored at RT. Objectives were to evaluate the yield, purity, and integrity of DNA extracted from whole blood samples stored at RT, low (−20°C), and ultra-low (−80°C) temperatures. Sheep (n = 4 [7 mL]) and human (n = 6 [4 mL]) whole blood samples were collected and aliquots stored at RT, −20°C, and −80°C. Blood samples at RT were stored utilizing bio-stabilization technology (DNAstable Blood and DNAgard Blood; Biomatrica, San Diego, CA) designed to protect genomic DNA in whole blood from degradation resulting from unprotected RT storage. Negative control samples were stored unprotected at RT. Genomic DNA was extracted by using the QIAamp DNA Blood Mini Kit (Qiagen, Valencia, CA). Quantification and purity of the extracted DNA was determined by spectrophotometry and the integrity was assessed following electrophoresis. The DNA yield was not influenced by a species × storage temperature interaction ($P = 0.84$). Similarly, storage temperature did not influence DNA yield ($P = 0.52$) and averaged 13.6 ± 1.2 ng/μL across all storage temperatures. Among samples stored protected at RT, species, type of technology utilized, and the interaction did not ($P > 0.13$) influence DNA yield with yield averaging 12.5 ± 1.2 and 12.7 ± 1.2 ng/μL for DNAgard and DNAstable, respectively. The 260/280 ratio was influenced by a species × storage temperature interaction ($P = 0.01$). In general, the 260/280 ratios were higher ($P < 0.05$) for human samples stored at low and ultra-low temperatures compared with sheep samples stored at similar low temperatures. In conclusion, ambient temperature-based bio-stabilization technologies may offer an alternative to traditional low temperature-based bio-specimen preservation and storage.

Key Words: blood, DNA, temperature

W55 Maximum differences analysis: An empirical method for genome-wide association studies. M. Cellesi, N. P. P. Macciotta,* G. Pulina, G. Gaspa, and C. Dimauro, *Dipartimento di Agraria, Universitá di Sassari, Italy.*

Genome-wide association studies have rapidly become the most popular method to discover associations between SNPs and quantitative traits. Marker significance is traditionally assessed by using the Bayesian or the frequentist approach. Both methods have positive and negative aspects. In the present study we suggest an empirical method which combines the simplicity of the frequentist approach with the reliability of Bayesian inference. We called this method maximum difference analysis (MDA). A total of 2,093 Italian Holstein bulls were genotyped with the Illumina BovineSNP50 BeadChip. Polygenic EBV for milk yield, fat and protein content were available. MDA starts by randomly choosing 1,500 animals and retaining the best 100 (B) and the worst 100 (W) animals for a particular trait. Relative genotypes frequencies for each marker were calculated for B and W group, respectively. Then the difference between genotype having the highest frequency in B and the corresponding frequency in W were calculated. In every single chromosome, the above mentioned differences were considered as a random variable and, after standardization, SNPs with difference higher than 1.96 standard deviations were retained as possible candidate for association. This procedure was repeated 5,000 times and the frequency (fi) of the previous detected association for each SNP annotated. A marker was considered significantly associated with the specific trait if $pi = fi/5000 > 0.99$. For milk yield, fat and protein, 93, 40 and 92 markers were selected, respectively. Several SNP were found to be significantly associated to more traits: 19 for milk and protein, 19 for milk and fat, 12 for fat and protein and 10 among all traits. Moreover, 19, 7 and 17 SNPs, for milk, fat and protein, respectively, were selected with $pi = 1$. The reliability of results obtained by MDA was confirmed by the detection of several SNPs located near genes known to affect the specific trait, as the DGAT1 and the casein cluster.

Key Words: gene association

W56 Adjustment of selection index coefficients and polygenic variance to improve regressions and reliability of genomic evaluations. P. M. VanRaden, J. R. Wright,* and T. A. Cooper, *Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD.*

In multi-step genomic evaluations, direct genomic values (DGV) are computed using either marker effects or genomic relationships among the genotyped animals, and information from non-genotyped ancestors is included later by selection index. The DGV, the traditional evaluation (EBV), and a subset breeding value (SBV) estimated using pedigree relationships among the genotyped animals are combined according to theoretical weights based on reliabilities of the 3 terms. In official yield trait evaluations of young Holstein bulls, the weights average 0.99 for DGV, 0.12 for EBV, and −0.11 for SBV. Alternative weights have been proposed by other countries to increase reliabilities and regressions of predicting future data from past. Most US regressions were close to expected values and increased when some weight was removed from the DGV and added to either the EBV or SBV or both. Reliabilities decreased slightly for Holsteins with weight added to either EBV or SBV, but reliability increased for some traits of Jerseys if weight was added to SBV. Maximum weights on DGV of 1.0, 0.9, and 0.8 were compared. For each 0.1 decrease, regressions increased by about 0.02. Regressions for a few traits were lower than expected, and limiting the DGV weight to 0.9 or 0.8 instead of the theoretical value of 1.0 helped bring the regressions into compliance with validation tests. Adjustments to polygenic variance also increased the regressions by about 0.02 for each 0.1 increase, but reliabilities were slightly reduced when compared with adjusting the selection index weights. Finding optimum percentages of polygenic variance required more computation and was less flexible than finding optimum weights, because recombining 3 terms in a final step is easier than re-estimating all marker effects. Conclusions are that index adjustments can help to pass genomic validation tests for some traits by removing small biases in regressions, but that the theoretical selection index weights currently in use are close to ideal.

Key Words: multi-step evaluation, direct genomic value, validation

W57 Use of canonical discriminant analysis to distinguish among three bovine breeds by using a low number of selected SNP markers. C. Dimauro,* M. Cellesi, R. Steri, S. Sorbolini, and NPP Macciotta, *Dipartimento di Agraria, Universitá di Sassari, Sassari, Italy.*

Multivariate statistical techniques are commonly used to synthesize genomic information in animal breeding studies. In the present work, the multivariate canonical discriminant analysis (CDA) was used to discriminate between 3 bovine breeds. Data consisted of 2,090 Holstein, 750 Brown, and 480 Simmental bulls genotyped by using the Illumina BovineSNP50 BeadChip. After data editing, SNP in common to the 3 breeds were 30,055. A sample of 30 randomly selected bulls (10 for each breed) were used as new observations in the cross-validation data set. When 3 groups are involved, CDA derives 2 canonical functions (CAN1 and CAN2) which are linear combination of the original variables (SNP genotypes coded as 0,1 and 2). Coefficients of the linear combination are the canonical coefficients (CC) and represent the correlation among SNP and canonical functions. CDA was first applied separately on the 29 bovine autosomes. For each chromosome, SNP with CC >0.90 in CAN1 and CC > 0.50 in CAN2 were selected. Results indicated that CDA was able to efficiently separate the 3 breeds also at chromosome level. At the end of the procedure, 295 SNP out of 30,055 were retained. These markers were then used to develop a CDA on the entire genome. The Mahalanobis distance test was highly significant ($P < 0.001$) for all comparisons (distances: Holstein vs. Brown 2,941, Holstein vs. Simmental 3,127, Simmental vs. Brown 410). In particular, CAN1, which accounted for 95% of the total variability, separated Holstein from Brown and Simmental bulls. This result could be due to the high selection pressure exerted on Holstein population and the 129 SNP with CC > 0.90 could be the related signatures. CAN2 was able to significantly separate Brown and Simmental groups. In this case 7 SNP with CC > 0.60 were found. Finally, individuals in the cross-validation data set were 100% correctly classified. The above described procedure could be therefore tested for developing a test for the traceability of breed products. Low-density SNP panels (295 markers in this work), with moderate price, could be specifically developed for routine analysis.

Key Words: genomic association

W58 Reliability of genomic breeding values at different reference population's designs when some or all animals are genotyped. M. Pszczola[1,3], T. Strabel*[3], J. A. M. van Arendonk[2], and M. P. L. Calus[1], [1]*Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Lelystad, the Netherlands,* [2]*Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands,* [3]*Department of Genetics and Animal Breeding, Poznan University of Life Sciences, Poznan, Poland.*

Reliability of genomic breeding values with different structure of a small reference population including ungenotyped animals was investigated. Data reflecting a dairy cattle population structure was simulated for a trait with heritability of 0.3. Reference populations were small and consisted of cows only. Reference populations consisted of highly, moderately, lowly, and randomly related animals by choosing appropriate family structure. Evaluated animals were one generation younger than the reference populations. Four scenarios in which reference population and evaluated animals were not genotyped (AA), reference population was genotyped and the evaluated animals were not genotyped (GA), reference population was not genotyped and the evaluated animals were genotyped (AG) and both groups were genotyped (GG). Reliabilities of direct genomic values were predicted deterministically using selection index theory. For GG, reliabilities were considerably higher than in the other cases. In AG, reliabilities were somewhat higher, than in GA. AG achieved substantially higher reliabilities than AA. Reliabilities increased with decreasing average relationship within the reference population. The main source of the gain in reliability is genotyping the evaluated animals, however, the benefit from genomic selection is substantially higher when all animals are genotyped.

Key Words: genomic selection, reliability, dairy cattle

W59 Dealing with uncertainty of dependent variables in genome wide association studies. S. Smith,* E. H. Hay, and R. Rekaya, *University of Georgia, Athens.*

In genome-wide association studies (GWAS) using multiple-step procedures, the dependent variable (DV) is often a pseudo-observation such as estimated breeding values (EBVs) or de-regressed proofs. Thus, these "estimated" DVs include a certain level of uncertainty. If the sampling errors (SE) attached to these variables are constant across all records, regression analyses will accommodate this situation without major difficulty. However, when SE are heterogeneous across observations, the case with pseudo-records used in GWAS in livestock applications, the situation is more complex. The residual terms of the regression models include 2 components, the SE due to estimation of the DV, i.e., EBVs, and white noise that will exist if it was possible to observe (measure) the DV. Unfortunately, this type of data are often analyzed using an ordinary least square (OLS) assuming homogeneous residuals or weighted least square (WLS) where both components of the residual are assumed to be heterogeneous when only the first component is. In this study we present a method for analyzing uncertain DVs when only one component (SE) of the residual term is heterogeneous with applications in GWAS. Further, we assumed SE to be either completely known or only known up to a proportionality constant to mimic scenarios of using EBVs as DVs. A real data set consisting of 1989 animals genotyped for around 56k SNPs was used. EBVs for growth and associated prediction error variance (PEV) and reliability were computed using phenotypic and pedigree information. After SNP selection using single marker analyses and stepwise regression, 209 SNPs were retained for association with growth EBVs. Four analyses were conducted: 1) OLS (M1); 2) WLS (M2); 3) WLS assuming only heterogeneous SE using the estimated PEV (M3) and 4) WLS assuming only heterogeneous SE using a transformation of the estimated reliabilities (M4). Using a 5-fold cross validation, the results (correlation between EBVs and the prediction) showed a superiority of M3. This superiority ranged from 3% between M3 and M4 to 8% between M3 and M1.

Key Words: uncertainty, genome-wide association, prediction error variance

W60 Increased use of young bulls in dairy cattle breeding programs. H. D. Norman, J. L. Hutchison,* and J. B. Cole, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Availability of genomic evaluations since 2008 has resulted in many changes in breeding programs. The contribution of young bulls (0.8 to 3.9 yr old) to those programs was investigated. The number of Holstein sires of young bulls doubled from 2008 (126 sires) to 2011 (276 sires); 14% of sons were sired by a young bull in 2008 compared with 40% in 2011. Corresponding values for Jerseys were 34 and 54 sires of young bulls in 2008 and 2011, respectively, with 19 and 40% sired by young bulls. From US breeding records from 2007 through 2011, 19,359,730 Holstein and 1,133,090 Jersey breedings were examined. Young bulls were used for 28% of Holstein breedings in 2007, 29% in 2008, 39%

in 2009, 43% in 2010, and 48% in 2011; annual percentages for young genotyped Holstein bulls were 0, 8, 36, 42, and 48%. Genotyped bulls accounted for 0, 26, 92, 98, and 99% of breedings to young Holstein bulls annually from 2007 through 2011. Young bulls were used for 25, 27, 31, 33, and 40% of Jersey breedings annually, with 0, 0, 22, 32, and 39% of breedings to young genotyped bulls; genotyped bulls accounted for 0, <1, 72, 98, and 98% of breedings to young Jersey bulls. Percentage of female progeny sired by young bulls was calculated by progeny birth year for 5,035,103 Holstein and 496,062 Jersey heifers. Young bulls annually sired 24, 23, 23, 33, and 40% of Holstein heifers born from 2007 through 2011 and 29, 27, 30, 33, and 35% of Jersey heifers. Mean sire age for Holstein progeny born in 2011 was 23 mo younger than in 2006 for bulls and 12 mo younger for heifers; corresponding values for Jerseys were 15 and 4 mo. Mean net merit from December 2011 weighted by number of breedings was $290 for 2008 breedings, $339 for 2009 breedings, and $361 for 2010 breedings of active Holstein bulls and $230, $483, and $532 for genotyped Holstein bulls (a difference of $60, $144, and $171, respectively). Corresponding values for Jerseys were $270, $286, and $324 for active bulls and $396, $448, and $510 for genotyped bulls (differences of $126, $162, and $186). Use of young bulls has greatly reduced the generation interval and improved the rate of genetic gain since implementation of genomic evaluations.

Key Words: breeding, service sire, genomics

W61 Accuracy and bias for final score in US Holsteins from adding genomic information on bulls and cows.

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Obtaining genomic information on animals should lead to a greater opportunity for earlier and more accurate selection. Selective genotyping of validation bulls will lead to a regression coefficient (b) for later daughter deviations on early genomic parent averages to be less than 1.0. A recent study by Olson, et al. (2011) indicates that the current expected b-value for US final score for bulls is 0.781. The objective of this study was to compare the change in accuracy and potential bias from adding genomic information on bulls and cows for final score of US Holsteins. A total of 39,741 animals (5,235 cows and 34,506 bulls) had either a final score themself or progeny with a final score. A SNP chip containing 42,503 usable markers was available for all genotyped animals. The full data set included 10,944,571 records in 2011. The reduced data contained 9,602,030 records in 2007. Validation animals were 760 young bulls born after 2004 and with at least 50 daughters in 2011 and 2,098 young cows born after 2006. Genomic breeding values were calculated with a single-step procedure. Including genotypes on bulls only, raised the R2 from 23.4 to 33.3 along with a slight increase in the b-value. Including genotypes on both bulls and cows improved the R2 to 34.2 and slightly lowered the b-value for the bulls. Including genotypes on bulls and cows improved the cow's accuracy (R^2) from 16.1 to 24.2 with a b-value that went from slightly overestimating the genomic breeding values to slightly underestimating it, i.e., 0.978 and 1.042, respectively. Inclusion of bull and cow genotypes in the single-step procedure improves the accuracy of selection with a small change in the indication of bias from the parent averages.

Key Words: genomic evaluation, final score, US Holstein

W62 SNPs that affect microRNA binding sites in the bovine ACACA gene are associated with polyunsaturated fatty acid (PUFA) content of Canadian Holstein cows.

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Bovine milk has beneficial lipids that contribute positively to human health. These lipids include some isomers of CLA, oleic and α-linolenic acids and represent a very small portion of the total fatty acids (FAs) in milk. FAs in milk arise from dietary sources or are synthesized de novo in the mammary epithelial cells through the action of enzymes including acetyl-CoA carboxylase-α (ACACA). Fat synthesis is a complex trait that is regulated by genetic, environmental and epigenetic (e.g., microRNA) factors. microRNAs are functional non-coding small RNA molecules that have emerged as important regulators of gene expression. microRNA dis-regulation has been shown to be associated with disease conditions in humans and production traits in farm animals. In this study, we identified 6 SNPs in the 3′UTR of the ACACA gene by sequencing 50 samples and genotyping of 150 samples from Canadian Holstein cows by Sequenom iPLEX Gold technology. The FA profiles of milk from the same cows were analyzed by GC and HPLC. In silico analysis showed that SNPs ACACA-80 A > G affected a binding site for bta-miR-126 while ACACA-83 C > T and ACACA-84 G > A disrupted the binding site for bta-mir-3432. Relationship between FAs and SNPs were analyzed using PROC MIXED of SAS (version 9.3) with genotype as fixed factor. Multiple comparisons of means was done with Turkey adjustment. Significant associations were found between SNPs, total PUFA and other FA isomers in the milks of Canadian Holstein cows. Cows ACACA-80 AA had higher concentrations ($P < 0.05$) of PUFA (2.902 ± 0.122) as compared with cows GG (2.333 ± 0.159) but similar to cows AG (2.576 ± 0.090). ACACA-80 AA also had significantly higher concentrations of C16:1T, C18:1n9c and lower content of total saturated FAs as compared with cows AG and GG. Similarly, cows ACACA-83 CT (3.126 ± 0.185) had significantly higher PUFA content as compared with ACACA-83 CC (2.608 ± 0.067) and ACACA-83 TT (2.256 ± 0.586). PUFA of cows ACACA-84 GG (2.839 ± 0.107) was also higher ($P < 0.05$) as compared with ACACA-84 AA (2.334 ± 0.158) and ACACA-84 AG (2.488 ± 0.129). SNPs ACACA-83 and 84 also affected the content of C16:1, C16:1T, C18:2n6cc, C20:3n6, C6:0, C8:0, C10:0 and C12:0. These results demonstrate that SNPs in the 3′UTR of the ACACA gene may be involved in the regulation of PUFA synthesis and as such may act as potential candidate genes for breeding for improved PUFA content of bovine milk. Our results further suggest that microRNA may be involved in the regulation of mammary milk FA synthesis. We are in the processing of validating our results with a larger data set.

Key Words: ACACA gene, Canadian Holsteins, SNP

W63 Genomic-polygenic evaluation of postweaning weight and ultrasound carcass traits in an Angus-Brahman multibreed population.

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The objectives of this study were to estimate the fractions of additive genetic variances for postweaning weight (PW) and 3 ultrasound traits explained by SNP included in the Illumina3k chip, to compare EBV rankings predicted using genomic-polygenic, genomic, and polygenic models, and to assess EBV trends as Brahman fraction of calves increased from 0 to 1 in an Angus-Brahman multibreed population. Ultrasound traits were ribeye area (UREA), percent of intramuscular fat (UPIMF), and backfat thickness (UBF). Trait measurements on 623 calves born between 2006 and 2010 were collected at the Feed Efficiency Facility of the University of Florida. Single-trait genomic-polygenic (GP) models were used to estimate variance components using Markov Chain Monte Carlo procedures (option VCE from program GS3). Fixed effects were contemporary group (year-pen), age of dam, sex of calf, age of calf, Brahman fraction of calf, and heterozygosity of calf. Random effects were additive SNP, additive polygenic, and residual. Subsequently, EBV were computed with option BLUP of program GS3 using GP models and models that included only genomic (G) or polygenic (P) effects. The fractions of the additive genetic variance explained by SNP in the Illumina3k chip were 0.09 for UREA, 0.38 for UBF, 0.06 for UPIMF, and 0.08 for UW. Rank correlations between EBV from GP and P models were high (0.89 to 0.99), and moderate (0.51 to 0.65) between EBV from G and P models. Regression coefficients for all models and traits showed that calf EBV tended to decrease as Brahman fraction of calves increased suggesting that calves with higher Brahman fraction were leaner, had smaller ribeye areas, and grew more slowly than calves with higher Angus fractions. The low fraction of additive genetic variances accounted for by the markers in the Illumina3k chip indicated that higher density chips would be needed to more completely account for additive genetic variation in multibreed populations.

Key Words: cattle, genomic, multibreed

W64 Genomic-polygenic evaluation of Angus-Brahman cattle for carcass traits with the Illumina 3K chip. M. A. Elzo*[1], G. Hu[1], C. A. Martinez[1], G. C. Lamb[1], D. D. Johnson[1], M. G. Thomas[2], I. Misztal[3], D. O. Rae[1], J. G. Wasdin[1], and J. D. Driver[1], *[1]University of Florida, Gainesville, [2]Colorado State University, Fort Collins, [3]University of Georgia, Athens.*

The objective of this research was to assess the effect of including genotypic information from the Illumina 3k chip on the genetic evaluation of animals for 5 carcass traits in an Angus-Brahman multibreed population using genomic-polygenic (GP), genomic (G), and polygenic (P) models. Fractions of additive genetic variances associated with markers in the Illumina3k chip were computed, and animal EBV rankings and EBV trends as calf Brahman percent increased from 0 to 100% were compared across models. Traits were hot carcass weight (HCW), dressing percent (DP), ribeye area (REA), fat over the ribeye (FOE), and marbling (MAB). Phenotypic and genotypic data were from 202 steers born from 2006 to 2010. Data were analyzed with single-trait models. All models had contemporary group (year-pen), Brahman fraction of calf, heterozygosity of calf, and slaughter age as fixed effects. Random effects were additive SNP (GP and G models), additive polygenic (GP and P models), and residual. Program GS3 was used to compute variance components and heritabilities with option VCE (Markov Chain Monte Carlo), and EBV using option BLUP. Heritabilities were 0.72 for HCW, 0.25 for DP, 0.53 for REA, 0.44 for FOE, and 0.23 for MAB. Fractions of additive genetic variance explained by Illumina 3k SNP were 0.08 for HCW, 0.47 for DP, 0.19 for REA, 0.27 for FOE, and 0.23 for MAB. Higher rank correlations existed between EBV from GP and P models (0.94 to 0.99; $P < 0.0001$) than between EBV from G and P models (0.78 to 0.84; $P < 0.0001$). Regressions of calf EBV on Brahman fractions were non-significant for all traits indicating that calves of comparable EBV for carcass traits existed across all breed compositions. The low fractions of additive genetic variances accounted for by the Illumina3k chip indicated that GP models would need to be used to compute EBV if this chip were used to help predict animal EBV, and that higher density chips would be needed to better account for additive genetic variation in multibreed populations.

Key Words: carcass, cattle, genomic

W65 Using low-density commercial DNA-marker panels on prediction accuracy for expected progeny differences of selection criteria: An application in a marker-assisted breeding program for Nellore cattle in Brazil. J. B. S. Ferraz*[1], F. M. Rezende[1], R. C. G. Silva[1,2], X. Wu[3], S. Bauck[2], J. P. Eler[1], and E. C. Mattos[1], *[1]University of Sao Paulo/FZEA/ZAB/GMAB, Pirassununga, SP, Brazil, [2]Igenity Livestock Production Business Unit, Merial Ltd., Duluth, GA, [3]Department of Animal Science, Univ. of Wisconsin, Madison.*

The objective of this study was to evaluate the effect of inclusion of molecular information on estimated accuracy for expected progeny differences of the following selection criteria of a breeding Nellore project in Brazil: weaning weight (WW), post weaning gain up to 18 mo (PWGAIN), scrotum circumference (SC) and muscle score (MUSCLE), when predicted molecular breeding values (MBV) of these traits, based on low-density SNP panels developed by Igenity in Brazil (released in June 2011), were included in the analysis. Low-density SNP panels were selected using the parallel Bayes CpiC package, in which a BayesC π model was used for feature selection and a BayesC model was used for post-selection statistical inference and cross-validation. (Co)variance components and genetic parameters were estimated using a large data set with 97,580 animals included in the A^{-1} matrix. Heritability were estimated to 0.19 for WW, 0.82 for MBV of WW, and genetic correlation between them was estimated to be $r_g = 0.36$. Heritability and genetic correlation for other characters were: 0.21 (PWGAIN), 0.86 (MBV of PWGAIN), with $r_g = 0.50$; 0.52 (SC), 0.67 for (MBV of SC), with $r_g = 0.33$; 0.20 for (MUSCLE), 0.70 (MBV of MUSCLE) with rg = 0.32. Further, those genetic parameters were applied to genetic evaluation analyses with single traits (considering phenotypes only in appropriate models) and 2 traits (phenotypes as trait 1 and MBV for the same trait as trait 2), using REML approach, in a large data set ($A^{-1} = 520{,}169$) and from that analysis new predictions of EPD were obtained. From the large data set, close to 3,500 animals were genotyped. BIF accuracies were calculated for all animals in single-trait analysis. The effect of including MBV on accuracy of prediction of marker-EPD varied with subgroups of animals as well as different traits: prediction accuracy obtained for young replacement bulls with genotypes showed an increase of up to 22%; similar increment of predictive accuracy was observed for bulls 13 progenies or more. It is hence concluded that selected low-density SNP marker panels was useful in marker-assisted selection programs for Nellore population analyzed.

Key Words: MAS, beef breeding program, impact on accuracy

W66 SNP AY428575.1:g.346G>A of the bovine *TCAP* gene: Genotyping with PCR-RFLP and occurrence in Nelore animals (*Bos indicus*) and Angus (*B. taurus*) × Nelore. B. Borges*[1], R. Curi[2], A. Tamanaha[2], and L. A. Chardulo[3], *[1]College of Agrarian and Veterinary Sciences, UNESP, Jaboticabal, SP, Brazil, [2]College of Animal Production and Veterinary Medicine, Animal Breeding and Nutrition Department, UNESP, Botucatu, SP, Brazil, [3]Bioscience Institute, Chemistry and Biochemistry Department, UNESP, Botucatu, SP, Brazil.*

Genetic mapping studies and physiological analysis have resulted in identification of candidate genes related to meat quality on beef cattle, including the titin-cap gene (*TCAP*). It encodes teletonin, a protein found at skeletal and cardiac muscles linked to the Z1-Z2 domains of titin. This protein is degraded into the *post mortem* period and influences the reduction of tenderness between 24 and 72 h after slaughter. The major objective of this work was genotyping the SNP AY428575.1:g.346G>A of the bovine *TCAP* gene by PCR-RFLP technique, and report its use for the first time. Using the forward primer 5′ GGGAGTGAGCAGTCAT-CATGGC 3′ and reverse primer 5′ AGAGGCAGCACCCGCTGGT 3′, amplification products of 517 bp were acquired. They were submitted to digestion with *Bts*CI enzyme, which resulted in the genotypes AA (approx. 177, 154, 128, and 58 bp), AG (approx. 305, 177, 154, 128, and 58 bp) and GG (approx. 305, 154 and 58 bp). A total of 118 Nelore (*B. indicus*) and 8 Angus × Nelore (*B. taurus* x *B. indicus*) animals were genotyped. The use of the PCR-RFLP for the genotyping of SNP of the bovine *TCAP* gene was inexpensive and robust, which will greatly facilitate analysis of this polymorphism by basic laboratory equipment and reagents when compared with the single-base extension method. There were slight variation among Nelore animals with just 1 genotype AG and 117 genotypes GG. In the same way, there were found 6 Angus × Nelore with genotype AG and 2 GG. These preliminary results suggest the worthlessness of SNP AY428575.1:g.346G > A of the bovine *TCAP* gene to association studies with traits of interest to Nelore breed and, probably, to the subspecie *B. indicus*. On the other hand, they show the viability of these studies with the crossbreed Angus × Nelore, with Angus and, possibly, to all subspecies *B. taurus*. Acknowledgments to FAPESP for financial support.

Key Words: beef cattle, candidate gene, meat quality

W67 Association study of heat shock protein 70 gene with serum biochemical indices in Sanhe cattle. Y. Wang*[1], L. Liu[1], Q. Xu[2], Q. Chu[3], Y. Yu[1], H. Wu[4], D. Wang[4], P. Yuan[4], and A. Liu[5], [1]*College of Animal Science and Technology, China Agricultural University, Beijing, China,* [2]*College of Biology, Beijing Jiaotong University, Beijing, China,* [3]*Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China,* [4]*Xiertala Breeding Farm, Hailaer Farm Buro, Hailaer, Inner Mongolia, China,* [5]*Hailaer Farm Buro, Hailaer, Inner Mongolia, China.*

Resistance to extreme cold is one of the distinct characteristics of Sanhe cattle, a dual purpose breed developed in Northern China. To quantify the ability of cold resistance and explore the genetic mechanism of cold resistance, some physiological and biochemical indicators in the serum were chosen and polymorphism of Heat Shock Protein 70 gene (HSP70) were screened, and the association between those indicators and polymorphism of HSP70 was analyzed. Blood samples from 170 Sanhe cows were collected and 6 biochemical indicators-corticosteroid (CORT), adrenocorticotropic hormone (ACTH), thyroxin (T4), triiodothyronine (T3), Glutathione peroxidase (GSH-Px) and erythrocyte potassium in the serum were tested. Pooled DNA sequencing method (36 unrelated Sanhe cows) was used for identifying the polymorphisms of promoter and exon in HSP70. Individual genotypes were detected using the MALDI-TOF-MS technique. For the association study, a fixed effect model considering parity, sire and genotype of each single SNP was employed. Descriptive statistics of CORT, ACTH, T4, T3, GSH-Px and erythrocyte potassium in Sanhe cattle were 277.79 ± 30.47 ng/mL, 23.81 ± 9.29 pg/mL, 66.43 ± 13.91 ng/mL, 1.18 ± 0.36 ng/mL, 777.73 ± 126.40 U/mL and 22.74 ± 2.48 mmol/L, respectively. Research showed that serum biochemical indices changes when animal are exposed to hot or cold environment, and variations were found in Sanhe cattle, so serum biochemical indices can be used as auxiliary indicators for assessing the degree of cold stress. Totally 13 SNPs (6 SNPs in promoter region and 7 SNPs in exons) were detected using pooled DNA sequencing method, and all were found polymorphic in the sampled population. Minimum allele frequency of these SNPs was 0.027–0.423. The association study showed that parity significantly ($P < 0.05$) effected CORT level and sire significantly ($P < 0.05$) effected ACTH level in all situations. Three novel SNPs were found significantly ($P < 0.05$) associated with some biochemical indices, namely A1679G with ACTH level, C620G with GSH-Px activity and C1784T with erythrocyte potassium concentration. Current results provide evidence that HSP70 gene is an important gene associated with serum biochemical indices, therefore, assumed to have influence on cold resistance ability.

Key Words: HSP70 gene, Sanhe cattle, serum biochemical index

W68 Molecular characterization of constitutive androstane receptor (CAR) and its association with feed efficiency of Nellore (*Bos indicus*) cattle. P. Alexandre, M. H. A. Santana, R. C. Gomes, J. B. S. Ferraz,* and H. Fukumasu, *College of Animal Science and Food Engeneering - Animal Breeding and Biotechnology Group (USP/FZEA/ZAB/GMAB), Pirassununga, SP, Brazil.*

The constitutive androstane receptor (CAR) was initially characterized as a key regulator of xenobiotic metabolism. CAR has also been implicated in various physiological pathways such as energy metabolism and homeostasis of lipids, triglycerides, cholesterol and other endogenous hydrophobic molecules. Here, our focus was to detect genetic polymorphisms (SNP) of CAR of Nellore beef cattle, predict their functional role and associate them to residual feed intake (RFI) and residual body weight gain (RIG), a recently proposed measure of feed efficiency. Genomic DNA was extracted from blood of 50 Nellore bulls and the entire CAR gene was amplified and sequenced with 8 pairs of primers. Molecular characterization was performed for polymorphism identification, phylogenetic analysis and prediction of functional consequences of SNPs. Also, statistical association with RIG was performed with PROC MIXED (SAS). We found 24 SNPs in CAR gene, being one in the promoter region, 8 exonic, 13 intronic and 2 SNPs after the 3′ UTR. We did not find any SNPs in the DNA binding domain of the receptor (DBD); however, 2 SNPs were found between DBD and the ligand binding domain (LBD), both being synonymous: SNP10 (Leu→Leu) and SNP11 (Ser→Ser). The LBD was the most genetically variant region presenting 5 SNPs, being 4 synonymous: SNP14 (Asp→Asp), SNP17 (Ala→Ala), SNP18 (His→His) and SNP19 (Ala→Ala); and 1 non-synonymous: SNP13 (Ala→Treo). No SNPs were found in exons 8 and 9, which codes for 3′UTR. Phylogenetic analysis demonstrated that exons from CAR gene are highly conserved between *Bos indicus* and *Bos taurus* and are closer to primates than to dog or chicken. The single SNP found upstream of CAR gene (SNP01 c.-81–176G>A) changed the transcription factor binding sites due the variation of G to A. Interestingly, this SNP was the only one associated with RIG ($P = 0.0221$). These results lead us to consider that CAR expression might be associated with the complex physiology of feed efficiency in Nellore. Efforts to comprehend the role of CAR on molecular pathways related to feed efficiency and validate this marker for RIG in Nellore are under investigation by our group.

Key Words: Nellore, RFI, SNP

W69 Assessment of 16 candidate genes for growth and maternal ability traits in Mexican Charolais cattle. L. A. Meza-García, V. I. Pacheco-Contreras,* G. M. Parra-Bracamonte, and A. M. Sifuentes-Rincón, *Laboratorio de Biotecnología Animal, Centro de Biotecnología Genómica, Instituto Politécnico Nacional, Reynosa, Tamaulipas, México.*

Maternal ability, birth and weaning weights, are some of the most important traits considered as selection criterion in Mexican cattle. They are complex and quantitative traits, and have shown significant association with some gene polymorphisms in different cattle breeds. Here, we evaluate the gene-trait association of a selected panel polymorphisms located at 16 candidate genes in a Mexican Charolais cattle herd to estimated their utility in gene assisted selection. Based on literature reports, we selected 24 polymorphisms located at POU1F1, FGF2, PRL, STAT5A, LEP, ABCG2, CCR2, BLG, CYP11B1, GHRL, GHR, GHRH, Prop1, NPY, UCP3, UCP2 genes, 24 RFLP-based procedures were designed to genotype 57 samples of Charolais cows with records for total maternal (TM), yield milk (YM), birth weight (BW) and weaning (WW) weight. Polymorphism was confirmed for 22 SNPs in the analyzed population. The effect of genotypes on the maternal ability (MA) (measured as TM and YM) and weight traits were analyzed using the least square analysis of the GLM procedure including genotype as fixed effect. No marker showed association with BW and 3 markers (GHR555, UCP2–380 and LEP3100) were significantly ($P \leq 0.05$) associated with MA and WW traits and 5 markers shows trends for these traits. Regression analyses were achieved to determine the allele substitution effect of associated markers on each trait (Table 1). Before these makers can be used to assist the Charolais selection, more studies with larger data sets are necessary to confirm the found associations and observed trends.

Table 1. Estimated allele substitution effect ± SE of 3 SNP on weaning weight (kg) and maternal ability traits (EBV kg)

SNP ID	Allele substitution	WW	YM	MT
GHR555	G>A	12.16 ± 5.53		
LEP3100	T>C		0.25 ± 0.50	0.23 ± 0.22
UCP2-380	G>C		−0.90 ± 0.48	

Key Words: Charolais cattle, polymorphisms, maternal ability

W70 Distribution of molecular markers and determination of molecular breeding values associated with feed efficiency, beef tenderness, and marbling in Senepol cattle.

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Molecular breeding values (MBV) for feed efficiency (FE; net feed intake), marbling (MAR), and tenderness (TEN) were obtained using a commercially available 56 genetic marker panel to compare the genetics of a group of Senepol bulls (n = 153) used as sires in Brazil, Colombia, Puerto Rico, St. Croix (US Virgin Islands) and in the continental US with the currently available MVP database for such economically relevant traits. In addition, the distribution of individual alleles associated with FE, TEN, and quality grade (QG) and its corresponding potential phenotypic differences (traditional GeneSTAR candidate gene panel; Pfizer Animal Genetics) were determined in another group of animals 75% to purebred Senepol (n = 47). The multinational sire sample (n = 153) showed MAR, FE, and TEN MBVs of −0.31, −0.45, and 0.44, respectively. The current Senepol breed reference MBV average for MAR, FE, and TEN are −0.02, −0.27, and −0.04, respectively, and the across breed average MBVs are 0.03 MAR, −0.15 FE, −0.02 TEN (for FE and TEN, lower MBVs are more desirable). For bulls (n = 47) genotyped for individual alleles, from 8 favorable alleles/stars (2 corresponding to thyroglobulin 5, TG5) for QG, 5 alleles were present and arranged in 10 different combinations corresponding to a 4.75% probability of their carcasses been classified as USDA Choice or better. For FE (8 favorable alleles/stars), 13 different allele combinations were present, which indicated a predisposition within these animals to consumed 1.62 Kg (out a maximum of 1.8 Kg for animals with all desirable alleles) less dry matter per day and have a similar or better weight gain than an animal without any desirable allele. For TEN, in average, it would be expected to have 0.53 kg less of Warner Bratzler shear force from these animals as compared with animals without a tender allele (6 favorable alleles/stars; test candidate genes = calpain-316, calpain-4751, and calpastatin). These results suggest that the Senepol breed have a genetic predisposition to gain weight efficiently and produce lean beef.

Key Words: Senepol, molecular breeding value, feed efficiency

W71 Function analysis of liver X receptor α regulating fatty acid synthesis in mammary epithelial cells of dairy goats.

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Liver X receptor α (LXRα) is a nuclear receptor of the transcription factor and known to play a crucial role in lipid metabolism such as bile acid and fatty acid synthesis in humans and rodents. However, very little information is available on the role of LXRα in the regulation of fatty acid synthesis in goat mammary glands. In this study, a novel cDNA was isolated from the mammary gland of a Xinong Saanen dairy goat and designated as goat LXRα. RT-PCR and RACE were used to obtain the full-length cDNA of LXRα, which is comprised 1654 bp with an ORF (open reading frame) of 1344 bp, the 5′-and 3′-UTR regions of 150 bp and 160 bp, respectively. The deduced amino acid sequence encodes 477 amino acids with a predicted MW of 50.4 kDa and a theoretical pI of 6.3. Additionally, homology search and sequence multi-alignment indicated that the putative goat LXRα amino acid sequence shares a high similarity with bovine, mouse, rat, pig and human counterparts. Bioinformatics predictions demonstrated that the LXRα protein, which is located in the nucleus containing characteristic signatures of nuclear receptor with DBD (DNA binding domain) and LBD (ligand-binding domain). Real-time quantitative PCR presented that LXRα was predominantly expressed in goat small intestine, liver, spleen and mammary gland. Treatment of goat mammary epithelial cells with different concentrations (0.01, 0.1, 1 μM) of T0901317, a synthetic agonist of LXRα, resulted in elevating SREBP1 (sterol regulatory binding protein 1) and FASN (fatty acid synthase) mRNA levels in response to the LXRα activation. The association between the different T0901317 concentrations and fatty acid compositions in goat mammary epithelial cells also was examined using gas chromatograph. The results showed that activation of LXRα significantly increased goat mammary epithelial cells C18:1 and C18:2 content, but did not affect SFA (saturated fatty acids). These discoveries are consistent with the notion that LXRα plays a key role in controlling lipogenesis and regulating UFA (unsaturated fatty acids) synthesis of goat mammary glands, which may prove useful in regulating milk fatty acid composition in lactating dairy goats.

Key Words: dairy goats, LXRα, fatty acid synthesis

W72 Structural and functional analysis of fatty acid synthase gene promoter of Xinong Saanen dairy goat.

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The objective of the study was to analyze the structure and function of fatty acid synthase (FASN) gene promoter in the mammary gland epithelial cells of Xinong Saanen dairy goat, and further explore the transcriptional regulatory mechanism of FASN gene. The biopsy mammary gland tissue samples were collected from 3 does during lactation for epithelial cell culture; all measurements on epithelial cells were replicated 3 time for statistical analysis by SPSS. The 5′ flanking region of goat FASN gene cloned from genomic DNA included a 591 bp region upstream of the transcription initiation site (+1), exon1, intron1 and partial exon2. TATA box and CAAT box, which are typical eukaryotic promoter elements, were located at −41 and −74 respectively. G and C accounted for 76% of the whole upstream region sequence, and 4 GC boxes (GGGCGG and CCGCCC) were found upstream of the TATA box. Bioinformatic analysis showed that there were potential transcription factor binding sites of LXR(−400), ER(−390), SREBP-1c(−150), NF-Y(−90) and E-box(−65) in goat FASN gene promoter. To define the core region of the FASN promoter, chimeric constructs containing serial 5′ and 3′ deletion sequences and the luciferase reporter gene were transfected into goat mammary epithelial cells. The luciferase activity was determined using dual-luciferase reporter assay system. The results indicated that the core region of FASN gene promoter was from −293 to −14 conferring basal transcriptional activity. Moreover, transcription factor binding sites of LXR, ER, SREBP-1c, NF-Y and E-box were mutated using overlap extension PCR. Site-directed mutagenesis analysis showed that binding sites of SREBP-1c, NF-Y and E-box could significantly downregulate the FASN gene promoter activity in goat mammary epithelial cells ($P < 0.05$), while binding sites of LXR and ER had no effect on the gene promoter activity. It is concluded that transcription factors including SREBP-1c, NF-Y and E-box were involved in regulating FASN gene at the transcriptional level.

Key Words: dairy goat, FASN gene promoter, site-directed mutagenesis

W73 Use of different statistical approaches to study genetic variability of OAR6 in sheep breeds farmed in Italy.

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Dense marker maps allow for the investigation of genomic regions that differentiate between breeds. In this work, 496 sheep belonging to 20 Italian sheep breeds were genotyped with the Illumina OvineSNP50 BeadChip. After data editing, 2,180 SNP located on chromosome 6 were analyzed with 4 different approaches. I) Fst Outlier Detection (FOD), implemented in the LOSITAN software, based on the comparison between Fst calculated on actual data and expected heterozygosity (He) and Fst under an island model. II) Composite Log-likelihood (CLL), based on calculation of CLL of the observed allelic frequencies across overlapping windows of 9 markers. III) Correspondence analysis (CA). VI) Canonical Discriminant Analysis (CDA). The different approaches were able to identify regions at OAR6 that expressed variation between breeds. Highest values for all statistics were found for a region spanning between 35 and 41 Mb known to harbour BMPR1b and ABCG2 loci. SNPs with a relevant discriminating power between breeds were also found at 76, 96 and 107 Mb, near to KIT, IL8 and SCD5 genes respectively. FOD detected 227 not neutral markers (17 under positive and 210 under balanced selection) using a confidence interval of 0.95. A total of 62 windows out of 242 were significant for CLL ($P < 0.01$). Several 85 and 135 SNPs exceeded empirical threshold for CA and CDA, respectively. The discriminating power was high for all methods and in general, they revealed a geographical pattern of variation between breeds. Moreover, each method provided specific information. FOD supplied a relatively low number of markers in divergent selection but it was able to identify loci under balanced selection. CA and CDA allowed a decomposition of total variability in different and uncorrelated variables that could be useful for the identification of genes influencing complex traits. The use of different statistical methods to study genetic variability between ethnic groups could provide indications about the adaptation to local conditions as well as the effect of selection.

Key Words: sheep breeds, SNP, statistical approaches

W74 Genotyping of five Chinese local pig breeds focused on meat quality by using PCR-RFLP based on halothane and Mx1.

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In recent years, due to the increasing demand for pork with high quality, a more convenient and fast way to test pigs is required for breeding, which enhances investigations on genetic variations associated with meat quality. So far, many genetic variations associated with meat quality have been investigated, such as myxovirus resistance protein 1 (Mx1), which was first found to be related to meat quality using samples from Chinese local pig breeds, and Halothane (Hal). Effects of Mx1 on meat quality of Chinese local pig breeds were demonstrated by Li in her Master's thesis in 2005 (Huazhong Agric. Univ. Wuhan, China), which was published in Chinese. The current study focuses on the use of RCR-RFLP of Hal and Mx1 for evaluating meat quality traits of several Chinese local pig breeds (Bama mini-pig, Huanjiang mini-pig, Lantang pig, Ningxiang pig and Xiangxi black pig including Daheping black pig, Pushi black pig and Taoyuan black pig) and Landrace pig (a foreign pig breed). The results indicated that the genotypes of Chinese local pig breeds were mainly shown as HalNN, while rarely in HalNn, rather than Halnn. The recessive allele (n) frequency in Chinese local pig breeds was significantly lower than that in Landrace pig. The recessive allele (B) frequency in the sixth intron of Mx1 in Chinese local pig breeds was generally higher than that in Landrace pig. The B frequency in the ninth intron of Mx1 was commonly higher in both Chinese local pig breeds and Landrace pig. In general, these findings have manifested that the Chinese local pig breeds, particularly Xiangxi black pig and Ningxiang pig, have a better meat quality.

Key Words: pig, nutrition, digestion

W75 Which housekeeping gene can be used in gene expression analysis in Chinese local pig breeds?

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Relative quantification real-time PCR (RT-PCR) is widely used for the quantification of mRNA expression level. The expression level should be normalized by using one or more reference genes. In this study, 3 frequently-used endogenous reference genes, including glyceraldehyde-3-phosphate dehydrogenase (GAPDH), β-actin (ACTNB), and 18S rRNA (18S), were evaluated by comparing their expression levels in 864 samples from 5 Chinese local pig breeds (Huangjiang mini-pig, Bama mini-pig, Taoyuan black pig, Lantang pig, and Ningxiang pig) and Landrace pigs (a foreign pig breed). The results, which were analyzed by Fisher's Least Significant Difference test after ANOVA using SPASS, showed that ACTNB and GAPDH had no significant different expression in overwhelming majority of the tissues investigated in the present study. We conclude that ACTNB and GAPDH had higher stable expression levels in various tissues, which indicated that both of them could be used as reference genes for the quantification of mRNA expression in some Chinese local pig breeds. For Chinese local pig breeds, ACTNB might be more suitable as a reference gene for target genes with high expression levels, while GAPDH might be better for target genes with low expression levels. Our findings also suggested that evaluation of reference genes is necessary for research among different local pig breeds. Otherwise, absolute quantification RT-PCR should be recommended.

Key Words: local pig breeds, mRNA expression, nutrition

W76 Genotype imputation accuracy in an F_2 pig cross using high-density and low-density SNP panels. J. L. Gualdrón Duarte*[1,3], R. O. Bates[1], C. W. Ernst[1], N. E. Raney[1], R. J. C. Cantet[3], and J. P. Steibel[1,2], [1]*Department of Animal Science, Michigan State University, East Lansing,* [2]*Department of Fisheries and Wildlife, Michigan State University, East Lansing,* [3]*Departamento de Producción Animal, Facultad de Agronomía, UBA - CONICET, Ciudad Autónoma de Buenos Aires, Buenos Aires, Argentina.*

High resolution SNP genotyping can be used for QTL mapping to facilitate meta-analysis across multiple populations. Typical swine F_2 populations have only a few founders (F_0), and a relatively small number of recombinations are expected in each generation. For that reason, genotyping the F_0 and F_1 generations with a high-density (HD) panel and typing the F_2 with a reduced number of tagSNP would enable high imputation accuracy of HD genotypes in the F_2 generation at a fraction of the cost. The goal of this study was to estimate imputation accuracy of F_2 genotypes when HD (44,752 SNP after data cleaning) genotypes are available for F_0 and F_1 generations. Starting with genotypes for F_0 and F_1 animals from the MSU Duroc × Pietrain resource population obtained using the Illumina Porcine SNP60 BeadChip, we simulated F_2 genotypes ($n = 932$) conditional on the real pedigree using a gene-dropping model. Subsequently, we applied 2 different methods to select tagSNP for F_2 animals: 1) statistical criteria based on pair-wise linkage disequilibrium on F_1 haplotypes, and 2) evenly-spaced markers. Imputation was performed assuming that F_0 and F_1 were typed at HD. Average imputation accuracy was calculated as the mean difference between observed and expected allelic dosage. We found that using panels of similar size, from evenly spaced selection or statistical selection resulted in similar imputation accuracy. When both F_0 and F_1 were typed at HD, imputation accuracy was approximately 0.97 if 2% of the HD markers, approximately evenly spaced every 2.1 Mb were used as tagSNP. Based on these results, we recommend using HD SNP genotyping in F_0 and F_1 and evenly spaced tagSNP panels consisting of at least 1200 tagSNP to obtain average inter marker distances of 2.1 Mb and to guarantee imputation accuracy above 0.97 in the F_2. Furthermore, forward imputation of HD-SNP in F_2 is appealing, since the resulting association tests could be combined across multiple populations using meta-analysis.

Key Words: imputation accuracy, F_2 cross, swine

W77 The proteome and mRNA expression of vimentin in the adipose tissue of broiler chickens. G. Kelley,* A. Stewart-Bohannon, F. Chen, X. Wang, and S. Nahashon, *Tennessee State University, Nashville.*

Increased fat deposition in broiler chickens is a major concern to poultry producers and consumers alike. Genomic approaches have been employed to discern the mechanisms of adiposity in food animals. These approaches have provided key transcriptional information depicting the possible role of gene sequences and their expression on fat deposition. However, they do not provide insight on the translational events that may contribute to adiposity although it is understood that proteins are the executants of most of most biological functions. We hypothesize that chicken adiposity 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 and to evaluate the mRNA expression of genes that encode these proteins. One hundred twenty 1-d-old broiler chickens were randomly assigned to floor pens and fed standard broiler diet until 8 weeks of age (WOA). At 8 WOA, experimental birds were 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 16 birds with the highest and lowest abdominal fat percentage 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 fat and lean birds ($P < 0.05$). Among them was vimentin, which was highly expressed in obese birds and was confirmed by Western blot. The mRNA abundance of vimentin was assayed at 8 WOA using Real Time-Polymerase Chain Reaction. A student t-test revealed no significant differences ($P > 0.05$) in the threshold cycles (Ct values) of vimentin between the lean and obese birds. The Ct values were 14.67 and 14.34 for the lean and obese birds, respectively. These results indicate that there are factors beyond the genome that influence vimentin expression in broiler chickens.

Key Words: adipose tissue proteome, broiler chickens, vimentin

Dairy Foods: Microbiology and Dairy Chemistry

W78 Viability of free and encapsulated *Lactobacillus acidophilus* ATCC 4356 in yogurt and artificial human gastric digestion system. F. Ortakci*[1,2] and S. Sert[2], [1]*Western Dairy Center Nutrition Dietetics and Food Sciences Department, Logan, UT,* [2]*Ataturk University, Erzurum, Turkey.*

The objective of this study was to determine the effect of encapsulation on survival of probiotic *Lactobacillus acidophilus* ATCC 4356 (4356) in yogurt and during gastric digestion. 4356 was added to yogurt in calcium-alginate microencapsulated or free form at a level of 8.26 and 9.47 log cfu/g respectively, and the influences of alginate microcapsules (1.5 to 2.5 mm) on sensorial characteristics of yogurts were also investigated. Survival of 4356 in simulated gastric and bile juices included incubation in 0.08 N hydrochloric acid (pH 1.5) containing 0.2% NaCl and a simulated bile juice consisting of 1.2% bile salts in MRS broth. There were similar and statistically significant ($P < 0.01$) reductions (~1 log cfu/g) in both free and encapsulated 4356 during 4 wk refrigerated storage of yogurts. When incubated for 2h in gastric juice, the free 4356 did not survive (>7 log cfu/g reduction). There was, however, greater survival of encapsulated 4356 with only a 3 log cfu/g reduction occurred. Incubation in simulated bile juice (6h) did not significantly affect ($P > 0.05$) the viability of both free and encapsulated 4356 due to the natural bile resistance of the bacteria. The addition of probiotic cultures either in free or alginate encapsulated forms did not significantly ($P > 0.05$) affect appearance and color, flavor and odor of the yogurts. There were, however, significant deficiencies ($P < 0.05$) in body and texture (graininess) of encapsulated 4356 containing yogurts. It was concluded that incorporation of free and encapsulated probiotic bacteria do not substantially change the overall sensory properties of yogurts and alginate microencapsulation using extrusion method greatly enhanced the survival of probiotic bacteria against artificial human gastric digestive system.

Key Words: probiotic, microencapsulation, artificial gastric system

W79 Complete genome sequence of *Bifidobacterium animalis* subspecies *lactis* BF-6. A. Baker[1], A. Negrete-Raymond[2], K. Polzin[1], M. Souza[2], Y. Yu*[3], J. Loquasto[3], J. Amos[3], and R. Roberts[3], [1]*Cargill Texturizing Solutions, Waukesha, WI,* [2]*Cargill Biotechnology Development Center, Navarre, MN,* [3]*The Pennsylvania State University, Department of Food Science, University Park.*

The primary objective of the present work was to sequence and evaluate the complete genome of *Bifidobacterium animalis* ssp. *lactis* BF-6, a common commercial probiotic originally isolated from the feces of a healthy human, and use this information to assess relatedness to other completely sequenced strains of the same subspecies. Genomic DNA was harvested and subjected to sequencing. Shotgun sequencing using 454 GSFlx Titanium pyrosequencing resulted in 20× coverage of the genome, which was assembled using Newbler into 24 contigs. The contigs were ordered and oriented with SeqMan software using the genome of *B. animalis* ssp. *lactis* DSM 10140 as a scaffold. After ordering, primers were designed on the ends of each contig and the intervening sequence was amplified by PCR. Amplicons were Sanger sequenced to close the gaps. For repeated elements, such as rRNA operons and transposons, long-PCR was conducted and the resulting amplicons were used as templates for additional nested PCR and sequencing reactions. The final genome was 1,938,607 base pairs (bp) in length with GC content of 60.48%. Annotation of the genome using the RAST and Artemis genome browser revealed the complete genome contains 1604 genes with a coding percentage of 85.9%, 4 complete rRNA operons and 52 tRNAs. Genome wide SNP analysis revealed BF-6 was highly similar to, but distinguishable from, other fully sequenced *B. animalis* ssp. *lactis* strains. The complete genome of *B. animalis* ssp. *lactis* BF-6 reported in this study provides additional insight into the phylogenetic organization of the *B. animalis* ssp. *lactis* taxon as well as into the biological and probiotic characteristics of this microorganism.

Key Words: *Bifidobacterium animalis* ssp. *lactis*, genome, SNP

W80 Growth of yogurt culture bacteria in the presence of two antimicrobials. M. Vives[1,2] and K. Aryana*[2,1], [1]*Louisiana State University,* [2]*Louisiana State University Agricultural Center.*

Antimicrobials such as potassium sorbate are added in the manufacture of dairy products such as flavored yogurts and process cheeses. Potassium nitrite and potassium metabisulfite have been reported to have an antimicrobial effect on pathogenic microorganisms such as *Clostridium botulinum, Listeria monocytogenes, Staphylococcus aureus, Escherichia coli* and *Pseudomonas fluorescens*. Potassium nitrite is commonly used in cured meats, canned cured meats, vacuum-packaged and fermented meats, bacon, cheese and seafood, while potassium metabisulfite is used in beverages and fruits. Yogurt is known for its health benefits, mainly due to the presence of its cultured bacteria. potassium nitrite and potassium metabisulfite are not commonly used in the dairy industry. How well the yogurt bacteria grow in the presence of 2 antimicrobials (potassium metabisulfite and potassium nitrite) at different concentrations is not well known. The objective was to study the influence of potassium nitrite and potassium metabisulfite at various concentrations, on the growth of *Lactobacillus bulgaricus* and *Streptococcus thermophilus*. Different concentrations of potassium metabisulfite and potassium nitrite (100, 1000, 10,000, 100,000, and 1,000,000 ppm) were added to MRS broth previously inoculated with *Lactobacillus bulgaricus* and *Streptococcus thermophilus* separately. Peptone water 0.1% w/v was inoculated with 1% (v/v) of freshly thawed *Lactobacillus bulgaricus* and *Streptococcus thermophilus* previously exposed to the different antimicrobial concentrations. The control did not have any concentration of either antimicrobial. Growth was determined by plating the different treatments and the control at 0, 24, 48 and 72 h of incubation of both microorganisms. Data were analyzed using Proc Mixed model of Statistical Analysis System with a repeated measures design. Three replications were conducted. All concentrations for both antimicrobials where significant for the growth of *Lactobacillus bulgaricus* LB-12 and *Streptococcus thermophilus* ST- M5 at 0, 24, 48 and 72 h ($P < 0.0001$). The highest concentration of potassium metabisulfite and potassium nitrite (1,000,000ppm) was significantly different from the rest of the lower concentrations, having the highest counts of bacterial populations for *Streptococcus thermophilus*. The effect of the antimicrobial at the highest concentration did not inhibit the growth of *Streptococcus thermophilus* at 72 h, but showed an exponential growth at this time period. Potassium metabisulfite and potassium nitrite did not negatively affect the growth of yogurt bacteria.

Key Words: yogurt, culture, antimicrobial

W81 Acquired resistance of yogurt culture bacteria to two different antimicrobials.

M. Vives[1,2] and K. Aryana*[2,1], [1]*Louisiana State University,* [2]*Louisiana State University Agricultural Center.*

A bacterial strain can said to be resistant if it can survive and multiply itself in the presence of an antimicrobial agent that would normally inhibit or kill this particular kind of microorganism. Potassium nitrite and potassium metabisulfite have been reported to have an antimicrobial effect on pathogenic microorganisms such as *Clostridium botulinum, Listeria monocytogenes, Staphylococcus aureus, Escherichia coli* and *Pseudomonas fluorescens*. Potassium nitrite is commonly used in cured meats, canned cured meats, vacuum-packaged and fermented meats, bacon, cheese and seafood, while potassium metabisulfite is used in beverages and fruits. Antimicrobials such as potassium sorbate are added in the manufacturing of several products such as flavored yogurts and process cheeses. Antimicrobials such as potassium nitrite and potassium metabisulfite are not commonly used in the dairy industry. Yogurt is known for its health benefits, mainly due to the presence of its cultured bacteria. Whether yogurt bacteria can acquire resistance to 2 different antimicrobials (potassium metabisulfite and potassium nitrite) is not known. The objective was to study the possibility of an acquired resistance of these 2 bacterial strains to higher doses of the 2 antimicrobial compounds after prior exposure to lower doses of these antimicrobials. Treatments consisted of the transfer of previously grown cultures at the lower concentrations i.e., 100 and 1000 ppm of both antimicrobials, after 24, 48 and 72 h, into 2 higher concentrations 10,000 and 100,000 ppm, of both antimicrobials and growth was measured after 0, 24, 48 and 72 h of incubation. Data were analyzed using Proc Mixed model of Statistical Analysis System with a repeated measures design. Experiments were replicated 3 times. There was a significant interaction effect between the antimicrobial × microorganism × treatment × transfer hour × growth hour, on the growth of the bacterial strains ($P = 0.0015$). There were significantly higher counts ($P < 0.005$) of *Streptococcus thermophilus* compared with the control. For *Lactobacillus bulgaricus* the growth was similar to the control which suggests there are no significant differences between the growth at higher concentrations and the control. *Streptococcus thermophilus* exhibited resistance to the higher doses of antimicrobial compounds.

Key Words: resistance, yogurt culture, antimicrobial

W82 Isolation of an oligotrophic *Lactobacillus* species that may be associated with late gas production and splits in cheese.

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A wide variety of facultative and obligate heterofermentative bacteria, including several lactobacilli, have been associated with late gas production in aged cheese. Such cheese can suffer from splits and slit defects during cheese storage, especially when storage temperature is increased to accelerate flavor development. The objective of this study was to identify bacteria in aged Cheddar cheese that causes late gas production. We isolated a novel heterofermentative *Lactobacillus* species (WDC04) following incubation on MRS agar at 6°C for 35 d. BLAST analysis against the 16S rRNA gene database of GenBank revealed WDC04 had 97% sequence identity with *Lactobacillus suebicus* strain CECT5917 (AJ575744), *Lactobacillus vaccinostercus* (AB218793), and an uncultured compost bacterial sequence (FN667177). Cellular morphology and colony morphology were consistent with related species. API CH50 fermentation panels showed a preference for utilization of ribose and galactose over other carbohydrate sources, and WDC04 is difficult to grow expect on MRS broth supplemented with galactose and ribose. As a nonstarter lactic acid bacteria (NSLAB), WDC04 ecologically falls into the category of being an oligotroph that undergoes slow growth in conditions of low nutrient availability. In contrast, lactococcal starter bacteria have copiotroph attributes and exhibit high growth rates when resources are abundant such as occurs in milk. In the harsh environment of ripening cheese (no residual lactose, low pH, low temperature and high salt concentration), viability of starter bacteria usually declines. At the same time, oligotrophic NSLABs utilize amino acids and bacterial debris to supply their energy needs, and will slowly increase in numbers until they are the predominant organism(s) of aged cheese microflora. Gas production by WDC04 was observed at 5 d in MRS broth incubated at 25°C with significant gas production by 9 d. Gas production was also observed after incubation for 28 d in MRS at 8°C. It was concluded that WDC04 is a potential cause of gas production during storage of cheddar cheese.

Key Words: cheese, nonstarter, heterofermentative

W83 Influence of various health beneficial spices on the acid tolerance of *Streptococcus thermophilus* ST-M5.

M. Sanchez-Vega*[1,2] and K. Aryana[2,1], [1]*Louisiana State University,* [2]*Louisiana State University Agricultural Center.*

There is a great deal of public interest in the use of herbal remedies. Garlic is said to be antibacterial, antiviral, and antifungal and also prevent cardiovascular diseases and some types of cancer. Ginger is effective against nausea and cardiovascular diseases and is also an analgesic and has antibacterial properties. Onion is effective against the common cold and reduces the risk of developing diabetes; it also has antiinflammatory, anticholesterol, anticancer and antioxidant properties. Many studies have been conducted using spice extracts, but the effect of pure spice juice has not been studied. According to some studies, spices might have the capacity of enhancing the growth of certain probiotic strains while acting as a bactericide for harmful bacteria. The main objective of this study was to elucidate the influence of garlic, ginger, and onion on the acid tolerance of *Streptococcus thermophilus* ST-M5. Freshly thawed culture was inoculated in acidified MRS broth at pH 2 and 1% v/v of freshly extracted spice juice was added. Control was without spice juice. Growth was determined hourly during 2 h of incubation at 37°C. The data were analyzed using Proc Mixed model with a Tukey adjustment of Statistical Analysis System. Experiments were replicated 3 times. All 3 spices showed a significant ($P < 0.05$) increase in counts at 0 h of incubation when compared with control. After 1 h of incubation, all 3 spices had significantly ($P < 0.05$) higher counts than control. After 2 h of incubation, ginger showed no significant ($P > 0.05$) difference compared with control (5.5 log cfu/mL), while there were slight yet significantly lower counts for garlic (4.3 log cfu/mL) and onion (5.1 log cfu/mL). Among the spices, ginger had the best overall effect. These 3 spices can be used with *Streptococcus thermophilus* enabling health benefits from both sources.

Key Words: spice, culture, acid tolerance

W84 Bile tolerance of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 subjected to mild sonication intensities at different temperatures.

M. Moncada*[1,2] and K. Aryana[2,1], [1]*Louisiana State University,* [2]*Louisiana State University Agricultural Center.*

Low sonication intensity is a non-destructive technique that consists on the application of low energy, high frequency (1–10 MHz) and power intensities below 1 W/cm2. It has been reported that the survival of lactic acid bacteria is increased with the application of "mild" sonication condition. One of the requirements for a bacterium to be called probiotic is the ability to survive the gastrointestinal stress factors such as acid and bile conditions. *Lactobacillus bulgaricus* is widely used in the fermentation of dairy products. The objective of this study was to determine the effect of various mild sonication intensities at different temperatures on bile tolerance of *Lactobacillus bulgaricus* LB-12. Freshly thawed *Lactobacillus bulgaricus* LB-12 culture was suspended in 0.1% peptone water and sonicated using a 13 mm diameter probe set at a maximum acoustic power output of 750 W, frequency 24 kHz. Before sonication, the inoculated samples were set at 3 temperatures (4, 22, and 40°C). Four sonication treatments with intensities of 8.07, 14.68, 19.83 and 23.55 W/cm^2 were performed in a random manner at the 3 different temperatures mentioned above. Control samples did not receive any sonication treatment. Bile tolerance of samples was determined every 2 h for 12 h of incubation. Data were analyzed using ANOVA of Statistical Analysis System. Three replications were conducted. At 4°C, bile tolerance of cultures subjected to control and 14.68 W/cm^2 was significantly ($P < 0.05$) higher compared with the rest of mild sonicated intensities. Bile tolerance at 22°C was significantly ($P < 0.05$) higher than at 4 and 40°C during the 12 h of incubation. Log reduction at 22 and 40°C showed that samples treated with mild sonication intensities had higher bacterial growth than the control. It is concluded that certain mild sonication conditions improved bile tolerance of *Lactobacillus bulgaricus* LB-12.

Key Words: sonication, culture

W85 A new approach to make milk calibration standards for electronic somatic cell counters.

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Our objective was to develop a procedure to make milk somatic cell count (SCC) reference materials for calibration of electronic somatic cell counters (ESCC). The key innovation was the use gravity separation to produce a naturally occurring high and low SCC milk. One batch of whole raw milk was separated into 2 portions. One portion was gravity separated at 4°C for 24 h and the second portion was centrifugally separated at 4°C to produce raw skim milk that was also gravity separated. The somatic cells concentrated at the top of both gravity separation tanks. Milk was collected from the top and the bottom of the tanks to produce a high and low SCC milk from each tank. These 4 bronopol preserved milks were analyzed using direct microscopic somatic cell count by 2 laboratories. A set 12 milk dilutions of the high SCC whole and skim milks were made (mass/mass) combinations of the high and low SCC skim and whole milks, respectively. The experiment was replicated 3 times. The range of SCC within a set was from approximately 5,000 to 950,000 somatic cells per mL. Two laboratories analyzed 3 sets of these milks per week by ESCC over a period of about 21 d of 4oC storage. ANOVA was used to determine the effect of laboratory, set type (skim or whole milk), and sample age on the observed electronic milk SCC. No effect of laboratory or set type ($P > 0.05$) on observed milk ESCC was detected. There was a mean decrease ($P < 0.05$) in ESCC with time of storage (about 7,000 cells per mL at 350,000 cells per mL during 2 weeks of refrigerated storage). Gravity separation can be used to produce a set of milk SCC reference standards with a wide range somatic cell count with 12 incremental SCC distributed evenly from low to high across the range.

Key Words: somatic cells, gravity separation, reference standards

W86 Freezing and thawing milk calibration standards for electronic somatic cell counters.

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Our objective was to determine the effect of freezing and thawing on electronic milk somatic cell count (ESCC) standards. Whole raw milk (350 kg) was pasteurized and split into 2 portions. One portion was gravity separated at 4°C for 22 h and the second portion was centrifugally separated at 4°C to produce skim milk that was also gravity separated. After 22 h the somatic cells were concentrated at the top of both gravity separation tanks. Stock solutions (3: high SCC skim and whole milk stock and a low SCC skim stock) were prepared and preserved (bronopol). Standards were formulated by diluting high SCC (whole or skim milk) stock with low SCC skim stock to make 1600 g of each of a series of 12 whole and 12 skim standards. The range of SCC was from approximately 2,000 to 1,150,000 SCC/mL and from 2,000 to 800,000 SCC/mL for the skim and whole milk sets, respectively. Half of the sets were kept refrigerated at a 4°C and the other half were frozen at −80°C for 24 h, and then moved to a −20°C freezer. On each day of analysis, 1 set of skim and 1 set whole refrigerated milks were tested and 1 set of skim and 1 set whole frozen milks were tested on 2 different cell counters in different labs. Refrigerated and frozen samples were put in the water bath at the same time and were analyzed when their temperature reached 40 to 42°C. Analysis was repeated 4 times during a 2 week storage and replicated 3 times. Effects of freezing, laboratory, set type (skim or whole milk), and sample age on the ESCC were determined. For the skim SCC standards there was no effect of freezing on mean ESCC during a 2 week period. For the whole milk SCC standards there was an effect of freezing with the frozen and thawed set having a mean SCC of about 6,000 SCC/mL lower than the unfrozen samples over a 2 weeks period. Skim milk SCC standards had a larger range of SCC than whole milk. Frozen and thawed skim standards may have better homogeneity with longer frozen storage time and avoid problems of oiling off during thawing and heating of milks.

Key Words: somatic cells, freezing, gravity separation

W87 Protease activity of *Streptococcus thermophilus* ST-M5 subjected to mild sonication intensities at different temperatures.

M. Moncada*[1,2] and K. Aryana[2,1], [1]*Louisiana State University,* [2]*Louisiana State University Agricultural Center.*

Streptococcus thermophilus is a bacterium used widely for the production of many fermented dairy products. Protease activity degrades the milk proteins to peptides and influence the quality characteristics namely texture and flavor of several aged dairy products. “Mild” sonication intensity is a technique that uses sound waves to cause cavitation in liquid solutions and may improve the permeability of the cell membrane. The objective of this study was to evaluate the influence of “mild” sonication intensities on protease activity of *Streptococcus thermophilus* at different temperatures. Freshly thawed *Streptococcus thermophilus* ST-M5 culture was suspended in 0.1% peptone water and sonicated using a 13 mm diameter probe set at a maximum acoustic power output of 750 W, frequency 24 kHz. Before sonication, the inoculated samples were set a 3 different temperatures (4, 22 and 40°C). Four sonication treatments with intensities of 8.07, 14.68, 19.83 and 23.55 W/cm^2 were performed in a random manner at the 3 different temperatures mentioned above. Control samples did not receive any sonication treatment. Protease activity was determined at 0, 12 and 24 h of incubation spectrophotometrically at 340 nm. The experimental design was completely randomized design. Data were analyzed using ANOVA of Statistical Analysis System.

Three replications were conducted. Differences of least squares means were used to determine significant differences at $P < 0.05$ for main effect (mild sonication intensity) and interaction effect (mild sonication intensity × time × temperature). Absorbance units increased over time from 0 to 24 h. At 4°C, protease activity of cultures subjected to 8.07 W/cm^2 was significantly ($P < 0.05$) higher than the control at 12 and 24 h. At 22°C the protease activity at all sonication intensities and all time points were lower than the control except for 19.83 W/cm^2 at 24 h. At 40°C, 23.55 W/cm^2 showed significant ($P < 0.05$) increase in protease activity compared with the control at 0, 12 and 24 h. The optical density (OD) values at 0, 12, and 24 h after using 23.55 W/cm^2 were 0.11, 0.16 and 0.17 absorbance units while OD values for control were 0.09, 0.12 and 0.15 absorbance units at 0, 12, and 24 h, respectively, at 40°C. *Streptococcus thermophilus* treated with some mild sonication intensities improved its protease activity.

Key Words: protease, culture, sonication

W88 Prediction of fatty acid chain length and unsaturation of milk fat by mid-infrared milk analysis.

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Our objective was to predict mean fatty acid chain length (mCL, carbon number) and mean fatty acid unsaturation (mUnsat, double bonds per fatty acid) of milk fat from mid-FTIR spectra. Calibration models for both parameters were calculated, using partial least squares, based on spectra for 268 samples collected over a period of 1.5 year. Of which 219 samples (largely herd milks) were selected to cover a wide variation in regional and dietary dependent milk fat composition. The set was complemented with 49 modified milks spanning an orthogonal set in fat, protein and lactose. Milks were analyzed for fat by ether extraction and fatty acid composition by GLC. Standard errors for calibration, determined using full cross validation (SECV) on the calibration set were 0.11 carbons for mCL and 0.012 double bonds for mUnsat. Validation was on the basis of an independent set of 47 milks, for which mean and range in mCL were 14.47, 14.00 to 14.85 carbons and mean and range in mUnsat were 0.319, 0.236 to 0.394 double bonds, respectively. The mean difference, standard deviation of the differences, relative coefficient of variation for prediction of mCL compared with GLC reference values was 0.056 carbons, 0.063 carbons, and 0.4%, respectively, and 0.003 double bonds, 0.011 double bonds, and 3.3%, respectively. Future work will determine if estimates of fatty acid composition by mid-FTIR can be used in real time to improve the accuracy of prediction of total fat content of milk.

Key Words: mid-infrared, fatty acids, chain length

W89 A ruggedness study: Casein content of milk by Kjeldahl analysis for milk concentrates and non-bovine milks.

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The objective of our work was to develop a modification of Association of Official Analytical Chemists International (AOACI) method 998.05 (optimized for a raw bovine milk matrix) so that it could be applied to milk concentrates and milks of other species (goat, sheep, and water buffalo). A ruggedness study was carried out that demonstrated that as concentration of protein in milk increased (either in bovine milk concentrates or in milks of other species), the amount of buffer needed in the noncasein nitrogen sample preparation method to achieve a filtrate pH of 4.6 increased. In the first part of the study using a series of bovine milk ultrafiltration concentrates, it was demonstrated that the method gave more consistent predictions of casein as a percentage of true protein when the NCN filtrate pH was between 4.5 and 4.6, regardless of total protein concentration. The study was designed with a series of UF retentates ranged from 3 to 9% protein but all contained the same casein as percentage of true protein, regardless of TP concentration. Thus, when the reagent concentration was correct the casein as a percent of true protein at all protein concentrations. When the amount of buffer added to the sample was not sufficient (i.e, the filtrate pH was too high), the filtrates were not clear. A polynomial equation was developed for prediction of the amount of acetic acid - sodium acetate buffer required to achieve pH for milk protein concentrations from 3 to 9% protein. The modified method was tested on goat, sheep, and water buffalo milks. The results of this study will be used as the basis for proposed changes in the official (AOAC and International Dairy Federation) methods for measurement of the casein content of milk to expand the scope of the method so it can be used to achieve accurate results for milk concentrates and milks of other species.

Key Words: casein, milk concentrates, sheep and goat

W90 A review of the pH influenced casein-whey protein interactions in heated milk.

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During the heat treatment of milk, denatured whey proteins associate to the casein micelle, affecting the functional properties of milk in downstream applications such as milk and yogurt. Although the specific mechanism of attachment is not entirely understood, after partial denaturation, β-lactoglobulin (β-LG) attaches via available sulfide groups to κ-casein (κ-CN). Additionally, there is conflicting evidence, apart from the more commonly accepted mechanism in which the κ-CN/β-LG complex is formed on the surface of the micelle, that may indicate that β-LG does not attach to κ-CN on the surface of the casein micelle, but rather that κ-CN first interacts with β-LG preferentially in the serum matrix and later the κ-CN/ β-LG complex can re-associate with the casein micelle. Furthermore, it is believed that α-lactalbumin (α-LA) does not attach directly to the micelle, but instead forms an association with β-LG portion of the κ-CN/β-LGcomplex, and is therefore dependent on this association to attach to the casein micelle. After heat-treatment and attachment, the milk matrix contains 3 types of whey proteins: native whey proteins, protein aggregates, and those aggregates that have formed an association on the surface of the casein micelle. The percentages of these whey protein-types are highly dependent on the extent of heat treatment (temperature and time) as well as milk pH. Methods have been used to separate and quantify these types of whey proteins in heated milk including acid separation, rennet separation, and ultracentrifugation. To quantify the whey protein forms in milk, different analytical methods can be used such as HPLC, capillary electrophoresis and gel electrophoresis. This work reviews the mechanism of the attachment of partially denatured whey proteins to the surface of the casein micelle, the various types of whey proteins that can be found in the milk matrix after heat treatment, as well as the various methods of determination and quantification of whey proteins.

Key Words: whey protein, casein, denaturation

W91 Gel-based shotgun proteomics analysis of cow milk fat globules. T. J. Yuan, J. Q. Wang,* Y. X. Yang, D. P. Bu, J. H. Yang, 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 was designed to characterize protein expression profiling of cow milk fat globules (MFG). Four different lysis buffers were applied to improve protein extraction from the cow MFG, and extracts were subjected to SDS-PAGE separation followed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) for identification and characterization. The result indicated different lysis buffers led to different quality of protein extraction and resolution. All 224 MFG proteins (MFGP) were identified by 2 or more unique peptide sequences. The identified MFGP ranges from 8 kDa to 546 kDa in molecular weight mass, and 4.61 to 11.36 in isoelectric point. The Gene Ontology (GO) classification for localization and function of these proteins was presented. Among all identifications, 69 were not reported before in bovine MFG or MFGM, and the majority of these proteins are involved in membrane and vesicular trafficking, cell signaling, immune function, protein synthesis, binding and folding, fat transport/metabolism, enzymatic activity or poorly defined functions. Our work presents a detailed picture of the cow MFG proteome at the physiological conditions based on gel LC-MS/MS analysis, providing a useful source for future studies on lactation biology and on physiopathological evaluation of the mammary gland on the basis of their proteomic assortment.

Key Words: milk fat globule, shotgun proteomics, Gene Ontology classification

Forages and Pastures III

W92 Chemical composition of oats straw treated with oxidizing and alkali-based agents. F. E. Miccoli[1,2], H. M. Arelovich*[2,3], R. D. Bravo[2,3], and M. F. Martínez[2,4], *[1]Facultad de Ciencias Agrarias, Universidad Nacional de Lomas de Zamora, Buenos Aires, Argentina, [2]Departamento de Agronomía, Universidad Nacional del Sur, Bahía Blanca, Argentina, [3]Comisión de Investigaciones Científicas (CIC), Buenos Aires, Argentina, [4]CERZOS-CONICET, Bahía Blanca, Argentina.*

Specific chemical treatments improve feeding value of straws by dissolving chemical bonds of cell wall components without affecting lignin content, which may be decreased by oxidizing agents. The objective was to evaluate the effect of oxidizing and alkali-based agents added in aqueous solution to improve feeding value of chopped oats straw (*Avena sativa*, OS). Treatments were CON (control); U = urea (4 g/100 g DM); SH = NaClO (1 g active Cl/100 g DM); SC = NaCl (4 g/100 g DM); and the combinations U-SH; U-SC; SH-SC and U-SH-SC. A volume of 30 mL of each solution was sprayed and homogenized with 100 g DM of OS, compacted and stored for 10, 20 or 30 d in 10 × 15 cm PVC cylinders. The storage temperature was 24.1 ± 1.8°C. After storage samples were dried (65°C), ground (2mm) and analyzed for IVDMD, CP, NDF, ADF and ADL. Data were analyzed as a factorial arrangement of treatments with 4 replicates and means were compared using Tukey's test. Interaction ($P < 0.01$) between chemical treatments and storage length was only found for CP and ADL. Thus IVDMD, NDF and ADF across storage lengths are reported on Table 1 since chemical treatment is the main factor. The CP concentration did not change within treatments without urea in any storage length, averaging 2.36%. However, U, U-SH, U-SC and U-SH-SC averaged 10.30% CP being 4.4 times greater than treatments without urea. The combination of urea with oxidizing and alkali-based agents (U-SH, U-SC and U-SH-SC) promoted even larger N retention in OS than U alone ($P < 0.05$). The main reduction of ADL was noted at 30 d storage length ($P < 0.05$) with SH-SC (4.43%) vs. CON (6.28%). Combined oxidizing and alkali-based agents substantially improved feeding value of OS.

Table 1. Effect of oxidizing and alkali-based agents on oats straw quality

Treatment	IVDMD	NDF	ADF
CON	47.38^{a}	79.57^{e}	44.37^{c}
U	52.10^{bc}	76.72^{cd}	43.27^{bc}
SC	49.77^{ab}	78.85^{e}	43.72^{c}
SH	49.91^{ab}	78.19^{de}	43.71^{c}
U-SC	54.00^{c}	74.49^{b}	41.34^{ab}
U-SH	53.23^{bc}	75.22^{bc}	41.59^{ab}
SC-SH	53.65^{bc}	73.67^{ab}	42.57^{bc}
U-SC-SH	54.11^{c}	72.26^{a}	40.32^{a}
SEM	0.91	0.38	0.44

$^{a–e}$Means in the same column with different superscripts differ ($P < 0.05$).

Key Words: oats straw, forage quality, chemical treatment

W93 In vitro true organic matter digestibility, partitioning factor, and ruminal microbial protein synthesis 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], M. Guerrero Cervantes[2,4], N. C. Vásquez Aguilar[1], F. G. Ríos Rincón[3,4], E. Gutiérrez Ornelas[1,4], and J. E. Treviño Ramirez[1], *[1]Universidad Autónoma de Nuevo León, Fac. Agronomía, San Nicolás de los Garza, NL, México, [2]Universidad Juárez del Estado de Durango, Fac. Medicina Veterinaria y Zootecnia, Durango, México, [3]Universidad Autónoma de Sinaloa, Fac. Medicina Veterinaria y Zootecnia, Culiacán, Sin, México, [4]Red Internacional de Nutición y Alimentación en Rumiantes, México.*

This study was conducted to evaluate the nutritional value of 3 crown rust (*Puccinia coronata*) resistant oat cultivars (CRR = L112, L124 and L164), released from the Agronomy Dept. of the University of Nuevo Leon, Mexico, and of 2 commercial crown rust susceptible cultivars (CRS = Guelatao and Chihuahua) using in vitro procedures. Whole plant samples were harvested April 2008 at 3 growth days (d), and grouped in a 2 × 3 factorial arrangement of treatments, with 2 groups of cultivars (CRR and CRS), and 3 growth stages (101, 110, and 117 d), in a complete randomized design, without accounting for single varieties. No crown rust disease infested any of the experimental plots. Incubations of 500 mg samples were set in 40 mL of a 1:2 mixture of rumen fluid from 3 fistulated sheep fed 75% alfalfa hay and 25% concentrate, and buffer solution, in calibrated 100 mL glass syringes at 39°C, to determine mL gas production at 24h (GP_{24h}). True in vitro dry matter degradability (TIVDMDegr) was determined after refluxing the 24h-incubation residuals in NDF solution. Partitioning factor (PF) was calculated as mg true degraded DM/GP_{24h}. Microbial protein (MP) synthesis was estimated measuring UV-spectrophotometrically the purine content (µmol) of additional freeze-dried 24h-incubation residuals. True in vitro OM digestibility (TIVOMDig) was determined after incubating 250 mg samples in a Daisy (ANKOM) fiber digester. There was an interaction ($P < 0.01$) for GP_{24h}, since beginning with similar values at 101 d (avg. 86.5 ± 1.8), GP_{24h} for CRS increased until 117 d (89.9 ± 2.2 SE), whereas CRR decreased to 74.3 ± 1.8 mL. TIVDMDegr increased ($P < 0.05$) at 117 d (58.1 ± 0.9%) compared with 101 and 110 d (avg. 42.8 ± 0.9%). The PF of CRR at 117 d was higher than CRS (3.80 ± 0.08 *vs* 3.35 ± 0.10, $P < 0.05$), however (interaction $P < 0.05$) PF was similar earlier (avg. 2.50 ± 0.08). TIVOMDig at 101 d was higher than 117 d (72.1 ± 0.8 *vs* 66.8 ± 0.8%, $P < 0.01$); no difference was found between CRR and CRS. There was increased MP of CRS compared with CRR at 110 (9.0 ± 0.6 *vs* 7.5 ± 0.5) and 117 d (8.1 ± 0.6 *vs* 5.8 ± 0.5 µmol) but (Interaction $P < 0.05$) MP was similar (avg. 6.0 ± 0.6) at 101 d. In conclusion, TIVOMDig was higher at 101 d than later. GP_{24h} and MP of CRS at 110 and 117 d were higher than CRR.

Key Words: oat forage, crown rust, ruminal digestibility

W94 On farm corn silage evaluation method and its validation in a field study. B. Andrieu,* A. Perilhou, and J. Sindou, *Lallemand SAS, Blagnac, France.*

Many silages present some preservation issues, but measuring silo parameters on farm is not always an easy practice. Therefore, a toolbox and its accompanying software (Corn Silage Investigation (CSI) software) were developed to allow a diagnosis of corn silage quality on farm. To validate the concept a large-scale field study was performed. 51 farms located in several areas of France were diagnosed using the toolbox. Temperature, pH and density were recorded as described by the method and the corresponding values were entered in the CSI-software. In addition, parameters describing the farm (breeding performance, field management) and the harvest (type of harvester, speed, yield and application of silage inoculants) were noted. Samples at specific sampling points were taken for chemical analysis (VFA, ammonia, feeding value, monopropylene glycol). Data from the field survey were subjected to 1-way ANOVA. For each farm the CSI-sofware provided a report in which their values were graphically depicted versus benchmarks, which facilitates interpretation of the data. Results from the field survey showed that 30% of the silos had a density lower than the target value (240 kg DM/m3). The density was correlated with parameters at harvest (weight of the tractor, harvest speed), specifications of the corn (DM and chop length) and bunker specifications. It was also recorded that 36% of the investigated silage was heating up (>3°C above ambient temperature). Treating the silage with an inoculant showed to be beneficial. Not only was the percentage of silages that showed heating lower (60% for non treated (NTS) vs 16% for treated silage (TS)), the average increase of temperature was also significantly lower (+8°C for NTS versus +1°C for TS, $P \leq 0.05$) as well as the maximum temperature reached (51°C for NTS versus 28°C for silage treated with *L. buchneri* 40788 versus 47°C for silage treated with *L. buchneri* 202118, $P \leq 0.01$). The toolbox and the CSI-software have proven a practical tool to evaluate the quality of silage. The field study confirms that good management of several parameters (silo design, harvest parameters, etc.) are essential for good silage quality. The addition of a silage additive such as *Lactobacillus buchneri* can help optimizing these good management practices.

Key Words: corn silage quality, field survey, *L. buchneri*

W95 Transgenic corn hybrids reduce fungi in silage. G. B. Neto*[1], T. M. dos Santos Cividanes[1], R. B. F. Branco[1], A. L. Fachin[2], M. C. Beraldo[2], and T. A. Bitencourt[2], [1]*Agência Paulista de Tecnologia dos Agronegócios da Secretaria da Agricultura e Abastecimento do Estado de São Paulo, Ribeirão Preto, São Paulo, Brazil,* [2]*Universidade de Ribeirão Preto, Ribeirão Preto, São Paulo, Brazil.*

The presence of fungi was evaluated in 4 hybrid maize silages, DKB 390 and AG 8088, with (GMO) or without (near-isogenic non *Bt*) the *cry*1Ab *Bacillus thuringiensis* gene. The GMO was not treated with insecticide, and the conventional hybrids received one deltamethrin (2.8%) application 42 d after planting. The harvest was done 95 d after planting. The experimental design was the randomized block with 5 replications in a 2 × 2 factorial arrangement. The GMO had a reduce incidence of fungi in the silage ($P < 0.001$). The total-count averages in the GMO and conventional hybrid silages for filamentous fungi were of 12×10^3 and 3.4×10^5 cfu/g and 13×10^3 and 1.1×10^6 cfu/g for yeast, respectively. However, grain, leaf and stalk ionizant radiation samples were tested for their capacity to inhibit the formation of fungi, such as *Aspergillus flavus, Penicillium sp, Fusarium oxysporum, Fusarium verticilloides*, and no significant differences were found ($P > 0.05$). Thus, the smaller fungi population in the GMO silage was attributed to a higher defense capacity of the plant against the armyworm *Spodoptera frugiperda*. The average damage caused by the *S. frugiperda*, determined in 25 plants per treatment through a visual scale from 0 (no damage) to 5 (dead plants), was of 1.04, 1.60, 1.52, 1.52, 1.68 in GMO and 2.08, 2.28, 2.68, 2.84 and 2.80 in conventional hybrids 15, 22, 29, 36 and 46 d after planting, respectively. Although the GMO was highly effective against *S. frugiperda* ($P < 0.001$), it was not as effective against *Helicoverpa zea* 71 and 78 d after planting ($P > 0.05$). The average damage caused by *H. zea*, determined through a visual scale from 0 (no damage) to 4 (severe damage), was of 0.72 and 1.04 in GMO and 0.84 and 0.96 in conventional hybrids, respectively. Insect damage in plants plays an important role in mold infestation because these events cause the disruption of the protective cell wall. This creates entry points for infective molds. In addition, it causes release of nutrients from the plant endosperm that can be used by molds for growth. The results indicate that the GMO studied likely indirectly reduces fungi populations in silage through reduced impact of armyworm infestations.

Key Words: armyworm, mold

W96 Effects of DM concentrations and inoculants on Jiggs and Tifton 85 bermudagrass silage. J. M. B. Vendramini*[1], A. T. Adesogan[2], L. E. Sollenberger[3], A. D. Aguiar[1], A. Valente[1], and P. Salvo[1], [1]*UF/IFAS Range Cattle Research and Education Center, Ona, FL,* [2]*Department of Animal Sciences, Gainesville, FL,* [3]*Department of Agronomy, Gainesville, FL.*

Bermudagrass is the main warm-season grass species preserved as silage or haylage by dairy producers in Florida; however, the nutritive value and silage fermentation parameters are often less than desirable. The objective of this study was to investigate the effects of DM concentrations on nutritive value and fermentation parameters of Jiggs bermudagrass (*Cynodon dactylon* L.) and Tifton 85 bermudagrass (*Cynodon* sp.) silages treated with sugarcane (*Saccharum officinarum*) molasses [1 kg molasses (DM)/50 kg forage (As fed)], Ecosyl inoculant [EcoSyl, MTD/1; 100 mg/50 Mg forage (As fed)], B 500 inoculant [*Lactobacillus buchneri*, 8 mg/kg forage (As fed)], or control. The experiment was conducted in Ona, FL. Tifton 85 and Jiggs plots were distributed in a randomized complete block design with 3 replicates. The data were analyzed using PROC MIXED with bermudagrass cultivars (main plot), DM concentrations (sub-plot), and inoculants (sub-sub-plot) as fixed effects, and block and its interactions as random effects. Forage was harvested with 4 wk regrowth and readily ensiled (22% DM) or wilted on the field for 4 h (53% DM). Forage was packed into a mini-silo at a density of approximately 400 kg fresh forage/m^3 and ensiled for 90 d. There were no effects ($P < 0.05$) of species, DM concentrations, or inoculants on CP concentrations (12.2%). Forage with greater DM concentration had greater in vitro true digestibility (IVTD; $P < 0.01$, SE = 1, 56 vs. 53% for 53 and 22% DM, respectively) and the molasses treatment resulted in forage with greater IVTD than the other inoculant treatments ($P < 0.01$, SE = 1, 58 vs. 53%). However, silage with greater DM concentration had greater pH ($P = 0.02$, SE = 0.6, 4.5 vs. 4.8 for 22 and 53% DM, respectively) and decreased lactic acid concentrations ($P < 0.01$, SE = 0.1, 3.8 vs. 2.9% for 22 and 53% DM, respectively). Silage treated with molasses had decreased pH ($P < 0.01$, SE = 0.04, 4.3 vs. 4.8), increased acid lactic concentrations ($P < 0.01$, SE = 0.05, 5.4 vs. 2.4), and decreased aerobic stability when compared with forage treated with Ecosyl, B 500, and control ($P < 0.01$, SE = 11, 205 vs. 288 h). Using molasses as an additive may improve the nutritive value and fermentation characteristics of bermudagrass silage.

Key Words: bermudagrass, silage, inoculant

W97 Effects of *Lactobacillus* inoculants and forage dry matter on the fermentation and aerobic stability of ensiled mixed-crop tall fescue and meadow fescue. X. S. Guo[1], D. J. Undersander[2], and D. K. Combs*[2], [1]*State Key Laboratory of Pastoral Ecosystem, Lanzhou University, Lanzhou, China,* [2]*University of Wisconsin, Madison.*

This study evaluated the effects of *Lactobacillus plantarum* with or without *Lactobacillus buchneri* on the fermentation and aerobic stability of a mixture of tall fescue and meadow fescue ensiled at different dry matter. The first cut was harvested at boot stage and second-cut grasses were harvested when 30 to 35 cm tall. Four DM content treatments of the first-cut were 17.9%, 24.9%, 34.6%, and 48.7%; and of second-cut were 29.1%, 36.3%, 44.1%, and 49.2%. Chopped grasses at each DM content were treated with 1) deionized water (control); 2) *L. plantarum* MTD1

(LP); 3) a combination of *L. plantarum* MTD-1 with *L. buchneri* 40788 (LP+LB). The application rate of each inoculant to the fresh forage was 1×10^6 cfu/g. Grasses were ensiled in vacuum sealed polyethylene bags for 60 d with 4 replicates for each treatment, and each bag contained 150 g of DM. Aerobic stability was defined as the time after bag opening for the silage temperature to increase by 2°C above ambient temperature. Data were analyzed by using the GLM procedure of SAS according to a randomized complete block design. Silages inoculated with LP+LB or LP had greater pH compared with untreated silages (5.07, 5.04, 4.86, respectively, $P < 0.05$). Lactate was greater in LP silage (5.25% DM) than control (3.75%DM) or LP+LB (2.84%DM) silages ($P < 0.05$). As silage DM increased, lactate in untreated and LP treated silages decreased, but increased in LP+LB treated silage ($P < 0.001$). Acetate concentration decreased with increased DM in all silages. LP+LB treated silage had the longest and control silage the shortest aerobic stability for both harvests. The greatest values in aerobic stability were observed in silages with highest DM content ($P < 0.05$). In this study, aerobic stability of grass mixes ensiled between 18% and 44% DM increased as DM% increased. LP and LP+LB inoculants improved aerobic stability of silages harvested between 18% and 44% DM.

Key Words: fescue, silage, inoculant

W98 Effect of corn silage sample handling on nutritional parameters measured by wet chemistry.

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Prior to ration balancing, nutritionists submit samples to a laboratory for analysis. Many times, samples must be shipped to the laboratory as services may not be readily available nearby. Shipping methods vary, thus the time that lapses between sample collection and sample analysis may range from a few hours to a few days. A study was undertaken to determine the effect of silage sample handling on nutritional parameters measured by wet chemistry at a commercial laboratory. Eleven silage storage bags were sampled with a silage probe. Each individual silage bag sample was thoroughly mixed and divided into 5 sub-samples that were treated as follows: 1.Silage sub-sample placed in air tight bag and iced immediately, taken to the laboratory within 3.5 h (ICE); 2. Silage sub-sample placed in airtight bag, taken to the laboratory within 3.5 h (NO-ICE); 3. Silage sub-sample placed in airtight bag, taken to post office for overnight delivery (24H); 4. Silage sub-sample placed in air tight bag, iced, taken to freezer overnight and taken to post office for overnight delivery (48HFZN); 5. Silage sub-sample placed in airtight bag, kept overnight at room temperature in garage and taken to post office for overnight delivery (48H). All 55 silage sub-samples were analyzed for pH, CP, ADF and heat damaged CP at a properly accredited commercial laboratory (Rock River Laboratory, Inc., Watertown, WI). Statistical analysis was performed using SAS with a model containing terms for silage bag number and treatment. Separation of treatment means was conducted using the Tukey-Kramer test. Silage pH did not differ among treatments and averaged 3.84. The CP content (%) for 48HFZN (7.39) was increased ($P < 0.03$) relative to ICE (6.97), NO-ICE (6.91), 24H (6.79) and 48H (7.1). The available CP (DM %) for 48HFZN (7.16) was increased ($P < 0.03$) relative to ICE (6.71), NO-ICE (6.69), 24H (6.57) and 48H (6.74). The ADF insoluble CP (% CP) was increased in 48H (5.09) relative to ICE (3.8), NO-ICE (3.11), 24H (3.32) and 48HFZN (3.12). There were no treatment effects ($P > 0.10$) for ADF or energy parameters. Samples arriving to the laboratory after 24 h post-sampling are subject to increases in CP content regardless of the handling method. Samples arriving to the laboratory after 24 h post sampling are subject to increases in heat-damaged protein when not kept cold or frozen. Data suggest that samples should arrive to the laboratory within 24 h post sampling in tightly sealed bags.

Key Words: corn silage, nutrients, sample handling

W99 The effect of ensiling duration on fatty acid profile and concentration of corn silage.

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The profile and concentration of fatty acids (FA) in feed has been shown to affect rumen function, and the yield of milk and milk components. The objective of this study was to evaluate the effect of ensiling duration on the profile and concentration of FA of corn silage. Treatments were a brown midrib (BMR) and a non-BMR silage hybrid (nBMR), both harvested at a normal DM (32%) and a high DM (41%). Forages were sampled, vacuumed and heat-sealed in storage bags (n = 5) and ensiled for 45, 90, 180, 270, or 360 d, before analyses. Fatty acids were analyzed by gas-liquid chromatography. Data were analyzed as a 5 × 2 × 2 factorial arrangement of treatments, with main effects of hybrid, DM at harvest, ensiling duration, and interactions of each. The total concentration of FA (DM basis) was 1.9%, 2.0%, 1.9%, and 2.20% after 0, 45, 90 and 180 d, respectively. After 270 d and 360 d, the concentration of FA was increased ($P < 0.01$) over d 0 and 90 d to 2.3%. Harvesting nBMR at a normal DM (1.3 ± 0.06%) resulted in lower ($P < 0.01$) FA concentration, than harvesting at a high DM (2.4 ± 0.06%). This difference was absent in BMR silages, averaging 2.5% and 2.3% for normal and high DM silages, respectively ($P > 0.05$). When the FA profile was examined, the concentration of total PUFA was lower in high DM BMR (50 g/100 g FA) than low DM BMR (53 g/100 g FA) and normal DM nBMR (53 g/100 g FA) ($P < 0.01$). Levels of total PUFA were highest in high DM nBMR (55 g/100 g FA). Total PUFA concentration was, on average, 52.7 g/100 g FA after 0 d, decreased ($P < 0.01$) to 49.9 g/100 g FA after 45d, then increased ($P < 0.01$) to 51.0 g/100 g FA, 54.8 g/100 g FA, 54.8 g/100 g FA and 55.3 g/100 g FA after 90, 180, 270 d, and 360 d, respectively. The mean concentration of linoleic acid and oleic acid was 48 and 25 g/100 g FA, respectively, averaged over all time points and silages, and remained steady over time. Linoleic acid was highest in high DM nBMR (51.2 g/100 g FA) and was lowest in normal DM nBMR (44 g/100 g FA, ($P < 0.01$). Linoleic acid concentration increased with time ($P < 0.01$) in all other silages, and this increase was most dramatic in normal DM nBMR. Total MUFA (g/100 g FA) were steady over time in nBMR silages, ranging from 24.4 g/100 g FA, before ensiling, to 23.2 g/100 g FA, after 360 d of storage. In BMR silages, total MUFA levels peaked after 45 d of ensiling at 29.0 g/100 g FA, then decreased steadily ($P < 0.01$) to 26.8 g/100 g FA. Levels of oleic acid remained steady over time in nBMR silages, but fluctuated over time ($P < 0.01$), peaking after 45 d of ensiling at 27.9 g/100 g FA, and decreasing to 26.1 g/100 g FA after 270 d. These results indicate that on a DM basis FA concentration in corn silage changes during ensiling. It remains to be determined, however whether such changes are an increase in actual FA yields or due to a reduction of non-FA material within the forage. Future work should examine whether these FA are present as free or esterified FA and if this changes during ensiling.

Key Words: corn silage, BMR, fatty acids

W100 Relationship between organoleptic characteristics, pH, and aerobic deterioration of alfalfa and orchard grass silages.

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The perception of organoleptic properties (OP; odor, color, structure and moisture) of silages by trained observers enables an easy subjective evaluation of quality. On the other hand, chemical properties (CP) as pH and aerobic deterioration (measured as CO_2 production $TPCO_2$, mmol CO_2 g^{-1} dry matter d^{-1}, measured during 5 d of exposure to air) are quantitative objective assessments of silage quality, but they are not easily available to small farmers. The aim was to estimate the relationship between OP and CP of 46 alfalfa (*Medicago sativa* L.) and orchard grass (*Dactylis glomerata* L.) silages. The experiment was carried out between June and August 2011, at Chapingo University, México. The silages resulted of the factorial combination of cutting at 2 different hours (8:00 and 14:00), 3 wilting times (0, 1 and 2 h) and 2 levels of bacterial inoculants (0 and 5g t^{-1}) with 4 replicates. Forage was ensiled in 200 L plastic containers, and opening of silos took place 60 d after ensiling. Perception of OP was carried out by 5 previously trained independent observers. The different OP were classified in 4 classes ranging between 1 (bad) and 4 (excellent). Silage samples were taken for measurement of pH and $TPCO_2$. Correlations analysis and principal components analysis were carried out. Correlation coefficients (r) among OP ranged between 0.57 and 0.87, while r between CP was 0.39; CP were negatively correlated with OP, r ranged between −0.34 (pH-odor) and −0.67 ($TPCO_2$ -moisture). Even though r were low, they were all significant ($P \leq 0.02$). Principal components analysis enabled the classification of silages according to their quality. The first 2 components explained 80% of the variation; the first component (70%) implied the negative relationship between CP and OP; according to the second component CP were positively related to odor and color and negatively related to moisture. Due to the close relationship between OP and CP it is concluded that small farmers might reliably use perception of OP for the evaluation of silage quality.

Key Words: *Medicago sativa*, *Dactylis glomerata*, principal components analysis

W101 Effect of rate of application of various commercial exogenous fibrolytic enzymes on preingestive fiber hydrolysis and release of sugars and phenolics from bermudagrass haylage.

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The objective was to examine effects of the dose rate of 5 commercial exogenous fibrolytic enzymes (EFE; E1, E2, E3, E4, and E5 containing 1506, 286, 3624, 1693 and 70 µmol/min/g endoglucanase activity, respectively) on fiber hydrolysis of a 4-wk regrowth of Tifton 85 bermudagrass haylage. Dose rates were 0x (Control), 0.5x, 1x, 2x and 3x; where 1x was the recommended rate of 10, 15, 2.25, 2.25, and 15 g/kg ground (1 mm) substrate, respectively. Enzymes were diluted in citrate-phosphate buffer (pH 6) containing sodium azide (0.02% w/v) and were applied in quadruplicate in 2 runs. Suspensions were incubated at 25°C for 24 h before addition of 15 mL of water followed by shaking for 1 h and filtration through a Whatman 451 paper. Data for each enzyme were analyzed separately as a completely randomized block design. The model included effects of dose, run, and the interaction. Linear (L), quadratic(Q) and cubic (C) polynomial contrasts and the PDIFF statement of SAS were used to evaluate means. Increasing the dose rate increased ($P < 0.05$) DM loss (%) of substrates treated with E3 and E4 (C), E1 (Q), and E2 and E5 (L); decreased ($P < 0.04$) the NDF (%) of all enzyme-treated substrates (C); decreased ($P < 0.01$) ADF (%) of E2, E3, E4 and E5 (C), and E1 (Q); decreased ($P < 0.02$) hemicellulose (%) of E2, E3 and E5 (C), and E1 and E4 (Q); decreased ($P < 0.03$) cellulose (%) of E2, E3, E4, and E5 (C), and E1 (Q); increased ($P < 0.01$) release of water soluble carbohydrates (WSC, %) from E2, E3, E4, and E5 (C), and E1 (Q) and increased ($P < 0.01$) release of ferulic acid (FER, µg/g) from E1, E2, E3 and E5(C), and E4 (L). Optimal doses for reducing the % NDF of E1, E2, E3, E4 and E5 were 2x (−6.7), 0.5x (−1.9), 3x (−8.3), 2x (−3.8) and 3x (−4.0), respectively. Optimal doses for increasing release (%) of WSC and (µg/g) FER were 3x (+5.9), 3x (+0.7), 3x (+5.1), 3x (+2.4) and 3x (+1.3) and 3x (+37), 0.5x (+6), 3x (+54), 2x (+11) and 2x (+30), respectively. Increasing dose rates beyond manufacturer recommendations increased fiber hydrolysis by enzymes to different extents.

Key Words: forage, enzyme, dose

W102 The effects of bacterial inoculants and enzymes on the fermentation, aerobic stability and in vitro organic matter digestibility characteristics of sunflower silages.

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This study was carried out to determine the effects of lactic acid bacteria, enzymes, and lactic acid bacteria+enzyme mixture on the fermentation, cell wall contents, aerobic stability and in vitro organic matter digestibility characteristics of sunflower silages. Sunflower was harvested at the milk stage of maturity. Treatments were: 1) control; 2) lactic acid bacteria (I; Global Nutritech Biotechnology LLC, Richmond, VA); 3) enzyme (E; Global Nutritech Biotechnology LLC, Richmond, VA); and 4) lactic acid bacteria+enzyme mixture inoculants (I+E; SILAID; Global Nutritech Biotechnology LLC, Richmond, VA). Inoculants were applied to silages at the rate of 6.00 log cfu/g. Treated chopped sunflower was ensiled in 1.0-l special anaerobic jars equipped with a lid enabling gas release only. The jars were stored at 25 ± 2°C under laboratory conditions. Three jars from each group were sampled for chemical and microbiological analysis at 2, 4, 8, 15 and 60 d after ensiling. At the end of the ensiling period, all silages were subjected to an aerobic stability test for 5 d by measuring pH, production of CO_2, and growth of yeast and mold. In addition, in vitro organic matter digestibilities of these silages were determined. Both treatments (I and I+E) increased characteristics of fermentation but impaired aerobic stability of sunflower silages compared with control ($P \leq 0.05$). Bacteria+enzyme treatment decreased both neutral detergent fiber and acid detergent fiber contents of silage compared with control ($P \leq 0.05$). In vitro organic matter digestibility was numerically increased for treated silages compared with control silages. In conclusion, I and I+E inoculants can be used for sunflower silages.

Key Words: sunflower, silage, inoculant

W103 The inoculation rate of a mixture of homo-fermentative and hetero-fermentative bacteria strains affects the aerobic stability of tropical corn (TC) silage.

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The objective was to evaluate the effects of inoculation rate of a microbial additive containing homo-fermentative and hetero-fermentative lactic acid-producing bacteria strains (LAPBI) on the ensiling characteristics and aerobic stability of TC fermented during 45 and 90 d (FD) at 27°C. Chopped TC (38.21% DM) was ensiled in 1.2 kg capacity micro-silos and assigned to 1 of 3 treatments (TRT); no additive, LAPBI applied at 10^5 or at 10^6cfu/g fresh forage. Three samples of fresh forage and silage from each TRT and FD were analyzed to determine pH and fermentation products. Statistical analysis was performed according to a Completely Randomized Design with a 3 TRT by 3 FD factorial arrangement. For aerobic stability, triplicate samples from each TRT and FD were placed in styrofoam containers lined with plastic. Temperature was measured at 6 h intervals from 0 to 108 h and at 124, 130, 134, 140, 148, 158, and 176 h. Data was analyzed using a split plot design with a 3 TRT by 2 FD by 26 h factorial arrangement using silo as the repetitive measurement. No significant ($P > 0.05$) responses on pH and fermentation characteristics were observed. After 45 d of ensiling and during the aerobic exposure (AE) period temperature was lower ($P < 0.05$) in TC treated with 10^6 cfu/g LAPBI than control or TC inoculated with LAPBI applied at 10^5cfu/g. After 90 d of ensiling temperature was lower ($P < 0.05$) in treated silages vs. control. The temperature of inoculated silages fermented during 45 and 90 d was lower ($P < 0.05$) vs. control from 54 to 84 h and from 90 to 108 h of AE, respectively. Compared with ambient temperature, after 45 d of ensiling temperature started to rise at 36 h of AE for control and silage treated with 10^5 cfu/g, whereas in silage treated with 10^6 cfu/g it occurred after 54 h. After 90 d of ensiling, inoculation with 10^6 or 10^5 cfu/g delayed the start of temperature rise for 78 or 72 h, whereas for untreated TC the delay was 66 h. In summary, inoculation of TC did not enhance the fermentation characteristics, but improved aerobic stability. A greater response in aerobic stability was observed with the higher inoculation rate.

Key Words: tropical corn silage, microbial inoculants, inoculation rate

W104 Infrared thermography to assess the relationship between corn silage quality and face temperature.

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Feedout exposes silage to air consequently reducing silage quality and resulting in environmental implications. The aim of the study was to evaluate the utilization of infrared thermography (IRT) to relate face temperature with quality loses and ethanol emissions, and develop a tool that allows us to act rapidly to improve management and hence reducing the negative effects of air exposure. A randomized complete block design was used with bunker silos as blocks and face temperatures as treatments. Corn silage storage in bunker silos were sampled in 18 commercial well managed dairy and beef farms. A hand portable infrared camera (Ti45, Fluke thermal imagers) was used to measure IRT in each silo at a fixed distance of 4 m. From this measurement, the locations of maximum (Hot) and minimum (Cold) temperatures were established in exposed silo face. At each point samples were taken using a forage sampler (between 0 and 50 and 50–100cm depth), frozen and analyzed for DM, OM, CP, pH and in vitro DM digestibility (DMD) at 6, 12, 24 and 48h of incubation (DAISY). As expected, temperature from hot to cold locations differed by 13.9 ± 3.5°C ($P < 0.01$). Although no differences in quality parameters and pH were detected between 0 and 50 cm depth, a reduction in OM was detected from 50 to 100 cm in hot areas ($P < 0.09$). DMD at 48h was lower ($P < 0.01$) both between 0 and 50 and 50–100 cm depth in hot areas, when compared with cold ones. Besides at 6h, DMD was higher in cold areas. Although strong correlations were no detected for temperature and quality parameters in the type of silos involved in this trial, we conclude that hot areas in silo faces represents reductions in DMD which could be detected by IRT technology.

Table 1.

	Sampling site			Sampling site		
	0-50cm (n=18)			50-100 cm (n=18)		
Variable	Hot	Cold	SE	Hot	Cold	SE
T°C	27.23^a	13.34^b	0.579	27.23^a	13.34^b	0.579
DM %	32.41	31.66	0.344	31.82	31.69	0.313
pH	4.06	3.99	0.053	3.98	3.98	0.009
% on DM Basis						
OM	92.92	93.21	0.172	93.15^b	93.61^a	0.145
CP	6.62	6.31	0.153	6.48	6.31	0.162
DMDh6	45.10	46.17	0.899	45.86^b	47.65^a	0.699
DMDh12	50.91	51.72	0.808	51.79	51.94	1.054
DMDh24	62.38	63.55	0.944	62.42	63.54	0.591
DMDh48	68.23^b	72.52^a	0.699	69.59^b	73.10^a	0.488

^{ab}Means within a row with unlike letters differ ($P < 0.09$). T = face temperature.

Key Words: corn silage, infrared thermography, quality

W105 Fermentative losses and yeasts population in sugarcane ensiled with different particle sizes.

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The objective of this study was to evaluate the gas losses, effluent production, dry matter recovery, pH and the dynamics of yeasts population in silages of sugarcane with different particle size (0.5; 1.0; 1.5 and 2.0 cm). The silages were evaluated during the storage period of 0, 3, 7, 14, 28 and 56 d of fermentation. Results were analyzed in a completely randomized design, with 3 replications, with time repeated measures, using plastic bucket like experimental silos. Statistical analyzes were developed using MIXED procedure of SAS 9.0. It was observed significant differences ($P < 0.01$) in gas production. Silage with particle size of 1.0 cm showed greatest losses (85.4 × 66.4, 72.3 and 61.2 g/kg on the silages of 0.5; 1.5 and 2.0 cm, respectively).The gas losses increased until 28 d of fermentation. There were no significant differences ($P > 0.05$) in the dry matter recovery among the treatments, but there was a reduction ($P < 0.01$) along the days of fermentation. Yeast population was higher in the silages with 1.0 and 1.5 cm of particle size, compared with the treatments with 0.5 and 2.0 cm (5.94 and 5.91 × 5.47 and 5.34 log cfu/ g forage, respectively). There were no effluents losses in this trial, due to the high dry matter content of the ensiled forage (390 g/kg). The pH of the silages decreased ($P < 0.01$) along the fermentation period, with average values of 5.13 at the ensilage moment, and 3.63 after 56 d of fermentation. Among the treatments, the silage with particle size of 0.5 cm present lower value of this variable. Particle size of 0.5 cm can reduce fermentative losses of the sugarcane silage.

Key Words: dry matter recovery, gas losses, pH

W106 A preliminary evaluation of corn silage affected by Hurricane Irene in 2011.

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Hurricane Irene caused severe flooding and (or) lodging of crops in the Northeastern US. The objective of this study was to evaluate the chemical composition and fermentation of corn silage harvested from 5 farms affected in Vermont. All forages had large amounts of silt on the plants at harvest. Forage was harvested 42–43 d after the hurricane and was ensiled in vacuumed and heat-sealed bags in quadruplicate per farm and allowed to ferment for 60 d at 25°C. All analyses were by wet chemistry methods. Forages averaged 34.3% DM (28.6 to 40.3%) and 6.8% CP (4.8 to 8.4%, DM basis) at harvest. Concentrations of ADF and NDF (corrected for ash) were normal. Ash content was higher than normal (4.2%, NRC, 2001) ranging from 6.2 to 24.7% (ave. 10.6%). The concentrations of Ca, P, K, and Mg were within normal ranges. High concentrations of Fe (ave. 3409 ppm, range 1256 to 4397 ppm) and Al (ave. 2211, range 1256 to 4397 ppm) were detected. Forages also contained 37%, 767% and 314% more Cu, Zn and Mn than normal, respectively. The numbers of yeasts, molds, and enterobacteria averaged 4.6, 3.8, and 6.6 $\log_{10}$cfu/g of fresh forage, respectively. Numbers of yeasts (3.2 $\log_{10}$cfu/g) decreased by 1 $\log_{10}$ cfu/g of silage whereas molds and enterobacteria were not detectable after ensiling. The average pH of silages was 3.85 (3.71 to 4.19). All silages had more lactic than acetic acid with the exception of 1 farm where this was reversed. Overall, the concentrations of lactic acid, acetic acid, and ethanol were within normal ranges and averaged 3.34, 1.27, and 0.94% of DM, respectively. Butyric acid was detected in silage from only 2 farms (range 0.05 to 0.22% DM). The chemical composition and content of heavy metals in silages were similar to that of the fresh forage. Vomitoxin was detected (0.5 to 1.4 ppm) in all silage samples from 2 farms while 15-acetyl deoxynivalenol (0.9 ppm) and zearalenone (2.1 ppm) was detected in 1 out of 4 samples from 1 of these farms. Corn silage affected by Hurricane Irene generally ensiled well, but contained high levels of ash and certain minerals which when fed long-term may have negative effects on animal performance.

Key Words: corn silage, cow

W107 Feeding red clover cut at sundown and harvested as baleage did not improve milk yield in late-lactation dairy cows.

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Forages cut at sundown (PM) generally yield higher concentration of nonstructural carbohydrates (NSC) than those harvested at sunup (AM). In late-lactation Holstein cows fed only forage, we showed that PM-cut alfalfa baleage increased milk yield compared with cows fed the AM-cut counterpart. In the current study, 12 multiparous and 2 primiparous Holstein cows averaging 238 DIM received a TMR containing, on a DM basis, either 65% PM- or AM-cut red clover (RC) baleage plus 35% of a common concentrate in a crossover design with14 d for diet adaptation and 7 d for sample collection. A well established RC field was split in 2 with one half cut at sundown and the second half at sunup the next day. The PM- and AM-cut RC baleages contained (g/kg DM): 103 vs.75.6 total ethanol soluble carbohydrates, 8.83 vs. 7.91 starch, and 112 vs. 83.5 NSC (total ethanol soluble carbohydrates + starch); baleage DM averaged 442 g/kg of fresh matter. Feeding late-lactation cows PM- vs. AM-cut RC baleage did not improve ($P > 0.05$) animal performance (see table below). However, MUN was lower ($P < 0.001$) in cows fed the PM- vs. the AM-cut RC indicating enhanced N utilization. Although cows were in late lactation, milk yield was relatively high (mean = 28 kg/d). Hence, the difference in NSC between RC baleages (28.5 g/kg DM) may not have been large enough to elicit a positive response in animal performance. Alternatively, the amount of concentrate fed may have offset the potential positive effect of the PM-cut RC baleage on improving milk yield. Research is needed to examine the interaction between forage NSC and dietary levels of concentrate.

Table 1. Milk yield and composition in cows fed TMR containing PM- or AM-cut red clover (RC) baleage

	TMR			
Item	PM-cut RC	AM-cut RC	SED	*P* > *F*
Milk yield, kg/d	27.7	28.3	0.57	0.28
DMI, kg/d	20.6	20.9	0.25	0.26
Milk fat, %	4.04	4.02	0.08	0.82
Milk fat yield, kg/d	1.10	1.10	0.04	0.89
Milk protein, %	3.26	3.27	0.02	0.67
Milk protein yield, kg/d	0.88	0.90	0.03	0.69
MUN, mg/dL	12.1	13.7	0.31	<0.001

Key Words: dairy cows, red clover, nonstructural carbohydrates

W108 The effect of feeding normal corn silage, BMR corn silage or 50:50 mixture of the two on the production performance of lactating cows.

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This study evaluated the feeding value of corn silage from a normal (NML, Mycogen TMF2W726, Dow AgroSciences, Indianapolis, IN), brown midrib (BMR, Mycogen F2F700) and a 50:50 mixture (MIX) of these 2 hybrids for lactating dairy cows. The NML and BMR were planted separately whereas MIX was planted in alternating rows of each hybrid. Corn was harvested at approximately 36% DM, chopped (~19 mm length), processed, and ensiled in bag silos for 6 mo. Twenty-four Holstein cows in early lactation were fed a TMR containing silage from one of the 3 corn hybrids (52% of DM) with alfalfa silage (5%), alfalfa hay (3%), and concentrate (40%) in a simultaneously replicated 3 × 3 Latin square design of experiment with 28 d periods. The chemical compositions of the corn silage were similar among hybrids except for 30-h in vitro NDF digestibility, which was lower for NML (61.48%) by 6.59 and 3.24 percentage units than BMR (68.07%) and MIX (64.72%), respectively. Milk production, percentage and yield of milk fat and protein, 3.5% FCM and ECM were not affected by treatments. Lactose was highest ($P < 0.05$) in the milk of cows fed the BMR (4.82%) silage, intermediate for NML (4.78%), and lowest for MIX (4.73%). The milk urea nitrogen (MUN) of cows fed NML (11.25 mg/dL) was higher ($P < 0.05$) than those cows fed BMR (10.27) and MIX (10.43) suggesting that there is more efficient use of dietary N for productive purposes when cows are fed BMR and MIX corn silage. Intake of DM was lower ($P < 0.05$) for cows fed BMR (26.7 kg/d) and MIX (26.9 kg/d) than NML (28.2 kg/d) silage. Feed efficiency was higher ($P < 0.05$) for the cows fed BMR (1.90) and MIX (1.84) than NML (1.73) corn silage. Growing

BMR and normal corn together produced silage with a chemical composition almost comparable to pure BMR and when fed to cows this mixture resulted in greater feed efficiency and lower milk MUN than cows fed normal silage.

Key Words: corn silage, cow, brown midrib corn

W109 Effects of an esterase-producing inoculant and chop-length on fermentation and aerobic stability of barley silage.

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Forage chop length affects packing density of silage and thus the penetration of air into the silo face. Inoculation of silage with *Lactobacillus buchneri* inoculants has been shown to improve the fermentation and aerobic stability of cereal silages. This study investigated the effects of forage chop length and an esterase-producing inoculant on fermentation characteristics, DM loss and aerobic stability of barley silage. Whole-crop barley (*Hordeum vulgare* L.; 31% DM) was chopped to theoretical lengths of 0.95 cm (SC) or 1.90 cm (LC) and ensiled with or without an inoculant containing esterase-producing *L. buchneri* LN4017, and *Lactobacillus plantarum* LP7109 and *Lactobacillus casei* (2.8×10^5 cfu/g forage) in mini silos. Silos were opened after 64 d of ensiling for determination of fermentation characteristics and assessment of aerobic stability over an 8-d period. Thermocouples were embedded in the d-64 silages to measure temperature over the period of assessment of aerobic stability. Data were analyzed by the mixed procedure of SAS in a 2 × 2 factorial design. Inoculation decreased ($P = 0.01$) pH in SC (pH = 3.87) but not LC (pH = 4.02) silage. Inoculated LC had higher ($P = 0.01$) acetic acid concentration (1.8% DM) compared with the inoculated SC (1.4% DM) silage. Lactic acid concentration was also higher ($P = 0.01$) in the LC (8.2% DM) than in SC (6.7% DM) silage regardless of inoculation. Lactic: acetic acid ratio was lower ($P = 0.01$) with inoculation of LC (4.6) compared with the ratio in the SC (4.5) silage. Regardless of chop length, inoculation increased ($P = 0.01$) lactic acid bacteria and decreased ($P = 0.03$) yeast populations. Neither chop length, inoculation nor their interaction affected silage DM losses. Short-chop silage remained stable during 8 d of aerobic exposure; however, the inoculated LC silage was stable for 7 d compared with only 4 d without inoculation. In both lengths of chop, the inoculant caused shifts in silage fermentation and lengthened the duration of aerobic stability in LC silage compared with the SC.

Key Words: aerobic stability, silage chop length, barley silage

W110 Effects of applying bacterial inoculant with different shooting height on fermentation quality of barley silage.

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This study was conducted to evaluate the effect of bacterial inoculant with the different shooting height on fermentation quality of barley silage. Barley forage (Yuyeon hybrid) was grown at Animal Research Unit, Gyeongsang National University, Jinju, South Korea. Barley forage (500 kg) was harvested at 25% DM with 2 different shooting heights (5 cm and 15 cm), chopped 5 cm length and divided 2 piles. One half of barley forage at each shooting height was used for no inoculant treatment and the other for inoculant treatment. The inoculant was applied at 1.2×10^3 cfu/g of forage (*L. plantarum*). The experiment was conducted in a 2 × 2 factorial design with 5 replications. Barley forage was ensiled into 10 L bucket silo for 2, 5, 7, 28, 49 and 100-d durations. Dry matter, CP, and NDF concentrations of barley forages at 5 cm and 15 cm of shooting height were 26.1, 7.03 and 58.4% vs. 24.9, 8.92 and 60%, respectively. Inoculant increased ($P = 0.001$) DM (20.2 vs. 19.2%) of barley silage ensiled for 100-d, but decreased ($P < 0.005$) CP, crude ash, NDF and ADF concentrations (8.1 vs. 8.8%, 7.7 vs. 8.2%, 55.1 vs. 58.4% and 35.8 vs. 38.9%, respectively). Increased shooting height increased ($P < 0.001$) CP concentration (9.2 vs. 7.7%), whereas decreased ($P < 0.05$) DM, crude ash, NDF, ADF and hemicellulose concentrations (19.4 vs. 20.0%, 7.7 vs. 8.2%, 54.6 vs. 58.8%, 35.8 vs. 38.8% and 18.8 vs. 20.1%, respectively). Yeast was decreased (9.5 vs. 7.0 $\log_{10}$ cfu/g, $P < 0.001$) by increasing shooting height. Increased shoot height in absence of inoculants had the decrease effects ($P < 0.05$) on acetate concentration (6.0 vs. 3.7%) and mold (5.6 vs. 4.5 $\log_{10}$ cfu/g), but the increase effects of lactate concentration (2.8 vs. 5.9%) and lactate to acetate ratio (0.5 vs. 1.6). However these measurements were not affected by shooting height with inoculant. Gel electrophoresis analysis and band mass after PCR amplification of DNA indicated higher *L. plantarum* in barley silage with applied inoculant and increased shooting height. Therefore, applying bacterial inoculant and increased shooting height can improved the fermentation quality of barley silage.

Key Words: barley silage, inoculant, shooting height

W111 Effects of bacterial inoculant and shoot height on fermentation quality of barley silage.

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This study was carried out to determine the effect of applying inoculant and shoot height on fermentation quality of barley silage. Youngyang hybrid barley forage was grown at Animal Research Unit, Gyeongsang National University, Jinju, South Korea, and harvest at 27% DM with 2 different shoot heights (5 cm and 15 cm). Approximate 500kg of barley forage with 5cm or 15cm shoot heights were chopped 5 cm length and divided 2 piles for with or without inoculant application at 1.2×10^3 cfu/g of forage (*L. plantarum*). A 2 (inoculant) × 2 (shoot height) factorial design with 4 replications was used in this study. Barley forage was ensiled into 10 L mini silo (3 kg) for 2, 7 and 100 d fermentations. Before ensiling, barley forages of 5 cm and 15 cm shoot heights had 25.7 vs. 28.6% of DM and 54.6 vs. 55.5% of NDF, respectively. After 100 d of fermentation, ash content decreased by applying inoculant (2.3 vs. 2.5%, $P = 0.021$) or increased shoot height (2.3 vs. 2.6%, $P = 0.008$), while ether extract (3.7 vs. 2.9%, $P = 0.069$) tended to increase with increased shoot height. By increase of shoot height, crude protein concentration decreased (8.8 vs. 8.2%, $P < 0.05$) in without inoculant, but increased (8.2 vs. 9.0%, $P < 0.05$) in with inoculant. The concentrations of ammonia N (0.32 vs. 0.23%, $P = 0.001$) and ammonia N of total N (23.4 vs. 16.9%, $P = 0.004$) were increased by applying inoculant, while propionate concentration (0.48 vs. 0.71%, $P = 0.004$) was decreased with increase of shoot height. Lactate concentration (2.9 vs. 4.9%) and lactate to acetate ratio (0.5 vs. 1.1) were increased ($P < 0.05$) by increased shoot height and applied inoculant, but no effects on them by increased shoot height and without inoculant. Gel electrophoresis and band mass after PCR amplification of DNA had shown higher *L. plantarum* in barley silage by inoculant application and increase of shoot height. These results indicate that Youngyang hybrid barley silage has better quality without *L. plantarum* irrespective of shoot height.

Key Words: barley forage, silage quality, fermentation indices

W112 Effects of inoculant blends on emissions of volatile organic compounds, oxides of nitrogen, carbon dioxide, ammonia, and dry matter losses in alfalfa silage.

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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 feedstuff were identified as a major source for volatile organic compounds (VOCs) and nitrogen oxides (NOx) which could be a contributor to ozone formation in this area. Gaseous losses from silages also affect feed quality and silage dry matter (DM) losses of 20–30% have been widely reported to occur in the SJV. These DM losses include gaseous losses of VOCs and NOx but also carbon dioxide (CO_2) and ammonia (NH_3). Microbial inoculants are utilized in silage to promote effective fermentation, and thus could affect the amount and species of gases emitted, dry matter losses from original material ensiled, and subsequently, animal performance. This study quantified the different VOCs, NOx, (CO_2), (NH_3) emitted from alfalfa silage (*Medicago sativa* L.) and DM losses after microbial inoculation for 60 d. Twenty-five mini-silos (22 L) were built and used in a repeated measures design over time. Five mini-silos were assigned to 5 treatments: (X) control, (A) heterofermentative, (B) homofermentative 1, (C) a mix of homofermentative and heterofermentative microbes, and (D) homofermentative 2. Emissions were measured using a photoacustic gas monitor and a NO/NO_2/NOx analyzer, using 5 L Teflon bags for gas collection. Concentrations of NOx, predominantly nitric oxide (7.35 ± 1.65 µg NOx-N g DM silage^{-1}) on treatment C were measured (p-value = 0.046). Ethanol and methanol were also detected but with no differences across treatments. No differences in DM losses were observed across treatments, however differences were observed over time (p-value = 0.03). Further studies in quantification and monitoring of these emissions are critical for assessment and therefore response to the specific needs of the air quality in the SJV.

Key Words: NOx, alfalfa silage, alcohols

W113 Screening of bacteriocinogenic lactic acid bacteria from tropical legume silage.

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Ensiling has been used worldwide to preserve the nutritional quality of field crops used as animal feeds. The objective of this work was to isolate and characterize bacteriocinogenic lactic acid bacteria (LAB) during the ensiling of Campo Grande *Sylosanthes* (a mixture of *Stylosanthes capitata* and *S. macrocephala*). Mini-silos made of plastic bags and containing 600 g of chopped forage added with increasing amounts of citrus pulp were used in this study. Samples (25 g) harvested at d 1, 7, 14, 28 and 56 of fermentation were serially diluted in Na-phosphate buffer and plated in selective MRS media containing purple bromocresol. Colonies of gram-positive bacteria that produced acid and were catalase negative were picked for further characterization. Antimicrobial activity was determined against *Listeria monocytogenes* ATCC 7644. The genetic diversity of selected isolates was determined by BOX-PCR fingerprinting and identification was achieved by phenotypic characterization and sequencing of the 16S rDNA. Two hundred and 50 6 cultures were isolated during the ensiling process and 83% (n = 214) of the isolates showed some antagonist activity against *L. monocytogenes*. From these, 22 isolates with simple growth requirements were grouped by BOX-PCR in 2 separate clades, which distinguished the isolates by the period of ensiling (first day and 14 d of fermentation). The fermentation pattern of 49 carbohydrates and the sequencing of the 16S rDNA indicated that the isolates with greater ability to compete during ensiling (n = 8) belonged to the species *Pediococcus pentosaceus*, *Pediococcus acidilactici* and *Lactobacillus plantarum*. The antimicrobial activity of acidic cell-free extracts obtained from *P. pentosaceus* MP6.16, *P. acidilactici* MP10.4 and *P. acidilactici* MP10.6 was sensitive to proteinases, indicating its proteinaceous nature. Based on the inhibitory activity against other gram-positive bacteria (e.g., *Staphylococcus*, *Micrococcus*, *Streptococcus*) and their simple growth requirements, the isolates obtained in this study could be tested as inoculants for legume silages. Financial support by CNPq and FAPEMIG.

Key Words: antimicrobial activity, *Listeria monocytogenes*, lactic acid bacteria

W114 Chemical composition and fermentation profile of *Brachiaria brizantha* and Campo Grande *Stylosanthes* mixed silages.

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The aim of this study was to evaluate the chemical composition, fermentation profile and dry matter recovery in *Brachiaria* grass silage with increasing levels of Campo Grande *Stylosanthes* (0, 10, 20 and 30%), with and without bacterial inoculant. The *Brachiaria* was harvested at 70 d of regrowth and the *Stylosanthes* at the pre-flowering stage. The inoculant used was Sil All C4 (Alltech Brazil). The material was ensiled in laboratory silos of 20 kg capacity, equipped with Bunsen valves. A 4 × 2 factorial arrangement of treatments (4 levels of *Stylosanthes* × with and without inoculant) was used, in a completely randomized design, with 4 replications. There was interaction effect ($P < 0.05$) of *Stylosanthes* levels and inoculants on dry matter (DM) content, effluent losses, dry matter recovery and mold and yeast populations. The DM content of silage with and without inoculant increased linearly with increasing levels of *Stylosanthes* in the silages. The crude protein (CP) content increased linearly while the neutral detergent fiber (NDF) content decreased linearly with increasing levels of *Stylosanthes* in the silages. The pH and NH_3-N content were affected only by *Stylosanthes* levels. There were effects ($P < 0.05$) of inoculant and levels of *Stylosanthes* on LAB populations. The DM recovery increased linearly with increasing levels of *Stylosanthes* in the silage without inoculant. However, in inoculated silage the maximum recovery of DM was found in silages containing 17% of *Stylosanthes* . We concluded that the Campo Grande *Stylosanthes* improves the nutritive value and reduces the losses of DM in mixed silages of *Brachiaria* and *Stylosanthes* . Financial support by CNPq and Fapemig

Key Words: ADF, NDF, pH

W115 Feedtech CustomChop F-20 enhances the fermentation characteristics of elephant grass (*Pennisetum purpureum*) after 45 d of ensiling.

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This study determined the ensiling characteristics and aerobic stability of *Pennisetum purpureum* (PP) fermented with or without a microbial additive containing the lactic acid-producing bacterial strains (LAPBI) *Lactobacillus plantarum* MiLAB 393; *Pediococcus acidilactici*, *Lactococcus lactic*, and *Enterococcus faecium*. Forage (23.43% DM) was chopped at 2.5 cm and assigned to 1 of the 2 treatments (TRT). Additive was added to weighed portions of PP and packed into PVC micro-silos (1.8 kg) to ferment for 45 d at 25 to 27°C. The LAPBI were applied to the forage at a rate of 2×10^5 cfu/g of fresh material. Five silos from each TRT were analyzed for pH, populations of lactic acid-producing bacteria (LAPB), fermentation products, and DM losses. Statistical analysis was a completely randomized design with a 2 additives by 2 d of ensiling (0 and 45) factorial arrangement of TRT. Tukey-test was used for mean separation. Temperature was monitored for aerobic stability determination at 29 6 h intervals (168 h total) in 5 samples from each TRT (1000 g). Statistics were performed as a split plot design with a 2 additives by 29 times as repeated measures factorial arrangement using silos replicates. Treated silage had lower ($P < 0.05$) pH and higher LAPB population than control (3.74 vs. 4.16 and 6.78 vs. 6.01 cfu/g, respectively). Lactic acid % and lactic acid:acetic acid ratio were higher ($P < 0.05$) in PP fermented with LAPBI than control (3.47 vs. 2.24 and 6.61 vs. 1.56, respectively). Acetic, butyric, and propionic acid % were lower ($P < 0.005$) in treated PP than control (0.71 vs. 1.47, 0.00 vs. 0.09, and 0.00 vs. 0.47, respectively). Forage treated with LAPBI also had a numerically lower NH_3-N/total-N ratio and DM losses associated with the fermentation process than untreated silage. In summary, addition of the LAPBI improved the fermentation characteristics of PP. Forage fermented with or without the microbial additive resulted in silage stable to aerobic conditions.

Key Words: *Pennisetum purpureum*, microbial inoculant, fermentation

W116 Intake and total apparent digestibility of nutrients of corn and *Stylosanthes* silages in diets for sheep.

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The Campo Grande *Stylosanthes*, native from Brazil, is one of the most important legumes of tropical and subtropical regions due to adaptation to low soil fertility. The objective of this study was to evaluate the nutrient intake and total apparent digestibility of corn and stylosanthes silages in diets for sheep. The experimental diets consisted of: 1- corn silage and concentrate (CS+C), 2- *Stylosanthes* silage and concentrate (StS+C) and 3- *Stylosanthes* silage exclusive (StS). The concentrate represented 50% of total DM of diets 1 and 2. Diets were formulated to be isonitrogenous, 12.0% CP on DM basis, similar to the content found in StS, 11.7% CP. The concentrate consisted of corn, soybean meal and a mixture of urea and ammonium sulfate 9:1 to adjust the CP content of diets due to differences in the CP content of silages. Twelve crossbred Santa Ines sheep, weighing on average 32.2 kg BW, were allotted in 4 3x3 Latin squares. The animals were kept in individual pens with protected feeders and wateriers. Each experimental period lasted 16 d, being 10 d for adaptation and 6 for collection of data and sample. It was performed 4 d of total collection of feces through tailored bags to the animals. The data were subjected to statistical analysis using the SAS. Intake of DM, CP and NDF was lower ($P < 0.05$) for animals fed StS compared with that observed for StS+C and CS+C which were similar (Table 1). Intake of EE was lower ($P < 0.05$) for animals fed CS+C compared with other treatments. Diets containing CS or StS, supplemented with concentrate can be considered nutritionally equivalent. Financial support by CNPq and Fapemig.

Table 1. Average daily intake and total apparent digestibility coefficients of dry matter (DM), crude protein (CP), neutral detergent fiber (NDF) and ether extract (EE) in the diets

	Intake (g/d)			Digestibility(%)		
Item	CS+C	StS+C	StS	CS+C	StS+C	StS
DM	1,047.3^{a}	958.9^{a}	557.9^{b}	74.1^{a}	64.3^{b}	40.1^{c}
CP	112.6^{a}	110.3^{a}	62.1^{b}	67.9^{a}	60,8^{b}	51.3^{c}
NDF	398.3^{a}	434.5^{a}	339.7^{b}	61.53^{a}	53.0^{b}	42.6^{c}
EE	11.9^{b}	13.5^{ab}	16.3^{a}	71.85^{a}	63.7^{b}	74.5^{a}

$^{a–c}$Means followed by the same letter in the row for intake and digestibility did not differ ($P > 0.05$) by Tukey's test.

Key Words: crude protein, dry matter, legume silage

W117 Condensed tannins concentrations of prairie legume forages at different phenological stages.

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Although studies have shown that condensed tannins (CT) at appropriate concentration improves protein utilization and prevents bloat in ruminant animals, information on CT content in different phenological stages and different portions of forages growing in North America prairie is still lacking. Objective of this study was to determine the CT concentration in legume forages at different phenological stages and plant portions. Whole plant samples of purple prairie clover (*Dalea purpurea* Vent., PPC), white prairie clover (*Dalea candida* Michx. ex Willd, WPC), sainfoin (*Onobrychis viciifoliav* Scop.) and Canadian milkvetch (*Astragalus Canadensis* L., CMV) were collected in 2011 from replicated small plots (n = 4) at different phenological stages: flowering and seed maturity stage. The samples were manually separated into leaf, stem and floral/seed pod plant portions depending on the phenological stage. Samples were freeze-dried, ground (1 mm) and analyzed CT by a modified Butanol-HCL procedure. Measurement of CT for every plant portion by phenological stage was done by legume forage and Proc Mixed proceduce of SAS was used to analyze data. Differences ($P < 0.05$) were observed between each plant portions for each phenological stage for PPC and WPC. Condense tannins were highest for floral/seed pod > leaf > stem. The highest average CT contents for PPC and WPC at flowering and floral/seed pod were 161.63 ± 5.58 g kg^{-1} DM and 149.53 ± 4.03 g kg^{-1} DM, respectively. For sainfoin the CT contents were different ($P < 0.05$) between plant portions and phenological stages with the leaf having the highest contents (78.41 ± 1.70 g kg^{-1} DM) and the stem having the lowest content (10.17 ± 0.48 g kg^{-1} DM). With the exception of the seed pod, no CT contents were detected for CMV in the leaf, stem or flower portions at any phenological stage. Results demonstrate that CT levels can be quite variable among legumes and were dependent upon phenological stage and plant portion. Time of grazing of these CT legumes is important to optimize ruminant performance and productivity.

Key Words: condensed tannins, legume forage, leaf, stem, floral/seed pod

W118 Mixing purple prairie clover with alfalfa reduced alfalfa N transforming to ammonia-N.

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Although mixing condensed tannin (CT)-containing forage with alfalfa (Alf) reduces protein degradation it is not known if this is due to the binding of CT to Alf protein. The objective of this study was to assess the effects of purple prairie clover (PPC) CT on N transformation of Alf during ruminal fermentation. Alfalfa was grown in a greenhouse in a nutrient solution containing ^{15}N labeled ammonium sulfate and harvested at the vegetative growth stage. Native PPC was harvested at the full-flower and early seeding stage. Both forages were freeze-dried, ground (1 mm) and then mixed in ratios (DM basis) of 0:100, 25:75, 50:50, 75:25 and 100:0. The forage mixtures were incubated in mixed rumen batch cultures in serum vials supplemented with or without polyethylene glycol (PEG) for 6, 12, 24 and 48 h. Gas and methane production, VFA, NH_3-N and NH_3-^{15}N were determined. Effect of CT was assessed by comparing differences in fermentation parameters between incubations with and without PEG. Data were analyzed statistically by ANOVA as a 5 × 2 factorial design using the MIXED procedureof SAS. A forage × PEG interaction was observed ($P < 0.05$) for gas production (ml/g DM), NH_3-N (mg/g DM) and NH_3-^{15}N (µg/g Alf ^{15}N) accumulation. Inclusion of PEG did not affect CH_4 or VFA production in any of the forage mixtures. However, gas production and accumulation of NH_3-N and NH_3-^{15}N were linearly ($P < 0.05$) increased (6, 12, 24 and 48 h) by PEG as the proportion of PPC increased in the forage mixture. The proportion Alf ^{15}N transformed to NH_3-^{15}N was reduced ($P < 0.001$) by PPC CT for 50:50 and 25:75 Alf-PPC mixtures at 12, 24, 48 but not 6 h of incubation. This indicates that PPC CT reduced transformation of Alf N to NH_3-N and that mixing PPC with Alf has the potential to improve the utilization of Alf protein by ruminants.

Key Words: condensed tannins, alfalfa, N transformation

W119 Effect of sainfoin condensed tannins on the N transformation of alfalfa forage preserved as silage.

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Our previous study demonstrated that ensiling fermentation was improved and protein degradation was reduced by mixing alfalfa and sainfoin during the ensiling process, presumably due to the presence of condensed tannins (CT) in sainfoin. The objective of this study was to assess the effects of sainfoin CT on the N transformation of alfalfa during ensiling. Freshly harvested vegetative alfalfa grown in greenhouse with nutrient solution containing ^{15}N labeled ammonium sulfate, and pre-buds-stage sainfoin from field plots were chopped and mixed manually to the ratio of (alfalfa:sainfoin; DM basis) 100:0, 75:25, 50:50 and 25:75. Each mixture was made in 6 portions and half of them were sprayed with polyethylene glycol (PEG) to deactivate CT. The PEG and non-PEG treated forages were then ensiled in laboratory silos. At d 7, 14 and 74 of the ensiling, triplicate silos were opened and the content was processed for laboratory evaluation. After 74-d ensiling, increasing proportion of sainfoin in the mixtures increased concentrations of lactic acid (L; $P < 0.001$) and total VFA (Q, $P < 0.001$), resulting in decreased silage pH (L; $P < 0.001$). Inclusion of PEG did not affect silage pH or concentration of VFA, but increased ($P < 0.01$) concentration of lactic acid. Interactive effects of forage × PEG were observed ($P < 0.05$) in concentrations of NPN (mg/g total N), ^{15}NPN (µg/g alfalfa N), NH_3-N (mg/g total N) and NH_3-^{15}N (µg/g alfalfa N). The concentrations of NPN and NH_3-N were linearly increased ($P < 0.05$) by PEG as the proportion of sainfoin increased. The inclusion of PEG also linearly increased ($P < 0.05$) concentrations of ^{15}NPN and NH_3-^{15}N as the proportion of sainfoin increased. The results demonstrated that co-ensiling sainfoin and alfalfa improved ensiling fermentation in laboratory silos and alfalfa protein degradation was decreased by sainfoin CT. Co-ensiling sainfoin and alfalfa has the potential to reduce alfalfa protein degradation and improve the silage quality.

Key Words: condensed tannins, alfalfa, silage

W120 Effect of application rate of a fibrolytic enzyme product on in vitro ruminal fermentation of three low-quality substrates.

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The effects of a fibrolytic enzyme product (Dyadic Xylanase PLUS, Dyadic Inc. USA) on the in vitro ruminal fermentation of 3 low-quality forages (rice straw, corn stover and grass hay) were investigated using batch cultures of mixed ruminal microorganisms. Five different treatments were tested: 0X (control), 0.5X, 1X, 4X and 10X (where 1X was the manufacturer recommended dose, 20 mg/g DM). Enzymes were applied directly onto the forages 24 h before incubation with buffered ruminal fluid at 39°C for 9 h. Four incubation runs were performed on different days. Gas production was measured at 3, 6, 9 h, and the main fermentation parameters were determined at the end of the incubation. Five concentrations of enzyme, 3 substrates, and the interaction of enzyme x substrate were included in the model as fixed effects, whereas incubation day was considered as a random effect. There were enzyme x substrate interactions for all the parameters measured, indicating different effects on each feed. All doses of enzyme product increased ($P < 0.05$) gas production after 3, 6 and 9 h of incubation for corn stover and grass hay, whereas only 10X increased ($P < 0.05$) gas production at 3 and 6 h for rice straw, compared with the control. All doses stimulated ($P < 0.05$) gas production after 9 h of incubation for the 3 substrates. Dry matter disappearance increased ($P < 0.05$) with doses 4X and 10X for the 3 substrates. Doses 0.5X, 1X and 4X decreased ($P < 0.05$) NH3 concentrations for the 3 substrates, but 10X had no effect ($P > 0.05$). Enzyme treatment increased ($P < 0.05$) total VFA production to 116, 120, 131 and 177% of control values for 0.5X, 1X, 4X and 10X, respectively, for grass hay, to 147, 173, 190 and 268% of control values for corn stover, and 125, 149, 160 and 282% of control values for rice straw. Acetate:propionate ratio decreased ($P < 0.05$) in grass hay and maize stover treated with any dose of the enzyme product, but in the case of rice straw, 0.5X, 1X and 4X doses increased ($P < 0.05$) this ratio and 10X decreased ($P < 0.05$) it, compared with the control. The results indicate that the pre-treatment of these low-quality forages with a wide range of doses of the fibrolytic enzyme has a positive effect on ruminal fermentation and the enzyme product is a good candidate to improve their digestibility.

Key Words: xylanase, low-quality forages, In vitro ruminal fermentation

Growth and Development III

W121 Effect of hay or corn silage in pre-weaned calf diets on eating behavior and rumen development. F. X. Suarez-Mena* and A. J. Heinrichs, *The Pennsylvania State University, University Park.*

The objective of this experiment was to study effects of including corn silage or grass hay in pre-weaned calf diets on rumen development and eating behavior. Male Holstein calves (n = 15, 43.60 ± 3.91 kg BW at birth) were housed in individual pens on rubber mats with no bedding. Water and calf starter (56% whole corn grain, 40% pelleted supplement, and 4% molasses; as is) were offered free choice, and milk replacer was fed to 12% of birth BW. Calves were randomly assigned to treatments, either calf starter as the only solid feed (S), starter plus chopped hay (H), or starter plus corn silage (CS), H and CS were also offered free choice. Solid feed was offered from d 2 of age. At 35 ± 1 d of age calves were euthanized and organs where harvested, emptied, rinsed and weighed to determine treatment effects on rumen development. Total 35 d DMI (milk replacer + starter + forage; 34.23 S, 33.10 H, and 34.08 CS ± 2.62 kg) and total starter intake (33 d; 11.65 S, 9.58 H, and 10.46 CS ± 2.18 kg) were not different ($P > 0.05$). Calves on H and CS treatments preferred starter over forage as total forage intake (33 d) was lower (kg; 0.86 ± 1.03 H, and 0.19 ± 0.13 CS, mean ± SD). In the last week, starter intake (5.14 S, 5.08 H, and 5.27 CS ± 1.10 kg), and starter plus forage intake (5.14 S, 5.46 H, and 5.35 CS ± 1.17 kg) were not different. Mass of reticulorumen (1.22 ± 0.07), omasum (0.23 ± 0.02), abomasum (0.56 ± 0.02), and liver (2.31 ± 0.11) as a percentage of BW were not different ($P > 0.05$). Papillae length (1.22 S, 1.28 H, and 1.18 CS ± 0.10 mm) and width (0.69 S, 0.75 H, and 0.73 CS ± 0.04 mm), rumen wall thickness (0.89 S, 0.99 H, and 0.80 CS ± 0.06 mm) and rumen contents pH (4.97 S, 5.31 H, 5.15 CS ± 0.11) were also not different ($P > 0.05$). High standard errors may be in part due to poor calf health as many calves from all treatments were treated for diarrhea and/or pneumonia, which had a negative effect on intake. This study shows that when palatable calf starter is available free choice, forage intake is minimal. Forage was not a palatable feed source for calves in this study.

Key Words: calf, rumen development, forage intake

W122 Exogenous palimitic and palmitoleic acids respond differently in stearoyl-CoA desaturase (SCD1) inhibited bovine adipocytes. A. K. G. Kadegowda,* T. A. Burns, and S. K. Duckett, *Clemson University, Clemson, SC.*

Objectives were to determine the effect of exogenous palmitoleic acid (C16:1) or palmitic acid (C16:0) with or without SCD-1 inhibitors on adipogenesis in primary bovine adipocytes. Bovine primary preadipocyte cultures were isolated from intermuscular fat of 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* DEX, 5 μ*M* troglitazone, 0.5 m*M* IBMX, and 10 m*M* acetate] for 2 d and from D2 to D12 without DEX and IBMX. From D0 to D6, cells were treated with SCD-1 inhibitors, sterculic acid (SA) or trans-10, cis-12 conjugated linoleic acid (CLA), at 0 or 50 μ*M* . In addition, from D2 to D6, cells were treated with (0 or 150 μ*M*) of C16:0 or C16:1 and harvested for fatty acid analysis by GLC and gene expression by RT-qPCR. The effect of the treatments on cell viability in differentiated cells was assayed using Cell Counting Kit-8. Glycerol-3-phosphate dehydrogenase (GPDH) activity was assayed to determine the effect on adipocyte differentiation. The treatment effects were analyzed by ANOVA using Proc Mixed of SAS 9.2. The C16:0 decreased ($P < 0.05$) total cellular fatty acid (FA) yield (minus supplemented FA) due to reduced cellular viability of differentiated adipocytes. In contrast, a similar decrease in total cellular FA content was seen in C16:1/CLA treatment without affecting cellular viability. Palmitic acid supplementation reduced ($P < 0.01$) GPDH activity compared with controls (3.09 ± 0.2 vs. 9.51 ± 0.2 nmol/mg protein.min), which was further exacerbated in SCD1 inhibited adipocytes (0.49 ± 0.2 and 0.9 ± 0.2 in SA and CLA treatments, respectively). In contrast, C16:1 increased GPDH activity (14.81 ± 0.2) which was reduced with CLA (4.17 ± 0.2). Compared with SA treated cells, C16:0 and C16:1 decreased the expression of fatty acid synthase, fatty acid elongase 6 and diacylglycerol acyltransferase. Furthermore, C16:0 increased *SCD1*; whereas C16:1 increased adipose triglyceride lipase. In summary, the results showed that the responses of lipogenic enzymes in bovine adipocytes differ when supplemented with C16:0 and C16:1, and with or without SCD1 inhibitors.

Key Words: adipocytes, gene expression, fatty acids

W123 Steroyl-CoA desaturase 1 (SCD1) inhibition decreases de novo fatty acid synthesis in primary bovine adipocytes. A. K. G. Kadegowda,* T. A. Burns, N. Tharayil, S. L. Pratt, and S. K. Duckett, *Clemson University, Clemson, SC.*

We have previously shown that sterculic acid [8-(2-octyl-1-cyclopropenyl) octanoic acid] (SA) and *trans*-10, *cis*-12 conjugated linoleic acid (CLA) inhibit SCD1 activity at 50 μ*M* concentration in primary bovine adipocytes. The objectives were to determine the effect of SCD1 inhibition on de novo fatty acid synthesis and expression of lipogenic and lipolytic genes. Bovine primary preadipocyte cultures were isolated from intermuscular fat of carcasses from 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* M dexamethasone (DEX), 5 μ*M* M troglitazone, 0.5 m*M* 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 0 or 50 μ*M* of SA or t10c12 CLA and harvested for gene expression by RT-qPCR. In addition, cells were incubated with acetate ($^{13}C_2$) from D4 to D6 to estimate lipogenesis using GLC-MS. The geometric mean of Eukaryotic translation initiation factor 3, subunit k (EIF3K) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was used for normalization of gene expression data. In acetate ($^{13}C_2$) supplemented cells, the mass isotopomer distribution analysis showed that the fractional synthesis rate [molar percent excess (MPE)/h]) of ^{13}C-16:0 was reduced in SA (0.49 ± 0.07, −51.2%, $P < 0.01$) and CLA (0.43 ± 0.07, −43.68%, $P < 0.01$) treatments compared with control (0.89 ± 0.07 MPE /h). Of the lipogenic genes, CLA treatment decreased the expression of *SCD1* ($P < 0.01$), acetyl-CoA carboxylase (*ACC*; $P < 0.05$), fatty acid synthase (*FASN*), whereas SA supplementation decreased the expression of *ACC* ($P < 0.05$). Both SA and CLA increased the expression of hormone-sensitive lipase ($P < 0.05$) known to be involved in lipolysis. The results showed that SCD1 inhibition by SA and CLA in the bovine adipocytes decreases de novo fatty acid synthesis by downregulating genes involved in lipogenesis and upregulating gene involved in lipolysis.

Key Words: SCD1, adipocyte, GLC-MS

W124 Metabolic differences in hepatocytes from Iberian and Landrace pigs.

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There are important differences when Iberian are compared with modern pigs in terms of metabolic activity, energy utilization and capacity of protein and fat deposition. In an attempt to partially explain differences we have used the primary culture of hepatocytes to evaluate the hepatic function and sensitivity to hormones without the interference of circulating blood factors. Hepatocytes were isolated from pure Iberian and Landrace pigs of similar body weight (n = 5; 25 kg BW), by collagenase perfusion and seeded into collagen-coated T-25 flasks. Monolayers were established in medium containing fetal bovine serum for 1 d and switched to a serum-free medium for the remainder of the culture period. Hepatocytes were maintained in William's E amended with β-mercaptoethanol (0.1 mM), glutamine (2 mM), antibiotics (gentamicin, penicillin, streptomycin and amphotericin B), DMSO (1ng/ml), dexamethasone (10–8 M), insulin (1 and 100 ng/ml) and glucagon (1 and 100 ng/ml) for 24–48h. IGF-1 synthesis, urea synthesis, gluconeogenesis, insulin and glucagon impact on glycogen content were determined. Gluconeogenesis was measured in glucose free Dulbecco's modified Eagle's medium with glucagon (100 ng/ml) and lactate (5 mM), pyruvate (5 mM) and alanine (5 mM). For urea synthesis, cells were cultured in basal medium amended with ammonium sulfate (2.5 and 5mM). All results were expressed relative to the protein content of the culture. As the metabolic activity may vary among pigs, data were analyzed using the PROC MIXED procedure of SAS. Although insulin and glucagon regulated glycogen content, the difference between breeds was not significant ($P > 0.10$). Nevertheless, gluconeogenesis, urea synthesis and IGF-1 synthesis were 69, 38 and 22% lower ($P < 0.05$), respectively, in hepatocytes from Iberian compared with Landrace. In conclusion, the genetic background should be considered when hepatocyte culture is used for metabolic studies.

Key Words: hepatocytes, metabolism, breed

W125 Effect of betaine and conjugated linoleic acid on porcine subcutaneous adipose tissue lipolysis.

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Betaine (Bet) and CLA have the potential to alter body composition in swine by decreasing body fat.The aim of the present study was determine if Bet and CLA have an effect on lipolysis in the adipose tissue of Iberian pigs. Five Iberian pigs were used (38kg BW). Adipose tissue samples were acquired following slaughter by electrical stunning and exsanguination. The adipose tissue was diced into strips and placed in Hanks' buffer (37°C, pH 7.4). In the laboratory, the strips were dissected clean of any extraneous muscle tissue and further separated into 1-cm cubes in a laminar flow hood. Adipose tissue explants (approximately 100mg) were prepared by slicing tissue cubes with a microtome. Tissue slices were blotted free of excess liquid, weighed, transferred to 6-well tissue culture with 2 mL of basal medium per well (DMEM/F12 (50:50), 25% bovine serum albumin, 25 mM HEPES, gentamycin, amphotericin B and penicillin-streptomycin) and incubated (5% CO2, 37°C) for one hour to wash away endogenous glycerol and fatty acids. Triplicate tissue slices were then incubated in test medium (Basal medium amended with 10mM Linoleic acid (control), 10mM 10-t, 12-c CLA, 10mM Linoleic acid + 200mM Bet and 10mM 10-trans, 12-cis CLA + 200mM Bet). To estimate the direct effects of CLA and Bet on lipolysis, incubations were performed for 2 and 72 h. To examine the ability of Bet or CLA to inhibit insulin's suppression of isoproterenol-stimulated lipolysis after acute and chronic exposure, the test medium was amended with 1 µM isoproterenol ± 10 nM insulin. Media glycerol concentration was measured at the end of the incubations. Data were analyzed by multifactorial ANOVA and mean separated by Fisher's LSD test. No effect of Bet or CLA on acute lipolysis was observed ($P > 0.10$). Nevertheless, adipose tissue supplemented with 10-t, 12-c CLA decreased (22%; $P < 0.05$) chronic lipolysis challenges compared with control. As expected, chronic exposure of adipose tissue to isoproterenol increased lipolysis (83%; $P < 0.05$), and insulin inhibited isoproterenol stimulated lipolysis (50%; $P < 0.05$). In conclusion, CLA decreased lipolysis in adipose tissue isolated from Iberian pigs while Bet had no effect in acute or chronic lipolysis.

Key Words: lipolysis, conjugated linoleic acid, betaine

W126 *T-box (Tbx)-2* is required for proliferation of osteoblast cells.

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Bone related diseases and injuries affect many livestock species and have an enormous impact on efficiency of production and quality of life. Transcription factors are key regulators of osteoblast function; however our understanding of this complex process is limited. We recently demonstrated that *Tbx3*, a transcription factor implicated in ulnar mammary syndrome, is required for osteoblast proliferation. However, the mechanisms by which a closely related member, *Tbx2*, regulates skeletal development is unknown. We hypothesized that *Tbx2*, like *Tbx3*, is required for proliferation of osteoblasts. We used SaoS-2 cells, osteoblast-like human osteosarcoma cell line, and mouse preosteoblast cells (MC3T3-E1). To evaluate the role of *Tbx2*, we knocked down *Tbx2* expression by transfecting SaoS-2 and MC3T3-E1 cells with species-specific, *Tbx2*-specific small interfering (si) RNA (66 nM) and determined cell proliferation by alamarBlue assay and bromodeoxyuridine (BrdU) incorporation. Surprisingly, although we were able to detect a signficiant knockdown of mRNA expression of *Tbx2* in MC3T3-E1 cells, we were unable to detect *Tbx2* protein in MC3T3-E1. However, we were able to detect *Tbx2* protein in the SaoS-2 cells, therefore the SaoS-2 cell model was used for further experiments. In SaoS-2 cells, *Tbx2* siRNA reduced *Tbx2* mRNA expression 90 ± 4% ($P \leq 0.01$) and protein by 62 ± 4% ($P < 0.01$). Cell number was reduced 29 ± 2% and BrdU incorproration was reduced 40 ± 2% in *Tbx2* siRNA transfected cells compared with control cells ($P < 0.001$). To determine if *Tbx2* is required for differentiation, we cultured control and siRNA transfected cells in media containing β-glycerophosphate and ascorbic acid and determined alkaline phosphatase (ALP) activity, a known marker of osteoblast differentiation. Knockdown of *Tbx2* did not alter ALP activity ($P \geq 0.50$). In conclusion, 1) similar to *Tbx3*, *Tbx2* is required for optimal proliferation of osteoblast cells, 2) *Tbx2* may not be required for differentiation of osteoblasts, and 3) *Tbx2* and *Tbx3* may have both redundant and distinct functions in regulating bone development.

Key Words: bone, *T-box*, osteoblast

W127 Comparison of feed form (pelleted vs. textured) on growing performance and rumen papillae development of dairy steers.

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The objective was to determine if feed form affects the growth performance of dairy steers from 13 to 24 wk of age and alters rumen papillae surface area. At 13 wk of age, 32 Holstein steers were blocked by weight and assigned to groups of 4 per pen (4 replicates per treatment). Pens were assigned to one of 2 grain mixes: pelleted (PL) or textured (TT, coarse mix of pellets and grains). Steers were limit fed 4.55 kg/d of the grain mixes (20% crude protein and 3.0 Mcal/kg, dry basis) with mixed grass hay offered, ad libitum. Body weight (BW, kg), hip height (HH, cm), heart girth (HG, cm), body length (BL, cm) measurements, and calculated body volume (BV, cm^3) were completed every 2 wk. No differences were detected for any of the growth measurements or total dry matter intake. Initial measures were 101 kg BW; 95 cm HH; 104 cm HG; 100 cm BL; and 318 cm^3 BV. Final measures were 212 kg BW; 116 cm HH; 133 cm HG; 135 BL; and 665 cm^3 BV. Average daily gain and feed to gain ratio were not different (1.3 kg/d and 3.9, respectively). At 24 wk of age, 2 steers were randomly selected from each treatment and euthanized to evaluate rumen papillae surface area. Rumen papillae of PL and TT had similar surface area for portions of the rumen identified as cranial ventral (57 and 38 mm^2, SE 8.7); cranial dorsal (13 and 11 mm^2, SE 3.8); and caudal dorsal (32 and 19 mm^2, SE 6.4). The caudal ventral region tended to be greater for PL steers (29 mm^2) compared with 15 mm^2 for TT fed steers (SE 3.3, $P = 0.10$). Empty rumen weight and content DM were 5.4 and 3.4 kg for PL; 5.0 and 2.6 kg for TT, respectively. Ruminal pH tended to be different: 6.3 vs. 6.9 for PL and TT, ($P = 0.15$). Histological analysis did not indicate differences by form of feed for mucosal surface length, sub-mucosa thickness, and muscle thickness measurements of the rumen determined via a digital image analysis program (CellSens Imaging Software; Olympus Corp.). Feed delivery form (pellets or textured) did not differentially influence calf growth performance, nor were there negative effects on rumen size, ruminal papillae surface area, or histology.

Key Words: rumen, papillae, pellets

W128 Effect of parenteral administration of glutamine on autophagy of liver cell and immune responses in weaned calves.

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The objectives of this study were to determine the effects of an increased jugular supply of L-Gln on postweaning growth, immune responses and autophagy of weaned calves. At 35d of age, 24 Holstein calves (initially 50 ± 2.3kg; 35 ± 2 d of age) were randomly allocated to 4 treatments, and each treatment included 5 male and 1 female calves. Holstein calves were assigned to treatments of 1) no L-Gln and milk supplementation, but infusion of 2 L of 0.85% NaCl solution, Control group [C] 2) no milk supplementation, but infusion high dose L-Gln (0.64g/kg BW/day) mixed with 2 L of 0.85% NaCl solution [H], 3) no milk supplementation, but infusion moderate dose L-Gln (0.32g/kg BW/day) mixed with with 2 L of 0.85% NaCl solution [M], 4) no milk supplementation, but infusion low dose L-Gln (0.16g/kg BW/day) mixed with 2 L of 0.85% NaCl solution [L]; each treatment was delivered 2 h/d for each of 7 consecutive days starting on d1 after weaning. The dose of L-Gln for calves were calculated from published data on i.v. infusion rates for sheep (Hoskin et al., 2001) and adjusted on the basis of metabolic BW. Feed and water were freely available to all calves. All calves were euthanized at the end of infusion 7 d for measurements of autophagy of liver cell and intestinal morphology. The ADG and growth rate increased quadratically ($P < 0.05$) with increasing infusions of Gln. Infusion N increased linearly in response to the graded amount of Gln infused ($P < 0.05$). At the end of infusion 7 d, a blood sample was collected into a 10 mL EDTA vacuum tube to analyze immunological assays. Infusion Gln increased the abundance of CD4 and the ratio of CD4/CD8 linearly, but decreased CD8 linearly ($P < 0.05$). Characterization of blood lymphocyte populations was performed by flow cytometry analysis. The urea N, Gln in plasma increased linearly with increasing Gln loads ($P < 0.001$). After harvest, Villi and their crypts were identified and measured in duodenum, jejunum, and ileum of each calf using standard histomorphometric methods. Infusion Gln also increased villus height and crypt depth of intestine quadratically ($P < 0.05$). In summary, the Gln supplied by milk replacer may be inadequate to meet calf metabolic demands under weaning physiological conditions.

Key Words: calf, L-Gln, autophagy

W129 Influence of hay type on ruminal papillae surface area of growing dairy steers from 13 to 22 wk of age.

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The objective was to determine if hay type affects ruminal papillae surface area and growth of dairy calves from 13 to 22 wk of age. At 13 wk of age, 72 Holstein steers were blocked by weight into groups of 6 per pen (6 replicates per treatment). Steers were fed 2 different hays ad libitum: grass (GR) or alfalfa (AF) along with a complete grower feed at 3.3 kg DM/d per head. GR was 9.9% CP, 35.0% ADF, and 57.1% NDF; and AF was 18.7% CP, 31.1% ADF, and 43.8% ADF, dry basis. Hay intakes of the pens were measured every 2 weeks. Measurements of full BW were completed every 2 wk, and hip heights (HH) were recorded at wk 13 and 22 of age. No significant differences were detected for any of the growth measurements. Initial BW and hip heights (HH) were 114 kg and 96 cm, and final weights were 195 kg with HH of 112 cm. The pooled feed:gain efficiency was 3.9 with an ADG of 1.2 kg BW/d. The total DMI (sum of forage and concentrate intake) was slightly greater for steers fed AF compared with GR during the final 2 weeks of the study (5.6 vs. 5.2 kg/d per head). The intake of hay was similar for each feeding rate of grower during wk 13 to 20, but 0.3 kg/d per head greater for AF during wk 20 to 22 of age. At 22 wk of age, 4 steers per treatment were euthanized to examine ruminal papillae surface area. The wet weight of the rumen contents was 26.7 vs. 19.7 kg for GR and AF, respectively ($P < 0.05$). Papillae surface area was measured at 4 regions: caudal dorsal, cranial dorsal, caudal ventral, and cranial ventral. Absorptive surface area was greater for steers fed AF compared with GR fed steers: caudal ventral (21.9 vs. 14.6 mm^2) and caudal dorsal (22.6 vs. 16.2 mm^2) regions ($P < 0.01$). No difference for the cranial dorsal region was detected, but a tendency for greater surface area of cranial ventral region ($P = 0.10$, 31.1 vs. 43.3, GR and AF, respectively). Overall, alfalfa hay resulted in greater papillae surface area of the rumen compared with grass hay.

Selection of the forage quality or type may have a significant impact on transitioning growing calves from all grain diets to higher forage diets.

Key Words: dairy calves, rumen papillae, growth

W130 Intake and performance of dairy heifers 12 to 24 wk of age following a full potential calf feeding program. J. A. Davidson,* D. C. Brown, and B. L. Miller, *LongView Animal Nutrition Center, Land O' Lakes Purina Feed, Gray Summit, MO.*

The objective was to determine optimal feeding recommendations for dairy heifers from 12 to 24 wk of age during transition from complete feeds to greater forage diets and maintain growth performance. At 12 wk of age, 46 heifers were blocked by birthdate into groups of 3 to 4 heifers per pen (6 replicates per treatment). Heifers were fed 2 different rates of complete grower feed (AMPLI-Calf Grower): 3.3 or 4.1 kg DM/d. Both groups received ad libitum chopped alfalfa hay (16% CP, 41% ADF, and 49% NDF, DM basis). Hay and grower feed intakes were measured daily. Measurements of full BW, hip heights (HH), heart girths (HG), and body lengths (BL) were completed every 2 wk, and BCS were recorded every 4 wk. No significant differences were detected for any of the growth measurements. Initial BW and HH were 104 kg and 98 cm. At 24 wk of age, heifers weighed 199 kg with HH of 113 cm, HG of 133 cm, and BL of 126 cm. Calculated body volume was 345 and 605 cm3 at 12 and 24 wk, respectively. The pooled feed:gain efficiency was 4.2 with an ADG of 1.1 kg BW/d. Final BCS was slightly greater for 4.1 kg DM/d grower feeding rate (3.30 vs 3.45, $P < 0.05$). Even though growth measurements were similar between feeding programs, intake was significantly influenced. The total DMI (sum of daily forage and concentrate intake) was greater for heifers fed grower at 4.1 kg DM/d (pooled across day of study: 5.2 vs 4.6 kg DM/d, $P < 0.01$). The intake of hay was similar for each feeding rate of grower during wk 12 to 14. However, the heifers at the reduced feeding rate of grower consumed more hay over time (treatment by day, $P < 0.01$). At 24 wk of age, heifers at the reduced feeding rate of grower were consuming 2.6 kg of DM/d as hay vs 1.5 kg DM of hay/d. Feeding 3.3 or 4.1 kg DM of AMPLI-Calf Grower per d did not significantly alter body growth performance of dairy heifers. However, the greater feeding rate delayed an increased consumption of the portion of total DMI as hay. The addition of the hay to the diet was great enough quality to maintain growth performance and transition the heifers to greater forage diets.

Key Words: dairy heifer, intake, growth

W131 Effects of milk feeding strategies on performance, ruminal development, and metabolic and hormonal profile of Holstein calves. B. F. Silper,* S. G. Coelho, A. M. Q. Lana, A. U. Carvalho, C. S. Ferreira, A. P. S. Franzoni, H. M. Saturnino, and R. B. Reis, *Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brasil.*

Brazilian dairy farms feed calves 4 L/d. Strategies between conventional and accelerated systems show an opportunity to improve development. The effects of milk replacer (MR) feeding strategies on weight gain, starter intake, ruminal development, metabolic/hormonal profile, organs and perirenal fat weights were evaluated (ethical committee - UFMG 44/2009). Male calves (n = 54) were individually bedded on tropical grass. Water and starter were provided at all times. MR (22.5% CP; 17.0% fat; 12.5% solids) was fed in 2 equal portions/d in 3 strategies: 4L-60d (4 L –500 g– MR/d during 60 d), 6L-29d/4L-60d (6 L –750 g– MR/d on the first 30 d and 4 L –500 g– MR/d from 30 to 60 d) and 6L-60d (6 L –750 g– MR/d during 60 d). Weaning was abrupt at 60 d age. Six calves/group were euthanized at 30, 60 and 90 d age. A completely randomized split-plot design was used for statistical analysis, with animals as random and time as repeated measures, means tested with SNK ($P = 0.05$). There were MR refusals in first month in all groups, but none in second month. Starter intake was not different among groups ($P > 0.05$) and increased with age ($P < 0.05$). Weight gain and feed efficiency were higher during first month in groups allowed more MR ($P < 0.05$). From 31 to 60 d age weight gain was equal ($P > 0.05$), after weaning it was higher in 6L-60d ($P < 0.05$). Weight gain increased each week, except on wk 5 in the group which had MR allowance reduced at d 30 ($P < 0.05$). Glucose, NEFA and IGF-1 were not influenced by MR feeding strategy ($P > 0.05$). Insulin was higher in 6L-60d ($P < 0.05$). Glucose and insulin increased and NEFA reduced with age ($P < 0.05$). Forestomach and perirenal fat weights, papillae length, and acetate, butyrate and N-NH$_3$ concentrations were not different ($P > 0.05$). Ruminal pH was higher and propionate concentration lower in 6L-60d ($P < 0.05$). Mitotic index of ruminal mucosa's basal stratum was higher in groups 6L-60d and 6L-29d/4L-60, as were abomasum, pancreas and liver weights ($P < 0.05$). Feeding calves 6 L MR/d during 60 d improved pre and postweaning performance without reducing starter intake or ruminal development. Research supported by FAPEMIG/APQ1839/09.

Key Words: starter intake, milk replacer, papillae

W132 Ontogenic changes of hepatic glucocorticoid and α_1- and β_2-adrenergic receptors in neonatal calves. D. Rohrbeck, J. Steinhoff-Wagner, E. Kanitz, and H. M. Hammon,* *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Neonatal calves, to a greater extent in preterm born, suffer from hypoglycemia after birth and have to adapt glucose metabolism by maturation. Plasma cortisol and catecholamines are elevated around birth and both hormones affect hepatic endogenous glucose production (eGP) by stimulation of glycogen degradation and gluconeogenic activity in liver. We have tested the hypothesis that the number of glucocorticoid (GR) and α_1- and β_2-adrenergic receptors (AR) in neonatal calves change with development and correlate with eGP. Male Holstein calves were born preterm (PT; 9 d before term) or term (T) and slaughtered 26 h after birth or were term born, fed colostrum (TC) and were slaughtered on d 4 (n = 7 per group). TC calves were fed twice daily at 8% of BW/d on d 1 and 10% of BW/d from d 2 onward. For measurement of eGP U-^{13}C-glucose (iv) was infused in PT and T calves directly after birth and in TC on d 3 of life and enrichment of U-^{13}C-glucose in blood plasma was measured. After slaughter, liver samples were snap frozen. For AR measurements membrane suspensions (2 mg protein/ml) were prepared and saturation binding assays were performed with increasing concentrations of (^{3}H)-prazosin and (^{3}H)-CGP-12177 for determination of α_1- and β_2-AR, respectively. For GR measurement the cytosol fraction (8 mg protein /ml) was incubated with increasing concentrations of (^{3}H)-dexamethasone. Maximal binding capacity (B_{max}) and binding affinity (K_D) were calculated. Data were analyzed by General Linear Model (GLM) of SAS with ontogenic stage as fixed. For GR, B_{max} was higher ($P < 0.05$) in TC than T and PT. B_{max} of α_1-AR significantly increased with maturation ($PT < t < TC$; $P < 0.05$). B_{max} of β_2-AR was higher ($P < 0.05$) in TC than in T and PT. K_D for β_2-AR was lowest ($P < 0.05$) in PT. B_{max} of GR and α_1- but not β_2-AR were positively correlated to eGP ($r = 0.61$; $P < 0.01$ and $r = 0.78$; $P < 0.001$). Results demonstrated that hepatic GR as well as α_1- and β_2-AR increase during early development in calves. GR and α_1-AR may be involved in stimulation of eGP by cortisol and catecholamines in neonatal calves. Supported by DFG, Germany.

Key Words: calves, ontogenic maturation, adrenergic and glucocorticoid receptors

W133 L-Arginine regulates expression of myokines and adipokines in myoblast and adipocyte cells.

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It is widely accepted that skeletal muscle and adipose tissue are not only the organs for energy storage and expenditure but also endocrine organs. Factors secreted from muscle (myokines) and adipose (adipokines), have important roles in the regulation of physiological actions in various tissues and organs. This study was conducted to investigate the effect of L arginine (Arg), a functional amino acid, on the expression of myokines and adipokines. Skeletal myoblasts (C2C12) and adipoblasts (3T3-L1) were cultured in high glucose Dulbecco modified high glucose Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS). Differentiation was induced by incubation in DMEM containing 2% horse serum (C2C12) or l-methyl-3-isobutylxanthine + dexamethasone + insulin (3T3-L1). The differentiated cells were treated with increasing concentrations of Arg for 12 h and the mRNA expression of myokines and adipokines was measured by reverse transcription (RT)-PCR. Data was analyzed by one way ANOVA. Myokine and adipokine gene expression exhibited time and Arg dose dependence. The expression of IL-15, BDNF, FGF21, EPO, and LIF increased ($P < 0.05$) during C2C12 differentiation. Leptin, adiponectin, TNF, apelin and resistin expression increased ($P < 0.05$) during 3T3-L1 differentiation. When the differentiated C2C12 and 3T3-L1 cells were cultured with Arg, the expression of IL-15, BDNF, Fstl, FGF21, LIF, leptin and adiponectin increased ($P < 0.05$), but the expression of TNF, IL-6 and apelin decreased ($P < 0.05$). Arg-induced expression of IL-15, BDNF, Fstl, FGF21, LIF, leptin, adiponectin, TNF and IL-6 was attenuated ($P < 0.05$) with 100 nM rapamycin or L-NAME. Insulin (100 nM) increased ($P < 0.05$) the effects of Arg on IL-15, BDNF and leptin expression in both cell types. The inhibitory actions of Arg on TNF and IL-6 expression were attenuated ($P < 0.05$) by 100 nM insulin. Results demonstrate that Arg regulates the expression of myokines and adipokines through mechanisms involving mTOR and NO signaling pathways.

Key Words: pigs, amino acids, expression

W134 Role of estrogen receptor-α (ER-α) and insulin-like growth factor receptor-1 (IGFR-1) in estradiol-stimulated proliferation of cultured bovine satellite cells.

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Estradiol (E2) enhances muscle growth in several species; however, the mechanism by which E2 enhances muscle growth is not known. Treatment with 10 nM E2 stimulates proliferation of cultured bovine satellite cells (BSC) and this is particularly significant because satellite cells are the source of nuclei needed to support postnatal muscle fiber hypertrophy and are thus crucial in determining the rate and extent of muscle growth. Treatment of BSC with 10 nM E2 significantly ($P < 0.05$) stimulates proliferation and insulin-like growth factor receptor (IGFR)-1β phosphorylation under conditions in which neither IGF-1 nor IGF-2 expression is increased. To further investigate the mechanisms by which E2 stimulates BSC proliferation, we have used small interfering (si) RNA to silence expression of estrogen receptor (*ER*)-*α* and assessed the effects on E2-stimulated proliferation and IGFR-1β phosphorylation in BSC cultures. Additionally, we have assessed the effect of using siRNA to silence *IGFR-1β* expression on E2-stimulated proliferation in BSC cultures. All experiments were repeated at least 3 times using cells from 3 different steers. Treatment of *ER-α*- or *IGFR-1β*-silenced cells with E2 does not significantly stimulate proliferation. Estradiol treatment for 30 min stimulates phosphorylation of IGFR-1β in control BSC cultures but does not stimulate IGFR-1β phosphorylation in *ER-α*-silenced cells. These results indicate that binding of E2 to ER-α results in phosphorylation and activation of IGFR-1β, which results in increased proliferation in BSC cultures. The fact that this occurs under culture conditions in which neither *IGF-1* nor *IGF-2* mRNA expression is increased strongly suggests that E2 activates IGFR-1β via a mechanism that does not involve increased IGF-1 or IGF-2 binding to the receptor.

Key Words: estradiol, satellite cells, bovine

Horse Species

W135 Trends in equine farm management and conservation practices. B. J. McIntosh* and S. A. Hawkins, *The University of Tennessee, Knoxville.*

It is widely recognized that horse farms often have unthrifty, weed infested and overgrazed pastures due to poor grazing management practices, including continuous grazing and overstocking. Poorly managed pastures and lack of appropriate waste management practices on horse farms contribute to surface water pollutant loads of sediment, nutrients, and pathogens. A survey consisting of 48 questions was distributed to participants of the Tennessee Master Horse Owner Program from 2008 to 2011 to identify potential educational needs, demographics and management practices of horse farms. Data are summarized as percentages or mean ± SE. The response rate was 89.0% and surveys (n = 121) were completed by respondents from 18 counties in TN and the states of MS, AR and AL. The respondents consisted of the following age ranges: less than 20 yr (6.6%); 20–29 yr (9.9%); 30–39 yr (6.6%); 40–49 yr (21.5%); 50–59 yr (43.8%); and 60–69 (12.4%). The majority of respondents were female (77.6%) compared with male (23.1%). Most of the respondents indicated involvement in the equine industry for more than 10 years (54.5%). The number of horses per farm was 5.0 ± 0.6 head with a range of 1 to 51. The area designated for pasture was 25.6 ± 0.8 acres. However, 48.8% of farms designated 10 or fewer acres for grazing. Continuous grazing was practiced by 51.5% of respondents. Pasture weeds were reported to be a problem by 78.1% of respondents. Soil testing for nutrient content was not practiced by the majority of respondents (58.4%). Respondents indicated equine were stabled with access to pasture for turnout (62.6%), housed on pasture continuously (36.6%) or stabled continuously (0.8%). The majority of respondents reported that stall waste was stored on bare ground in uncovered piles (89.8%). Mud was reported to be an issue in high animal traffic areas during periods of wet weather on the majority of farms (80.5%). The management practices indicated by the respondents in this study may lead to pollution due to erosion, surface water runoff, or leaching of N or P and volatilization of N from animal waste. This study indicates there is a need for educational programs that target best management and conservation practices for equine farms to reduce adverse environmental impact.

Key Words: equine, management, conservation

W136 The effects of feed-borne *Fusarium* mycotoxins on the presence and severity of equine gastric ulcer syndrome and the efficacy of a glucomannan mycotoxin adsorbent. M. Mortson,* G. Girgis, H. Staempfli, A. Gallastegui, and T. K. Smith, *University of Guelph, Guelph, Ontario, Canada.*

Standardbred racehorses have a high prevalence of ulcer development ranging from 40 to 80%. Consumption of mycotoxin-contaminated diets can have a negative effect on equine health. A study was conducted to determine the effect of feed naturally contaminated with *Fusarium* mycotoxins on the presence of equine gastric ulcer syndrome (EGUS). Feed intake, body weight (BW) gain and serum hematological and biochemical parameters were evaluated as well as and the efficacy of a glucomannan mycotoxin adsorbent (GMA) (Integral, Alltech Inc., Nicholasville, KY). Nine standardbred mares at maintenance, of similar age, were assigned to one of 3 dietary treatments for 28 d with a 21 d recovery, in a replicated 3x3 Latin Square design. Each horse was housed in individual stalls and received limited turnout daily. Dietary treatments included a control, a contaminated diet and a contaminated diet + 0.2% GMA. The 2 contaminated diets ranged from 8.1 to 10 ppm deoxynivalenol and 1.2 ppm zearalenone, along with minor quantities of aflatoxin and fumonisin. Gastroscopies were performed and biopsies collected every 2 weeks during the experimental period. Day 0 ulcer scores ranged from 0 to 1 on a scale of 4 across treatment groups. Histological evaluation of the tissue biopsies showed inflammation of the glandular mucosa across treatments with varying distribution in the contaminated and GMA diets. Data was analyzed using a 2-way ANOVA including horse, diet and day in the statistical model ($P < 0.05$). A slight decrease in feed intake was observed in the contaminated groups compared with the control although the results were not statistically significant. BW gain was not affected by diet. Diet significantly altered serum anion gap ($P = 0.033$) and thymidylate synthase activity ($P = 0.046$) when comparing the control to the contaminated and GMA diets. It was concluded that horses tolerated this level of mycotoxin challenge with respect to BW and feed intake but histological changes in the gastric mucosa were evident.

Key Words: *Fusarium* mycotoxins, horses, equine gastric ulcer syndrome

W137 Comparison of high fat, high fiber, and high starch diets on serum levels of insulin, IGF-1, and glucose in growing horses. C. A. Craige,* S. R. Cooper, L. J. Spicer, and S. T. Kawcak, *Oklahoma State University, Stillwater.*

The objective of this study was to examine the effects of high fat, high fiber, and high starch diets on serum insulin, IGF-1, and glucose levels in growing horses. Yearling Quarter Horse fillies and geldings were randomly assigned into one of 3 treatment groups and individually fed 3 concentrates (each containing 4.0 Mcal/kg DE and 20% CP and fed at 2–3% of BW): 1) high fat (FT; 13% fat, 1% starch; as-fed basis: 90% alfalfa pellets (AF), 10% soybean oil; n = 6), 2) high fiber (FB; 3% fat, 1% starch; as-fed basis: 100% AF; n = 6) or 3) high starch (ST; 4% fat, 20% starch; as-fed basis: 50% AF, 20% ground shelled corn, 20% wheat middlings, 8% soybean meal, 2% minerals; n = 5). Each diet was formulated to contain approximately 20% CP to match the protein level of the FB diet. Diets were fed at 0700 h and 1800 h for 60 d. All horses were allowed 2 h of turn out exercise per day and weighed weekly. After 30 d (feed period 1) and 60 d (feed period 2) of treatment, blood samples were collected starting 15 min before (T-15) and 30 (T30), 60 (T60), and 180 (T180) min after the 0700 h feeding. Serum insulin, IGF-1, and glucose levels were analyzed using MIXED procedure of SAS in a split-split plot design. Main effects of diet, feed period, and time relative to feeding influenced ($P < 0.05$) serum insulin and glucose levels. Within a treatment, glucose concentrations increased postprandially ($P < 0.01$), peaking at T60. A subsequent decrease ($P < 0.01$) in glucose levels was observed until T180. Insulin concentrations were greater ($P < 0.05$) at T60 and T180 in horses fed ST diets compared with FB and FT diets (diet x time, $P < 0.001$). Serum IGF-1 concentrations tended ($P < 0.10$) to be influenced by diet x feed period. Serum IGF-1 levels in horses fed the ST diet tended to increase ($P < 0.10$) from feed period 1 to 2, but did not change in horses fed FT and FB diets. Serum IGF-1 levels did not differ among groups in feed period 1. In feed period 2, horses fed the ST diet tended to have greater ($P < 0.10$) IGF-1 levels (251 ± 25 ng/mL) than horses fed the FT (187 ± 23 ng/mL) or FB (187 ± 23 ng/mL) diets. Overall, the effects of ST diet on serum insulin and glucose were manifested acutely during feeding, whereas the effect of the ST diet on serum IGF-1 took 60 d to develop and was not acutely affected by feeding.

Key Words: equine, IGF-1, insulin

W138 Horses decrease water intake when supplements are added to drinking water. M. E. Gordon,* B. L. Miller, and M. L. Jerina, *Land O'Lakes Purina Feed LLC, Gray Summit, MO.*

The objective of this study was to test the hypothesis that horses decrease water intake when supplements are added to water. Six mature Quarter Horses (564.5 ± 44.0 kg, BW ± SD) were acclimated to drinking water from buckets over a 7 d period, and then offered both plain water (PW) and water with one of 4 different supplements (SW) in a block design. Each treatment period lasted for 5 d, and horses had a 2 d period between treatments when only PW was offered. Supplements included 2 electrolyte preparations (Farnam Apple Dex and Land O'Lakes Calf electrolyte), a vitamin/mineral (Farnam Red Cell) and a joint additive (Finish Line Fluid Action). All supplements were offered at a rate of 28 g per 18.93 L of water. Water intake from buckets was recorded via weight and replenished at 0700 and 1800. Horses were fed 1% BW grass hay and 3.6 kg of commercial pelleted diet daily throughout the trial, split into 2 feedings. Horses had ad libitum access to plain white salt in block form and were housed individually in stalls with attached dry lot paddocks. An incomplete block design was used to test the effect of supplements in water on water intake, utilizing ANOVA with mixed models (SAS 9.2 2010). Least squares means were compared with Fisher's least significant difference ($P < 0.05$). There was an effect of adding supplements to water ($P < 0.0001$), as horses preferred PW with mean daily intake of 11.92 ± 0.893 L versus 4.86 ± 1.785 L for SW. There was no difference within the supplement treatments for water intake ($P < 0.05$). There was a trend for water intake to be affected by time of day ($P = 0.0583$), with the greatest volume consumed overnight. This trend may have been influenced by timing of water weighing and replenishment and/or housing management conditions. In this study, horses drank over twice the amount of PW versus SW. Therefore, adding supplements to water can decrease intake in horses and may cause horses to become dehydrated. This may lead to poor performance or other adverse health effects in horses.

Key Words: equine, water intake, supplements

W139 The effects of coprophagy on the hindgut bacterial community of neonatal foals. L. A. Strasinger*[1], L. M. Lawrence[1], M. D. Flythe[2,1], G. L. Gellin[2], M. Brummer[1], B. E. Davis[1], and L. R. Good[1], [1]*University of Kentucky, Lexington,* [2]*United States Department of Agriculture, Agricultural Research Service, Forage-Animal Production Research Unit, Lexington, KY.*

How and when foals establish their hindgut bacterial community has received little attention from researchers. The aim of this study was to determine if coprophagy of maternal feces is essential for bacterial colonization of the foal′s digestive tract. Eight mare and foal pairs were randomly allocated into 2 treatment groups, allowed access to maternal feces (allowed, n = 4) and restricted access to maternal feces (restricted, n = 4). For at least the first 96 h after parturition, foals in the allowed group were monitored via video surveillance and the number of bouts of coprophagy was recorded. In the restricted group, each pair was constantly observed by an attendant for the 96 h following parturition, and mare feces was removed immediately following defecation. Starting with the passing of the foal′s meconium, fecal samples were taken from the mare and foal during the first 4 d. Samples were immediately frozen then later subjected to PCR-denaturing gradient gel electrophoresis (PCR-DGGE). Comparisons of each mare and foal was made using Dice′s index and cluster analysis, and reported as percent similarity. Foal body weights were measured every day a fecal sample was taken. Foals in the allowed group ate mare feces as early as 27 h after birth. When PCR-DGGE was performed on the meconium of newborn foals (d 0), no bands were observed and % similarity between mares and foals was 0 for both groups. By d 2 and 4 the number of bands had increased ($P < 0.01$), but there was no effect of time × treatment ($P > 0.05$). The average foal to mare similarity increased over time ($P < 0.05$) but there was no time × treatment interaction ($P > 0.05$). The % similarity between foals and their dams was 47 ± 16.8 (mean ± SD) for allowed group and 48 ± 6.3 for restricted group by d 2. The similarity between mare and foals on d 4 was to 62% ± 9.1 for allowed and 55% ± 10.3 for restricted. On d 14 restricted foals had an average daily gain of 2.06kg/d, while the allowed foals gained 1.77 kg/d ($P > 0.05$). Restricting access to maternal feces in the neonatal period did not appear to alter the diversity of the foal′s hindgut bacterial community by d 4.

Key Words: horse, neonates, microbiome

W140 Influence of maternal plane of nutrition and arginine supplementation on mares and their foals: Foaling parameters. K. N. Winsco*[1], J. A. Coverdale[1], C. J. Hammer[2,3], K. L. Gehl[1], A. E. Hanson[1], J. L. Lucia[1], and A. N. Wolford[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 determine the effect of plane of nutrition and arginine supplementation on foaling parameters, 32 mares (468 to 668 kg BW; 3 to 19 yr) were blocked by expected foaling date and randomly assigned within block to treatments which were arranged as a 2 × 2 factorial with 2 planes of nutrition, moderate (Mod; 0.5% BW AF grain/d) or high (High; 1% BW AF grain/d) and 2 levels of L-arginine supplementation, 0.21 g/kg/d (Arg) or no supplemental Arg (Con; L-alanine to maintain isonitrogenous diets). Treatments began 110 d before expected foaling date and terminated at parturition. Mares were housed by block and allowed ad libitum access to water and coastal bermudagrass (*C. dactylon*) hay, and fed commercial grain 2 × /d in individual stalls. Parturition was observed and the following foaling parameters were recorded: time of water break to birth, time to stand, and time of birth to placenta expulsion. Total length of gestation was calculated and placenta weight was recorded. Additionally, total colostrum volume (CV), specific gravity (SG), and Brix% of colostrum were measured. Physical measurements were also obtained which included mare BW, foal BW, foal wither and hip height, and foal body length. Data were analyzed using PROC GLM of SAS with main effects tested being plane of nutrition (Nutr), amino acid (AA), time, and their interactions. Significance was declared when $P \leq 0.05$ and a trend toward significance declared when $P \leq 0.10$. There was no influence of Nutr or AA on gestation length, foaling parameters, physical measurements, ratio of placenta to mare BW, placenta to foal BW, and ratio of foal BW to mare BW ($P \geq 0.15$). Maternal plane of nutrition tended to influence CV ($P \leq 0.08$) with Mod mares having greater volume compared with High. There was an influence of Nutr ($P \leq 0.03$) on colostrum quality indicated by greater SG in High mares compared with Mod. In summary, these data indicate that maternal plane of nutrition in late gestation affects colostrum volume and quality estimates, while arginine supplementation had no effect on foaling parameters, colostrum, or foal physical characteristics.

Key Words: pregnant mares, parturition, arginine

W141 Mineral concentrations of cool season grasses as affected by specie and season. A. L. Fowler,* L. M. Lawrence, S. H. Hayes, and S. R. Smith Jr., *University of Kentucky, Lexington.*

In pasture-based horse production systems in Central Kentucky the concentrate is the primary source of many minerals imported onto the farm, including phosphorus (P), potassium (K) and copper (Cu). By complementing the minerals in the concentrate with the minerals provided by the pasture, a reduction in mineral importation to the farm might be achieved. To develop a synchronized feeding program, factors affecting the concentration of minerals in the forage must be assessed. To this end, 2 studies were conducted. In experiment 1, replicated plots of 5 cool season grasses were sampled in early May to assess differences in the concentrations of calcium (Ca), P, Cu, K and the Ca:P ratio among species. Multiple samples of perennial ryegrass (n = 12), timothy (n = 12), tall fescue (n = 7), festulolium (n = 4), and orchardgrass (n = 4) were collected from experimental plots seeded the previous fall. Effect of grass specie on mineral content was determined using ANOVA. Ca concentrations ranged from a high of 0.73% in perennial ryegrass to a low of 0.49% in timothy ($P < 0.0001$). Festulolium and perennial ryegrass had the highest concentrations of P (0.46% and 0.46%, respectively), while timothy had the lowest (0.33%; $P < 0.0001$). There were no differences in the Ca:P ratio among species ($P > 0.05$). Timothy had the highest concentration of Cu and perennial ryegrass, festulolium, and tall fescue had the lowest concentrations ($P < 0.0001$). Perennial ryegrass, festulolium, and orchardgrass had higher concentrations of K than tall fescue and timothy ($P < 0.0001$). In experiment 2, samples of 8 tall fescue cultivars were collected from experimental plots in early May and late September to evaluate seasonal differences in the concentrations of Ca, P, Cu, K and the Ca:P ratio. No differences were found in mineral concentrations between spring and fall ($P > 0.05$). When synchronizing mineral content between pasture and concentrate, it might be beneficial to select pasture varieties that contain a higher concentration of necessary minerals to reduce the need for mineral supplementation of the diet and thus reduce the importation of nutrients to the farm.

Key Words: horse, calcium, phosphorus

W142 Effects of late gestation on conformation and movement in mares.

H. Roberts,* J. M. Reddish, and K. Cole, *Department of Animal Sciences, The Ohio State University, Columbus.*

Studies have shown that conformation, soundness and external weight distribution can affect a horse's movement. These factors can also influence the viability of the mare as a breeding animal. The effects of internal weight as opposed to external weight distribution have not yet been evaluated. During pregnancy, mares typically gain approximately 10% of their body weight (BW), with the majority of the weight gain occurring during the last 3 mo of gestation. The objective of this study was to evaluate the effects of increased BW during late gestation on conformation and movement in Quarter Horse mares. Each mare (n = 5) was videotaped in hand at the walk and trot tracking to the left and right on a flat surface on d 270, 285, 300, 315 and 330 of gestation, within 12 h of foaling, and d 15 and 30 postpartum. The camera was positioned at a height of 3.0 m and 8.6 m away from and perpendicular to the line of travel. Each horse was photographed from the left and right lateral view along with a plantar view of the left front and rear hoof. Videos and photographs were analyzed using OnTrack Equine software for hoof width, shoulder and hip angle, maximum knee and hock angle at the walk and trot, and stride length at the walk and trot. Data were analyzed using the PROC MIXED procedure of SAS. A P value of ≤0.05 was considered statistically significant. Average gestation length was 341.8 ± 8.9 d. BW increased by an average of 4.5% in the mares between d 270 of gestation and foaling then decreased after the birth of the foal and passage of the placenta ($P = 0.059$). Conformation of the shoulder and hip were not influenced by increased BW during late gestation ($P > 0.05$). Similarly, BW did not influence conformation of the hoof, as measured by hoof width ($P > 0.05$). Stride length at the walk and trot were not influenced by BW ($P > 0.05$). Knee and hock angles recorded at the walk and trot also were not influenced by BW ($P > 0.05$); however, there was a tendency for these measurements to decrease between d 330 of gestation and 15 d postpartum. In summary, increased BW during late gestation did not influence the conformation or movement of mares in this study.

Key Words: horse, movement, gestation

W143 Exercise response in unfit horses of different selenium status.

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Glutathione peroxidase (GPx) plays an important role in the neutralization of hydrogen peroxide which can generate hydroxyl radicals known as reactive oxygen species (ROS). Exercise has been shown to increase ROS as well as alter GPx activity post exercise. This study aimed to evaluate the effect of Se status on the response of unfit horses to mild exercise. Twenty 5 mature horses that had received one of 4 dietary Se treatments for 29 wk were used. The 4 dietary treatments were low Se (LS, n = 6), adequate Se (AS, sodium selenite, n = 6), high organic Se (SP; Sel-Plex, Alltech, Nicholasville, KY, n = 7) and high inorganic Se (SS, sodium selenite, n = 6). Total dietary Se for LS, AS, SP and SS was 0.07, 0.14, 0.3 and 0.3 ppm respectively. The basal diet consisted of low Se pasture, hay, cracked corn and a balancer pellet either low (LS, SP, SS) or adequate (AS) in Se. The SP and SS supplements were top dressed on the balancer pellet. Prior to the exercise test blood Se was higher ($P < 0.01$) for SP and SS (255 and 240 ng/mL) than AS and LS (195 and 125 ng/mL). Vitamin E status was adequate and similar between groups ($P > 0.05$). The exercise test, conducted in a 6 horse exerciser (Stratton Equine Enterprise Inc., Lexington, KY), consisted of walking and trotting, covering 4.41 km in 36 min. Blood samples were taken pre-, 0, 4 and 24 h post exercise to evaluate blood GPx activity, serum malondialdehyde (MDA) as indicator of oxidative stress, serum creatine kinase (CK) and aspartate aminotransferase (AST). Data were analyzed as ANOVA with repeated measures (SAS 9.2). There was an effect of treatment ($P < 0.05$) and treatment x time ($P < 0.05$) for GPx. Post exercise GPx decreased in LS and did not recover by 24 h, while remaining unchanged in AS. Post exercise GPx increased in SP and decreased in SS, but both returned to pre values at 24 h. At 24 h MDA was elevated in all groups (time $P < 0.05$). MDA was lower at 4 h in SP compared with AS (treatment x time $P < 0.05$). CK and AST were unaffected by Se status ($P > 0.05$). Overall Se status did not have a substantial effect on response to exercise in unfit horses, but the differences in post exercise GPx response may warrant further investigation.

Key Words: equine, GPx, MDA

W144 The effect of antibiotic administration on fermentative characteristics of equine feces.

B. E. Davis*[1], L. M. Lawrence[1], M. D. Flythe[2,1], S. H. Hayes[1], C. Wilson[1], A. L. Fowler[1], M. Brummer[1], and L. A. Strasinger[1], *[1]University of Kentucky, Lexington, [2]United States Department of Agriculture, Agricultural Research Service, Forage-Animal Production Research Unit, Lexington, KY.*

Horses are often treated with antibiotics in response to wounds or respiratory disease. Antibiotic use is occasionally associated with diarrhea, suggesting a disruption of the normal hindgut microflora. Not all horses receiving antibiotics develop diarrhea, but it is not known whether antibiotic treatment alters fermentation in the hindgut. Therefore, this study was designed to look at the effect of 2 commonly used antibiotics on the functional capacity of the microbial community of the equine hindgut. Horses ranging from 2 to 14 y, were blocked by age and gender into 6 blocks of 3 horses each. Within block horses were randomly assigned to 1 of 3 treatments: CO (no antibiotic; n = 6), ST (trimethoprim-sulfadiazine, oral, 30 mg/kg; n = 6) and CF (ceftiofur sodium, IM, 2.2 mg/kg; n = 6). Each block consisted of a 21 d adaptation, a 7 d treatment, and a 7 d withdrawal period. Feed refusals were weighed back and recorded on the last week of adaptation and during the treatment and withdrawal periods. Fecal samples were collected during each block and were analyzed for pH and DM. In vitro dry matter disappearances (IVDMD) of tall fescue, orchard grass and alfalfa hay were measured using fresh feces from each horse as the inoculum. In vitro gas production (IVGP; mL/g of substrate) from alfalfa hay was also measured using fresh feces as the inoculum. Data were analyzed using repeated measures ANOVA in the mixed procedure of SAS version 9.2. No horses exhibited diarrhea during the study. No differences in feed refusals were found between treatments ($P > 0.05$). There were no treatment or time x treatment effects on fecal DM ($P = 0.51$), fecal pH ($P = 0.78$) or IVGP ($P = 0.30$). Furthermore, treatment did not affect IVDMD of tall fescue, orchard grass, or alfalfa hay respectively ($P = 0.20$; $P = 0.21$; $P = 0.28$). Treatment with CF and ST did not induce changes in the in vitro fermentation associated measurements made in this study, without onset of diarrhea.

Key Words: diarrhea, IVDMD, fermentation

W145 Effects of probiotic supplementation on stress and immune responses in horses.

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Today's horse management practices often include restricted access to forage and feeding large quantities of grain in a limited number of meals throughout the day. These practices may create physiological and psychological stress in the horse, leading to increased cortisol production which may alter gastrointestinal microflora and immune responses. In this study, 12 Quarter Horses (1.6 ± 0.6 yr) were used to evaluate the effects of probiotic supplementation on stress and immune response to tetanus toxoid vaccination. Horses were randomly assigned to one of 2 treatment groups: Probiotic or Control. All horses received 0.5% BW of a 14% CP pelleted concentrate, with water and mixed grass hay ad libitum. Horses in the probiotic treatment group were fed a target dose of 10^7 cfu/(45 kg of BW x d) of a mixed culture containing *L. acidophilus*, *L. casei*, *L. plantarum*, and *E. faecium* throughout the study. After 45 d, horses were vaccinated against tetanus toxoid and blood samples were taken on d 0, 7, 14, 21 and 28 d post-vaccination to determine tetanus antibody titers. On d 28 post-vaccination, horses were transported for 15 min and blood samples to determine cortisol concentrations were taken by jugular venipuncture immediately before and after transport. Tetanus antibody titers and cortisol concentrations were analyzed using the PROC MIXED procedure of SAS. A P value of ≤0.05 was considered statistically significant. By d 7 post-vaccination, all of the horses in the study were fully protected against tetanus, regardless of treatment. Although no differences in cortisol production were found across treatment groups, cortisol concentrations increased significantly after transport for 15 min within the control group ($P < 0.05$). Denaturing gradient gel electrophoresis (DGGE) analysis of fecal samples revealed no differences in the microbial profiles of the horses due to probiotic supplementation. However, the microbial profiles of horses of comparable age showed similarities in banding patterns. Overall, probiotic supplementation did not influence gastrointestinal microflora, cortisol response to transport stress, or antibody response in this study.

Key Words: horse, probiotic, antibody response

W146 Biochemical markers of bone metabolism in growing Quarter Horses fed a higher starch versus a higher fat diet.

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The objective of this study was to determine if diet affects serum concentrations of osteocalcin (OC, marker of bone formation) and carboxy-terminal pyridinoline cross-linked telopeptide region of type I collagen (ICTP, marker of bone resorption) in growing Quarter Horses (QH) during the first 2 years of life. Eleven QH foals (5 fillies, 6 colts) housed in dry lot paddocks and individual stalls were fed either Omolene 300 (n = 5) (16% CP, 5% fat, 6.5% fiber, 29.4% starch, 10.6% WSC, 3.4 Mcal/kg) or Ultium Growth (n = 6) (15.5% CP, 9.5% fat, 13% fiber, 16.6% starch, 10% WSC, 3.7 Mcal/kg; analyses by Dairy One, Ithaca, NY). Foals were creep fed beginning at d28, starting with 0.23 kg/d and increased by 0.23 kg every 2 d until intake reached 3.6 kg/h/d, not exceeding 0.45 kg/mo of age before weaning at wk20. Foals consumed grass hay along with their dams and received 1% BW in grass hay post-weaning. Blood serum was collected at birth (d0) and at 6 wk intervals thereafter through wk102 (2 yr) and analyzed for OC (Metra Osteocalcin, Quidel Corporation, CA) and ICTP (ICTP RIA, Orion Diagnostics, Oulunsalo, Finland). A completely randomized factorial split-plot design was used to test the effect of diet, sex, and weaning. Analysis of variance was done with mixed models (SAS 9.2 2010) and least squares means compared with Fishers LSD ($P < 0.05$). There were no differences due to diet or sex for OC ($P = 0.60$, $P = 0.16$) and ICTP ($P = 0.48$, 0.10), but OC was higher in fillies than in colts before weaning ($P = 0.03$). In all horses, both OC and ICTP rose after birth, peaking at wk6 for OC (132.74 ± 11.2 ng/ml) and ICTP (24.26 ± 0.6 µg/L), and were higher before weaning compared with post-weaning levels ($P < 0.0001$). OC returned to d0 levels (86.03 ± 9.4 ng/mL) by wk18 ($P < 0.05$) and fell and remained below d0 levels by wk42 ($P < 0.05$). ICTP returned to d0 levels (21.82 ± 0.6 µg/L) by wk18 ($P < 0.05$) and fell and remained below d0 levels by wk24 ($P < 0.05$). Although feeds higher in starch and sugar have sometimes been implicated in metabolic bone problems in growing horses, these results suggest that bone formation and resorption are not affected by dietary starch and sugar levels in the current study.

Key Words: equine, osteocalcin, ICTP

W147 Anthelmintic resistance testing and training on horse farms in the Southeast.

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A total of 487 horses on 11 NC farms, 5 SC farms, and 9 VA farms were used for training agricultural professionals in and conducting fecal egg count (FEC) reduction testing for gastrointestinal nematode (GIN) parasite anthelmintic resistance. Horses (249 females, 238 males) of various breeds averaging 519 ± 6 kg BW and 11.3 ± 0.4 yr of age (range 1 to 34 yr) were used. Animals were assigned to treatment to account for preliminary fecal egg count (FEC), sex, breed type and age as possible. Ivermectin (Zimecterin; IVM; n = 246) and pyrantel (Strongid; PYR; n = 241) were used as labeled for BW (measured by equine weigh tape) plus 15% with doses rounded up to the nearest 22.7 kg (50 lb). Ninety horses on 12 farms were used in a switchback design but analyzed as independent data points. At treatment (d 0) and at d 14, fecal samples were collected after defecation for FEC using the Modified McMasters technique with a sensitivity of 8 eggs per gram (epg). Reduction in FEC

(RED) were calculated as ((FEC before trt — FEC after trt)/FEC before trt) x 100% for animals with d0 FEC of at least 40 epg (n = 472). Treatment was considered effective with RED of >80% for PYR and >90% for IVM. On 14 farms, for horses for which treatment was considered effective, fecal samples were collected every 14 d until FEC increased to below effective RED level (egg recovery period; ERP). Using SAS, Chi Square analysis and Wilcoxon Rank Sum testing was conducted. For random samples from 7 farms, individual McMaster chamber FEC was recorded; the CV for those samples averaged 22.1% for all farms. Overall, d0 FEC averaged 639 ± 30 epg. The average RED was greater ($P < 0.01$) for IVM (99.5%) than PYR (63.8%). For individual horses, IVM was effective in 99.2% of the horses tested while PYR was only effective in 57%. The average ERP was 53.4 ± 2.4 d for IVM and 46.0 ± 3.1 d for PYR. As previously reported in other states and livestock species, this study confirms GIN resistance to PYR on NC, VA, and SC horse farms. At least 10 agricultural professionals were trained in equine GIN anthelmintic resistance testing, resulting in overall decreased anthelmintic use on horse farms.

Key Words: anthelmintic resistance, horse, ivermectin

Lactation Biology III

W148 Estradiol enhances apoptosis in bovine mammary epithelial cells in vitro. L. Yart*[1,2], L. Finot[1,2], V. Lollivier[2,1], P. G. Marnet[2,1], and F. Dessauge[1,2], *[1]INRA, UMR1348 Pegase, Saint-Gilles, France, [2]Agrocampus Ouest, UMR1348 Pegase, Rennes, France.*

Previous studies conducted on mid- or late-lactation dairy cows showed that the administration of exogenous estradiol induced a severe decrease in milk yield and accelerated mammary gland involution. However, the effects of estradiol on mammary epithelial cells remained unknown. The aims of this study were to investigate the in vitro effects of estradiol (i) on a bovine mammary epithelial cell line (Mac-T) and (ii) on apoptose-induced bovine mammary epithelial cells. In the first part of this study, the Mac-T cells were treated with increasing doses of estradiol (10^{-6}, 10^{-5}, 10^{-4}, and 10^{-3} M), during increasing times (6h, 12h, 24h and 48h). It appeared that the higher treatment doses of estradiol (10^{-4} and 10^{-3}M) reduced the cell proliferation by 8 and 19% respectively at 24h and by 5 and 10% respectively at 48h, and induced apoptosis of the mammary epithelial cells. In the second part of this study, the Mac-T cells were either treated with estradiol (E_2, 10^{-4}M) or with camptothecin (Ct, 10 μM) to induce apoptosis or with camptothecin combine with estradiol (Ct+ E_2), during increasing times (2h, 6h, 24h and 48h). After 6h of treatment, we observed an increase in apoptotic markers (Caspase 3 activity and Annexin V-positive cell rate) in both Ct and Ct+ E_2 treatment batches. This increase was more important in the Ct+ E_2 treatment batch at 6h (+ 61.5%) and 24h (+ 9.8%) compared with the Ct treatment batch. Taken together, these results suggest that estradiol reduces mammary epithelial cells expansion and enhances apoptosis pathways in vitro.

Key Words: estradiol, mammary epithelial cell, apoptosis

W149 Evaluation of mitogenic properties of colostrum and colostrum replacer (CR) on growth of bovine mammary epithelial cells (BMEC) in vitro. K. E. Stemm,* C. M. Jones, J. L. Collier, and R. J. Collier, *University of Arizona, Tucson.*

Ingestion of colostrum is necessary for neonatal calves to develop a functioning immune system. A viable alternative source of immunoglobulins for management and safety reasons is colostrum replacer (CR). Colostrum has also been implicated in improved milk yield at maturity, possibly due to increased mammary growth. A comparison of mitogenic effects of colostrum versus CR has yet to be established. In this study, pooled whole colostrum (WC) from a commercial dairy was compared with Convert ImmPower Colostrum Replacer supplied by Agrarian Marketing (Middlebury, Indiana). A clonal BMEC cell line (MAC-T), was used to screen potential mitogenic agents in colostrum. Concentrations of DNA were determined by CyQuant DNA Assay (Life Technologies, Grand Island, NY) and by proxy mitogenic activity. Protein concentrations of WC and CR were 187.01 and 181.56 mg/mL, respectively, and therefore treatments were delineated as percentages by weight. Cells treated with 10% WC or CR exhibited a decline in cell numbers ($P < 0.05$). Therefore, only treatments of 1% and 5% WC or CR were utilized. The treatment of MAC-T cells with WC or CR at 1 or 5% produced higher DNA concentrations than cells that were untreated, ($P < 0.05$). The use of WC at 1% provided the best growth results, which was not different from the normal in vitro growth media, containing 10% FBS and insulin. When the comparison was made between the 2 treatments, WC promoted more growth than CR at 1%, ($P < 0.001$). The mitogenic agents epidermal growth factor (EGF) and insulin-like growth factor I (IGF-I) were then added to CR to determine if it improved mitogenesis. The addition of 25 ng/ml EGF and 100 ng/ml IGF-I alone and in combination with 1% CR promoted growth of cells greater than 1% CR alone, ($P < 0.001$), but not different from 1% WC ($P < 0.05$).

Key Words: colostrum replacer, mitogen, mammary cells

W150 Effects of intra-mammary infusions of casein hydrolysate, EGTA, and lactose at drying-off on mammary gland involution. B. Ponchon*[1], P. Lacasse[2], N. Silanikove[3], S. Ollier[2], and X. Zhao[1], *[1]Department of Animal Science, McGill University, Sainte-Anne-de-Bellevue, QC, Canada, [2]AAFC-Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada, [3]Volcani Center, Bet Dagan, Israel.*

The transition from lactation to the dry period in dairy cows is a period of high risk for acquiring new intra-mammary infections. This risk is reduced when the involution of the mammary gland is completed. Consequently, strategies that accelerate the involution process after drying-off could reduce the incidence of mastitis. The objective of this study was to assess the effect of 3 different treatments on mammary gland involution markers. Each quarter of 8 Holstein cows in late lactation was randomly assigned at drying-off to an intra-mammary infusion of iso-osmotic solutions of a casein hydrolysate (CNH; 70mg), EGTA (5.7g), lactose (5.1g) or saline (control). Milk samples were collected on the last 2 d before and 1, 3, 5, 7, 10 and 14 d after the last milking. Milk somatic cell count (SCC), lactoferrin and BSA concentrations gradually increased ($P < 0.001$) during the first 2 weeks following the last milking whereas milk citrate concentration decreased ($P < 0.001$). The increases in SCC, lactoferrin and BSA concentrations after the last milking were similar in quarters infused with saline and lactose. Intra-mammary infusion of CNH hastened the increase in SCC and BSA and their concentrations were greater ($P < 0.05$) than in milk from control quarters on d 1, 3, 5 and 7. Similarly, the CNH treatment induced a faster rise of lactoferrin concentration, which was greater ($P < 0.05$) than in milk from control quarters on d 1, 3 and 5 after the drying-off. Milk citrate concentration was unaffected by CNH but the citrate:lactoferrin ratio was lower ($P < 0.05$) in CNH-treated quarters at d 3 and 5 than in control quarters. Infusion of EGTA increased SCC on d 1 and 3 but it had no effect on the other parameters. This study suggests that an intra-mammary infusion of CNH at drying-off hasten the involution of the mammary gland.

Table 1. Milk SCC, BSA and lactoferrin concentrations and citrate:lactoferrin ratio 3 days after drying-off

	Control	CNH	EGTA	Lactose
SCC (x 1000)	182	3 162*	436*	323
BSA (g/L)	1.14	2.63*	1.37	1.48
Lactoferrin (G/L)	0.73	1.26*	0.76	0.78
Citrate:Lactoferrin	3.64	1.58*	2.94	2.25

*Different from control ($P < 0.05$).

W151 Expression of amino acid transporter LAT1 and the regulation by prolactin in mammary gland of dairy cow.

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System L-amino acid transport mediates the uptake of aromatic neutral amino acids and nutritionally essential amino acids. This study was to reveal the relationship between the expression of system L-amino acid transporter LAT1 and the development of dairy cow mammary gland, and illuminate the regulation mechanism of prolactin (PRL) to LAT1 expression. We used Western blotting and immunofluorescence triple staining technology to detect the expression of LAT1 and its auxiliary protein 4F2hc at 4 development stages of dairy cow mammary gland tissue, including virgin, pregnant, lactation, involution. The effect of prolactin on the expression of LAT1 was determined by qRT-PCR and Western blotting in dairy cow mammary epithelial cells during mid-lactation. Subsequently, we silenced the prolactin receptor (PRLR) gene by siRNA interference technology in dairy cow mammary epithelial cells, and detected the PRLR gene silencing effect silencing and the expression of LAT1 by qRT-PCR and Western blotting. We also tested Î^{2}-casein in mammary epithelial cells by high performance liquid chromatography (HPLC). Immunofluorescence results showed that LAT1 and 4F2hc co-expressed in the apical and basolateral membrane of duct and acinus epithelium at different stages of mammary gland. The expression of LAT1 and 4F2hc were significantly upregulated during lactation ($P < 0.05$). LAT1 mRNA expression were greatly increased prolactin dose range (5, 10, 20, 40 and 60 Î1/4g/ml), and LAT1 had the highest expression level at 20 Î1/4g/ml prolactin stimulation group. This result conformed to the result of Western blotting. In siRNA-PRLR transfection group, the expression of LAT1 exhibited a differentially reduction ($P < 0.05$). In addition, both secretion of Î^{2}-casein and cell activities were also obviously decreased in transfected cells. These results indicated that PRL-PRLR signaling pathways were most likely to play a major role in the regulation of LAT1 expression during lactation, and LAT1 may play a role during the development and lactation of dairy cow mammary gland.

Key Words: dairy cow, mammary epithelial cells, LAT1

W152 Bzw2 promotes proliferation and lactation of mammary epithelial cell in dairy goat.

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Mitosis of mammary epithelial cell is the foundation of mammal lactation. We developed a strategy of combined application of serial analysis of gene expression (SAGE) tags for gene identification (GLGI) to screen and identify genes influenced lactating ability of mammary epithelial cell in the dairy goat. The Bzw2 gene was found as a candidate gene related to lactation by screening Long-SAGE library of mammary gland in the dairy goat. This study was to identify the Bzw2 gene function during lactation in the dairy goat mammary gland. The Bzw2 gene was cloned by SMART RACE from Long-SAGE tag. The mRNA level of Bzw2 was relatively higher in early lactation than in other development stages of the mammary gland. The proliferation of mammary epithelial cell was inhibited by transfecting specific shRNA of Bzw2, The mRNA level of Stat5, Csn2 and Prlr were also downregulated, which would suggest that the productivity of the mammary epithelial cell was attenuated after Bzw2 RNAi. The reduction of mammary cell growth and lactation by Bzw2 RNAi are rescued through overexpression of Bzw2. These results revealed that Bzw2 might play an important role in lactation though the molecular mechanism which was still to be discovered by studies.

Key Words: Bzw2, mammary epithelial cells;, RNAi

W153 CLA and diet induced milk fat depression reduces milk fat across the entire day.

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Recently a circadian rhythm of milk and milk component synthesis has been characterized that is partially dependent on the timing of feed intake. Our objective was to determine if inhibition of milk fat synthesis during diet-induced milk fat depression occurred to a higher degree during certain phases of the day. A retrospective analysis was conducted of 2 experiments that induced milk fat depression while milking cows at equal intervals, 3 times per day. The response at each milking was analyzed using the Proc Mixed procedure of SAS with a repeated statement. The model included the fixed effect of treatment, milking time, and the interaction of milking time and treatment and the random effect the cow and period. The subject was cow by period with the ARH1 covariance structure. In Experiment 1, 9 multiparous cows were arranged in a 3 × 3 Latin square design. Treatments were control TMR, control TMR plus 3 d intravenous infusion of 7.5 g/d of trans-10, cis-12 conjugated linoleic acid (CLA), and a low forage and high fat diet for 10 d. In Experiment 2, 10 multiparous ruminally cannulated cows were arranged in a replicated design and milk samples were collected during a control period or after 5 d of abomasal infusion of 10 g/d of CLA. In Experiment 1 there was a significant effect of treatment and milking for milk fat concentration and yield ($P < 0.001$ and $P < 0.05$, respectively), but no interaction of milking time and treatment. In Experiment 2, there also was an effect of treatment and milking time on milk fat concentration ($P < 0.05$) and no treatment by milking time interaction. There was a treatment, but no milking time or treatment by milking time interaction on milk fat yield. Milk fat percent was 0.48 and 0.28 percentage units lower at the morning milking than the afternoon milking in Exp. 1 and Exp. 2, respectively. A daily rhythm of milk fat concentration and yield can be observed in cows milked 3 times a day. However, diet-induced milk fat depression decreases milk fat yield equally over the day.

Key Words: milk fat, CLA, circadian

W154 Dairy cows having various levels of *cis*-9, *trans*-11 CLA de novo synthesis differently express proteins in milk epithelial cells.

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The objective of this study was to associate cows having various levels of *cis*-9, *trans*-11 CLA to different protein expression profiles of milk epithelial cells. Morning milks were collected individually from 26 multiparous Holstein cows in their third or fourth lactation fed the same diet. Total milk lipids of each sample were extracted following the Folch method and the lipid methyl esters were quantified by GC with a SP-2560 fused silica capillary column. Milk epithelial cells were extracted from the fresh milk by the Boutinaud method. All data were evaluated by GLM of SPSS using ANOVA. On the basis of *cis*-9, *trans*-11 CLA contents, the animals were grouped into group I (0.59% of total lipids;

n = 7), II (0.85% of total lipids; n = 8) and III (1.02% of total lipids; n = 11). Protein aliquots extracted from milk epithelial cells were pooled in each group. Differences in protein expression among these groups were compared with 2-DE. The differently expressed spots (III/I; ≥ 2 or ≤ 0.5) were identified using ESI-Q-TOF and a protein search engine. Although animals were offered the same diet, the content of *cis*-9, *trans*-11 CLA in group III (1.02 ± 0.10%) was twice as high as that in group I (0.59 ± 0.14%) ($P < 0.05$). The groups I, II and III showed significant differences in the protein expression profiles of milk epithelial cells ($P < 0.05$). One upregulated (CATHL5) and 3 downregulated proteins (ANXA1, ZWINT, CSN3) were found and they varied similarly as the pattern of *cis*-9, *trans*-11 CLA contents. In conclusion, the different levels of *cis*-9, *trans*-11 CLA de novo synthesis of dairy cows may associate with these identified proteins expressed in milk epithelial cells.

Key Words: *cis*-9, *trans*-11 CLA de novo synthesis, protein expression profiles, purified milk epithelial cells

W155 Modification of protein synthesis of bovine mammary epithelial cells induced by heat shock. H. Hu, J. Q. Wang,* D. P. Bu, L. Y. Zhou, and P. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing.*

The objective of this study was to determine the effect of heat stress on protein synthesis by Chinese bovine mammary epithelial cells (CMEC). The CMEC has been identified to be a normal and available epithelial cell line. The CMEC cultured in vitro were exposed to 42°C for 0.5, 3, 5, 8, 12 h, and controls were exposed to 38°C. Heat shock protein (Hsp) and casein expression of gene and protein were detected by qRT-PCR and ELISA, separately. The mean, SD, and *P* values were calculated from triplicated experiments using SARS (9.0). The Student's *t*-test was used to calculate *P*-values for comparison, and the significant statistics was set at a *P*-value < 0.05. The transcription of Hsp genes (*hsp27*, *70* and *90*) was enhanced ($P < 0.05$) as of 0.5 h of heat stress. The peak of transcription was observed at 3 h after the onset of thermal treatment. Although the transcription rates returned subsequently to baseline values, they were still upregulated ($P < 0.05$) compared with controls at 12 h. The expression of Hsp27, 70 and 90 increased at different rates. The expression of Hsp27 and Hsp70 increased gradually during the first 8 h, and then decreased, yet all values were higher than those of the control over the entire thermal stress period ($P < 0.05$). On the other hand, the Hsp90 expression only increased at 8 h. Among the Hsp, Hsp70 was acutely synthesized, and the transcription and protein expression of Hsp70 were 10 times and 3 times greater than the control group at 0.5 h and 8 h, respectively. The major milk protein genes β-casein (*CSN2*) and butyrophilin (*BTN1A1*), which are markers for the secretion capacity of bovine mammary epithelial cells, were both downregulated with heat stress from 0.5 h to 12 h ($P < 0.05$). Total casein synthesis decreased from 3 to 8 h ($P < 0.05$), corroborating the decline in milk protein secretion. Results suggest that under heat stress, normal biological activities of CMEC are disturbed and the decrease in milk protein synthesis of epithelial cells contributed to synthesize heat shock proteins thereby protecting cells from heat damage. This result might potentially explain the reduction of milk formation induced by heat stress.

Key Words: mammary epithelial cells, heat stress, heat shock protein

W156 Choline and methionine affect oxidative stress in a bovine mammary epithelial cell line. L. Pinotti*[1], E. Skrivanova[2], R. Rebucci[1], E. Fusi[1], F. Cheli[1], and A. Baldi[1], [1]*Department of Veterinary Sciences and Technology for Food Safety, Università degli Studi di Milano, Milan, Italy,* [2]*Institute of Animal Science, Prague, Czech Republic.*

The aim of the present study was to investigate the role of choline and methionine in modulating the oxidative stress induced by hydrogen peroxide in bovine mammary epithelial cells. The BME-UV1 cell line has been used as an in vitro model of the bovine mammary epithelium. Cells were incubated with choline and methionine at 2 different concentrations: LowCM,500 µM and 715 µM for choline and methionine, respectively, or HighCM, 1000 µM and 1430 µM, for choline and methionine, respectively. The ratio between choline and methionine has been established on a molar basis. In both treatments, the cells were cultured in presence of insulin (1 µg/ml). In dose response experiments, cells were exposed to increasing concentrations of hydrogen peroxide (0 to 500 µM) to establish the half lethal concentration (LC50) of hydrogen peroxide for the BME-UV1 cell line. Cell proliferation (MTT test) was measured at different incubation times (24, 48 and 72h), whereas apoptosis (TUNEL) was measured at 48h. Incubation time affected the response to hydrogen peroxide. At the lowest range of hydrogen peroxide concentration tested (15.62 to 62.5 µM) choline and methionine significantly ($P \leq 0.05$) enhanced cell viability on average by 19%, 21% and 25.8% after 24, 48 and 72h, respectively. Supplemental choline and methionine in the medium exerted a dose dependent effect on apoptosis of BME-UV1 cells: percentages of apoptotic cells were 0.42%, 1.35%, in HighCM and LowCM treated cells, respectively, whereas apoptosis in hydrogen peroxide treated cells was 6.81% for the same range of hydrogen peroxide concentration tested. Our results indicate that choline and methionine could play a role in counteracting oxidative damage induced by hydrogen peroxide in bovine mammary epithelial cells, even though the exact mechanism merits further investigations.

Key Words: choline, methionine, bovine mammary epithelial cell

Nonruminant Nutrition: Feed Additives

W157 Effects of dietary Aviplus-S supplementation on growth performance, fecal characteristics, and blood profiles in weanling pigs. J. H. Cho,* L. Yan, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choongnam, South Korea.*

A total of 150 weanling pigs [(Landrace × Yorkshire) × Duroc, BW = 6.76 ± 0.61 kg] were used in a 42-d trial to investigate the effects of dietary Aviplus-S supplementation on growth performance, fecal score, fecal moisture, fecal pH, and blood profiles. Pigs were randomly assigned to 1 of 5 treatments according to BW. Dietary treatments were NC, basal diet (without antibiotics); PC, NC + 39 mg/kg tiamulin; AS1, NC + 0.05% Aviplus-S; AS2, NC + 0.1% Aviplus-S; AS3, NC + 0.2% Aviplus-S. Aviplus-S is based on a mixture of citric (25%) and sorbic (16.7%) acids, thymol (1.7%) and vanillin (1.0%). All pigs were housed in an environmentally controlled room and allowed ad libitum access to feed and water. All statistical analyses were conducted in accordance with a randomized complete block design, using the GLM procedures of SAS software package (1996). During d 0–7, ADFI was reduced ($P < 0.05$) in AS1 treatment compared with PC treatment, and G/F in AS1, AS2 and AS3 treatments were higher ($P < 0.05$) than those in NC and PC treatments. During d 7–21, lower ($P < 0.05$) ADFI was noted in AS1 and AS2 treatments than that in PC treatment, and no differences ($P > 0.05$) in ADG and G/F were observed among treatments. During d 21–42, pigs fed the PC diet had a higher ($P < 0.05$) ADG than those fed the NC diet, and the G/F was higher ($P < 0.05$) in PC treatment than those in NC and AS1 treatments. Overall, the ADG and G/F in PC treatment were higher ($P < 0.05$) than that in NC treatment. Fecal scores were reduced ($P < 0.05$) in AS2 treatment compared with NC treatment. Fecal moisture was unaffected ($P > 0.05$) by dietary treatments. Fecal pH was decreased ($P < 0.05$) in AS1 and AS2 treatments compared with NC treatment at d 7, and fecal pH was reduced ($P < 0.05$) in AS1, AS2 and AS3 treatments compared with NC and PC treatments at d 21. No differences ($P > 0.05$) were observed in blood profiles among dietary treatments. In conclusion, Aviplus-S could be used as an alternative for antibiotics in weanling pigs.

Key Words: Aviplus-S, growth performance, weanling pigs

W158 Effects of Alcopro supplementation as energy source on growth performance, nutrient digestibility, and blood characteristics in growing pigs. J. H. Cho*[1], P. Y. Zhao[1], K. D. Yang[2], S. W. Han[2], and I. H. Kim[1], [1]*Dankook University, Department of Animal Resource & Science, Cheonan, Choongnam, South Korea,* [2]*WooGene B&G, Seoul, South Korea.*

A total of 96 growing pigs [(Landrace × Yorkshire) × Duroc, BW = 26.12 ± 1.21 kg] were randomly allotted to 1 of 3 dietary treatments (8 replicate pens per treatment with 4 pigs per pen) to investigate the effects of Alcopro supplementation as energy source on growth performance, nutrient digestibility, and blood characteristics. This experiment lasted for 42 d. All the pigs were housed in an environmentally controlled room with a slatted plastic floor in 24 adjacent pens (1.8 × 1.8 m). Dietary treatments included: 1) CON (basal diet with 4% tallow), 2) A1 (basal diet with 2% tallow + 1% Alcopro + 1% corn), 3) A2 (0% tallow basal diet + 2% Alcopro + 2% corn). Alcopro is based on ethyl alcohol containing energy source (about 10,000 kcal/kg ME) and digestive enzymes for livestock. Data were analyzed using GLM procedures of SAS (1996), with each pen being used as the experimental unit, and the means of the treatments were compared by Duncan multiple range test. No significant difference ($P > 0.05$) was observed on the energy level changed between A1 (1% Alcopro) and A2 (2% Alcopro) diets during 4 d storage at the room temperature. No difference ($P > 0.05$) was observed on ADG, ADFI, and G/f throughout the experiments. However, pigs fed the A1 and A2 diets led to 72g (5%) and 65 g (4%) higher ADFI than those fed the CON diet, although the difference did not reach the significant level. No difference ($P > 0.05$) was observed on the apparent total tract digestibility of DM, N, and energy among treatments. There was no difference ($P > 0.05$) in the concentrations of WBC, RBC, BUN, creatinine, and Lymphocyte percentage during the experimental period. In conclusion, no negative effects were observed when Alcopro® was supplemented as energy source in growing pigs. This study indicated that Alcopro® could be used as an energy source for growing pigs and could partly replace tallow in the pig industry.

Key Words: Alcopro, growing pigs, growth performance

W159 Effects of Calibrin-Z on weanling pigs fed diets with no mycotoxin contamination. F. Chi[1], S. L. Johnston*[1], and D. C. Mahan[2], [1]*Amlan International Inc., Chicago, IL,* [2]*The Ohio State University, Columbus.*

Some clay-based mycotoxin binders have been shown to bind nutrients. However, in previous research Calibrin-Z (CAZ) has been shown to increase nutrient digestibility and has shown a tendency to improve feed efficiency. This would seem to indicate that CAZ either did not bind nutrients or might bind nutrients and release them during passage through the digestive tract leading to higher availability. In the current experiment 160 weanling pigs were used to evaluate the effects of CAZ in diets that had no mycotoxin challenge. The treatments were: 1) control diet; and 2) the control diet with 0.2% CAZ added. Treatment diets were fed from d 0 to d 35 post-weaning (average initial wt = 6.79 kg). There were 16 pens of 5 pigs each on each treatment, pen was the experimental unit. Diets were complex nursery feeds with 3 dietary phases: d 0–7, d 7–21, and d 21–35. The responses to CAZ added at 0.20% of the diet were analyzed in all replicates, the 7 lightest weight replicates, and the 9 heavier weight replicates. There was a numerical advantage ($P = 0.11$) for average daily gain in the 7 to 21 d period when CAZ was fed to all pigs, with values of 513 and 538 g per day for pigs fed the control diet or the control diet + CAZ, respectively. This was mainly due to a numerical advantage ($P = 0.06$) when CAZ was fed to the heaviest pigs. There was no other effect on growth performance with overall values for average daily gain of 525 g or 532 g, for daily feed intake of 783 g or 785 g, or gain:feed of 672 g/kg or 679 g/kg, for pigs fed the control diet or the control +CAZ respectively. At d 21 and 35 of the experiment pigs in 6 replicates were bled and plasma urea nitrogen concentrations were analyzed. There was no difference ($P = 0.19$) between plasma urea nitrogen concentrations on d 21 but it was significantly ($P < 0.01$) higher on d 35 in pigs fed diets containing CAZ, with values of 33.0 and 38.7, mmol/l. These results may indicate that there was higher amino acid availability when pigs were fed CAZ.

Key Words: feed efficiency, Calibrin-Z, plasma urea nitrogen

W160 Bovine lactoferrampin-lactoferricin produced by *Pichia pastoris* fed-batch fermentation improves intestinal microflora in weaned piglets. X. S. Tang and Y. L. Yin,* *Institute of Subtropical Agriculture, the Chinese Academy of Sciences, Changsha, China.*

The chimera of bovine lacroferrampin and lactoferricin, a promising alternative to antibiotics, namely lactoferrampin-lactoferricin (LFA-LFC) has stronger activity than its constituent peptides. In this study, LFA-LFC was produced by fed-batch fermentation in recombinant strain *P. pastoris* (KM71) XS10 constructed by our group. Uniform design U6(64) was used to optimize the fermentation conditions. The target peptide was purified by cation-exchange and size-exclusion chromatography, and identified by antimicrobial activity assay and MALDI-TOF MS. Then the purified sample was added into diet for weaned piglets at 21 d of age. After the following 21 d experimental period, lactobacilli, bifidobacteria and *E. coli* of gut were quantified by real-time PCR. The data were subjected to one-way ANOVA and least significant difference was performed to identify differences among the groups using the SPSS 15.0 program. Results showed that approximately 85 mg of LFA-LFC was secreted into 1 L of medium under the optimized conditions. Purified peptide with a purity of 91% showed antimicrobial activities against all the tested *E. coli* and had the same molecule mass as target peptide. Compared with control group, LFA-LFC group increased the ratio of lactobacilli and bifidobacteria ($P < 0.01$) in gut of piglets including stomach, duodenum, jejunum, ileum, colon and cecum. LFA-LFC group decreased the ratio of *E. coli* in stomach, duodenum and jejunum. These results show that diet supplementation with LFA-LFC can improve gut microbiota in weaned piglets.

Key Words: pig, antimicrobial peptide, microflora

W161 Effects of feeding capsicum oleoresin, garlicon, or turmeric oleoresin on gene expression of ileal mucosa of pigs. Y. Liu*[1], M. Song[1], T. M. Che[1], J. A. Soares-Almeida[1], J. J. Lee[1], D. Bravo[2], C. W. Maddox[1], and J. E. Pettigrew[1], [1]*University of Illinois, Urbana,* [2]*Pancosma SA, Geneva, Switzerland.*

This study was conducted to characterize the effects of 3 plant extracts on gene expression in ileal mucosa of weaned pigs. Weaned pigs (n = 64, 6.3 ± 0.2 kg BW, 21 d old) were housed in individual pens for 15 d: 4 d before and 11 d after the first inoculation (d 0). Treatments were in a 2 × 4 factorial arrangement: with or without an F-18 *E. coli* challenge and 4 diets (a nursery basal diet (CON), 10 ppm of capsicum oleoresin (CAP), garlicon (GAR), or turmeric oleoresin (TUR)). Total RNA (4 pigs/treatment) was extracted from ileal mucosa of pigs at d 5. Double-stranded cDNA was amplified, labeled, and further hybridized to the Affymetrix GeneChip Genome Array. Microarray data were analyzed in R using packages from the Bioconductor project. Differential gene expression was tested by fitting a mixed linear model equivalent to a 2 × 4 factorial ANOVA using the limma package. Bioinformatics analysis was conducted by DAVID Bioinformatics Resources. Three pairwise comparisons were made in the sham group: CAP vs. CON, GAR vs. CON, and TUR vs. CON. Compared with the CON, feeding CAP altered the expression of 490 genes (280 up, 210 down), feeding GAR altered the expression of 35 genes (17 up, 18 down), while feeding TUR altered the expression of 327 genes (232 up, 95 down). Compared with the CON, feeding CAP and TUR increased ($P < 0.05$) the expression of genes related to membrane and tight junctions, suggesting enhanced gut mucosa health, but decreased ($P < 0.05$) the pathway of cell cycle. Feeding GAR and TUR enhanced ($P < 0.05$) the expression of genes associated with immune responses, indicating feeding these plant extracts may stimulate the immune responses of pigs in the normal conditions. These findings may explain, at least partially, why diarrhea was reduced in pigs fed plant extracts in the sham group. In conclusion, plant extracts regulated the expression of genes in ileal mucosa of pigs, perhaps providing benefits by enhancing the gut mucosa health and stimulating the immune system.

Key Words: gene expression, plant extracts, weaned pigs

W162 Productive performance in post-weaned pigs conditioned by pre and postnatal porcine digestive peptides (PDP) exposure through maternal diet. J. Figueroa*[1], D. Solà-Oriol[1], E. Borda[2], S. A. Guzmán-Pino[1], and J. F. Pérez[1], [1]*Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain,* [2]*Bioibérica, Barcelona, Spain.*

Piglets present neophobia to unfamiliar ingredients at weaning. Preferences for a novel feed or flavor may be acquired as a result of the transmission of volatile compounds of maternal diet to the amniotic fluid and milk. The aim of the present study was to explore the influence of pre- and postnatal exposure to porcine digestive peptides (PDP) via maternal diet on the productive performance of post-weaned piglets fed a diet containing the same PDP. A total of 240 male/female post-weaned pigs were used in this experiment. Half of animals came from mothers that during late gestation (14d) and lactation (28d) ate 2% PDP in their diets. The other 120 piglets came from mothers fed an iso-caloric and iso-proteic diet but without PDP inclusion in these periods. Piglets were distributed into 4 blocks by initial weight. Within each block, pigs were distributed in pens for a balanced body weight. Each block consisted of 6 pens of 10 animals. All animals received a common weanling diet containing 2% of PDP in the pre-starter (0–14d) and starter (15–35d) specification during the transition period. Feed intake and body weight were weekly measured to calculate average daily feed intake (ADFI), average daily gain (ADG) and feed:gain ratio (FGR). Data were analyzed by using the GLM procedure of SAS. Piglets coming from sow's diets supplemented with PDP tend to showed higher ADFI during the 15–35d period (740 vs. 693g; $P = 0.07$). Similarly results were observed for ADG in piglets coming from PDP-treated sows during the 0–14d period (144 vs. 137g) and during the 15–35d period (502 vs. 471g; $P < 0.06$). No differences were observed for FCR along the experimental period. Therefore the final body weight at the end of the starter phase tended to be higher for those animals coming from mothers fed PDP supplemented diets (20.1 vs. 19.3kg; $P = 0.1$). These results suggest that pre and postnatal exposure to PDP via maternal diet may influence piglet performance in the presence of the same cues probably due to the positive association of the uterine or milk experience with these feed components.

Key Words: pigs, flavors, maternal-transference

W163 Effects of chitosan nanoparticles loaded with chromium ions on growth, blood metabolites, immune traits and tissue chromium in finishing pigs. M. Q. Wang,* C. Wang, H. Li, Y. J. Du, W. J. Tao, S. S. Ye, and Y. D. He, *Animal Science College of Zhejiang University, Hangzhou, Zhejiang, China.*

Nanocomposite materials have a higher surface area and smaller size than typical materials, and they exhibit electrical, magnetic, mechanical and biological characteristics which may enhance mineral absorption. The present study was conducted to investigate the effects of chitosan nanoparticles loaded with chromium ions (CNP-Cr) on carcass characteristics, pork quality and lipid metabolism in finishing pigs. A total of 120 crossbred barrows (66.06 ± 1.01 kg initial BW) were randomly divided into 4 treatment groups, with 4 pens of 10 pigs per group. Pigs were fed a basal diet (corn-soybean meal, 10.5 g/kg of Lys) supplemented without (control), or with 100, 200 or 400 µg/kg Cr from CNP-Cr. All pigs were given free access to feed and water. Eight pigs from each treatment were selected to collect blood and tissue samples after 35 d on trial for analysis of blood metabolites, immune traits, and tissue chromium concentrations. Results suggested no significant differences in growth performance between control and CNP-Cr-treated groups. Supplementation of 200 µg/kg CNP-Cr decreased serum glucose ($P < 0.05$). Serum immunoglobulin A was increased with supplementation of CNP-Cr ($P < 0.05$). Serum immunoglobulins G and M in pigs receiving 400 µg/kg CNP-Cr and serum complement in pigs receiving 100 µg/kg CNP-Cr were increased ($P < 0.05$). CNP-Cr supplementation increased chromium content in blood, longissimus muscle, heart, liver, kidney and pancreas in a linear fashion ($P < 0.05$). These results suggest that dietary supplementation of Cr as CNP-Cr affects serum glucose and immune status, and increases tissue Cr content of muscle and selected organs in finishing pigs.

Key Words: chromium, immune trait, blood metabolite

W164 Effects of fermented chlorella supplementation on growth performance, nutrient digestibility, and blood characteristics in growing pigs.

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A total of 96 growing pigs [(Landrace × Yorkshire) × Duroc, BW = 26.58 ± 1.41 kg] were used in a 6-week feeding trail to evaluate the effects of fermented chlorella (FC) supplementation on growth performance, nutrient digestibility, and blood characteristics. Pigs were randomly allotted into 1 of 4 dietary treatments with 6 replicate pens per treatment and 4 pigs per pen. Dietary treatments were: 1) NC, basal diet (without antibiotics); 2) PC, NC + 0.05% tylosin; 3) FC01, NC + 0.1% FC, and 4) FC02, NC + 0.2% FC. All diets were formulated to meet or exceed NRC (1998) recommendations for growing pigs. All the pigs were housed in an environmentally controlled room with a slatted plastic floor. Each pen was equipped with a 1-sided self-feeder and a nipple drinker, pigs were allowed ad libitum access to feed and water throughout the experimental period. Pigs fed the PC diet had a higher ($P < 0.05$) ADG than those fed the NC diet. No differences ($P > 0.05$) were observed in ADFI and G/f among dietary treatments throughout the experimental period. The apparent total tract digestibility (ATTD) of DM in PC treatment was higher ($P < 0.05$) than that in NC treatment. However, no difference ($P > 0.05$) was noted in the ATTD of N and energy among treatments. The concentrations of RBC, WBC, IgG, AST, ALT, and lymphocyte percentage were unaffected ($P > 0.05$) by dietary treatments. Fecal moisture content and fecal pH were also not affected ($P > 0.05$) by dietary supplementation with FC. In conclusion, the application of FC had no negative effects on growth performance, nutrient digestibility, and blood profiles in growing pigs, further studies should be conducted to confirm the growth promoting effect of FC in growing pigs.

Key Words: fermented chlorella, growing pigs, growth performance

W165 The efficacy of using the external marker LIPE to predict digestibility values in Nile tilapia (*Oreochromis niloticus*) fed contrasting diets.

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Measuring diet digestibility of formulate feeds is essential to determining which diets will maximize growth and feed conversion ratios (FCR). Inert dietary digestibility markers are one such method used to determine dry matter digestibility (DMD), organic matter digestibility (OMD), crude protein digestibility (CPD) and the digestibility of digestible energy (DDE) within diets. The main objective of this study was to determine whether the dietary marker LIPE can be successfully utilized as a digestibility marker in fish nutritional studies, by examining its efficacy in predicting digestibility values of juvenile Nile tilapia (*Oreochromis niloticus*) fed contrasting diets. Three treatment diets were formulated (low fat/low starch, high fat, high starch) each containing LIPE and chromic oxide at 0.1 g/kg and 1 g/kg respectively. Diets were randomly assigned to 12 tanks suitable for collection of feces via the Guelph method. Four replicates were used and each tank contained 15 juvenile tilapia. The experiment itself was a split-plot design with diets allocated to the main plots and method of assessing digestibility to the subplots. Data were analyzed using the MIXED model of SAS. Means analysis was used to assess the effect of diet, marker and diet × marker interaction on marker performance. LIPE® and chromic oxide were evaluated against actual values across all treatment groups using 2 statistical methods; linear regression and measures of deviation. Diet x marker interaction was found to be significant ($P \leq 0.05$) for DMD ($P = 0.02$), OMD ($P < 0.01$) and DDE ($P = 0.05$), but was not significant for CPD ($P = 0.06$). CPD was influenced by method ($P < 0.01$). Linear regression showed both LIPE® and chromic oxide predicted values to be weakly correlated with actual values for DMD, OMD, CPD and DDE. Measures of deviation analysis suggested both LIPE® and chromic oxide to overestimate DMD, OMD, CPD and DDE. It can be concluded that both LIPE and chromic oxide were poor markers of apparent energy and nutrient digestibility in juvenile Nile tilapia fed contrasting diets.

Key Words: feed formulation, Nile tilapia, marker performance

W166 Validation of the external marker Nanolipe as an indicator of apparent nutrient and energy digestibility in juvenile Nile Tilapia (*Oreochromis niloticus*).

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Nanolipe is a new, never before tested, external marker created for use in fish digestibility studies. Nanolipe was evaluated in juvenile Nile Tilapia (*Oreochromis niloticus*) against the traditional methodologies of total collection and titanium(III) oxide. The experiment was a split plot design with 3 contrasting diets (low fat/low starch, high fat, high starch) representing the main plots and 3 different marker methods (total collection, titanium(III) oxide, Nanolipe) representing the subplots, with 4 replicates. Twelve tanks were used, each containing 15 juvenile fish (35 ± 6.6 g). Feces were collected via the Guelph method. Dry matter, organic matter, crude protein and digestible energy digestibilities were assessed. Means analysis was used to assess the effect of diet, marker and diet × marker interaction on marker performance. Nanolipe and titanium(III) oxide were evaluated against actual values using 3 statistical methods; concordance correlation, linear regression and measures of deviation. Nanolipe was found to overestimate digestibility for all dietary components assessed in the low fat/ low starch and high fat diets, but underestimated digestibility for the high starch diet. Titanium(III) oxide was found to underestimate digestibility for all dietary components assessed in the low fat/low starch, high fat and high starch diets. Diet × marker interaction was found to be significant ($P > 0.05$) for both Nanolipe and titanium(III) oxide for all dietary components assessed in all of the low fat/ low starch, high fat and high starch diets. Both Nanolipe and titanium(III) oxide predicted values of estimate digestibility, for all dietary components, were poorly correlated with actual values by concordance correlation. Linear regression showed a significant correlation between Nanolipe and actual values for dry matter digestibility ($R^2 = 0.54$), but a poor correlation between Nanolipe and actual values for digestible organic matter ($R^2 = 0.37$), crude protein ($R^2 = 0.38$), and digestible energy ($R^2 = 0.17$). Measures of deviation analysis showed Nanolipe to over predict the digestibility of dry matter, organic matter, crude protein and digestible energy compared with actual values, while titanium(III) oxide consistently under predicted the digestibility of all dietary components assessed. It can be concluded that both Nanolipe and titanium(III) oxide were poor markers of apparent nutrient and energy digestibilities in feeds utilized by juvenile Nile tilapia. Further studies are evidently needed to understand the exact mechanisms of diet × marker interactions.

Key Words: diet composition, Nile tilapia, markers

W167 Total serum cholesterol and triglycerides concentrations in broilers fed with diets containing different sources of oil associated with conjugated linoleic acid (CLA). V. C. da Cruz*[1], R. F. de Oliveira[1], G. do Valle Polycarpo[2], V. B. Fascina[3], L. H. Zanetti[1], G. A. M. Pasquali[1], R. Crivellari[1], L. C. Carvalho[1], and C. C. do Valle Polycarpo[4], *[1]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil, [2]University of São Paulo, Pirassunga Campus, Pirassununga, São Paulo, Brazil, [3]São Paulo State University, Botucatu Campus, Botucatu, São Paulo, Brazil, [4]São Paulo State University, São José do Rio Preto Campus, São José do Rio Preto, São Paulo, Brazil.*

This study was carried out at São Paulo State University, Dracena Campus, Brazil, to evaluate total serum cholesterol and triglycerides concentrations of broilers at 21 and 42-d of age, fed with diets containing 2 levels of CLA (0.5% and 1.0%) associated to 3 oil sources (soybean oil, fish oil and linseed oil). A total of 840 1-d-old male Cobb chicks were distributed in a completely random design with 7 treatments and 4 replications. Broilers received the following treatments: T1- control diet without adding oils and CLA; T2- diet containing soybean oil associated to 0.5% CLA; T3- diet containing fish oil associated to 0.5% CLA; T4- diet containing linseed oil associated to 0.5% CLA; T5- diet containing soybean oil associated to 1.0% CLA; T6- diet containing fish oil associated to 1.0% CLA; T7- diet containing linseed oil associated to 1.0% CLA. At 21 and 42-d of age, 8 birds per treatment were killed for collection of 5 mL of blood through the wing brachial vein. No significant effects of treatments were observed for total serum cholesterol ($P > 0.05$) and triglycerides ($P > 0.05$) concentrations in the periods of 21 and 42 d of age. These results can be explained by the good nutritional quality of oil sources used in this research, which are rich in unsaturated and polyunsaturated fatty acids. The inclusion of CLA in the feeding of broilers seems to have influence on lipid metabolism, with positive effects or not, depending on the supplementation phase and the oil source used. In conclusion, the total serum cholesterol and triglycerides concentrations are not altered by CLA and by dietary lipid sources. The mechanisms of action of CLA about the metabolism of fats are not completely known; therefore further research related to cholesterol and triglyceride levels in broiler diets is needed.

Key Words: poultry, oil sources, serum lipids

W168 Effect of dietary oregano (*Origanum vulgare* L.) essential oil on growth performance of broiler chickens fed with diets of different metabolizable energy levels. **E. van Eerden[1], L. Star[1], P. van der Aar[1], and L. Z. Jin*[2],** *[1]Schothorst Feed Research, Lelystad, the Netherlands, [2]Meriden/Meritech Biotech, Guangzhou, China.*

This study was to investigate the effect of dietary oregano (*Origanum vulgare* L.) essential oil on body weight, feed conversion rate and mortality of broiler chickens fed with diets of the 4 different metabolizable energy levels. A total of 960 one-day-old male Ross 308 broiler chickens were divided into 8 treatments and each treatment had 6 replicates with 20 broilers each. The 8 treatments were arranged to 2 × 4 factorial trial design with supplementation of an oregano essential oil (Orego-Stim, Meriden, UK) at 2 levels (0 and 150 g per ton of feed) and 4 energy levels (standard, standard minus 0.33%, 0.66% and 1.0% fat). During the starter phase (d 0 to 15), all diets had the same energy level. The energy treatments were implemented in the grower phase (d 15 to 30) and the finisher phase (d 31 to 36). All parameters were evaluated by ANOVA using Genstat statistical software. Treatment means were compared by the least significant difference (LSD). The results demonstrated that the addition of oregano essential oil resulted in a significantly ($P < 0.05$) higher body weight gain and lower feed conversion ratio in the starter phase. Feed conversion ratio showed a significant effect of energy level ($P = 0.041$) and a near-significant trend of oregano essential oil ($P = 0.052$) in the grower phase. The lowest energy levels had the highest feed conversion ratios, whereas addition of oregano essential oil tended to result in a lower feed conversion ratio in the grower phase. In the overall production period the result showed that there is no significant differences of body weight gain, feed conversion ratio, final body weight, or mortality between the control group and the treatment group of broilers fed with ME-reduced diet supplemented with the oregano essential oil.

Key Words: oregano essential oil, broilers, energy level

W169 Growth performance, nutrient digestibility, and carcass traits of rabbits fed diets added with DDGS or hemicellulases and glucanases. H. Bernal Barragán*[1,4], J. E. Gallegos Balderas[1], M. A. Liñán González[1], C. A. Hernández Martínez[1], F. G. Ríos Rincón[2,4], M. A. Cerrillo Soto[3,4], N. C. Vásquez Aguilar[1], and A. S. Juárez Reyes[3,4], *[1]Universidad Autónoma de Nuevo León, Fac. de Agronomía, San Nicolás de los Garza, NL, México, [2]Universidad Autónoma de Sinaloa, Fac. de Medicina Veterinaria y Zootecnia, Culiacán, México, [3]Universidad Juárez del Estado de Durango, Durango, México, [4]Red Internacional de Nutrición y Alimentación en Rumiantes, México.*

A trial was conducted to evaluate the effect of 2 levels of DDGS (0 and 30%) and of enzymes hemicellulase+glucanase, (Hemicell, ChemGen, MD, USA; and Porzyme tp100, Danisco, Marlborough, UK), added either at 0 or 0.50 kg/ton of each enzyme, upon growth, nutrient digestibility and carcass traits of rabbits. Twenty-two 53-d old (initial BW = 1.178 kg) crossbred rabbits (California × New Zealand) of both sexes were individually allocated in cages, according to a 2 × 2 factorial arrangement of treatments, in a complete randomized design, with 5 or 6 replicates per treatment. Water and pelleted diets (17.4–18.5% CP, 16.9–25.4% NDF, 3.5–4.9% fat) based on alfalfa hay, grounded sorghum grain, soybean meal and a commercial vit+min mix, were fed ad libitum. During the third week, feces were quantitatively collected for determination of nutrient digestibility. After 28 d, rabbits were slaughtered and carcasses evaluated. There was an interaction ($P < 0.05$) for average daily gain (ADG), since enzymes caused an increase of ADG (26 to 32 g/d) in the diets with DDGS, but a reduction (from 31 to 25 g/d) in the DDGS-free diets. Feed intake and feed conversion rate were not influenced by main factors. No differences ($P > 0.05$) were detected in dry matter digestibility (avg. 71.6%), NDF (avg. 28.4%) and ADF (23.6%). However, enzyme increased lignin digestibility (15–19 percentage units) depending upon DDGS level of the diet (interaction $P < 0.05$). Protein digestibility was higher (74.8 vs. 70.5%; $P < 0.05$) with DDGS inclusion.

Carcass yield nor *Longissimus dorsi* were not different among treatments ($P > 0.05$). Enzyme addition to DDGS-free diets resulted in higher ($P < 0.05$) proportion of carcass forequarter (12.6%) compared with rabbits fed DDGS-diets (11.2%), but forequarter was similar (avg. 12.2%) in both enzyme-free diets (Interaction $P < 0.05$). Rabbits fed diets without DDGS or enzyme had less hindquarter (27.1% of carcass) than other diets (avg. 29.3%; Interaction $P < 0.05$). Results help to understand action mechanisms of hemicellulases and glucanases enzymes added to DDGS containing diets for growing rabbits.

Key Words: rabbits, DDGS, carcass traits

W170 Evaluation of n-3 fatty acid and probiotic supplementation on growth performance, nutrient digestibility, blood characteristics, relative organ weight, and breast meat characteristics in broilers. L. Yan,* S. M. Hong, and I. H. Kim, *Department of Animal Resource & Science, Cheonan, Choongnam, South Korea.*

A total of 720 1-d-old broilers were used in a 28 d experiment to determine the effects of n-3 fatty acid and probiotic supplementation on growth performance, blood characteristics, relative organ weight and breast meat characteristics. Birds were randomly allotted to 1 of 4 treatments in a 2 × 2 factorial arrangement with 2 levels of fish oil (0 or 3%) and probiotics (0 or 0.2%) (1.0×10^{10} viable spores/g of *Bacillus subtilis* endospores and 1.0×10^{9} viable spores/g of *Clostridium butyricum*). Each treatment was fed to 12 replications with 15 broilers per replication. Diets were isolysinic and isocaloric by manipulation of soybean meal and soy oil. In this study, supplementation of salmon oil did not affect ($P > 0.05$) the growth performance and nutrient digestibility throughout the experiment. Dietary probiotic supplementation increased ($P < 0.05$) the body weight gain, feed conversion and apparent total tract of DM digestibility. No difference was observed ($P > 0.05$) in the relative weight of liver, spleen, bursa and breast muscle to the body weight; however, abdominal fat was significantly reduced ($P < 0.05$) with the inclusion of salmon oil or probiotic supplementation. Broiler fed the probiotic supplemented diet had a lower ($P < 0.05$) cholesterol and triglyceride concentration than the non-probiotic diets, whereas the inclusion of salmon oil did not affect the cholesterol and triglyceride concentration. An interactive effect ($P < 0.05$) was observed on the cholesterol concentration. Furthermore, dietary supplementation of salmon oil led to a higher ($P < 0.05$) eicosapentaenoic acid (EPA), docosahexaenoic acid (DHA), total n-3 fatty acid, total polyunsaturated fatty acid but lower n-6:n-3 ratio. The inclusion of probiotics increased ($P < 0.05$) EPA concentration compared with non-probiotic supplemented diets. An interactive effect of probiotic and salmon oil was observed on the EPA concentration. In conclusion, dietary salmon oil supplementation could alter the fatty acid composition in breast muscle of broilers without affecting its growth performance. Dietary probiotics could increase the growth performance and affect the fatty acid concentration in breast muscle. A synergistic effect of salmon oil and probiotic could be observed on the fatty acid composition in broilers.

Key Words: broilers, n-3 fatty acid, probiotic

W171 Effects of YGF-251 extract supplementation on egg production, egg weight, egg quality, blood characteristics, and fecal noxious gas emission in laying hens. S. C. Kim,* S. Zhang, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choongnam, South Korea.*

A total of 288 46-week-old ISA-brown laying hens were used in a 6-week trial to evaluate the effects of YGF-251 extract supplementation on the egg production, egg weight, egg quality, blood characteristics, and fecal noxious gas emission. Hens were randomly assigned to 4 treatments with 6 replications (12 layers per replication) per treatment. Dietary treatments were: 1) CON, basal diet; 2) T1, CON + 0.05% YGF-251 extract; 3) T2, CON + 0.1% YGF-251 extract, and 4) T3, CON + 0.15% YGF-251 extract. YGF-251 extract consists of *Phlomis umbrosa* Turez, *Cynanchum wilfordii* Hemsl, *Zingiber officinale* Rosc., *Platycodi Radix* with 5% active ingredient. All diets were formulated to meet or exceed NRC (1994) recommendations for laying hens, protein levels and amino acid compositions were adjusted according to the compositions of YGF-251 at the expense of corn and soybean meal. All statistical analyses were conducted in accordance with a randomized complete block design, using the GLM procedures of SAS software package (1996). Overall, egg production in T3 treatment was higher ($P < 0.05$) than that in CON treatment. No differences ($P > 0.05$) were observed in eggshell color, gravity, shell strength, yolk height, yolk color, haugh unit, shell thickness among dietary treatments. Egg weight was unaffected ($P > 0.05$) by YGF-251 extract treatments. Total protein concentration in blood was higher ($P < 0.05$) in T1 treatment than those in CON and T3 treatments at 2 week. However, there were no differences ($P > 0.05$) in the concentrations of RBC, WBC, IgG, and lymphocyte percentage among dietary treatments throughout the experiment. Supplementation with YGF-251 extract in diets decreased ($P < 0.05$) fecal ammonia emission compared with CON treatment at 6 week. However, hydrogen sulfide, total mercaptans and acetic acid emission were not affected ($P > 0.05$) by dietary treatments. In conclusion, dietary supplementation with 0.15% YGF-251 extract could improve egg production, and decrease fecal ammonia emission in laying hens.

Key Words: egg quality, laying hens, YGF-251 extract

W172 Growth performance and carcass characteristics of Japanese quail fed different levels of zeolite. J. J. Portillo,* J. L. Bolado, A. Estrada-Angulo, B. I. Castro, D. Urías-Estrada, A. Aguilar-Hernandez, C. B. Castro-Tamayo, and F. G. Rios, *FMVZ-UAS, Culiacan, Sinaloa, Mexico.*

This study was conducted to determine the effect of dietary zeolite addition on productive performance of Japanese quail (Coturnix coturnix japonica) during the fattening phase. A total of 256 chicks (1 d of age; unsexed, BW 10.2 g) were allotted to 16 cages (16 quail/pen) in a completely randomized design. Four dietary treatments were based on an isoproteic (28% CP fed d 1 to 14, and 21.5% CP fed d 15 to 35) and isocaloric (2900 ME kcal/kg) basal diet composed of ground corn, soybean meal, soybean oil, sea salt, limestone, orthophosphate, methionine, lysine, Ca, P, vit + min premix. Zeolite was added to the basal diet at 0, 0.5, 1.0 or 1.5% to produce the 4 dietary treatments. After 35 d of feeding, quail were selected based on weight and dressing percentage, with 4 females and 4 males per treatment. ANOVA was performed for a model of completely randomized design with repeated measures for productive response variables, and additionally, slaughter weight was included as a covariate for analysis of carcass variables. Results suggest the inclusion of zeolite in finishing diets does not improve growth performance ($P > 0.50$), although the response changes with time of fattening ($P < 0.01$). Hot carcass weight (127 to 130 ± 2.15 g), dressing percentage (57.6 to 59.3 ± 0.45%) and liver weight per 100 g of quail BW (2.14 to 2.38 ± 0.10 g) were unaffected by the inclusion of dietary zeolite. These results suggest that zeolite supplementation up to 1.5% in fattening diets of quail does not improve growth performance or carcass responses.

Key Words: zeolite, *Coturnix coturnix japonica*, carcass

Nonruminant Nutrition: Management

W173 Appetite stimulants on diets of lactating sows. A. Rodríguez,* A. Pineda, E. Toledo, and A. Borbolla, *Department of Animal Production: Pigs, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, D.F. México City, México.*

This study evaluated the effect of appetite stimulating ingredients and feed additives on feed consumption and body condition of lactating sows and their litters. Forty-four sows (11 sows/treatment) were randomly assigned to 4 experimental treatments, using a randomized complete block design, with parity as the blocking factor. Four treatments were used in this study: C (control, basal diet for lactating sows), B (basal diet + 1 kg/ton of a phytogenic additive, containing essential oils of oregano, anis and citrus peels mixed with chicory), F (basal diet + 1 kg/ton of homeopathic additive containing natural active substances from plants of the poppy family, such as tetterwort, bloodroot, plume poppy, etc.), and P (basal diet + 5 kg/ton of animal plasma). Diets were fed ad libitum during lactation (22.9 ± 0.2 d). Feed consumption (FC), weight loss (WL) and backfat loss (BL) were measured in each sow. BL was measured at the last rib in the P2 point, upon entering the farrowing room and at weaning, using a Renco® ultrasound (Lean-Meater series 12, Minneapolis, MN, USA). WL was estimated by weighing each sow at entering the farrowing room and at weaning. Weight gain in litters was also evaluated. The resulting data were analyzed using the statistical program SPSS 17.0. There were no differences ($P > 0.05$) for any of the variables evaluated. The FC was similar for all treatments (C = 108.2 kg ± 6.76, B = 114.2 kg ± 5.93, F = 112.7 kg ± 5.93 kg and 112.4 ± P = 6.79). BL showed no differences ($P > 0.05$), among treatments; however, sows receiving both additives and animal plasma had a lower BL, compared with the control group (B = 1.3 mm ± 0.3, F = 1.6mm ± 0.34, P = 1.7 mm ± 0.27 and C = 2.5 mm ± 0.29, respectively). Similarly, the WL did not differ ($P > 0.05$) for any treatment; however, sows receiving the phitogenetic and homeopathic additives, lost the least weight (C = 22.6 ± 3.53 kg, B = 9.9kg ± 3.09, F = 14.9 kg ± 3.53, P = 19.1Kg ± 3.55). The initial weight of all litters was similar ($P > 0.05$) for all experimental groups (C = 18.6 ± 1.27 kg, B = 18.1 ± 1.11 kg, F = 16.4 kg ± 1.06, P = 18.1 kg ± 1.27); and no effect ($P > 0.05$), was observed in this parameter after weaning (C = 60.8 ± 5.16 kg, B = 55.5 ± 4.52 kg, F = 54.7 kg ± 4.52, P = 64.9 kg ± 5.18). These results indicate that under the rearing conditions used in this study, it is not necessary to use these appetite stimulants, although additional studies are needed.

Key Words: feed consumption additives, sows, litters

W174 Reproductive response of sows in lactation anoestrus to additional organic chromium intake and postweaned GnRH-A application. S. A. Félix[1], J. A. Romo[1], J. M. Romo[1,2], H. R. Güemez[1,2], and R. Barajas*[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Granja Porcina La Huerta, Culiacán, Sinaloa, México.*

Three hundred sixty-eight hybrid multi-parturient sows were utilized to determine the reproductive response of sows in lactation anoestrus to additional organic chromium intake and post weaned GnRH-A application. The study was performed from November 2010 to October 2011 in Culiacan, Sinaloa localized in the Northwest of Mexico. In agreement with a completely randomized experimental design with a 2 × 2 factorial arrangement, Sows were randomly assigned to one of 4 the treatments: 1) Feeding with a lactating corn-soybean meal based-diet, during period of lactation and first 7 d post weaning, and 1 mL-Injection of sterile saline solution 24 and 48 h post weaning (CTRL; n = 96); 2) Diet similar to control and application of 25 µg of GnRH-A at 24 and 48 h post weaning (GnRH-A; n = 84); 3) Diet similar to control plus 400 ppb of additional organic chromium supplementation during lactation time and 1 mL-Injection of sterile saline solution 24 and 48 h post weaning (Cr; n = 85); and 4) Diet similar to control plus 400 ppb of additional organic chromium supplementation during lactation time and application of 25 µg of GnRH-A at the 24 and 48 h post weaning (CrGnRH; n = 103). A GnRH-A x Cr interaction ($P < 0.01$) on interval weaning to estrus was observed, where Cr alone had not effect respect to CTRL, and GnRH-A application lengthened the interval weaning to estrus (5.1 vs. 4.5 d for GnRH and CTRL, respectively), however, when GnRH was applied joint with Cr supplementation (CrGnRH treatment), the length of the interval weaning to estrus was similar to observed in CTRL sows (4.5 vs. 4.4 d for CRTL and CrGnRH treatment, respectively). Treatments had not effect ($P > 0.10$) on the farrowing rate, litter size and the litter weight at the born time. We conclude that postweaned GnRH-A application lengthens the interval weaning to estrus, and the additional intake of organic chromium during lactation time appears to reduce the effect of GnRH-A application on the length of interval weaning to estrus in multi-parturient sows.

Key Words: sows, GnRH-A, reproductive response

W175 Feeding high fiber diet improves productive and reproductive performances of sows. A. Woldeghebriel,* M. Mama-Nodeli, T. Barios, and B. Pope, *North Carolina A&T State University, Greensboro.*

Sows (n = 36) in early gestation were used to determine the effects of feeding different sources of fiber and how these effects may relate to piglet performance. The experimental design employed 4 diets and 9 individually housed sows per diet. The sows were randomly assigned to 1 of 4 diets. Diets included a corn-soybean meal basal diet as the control (CON), and 3 antibiotic-free, high-fiber diets (D1, D2 and D3) each containing 5% sugar beet pulp plus one of the following: 1:2, 1:1, and 2:1 oat to barley ratios. Diets were formulated to contain similar amounts of protein (14% CP) and energy (3.145 Mcal DE/kg), but the fiber content of the CON diet was lower than the average of the high-fiber diets (8.38% vs. 22.40% NDF). All sows were fed the low-fiber diet for the first 84 d of gestation and randomly assigned to 1 of 4 diets for the next 30 d. This means that sows continued receiving either the low fiber (229 g of NDF/d) or high fiber (612 g of NDF/d) diets until farrowing. Each sow received 2.73 kg of feed per day during gestation and 2.73 kg 3 times per day during lactation. Sows were weighed initially, weekly during gestation, after farrowing and when piglets were weaned. Litter sizes and weights were also recorded at birth and weekly for up to 2 weeks post-weaning. Data collected were analyzed using SAS procedure where animals were considered random effects, and diet means were used to compare treatment effects. Results of the study indicated that average litter size at birth in high fiber-fed sows increased by 0.28 pig/sow/y. Litter growth rates were not affected by diet. However, average litter weights at birth and at weaning from high fiber-fed sows were 0.60 and 2.24 kg, respectively, being higher than in CON-fed sows. Average litter weight from high fiber-fed sows was also higher ($P < 0.05$) during the first week of lactation than during the second, but not the third week of lactation. In conclusion, results of the current study indicate that feeding sows with high fiber diet during the last 30 d of gestation had beneficial effects to both the litter and the sow itself.

Key Words: sow, lactation, dietary fiber

W176 Effects of dietary fat and protein quantity from different feedstuffs on litter gain. K. Koch*[1], L. Chu[2], K. Kalscheur[1], R. C. Bott[1], and R. C. Thaler[1], [1]*South Dakota State University, Brookings,* [2]*China Agricultural University, Beijing, China.*

A sow lactation study was performed to evaluate the effects of different quantities of fat and protein inclusion in lactation diets on litter gain and milk composition. Ninety-six sows and 3 dietary treatments were used in a complete randomized design. Sows used were of mixed parity (0–8), and litters were standardized within dietary treatment. Lactation length was standardized to 18 d. Treatments were low fat, high protein (LH, n = 32), comprised of corn and soybean meal; medium fat, low protein (ML, n = 31), comprised of corn and a co-extruded corn and soybean product; and high fat, high protein (HH, n = 33), comprised of corn, soybean meal and added soy oil. Fat quantities were provided at 2.51%, 5.30% and 8.96% of the diet (DM basis) in the low, medium, and high levels, respectively. Protein quantities were 19.36% and 20.50% of the diet (DM) for the LH and HH treatments and 12.14% of the diet (DM) for the ML treatment. Data were analyzed using PROC MIXED of SAS (SAS Inst. Inc., Cary, NC) with diet being a fixed effect. Litter gain was estimated by determining the difference of average litter weight at birth and at weaning, adjusted for the number of piglets. There was an effect on litter gain due to treatment ($P < 0.05$). Litter gain was approximately 4.61, 4.22 and 5.02 kg per piglet, for LH, ML, and HH, respectively. Upon weaning at d 18, 8 sows per treatment were randomly selected to determine if diet affected milk fat concentration. Sows selected had similar body condition scores (2.6 ± 0.1) at the start of the experiment. Milk fat concentration was 6.22 ± 0.51%, 6.70 ± 0.50% and 7.63 ± 0.12% for the LH, ML and HH treatments, respectively. Treatment had no effect on milk fat concentration ($P > 0.198$). Parity was included as a covariate and no effect was demonstrated on litter gain ($P > 0.195$) or milk fat ($P > 0.839$) concentration. Therefore, litter gain may be improved by elevated fat levels in lactation diets, when protein is provided at high level, but there is no effect on milk fat concentration.

Key Words: sow, lactation, fat

W177 The effects of blends of sensory functional ingredients on feed intake and growth in juvenile pigs during a food transition. C. Clouard[1], V. Noirot*[2], M. Champagnac[2], P. Etienne[2], D. Éclache[2], MC Meunier-Salaün[1], and D. Val-Laillet[1], [1]*INRA, UMR1079 SENAH, Saint Gilles, France,* [2]*Laboratoires Phodé, Terssac, France.*

When exposed to a novel diet during food transition, pigs often decrease spontaneously their feed intake, which can lead to impaired growth. The related experiment was conducted by the INRA team of UMR1079 SENAH (Saint Gilles, France). The objective was to identify blends of sensory functional ingredients based on aromatic active principles and plant extracts, formulated by Laboratoires Phodé (Terssac, France), that were likely to improve feed intake during food transitions. The spontaneous feed intake of 24 juvenile female pigs, housed in individual pens, was assessed during a food transition. After 9 d during which they were fed with a familiar starter diet, the pigs were divided into 3 experimental groups and fed with an unfamiliar grower diet added with either the N1 blend, the N3 blend, or without supplementation (control: C). The mean amount of food consumed and the mean body weight of the animals were compared between treatments using non-parametric Kruskal-Wallis tests. After the transition day, no difference in the mean feed intake and in the mean body weight per week was observed between the groups ($P > 0.05$). On d 10 (i.e., the transition day), compared with the consumption of the starter diet on d 9, the consumption of the C diet was 10.31% lower, while the consumption of the N3 diet was only 5.46% lower and the consumption of the N1 diet was 3.77% higher. However, the difference of consumption between d 9 and 10 was not significant ($P > 0.05$), due to high inter-individual variability. Albeit the adjunction of the functional ingredients in the novel diet did not increase feed intake or weight gain in these experimental conditions, N1 was likely to maintain a normal consumption the day of the food transition. Further investigations using an increased number of pigs would have counterbalanced the effects of individual variability and would have been likely to result in more significant results in terms of food intake and preferences.

Key Words: functional feed ingredients, pigs, food transition

W178 Effects of genotype and dietary oil supplementation in pigs. 1. Growth performance and carcass traits. T. M. Bertol*[1], J. V. Ludke[1], R. M. L. de Campos[2], N. N. Terra[3], E. A. P. de Figueiredo[1], A. Coldebella[1], and J. I. dos Santos Filho[1], [1]*Embrapa Suínos e Aves, Concórdia, SC, Brazil,* [2]*Fundação Universidade Federal do Vale do São Francisco, Petrolina, PE, Brazil,* [3]*Universidade Federal de Santa Maria, Santa Maria, RS, Brazil.*

A 42-d study was carried out to evaluate the effect of genotype (GEN): terminal sire line Duroc × F1 (DC×F1); terminal sire line Embrapa MS115 × F1 (MS115×F1); and MS115 × Moura (MS115×MO) and 3 dietary oils (DIET): 3% soybean oil (SBO); 3% canola oil (CAN); and 1.5% canola oil + 1.5% flax oil (CAN+FLX), on pig growth performance and carcass traits. Ninety animals (45 barrows and 45 gilts) averaging 130.7 ± 3 d of age were utilized, 15 barrows and 15 gilts of each GEN per diet. The ANOVA model included block (initial weight), sex, GEN, DIET and interactions of second and third order. Means were compared by protected *t*-test ($P < 0.05$). There was no DIET effect ($P > 0.05$) on growth performance and carcass traits. Final weight (FW), average daily gain (ADG) and daily feed intake (DFI) were higher ($P < 0.001$) in DCxF1, with the lowest values observed in the MS115×MO pigs (FW = 122.4 ± 0.85^a, 112.8 ± 1.38^b, 96.8 ± 1.30^c kg; ADG = 1.090 ± 0.018^a, 0.987 ± 0.019^b, 0.828 ± 0.015^c kg; DFI = 3.415 ± 0.053^a, 3.033 ± 0.056^b, 2.725 ± 0.059^c kg, for DC×F1, MS115×F1 and MS115×MO, respectively). Feed conversion ratio was higher ($P < 0.01$) in the MS115×MO pigs than in the other GEN. The highest ($P < 0.001$) hot carcass weight was found in the DC×F1 and the lowest in the MS115×MO pigs. The MS115×F1 pigs had the lowest ($P < 0.001$) backfat thickness (BF) and the MS115×MO showed the lowest ($P < 0.001$) loin depth (LD) (BF = 22.75 ± 0.71^a, 17.09 ± 0.63^c, 20.46 ± 0.86^b mm; LD = 62.04 ± 0.74^a, 63.35 ± 1.21^a, 54.52 ± 1.11^b mm). The GEN by DIET interaction was significant ($P < 0.05$) for carcass lean percentage (LP), with the highest ($P < 0.05$) LP provided by CAN diet in the DCxF1 pigs and by SBO DIET in the MS115×MO pigs, while no differences were observed ($P > 0.05$) among DIET in the MS115×F1 pigs. For the GEN effect within DIET, the MS115×F1 pigs showed higher ($P < 0.05$) LP than the other GEN, regardless the DIET. In conclusion, the type of oil did not influence growth but did affect carcass traits, depending upon genotype. DC×F1 pigs showed the best growth performance and MS115×MO the worst. The MS115×F1 GEN had the best carcass quality.

Key Words: canola oil, flax oil, soybean oil

W179 Improving feed efficiency in fattening pigs through sensorial stimulation.

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Interest in strategies to improve feed efficiency and prevent excessive fat deposition in fattening pigs is growing. We hypothesized that triggering sensory and gastrointestinal satiety through flavoring compounds may contribute to achieve such a goal by reducing over-consumption of feed without compromising animal growth. To test this hypothesis, an experiment was conducted in which a flavoring composition developed to induce satiety (SAT) was added into the diet of fattening pigs. One hundred and 44, mixed sex (50:50) pigs [Duroc × Landrace (sow line) × Pietrain (boar line); 49 ± 4.55 kg BW] were distributed into 48 pens (3 animals/pen) and 4 blocks of BW, and fed ad libitum either a control diet or the same diet treated with SAT (750 ppm) during the last 49 d before slaughter. Animals were individually weighed on d 0, 21, 35 and 49 and feed intake was recorded every week from d 0 to d 49. Data (BW, ADG, ADFI, GFR) were analyzed as a mixed-effect model with repeated measures in time in which pen was treated as a random effect and diet, block, sex and their interactions were considered fixed effects. Analyses were carried out using the MIXED procedure of SAS. No interactions ($P > 0.5$) were observed for any of the measured parameters. In addition, no differences were observed for BW($P > 0.7$) and ADG (745 vs. 746 g/d;$P > 0.8$) between treatments. The addition of SAT into the diet, however, reduced ($P < 0.02$) ADFI by 6% (2437 vs. 2287 g/d) resulting thereby in a 7% improvement ($P < 0.05$) in GFR (0.30 vs. 0.32). In conclusion, the inclusion of a satiety-inducing flavor in pig finishing diets improved feed efficiency through the reduction of feed intake without affecting body weight gain.

Key Words: efficiency, flavor, satiety

W180 Gene expression of myosin heavy chain isoforms and β-adrenergic receptors induced by ractopamine feeding duration in finishing pigs.

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Ractopamine (RAC) is fed to finishing pigs to increase muscle mass and decrease fat deposition, to improve feed efficiency and carcass value. To understand how RAC feeding induces skeletal muscle growth, 80 finishing barrows were used to evaluate the time-dependent effect of RAC feeding on myosin heavy chain (MyHC) isoforms (I, IIa, IIx and IIb), β1-adrenergic receptor (AR) and β2-AR mRNA abundance. Pigs were blocked by initial BW (69.42 ± 1.24 kg) and assigned randomly to 5 treatments, with 8 replicates per treatment and 2 pigs per pen. Dietary treatments consisted of corn and soybean meal diets containing no RAC (control) for 28 d and 10 mg/kg RAC for 7, 14, 21, or 28 d before slaughter. Longissimus muscle samples were collected immediately post-exsanguination, snap frozen in liquid nitrogen and stored at −80°C until processed for gene expression analysis. Total RNA was extracted and the mRNA expression was determined by quantitative real-time RT-PCR. Relative gene expression ratio was calculated with the Pfaffl's method, using 18S rRNA as reference gene. Statistical analyses were performed by ANOVA using the GLM procedure of SAS. Linear and quadratic responses were determined utilizing polynomial orthogonal contrasts. Although β1-AR mRNA abundance was not affected ($P > 0.05$) by RAC treatment, increasing RAC feeding duration tended to decrease β2-AR expression (1.39, 1.03, 0.83, 0.83, 0.62 ± 0.15; $P = 0.08$). Expression of MyHC I decreased linearly (1.81, 1.72, 1.53, 0.98, 0.94 ± 0.20; $P = 0.02$), whereas MyHC IIb mRNA expression increased linearly (0.32, 1.05, 1.20, 1.41, 1.79 ± 0.16; $P = 0.001$) as RAC feeding period increased. Conversely, transcript abundance of MHC IIa and IIx did not differ ($P > 0.05$) between treatments. These results suggest that RAC feeding alters the MyHC isoform gene expression profile, and that the responses might be mediated by β2-AR.

Key Words: β-adrenergic agonist, skeletal muscle growth, swine

W181 Influence of pellet size on pellet quality and performance and nutrient utilization of broilers.

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The importance of physical quality of pellets in improving growth is well recognized in the broiler industry. High conditioning temperatures during pelleting increase pellet quality, but decrease nutrient availability. This study tested whether manipulation of pellet diameter and length, at low conditioning temperature, would influence quality of pellets, and performance and nutrient utilization of broilers. total of 192, 10-d old birds were used in a 2 × 2 factorial arrangement to evaluate pellet diameter (3 or 4.76 mm) and pellet length (3 or 6 mm). Wheat-based grower (d 10 to 21) and finisher (d 22 to 42) broiler diets were formulated to meet Ross 308 strain recommendations. Diets were steam-conditioned at 60°C before pelleting. In grower and finisher diets, improvements in pellet durability index and pellet hardness with increasing pellet length were greater ($P < 0.05$) in pellets with 3-mm diameter than those with 4.76-mm. Increasing pellet length from 3 to 6 mm increased ($P < 0.05$) apparent ME value (3322 vs. 3288 kcal/kg DM). Neither main effects of pellet diameter and length nor the interaction were significant for ileal digestibility of nitrogen and starch. During the grower period, birds fed pellets of 6-mm length had greater weight gain ($P < 0.05$; 745 vs. 725 g/bird) and better feed conversion ($P < 0.05$, 1.427 vs. 1.446 feed/gain) than those fed 3-mm long pellets. Feed intake was unaffected. During the finisher phase and over the whole trial (d 10 to 42), neither the main effects nor the interaction were significant for weight gain and feed intake. Pellet length had no effect on feed conversion for 3-mm diameter pellets; however, increasing pellet length from 3 to 6 mm improved ($P < 0.05$) feed conversion at 4.76-mm pellet diameter (1.755 vs. 1.792 feed/gain, finisher phase; 1.675 vs. 1.706 feed/gain, whole trial). Overall, best pellet quality was achieved in 6 mm long and 3 mm diameter pellets, while best performance was in broilers fed 6-mm pellets that were 4.76 mm wide. When low conditioning temperatures are used to optimize nutrient availability, it seems a longer pellet is better, but choice of die size creates a trade-off between pellet quality and bird performance.

Key Words: broiler, pelleting, growth

Nonruminant Nutrition: Minerals and Vitamins

W182 Effects of increasing inclusion of supplemental magnesium oxide (MgO) on laying performance and eggshell quality in 72-week-old brown egg-laying hens. C. H. Kim, I. K. Paik, and D. Y. Kil,* *Department of Animal Science and Technology, Chung-Ang University, Anseong-si, Korea.*

In our previous experiment, increasing level of supplemental MgO in diets improved the eggshell quality in 46-week-old laying hens. However, such an effect has not been determined in aged laying hens that may encounter more problems in eggshell quality than young laying hens. The objective of this experiment, therefore, was to investigate the effect of increasing inclusion of supplemental MgO in diets on laying performance and eggshell quality in aged laying hens. A total of 640 Hy-Line Brown laying hens of 72 weeks of age were assigned to 1 of 4 dietary treatments with 4 replicates in a completely randomized design. Each replicate consisted of 40 hens raised in 2 hens per cage. The basal diet contained 0.16% Mg and 3 levels of 0.10, 0.15, and 0.20% MgO (60% Mg) were supplemented to the basal diet. All other nutrients and energy were included to meet or exceed NRC requirement estimates for laying hens. Laying performance was recorded daily and summarized for a 5-week feeding trial. Eggshell quality was measured in 20 eggs collected randomly from each replicate on the last day of each week during 5 weeks and the data were pooled. Results indicated that increasing inclusion of supplemental MgO increased (linear, $P < 0.05$) eggshell strength and decreased (linear and quadratic, $P < 0.01$) broken and shell-less egg production. However, there was no difference in eggshell thickness among treatments. Hunter lightness (L*) and redness (a*) values in eggshell decreased (linear, $P < 0.05$) as inclusion of supplemental MgO increased. Feed intake, feed conversion ratio, hen-day egg production, egg weight, egg yolk color, and Haugh unit were not affected by dietary treatments. The concentrations of Mg in eggshell increased (linear, $P < 0.01$) with inclusion of supplemental MgO, but those of Ca, P, and Fe in eggshell were not influenced by dietary treatments. In conclusion, inclusion of supplemental MgO improves eggshell strength and color with no effect on laying performance in aged laying hens.

Key Words: aged laying hens, eggshell quality, magnesium oxide

W183 Evaluating the impact of pre-weaning calcium and phosphorus supplementation on growth performance and carcass characteristics of low and high birth-weight pigs. P. L. Y. C. Chang*[1], C. H. Stahl[1,2], and E. van Heugten[1], [1]*Department of Animal Science, North Carolina State University, Raleigh,* [2]*Laboratory of Developmental Nutrition, North Carolina State University, Raleigh.*

Neonatal Ca and P deficiencies affect growth performance and the activity of the tissue-specific stem cells responsible for lifetime muscle and bone growth. This study evaluated the effect of direct oral supplementation of Ca and P to nursing pigs on growth performance and carcass characteristics. From commercial sows (n = 52), 2 light-weight pigs (LW, 1.52 ± 0.04 kg BW) and 2 heavy-weight piglets (HW, 2.14 ± 0.04 kg BW) were selected at d 3 of age. Within sow, 1 of the LW and 1 of the HW piglets were orally supplemented once daily with 2 mL of a $CaPO_4$ solution that provided 240 mg Ca and 182 mg P. The remaining LW and HW pig from each litter orally received 2 mL of a placebo. Pigs were weaned at 22.5 d of age and were randomly allotted to pens (3 to 5 pigs per pen) according to sex, supplementation, and birth weight. Pigs were fed 3 diet phases in the nursery (44 d) and 3 diet phases in the finisher (98 d). At the end of the study carcass characteristics were determined using ultrasound. Pigs in the HW group were heavier ($P < 0.001$) at weaning (6.3 vs. 4.7 kg), at the end of the nursery (29.1 vs. 23.7 kg), and at the end of the finisher (121.0 vs. 108.1 kg). Heavy birth weight pigs grew faster ($P < 0.01$; 518 vs. 430; 938 vs. 861; 808 vs. 728 g/d for nursery, finisher, and overall), consumed more feed (0.70 vs. 0.57; 2.44 vs. 2.20; 1.90 vs. 1.69 kg/d for nursery, finisher, and overall) and had greater ($P < 0.01$) loin eye area (19.5 vs. 17.7 cm^2) and daily lean gain (377 vs. 350 g/d). Pre-weaning supplementation with $CaPO_4$ did not affect ADG, ADFI, G/F or any of the carcass traits. In conclusion, increased birth weight of pigs greatly enhanced pig performance to market weight; however, pre-weaning supplementation with $CaPO_4$ did not improve performance of either LW or HW piglets. This work does not support the hypothesis that low birth weight pigs receive inadequate Ca and PO_4 nutrition during the nursing period.

Key Words: nursing pigs, pre-weaning nutrition, $CaPO_4$ supplementation

W184 Bone ash and strength traits of young pigs fed diets with no supplemental vitamin D were compromised within a four-week trial. L. A. Rortvedt,* D. K. Schneider, and T. D. Crenshaw, *University of Wisconsin-Madison, Madison.*

Last year we reported > 30% reduction in growth and whole body skeletal traits in pigs fed diets without supplemental vitamin D (D) during a 4-wk trial. Excess dietary Ca and P did not alleviate D responses. A method to detect kyphosis via DXA was reported, but individual bones were not assessed. The current objective was to evaluate the effect of diets on individual bone traits. In 2 trials (n = 72 ea) pigs were weaned (~3 wk) and fed diets with no supplemental D for 1 wk, then 1 of 8 diets (corn-SBM) for 4 wk. Treatments, arranged as a 2 × 2 × 2 factorial, included diets supplemented 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 (n = 24/trial) were euthanized, femurs and tenth ribs were excised. Femurs were scanned by DXA (GE Lunar Prodigy) to determine bone mineral content (BMC, g/bone) and density (BMD, g/cm^2), then subjected to a 4-point bending test to assess strength. Ribs were dried, de-fatted, and combusted (700°C) to determine ash. Femur BMC was reduced ($P < 0.01$) by > 50% in pigs fed -D vs +D, but responses depended on dietary Ca and P. Additional Ca and P increased femur BMC in pigs fed +D, but not -D ($P < 0.05$). Femur bending moments (BM) and rib ash (g and %) responded in similar patterns as femur BMC. Femurs from pigs fed +D vs -D had decreased ($P < 0.01$) strain, but responses did not depend on Ca or P. In conclusion, individual bone traits responded similarly to dietary D, Ca, and P as whole body DXA responses. Dramatic responses to dietary vitamin D within a 4 wk trial were not expected and may reflect carry-over effects of sow diets.

Table 1.

VitD, 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
Femur BMC, $g^{a, b, c, d, e}$	8.80	9.51	10.59	9.90	13.51	15.83	16.02	20.60	0.77
BM, kg-$cm^{a, b, c, d, e}$	235	306	354	360	410	567	571	809	39.9
Strain, cm/cm^{a}	0.240	0.249	0.193	0.240	0.156	0.140	0.140	0.120	0.026
Rib ash, $g^{a, b, c, d, e}$	1.010	0.958	1.088	0.999	1.445	1.710	1.842	2.251	0.091
Rib ash, $\%^{a, e}$	42.59	38.81	41.70	40.37	47.01	49.10	48.82	51.17	0.84

a. D, $P < 0.01$; b. Ca, $P < 0.05$; c. P, $P < 0.05$; d. D*Ca, $P < 0.05$; e. D*P, $P < 0.01$; f. D*Ca*P, $P < 0.05$.

Key Words: kyphosis, Ca, P

W185 Estimates of relative bioavailability of monocalcium and dicalcium phosphates based on whole body DXA scans to determine the efficiency of dietary P use by growing pigs.

P. T. Merkatoris,* L. A. Rortvedt, and T. D. Crenshaw, *University of Wisconsin, Madison.*

Monocalcium phosphate (MCP) is a less expensive source of P than dicalcium phosphate (DCP). However, the relative bioavailability of P between the 2 sources may not be equal. The current experiment was designed to access the relative bioavailability of P in MCP and DCP based on a slope-ratio assay using growth, femur ash, and calculations derived from dual energy x-ray absorptiometry (DXA, GE Lunar Prodigy) scans to determine mineral retention and efficiency. Crossbred barrows (n = 35) were fed standard diets until ~10 kg then randomly allotted within weight blocks to 1 of 7 treatments. Treatments included a basal, corn-SBM diet with no supplemental inorganic P (0.39% P) and 3 diets formulated to supply 0.05, 0.10, or 0.15% added P from either MCP or DCP. Pigs were individually housed and allowed continuous access to feed and water except for an overnight fast before DXA scans on d 0 and 20. Skeletal gain (gBMC) was calculated as the difference in d 20 and d 0 whole body bone mineral content (BMC, g) derived from DXA scans. Assuming a distribution of Ca (99%) and P (80%) in the whole body, Ca and P retentions were calculated assuming 38% Ca and 18% P in bone ash. Efficiency of Ca and P retention was calculated as the ratio of nutrient retained to nutrient consumed. Relative bioavailability of MCP vs DCP were based on the ratio of linear slope coefficients calculated for various criteria shown below. Criteria based on assessment of bone traits (femur BMC, gBMC, P efficiency) predicted 9 to 29% higher relative bioavailability for MCP than DCP. However, traits based on growth and feed consumption (ADG, FG ratio) predicted 5 to >35% higher bioavailability of P from DCP vs MCP. Reasons for a discrepancy in relative bioavailability estimates among criteria were not obvious.

Table 1.

Trait	Intercept	Basal	DCP	MCP	R^2	MCP/DCP
ADG	0.0379	0.1432	0.1341	0.1273	0.872	95.0
FG ratio	1.7442	−0.0190	−0.0541	−0.0340	0.090	62.8
gBMC	−1.8927	0.6943	1.3705	1.6362	0.734	119.4
P efficiency	0.0008	−0.0328	0.0529	0.0683	0.598	129.0
Femur BMC	3.2918	0.9628	1.7320	1.8849	0.751	108.8

Key Words: Ca retention, P retention, slope-ratio assay

W186 Effects of sulfur concentration in diets containing distillers dried grains with solubles on carcass characteristics and tissue mineral concentrations in growing-finishing pigs.

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The objective of this experiment was to determine if concentration of S in diets containing distillers dried grains with solubles (DDGS) affect carcass characteristics, loin quality, and tissue S, Se, and Cu concentrations in growing-finishing pigs. A total of 120 growing barrows (34.2 ± 2.3 kg BW) were allotted to 3 dietary treatments with 10 replicate pens and 4 pigs per pen in an 84-d experiment. The control diet was based on corn and soybean meal (0.14% S, 0.19 mg/kg Se, and 15.3 mg/kg Cu). The DDGS diet was formulated with corn, soybean meal, and 30% DDGS (0.16% S, 0.32 mg/kg Se, and 14.0 mg/kg Cu). The DDGS-S diet was similar to the DDGS diet, except that 1.10% CaSO4 (16.2% S) was added to this diet (0.37% S, 0.35 mg/kg Se, and 13.8 mg/kg Cu). Organ weights and loin quality, 24-h pH, drip loss, loin subjective color, marbling, and firmness did not differ among treatments, but loin redness (a*) was greater ($P < 0.05$) for pigs fed the control diet than for pigs fed the DDGS-S diet. Concentrations of S in hair, liver, heart, loin, and all other tissues did not differ among treatments, but urinary S concentration was greater ($P < 0.05$) for pigs fed the DDGS-S diet than for pigs fed the other diets. Pigs fed the DDGS diet or the DDGS-S diet had greater ($P < 0.01$) Se concentrations in hair, liver, heart, and loin than pigs fed the control diet, but liver concentrations of Cu did not differ among treatments. In conclusion, inclusion of 30% DDGS in diets fed to growing-finishing pigs does not influence carcass characteristics or tissue S concentrations regardless of S concentration in the diet, and excess dietary S is excreted in the urine. In contrast, because of the greater concentration of Se in DDGS compared with corn and soybean meal, tissue concentrations of Se are increased if DDGS is included in the diet. However, liver concentrations of Cu are not influenced by dietary DDGS.

Key Words: distillers dried grains with solubles, selenium, sulfur

Physiology and Endocrinology III

W187 Effects of ruminally digested and undigested snakeweed extracts on female Sprague-Dawley rats. R. A. Halalsheh,* D. M. Hallford, and T. T. Ross, *New Mexico State University, Las Cruces.*

Two studies were conducted to examine effects of snakeweed (SW) extracts (evaporate residues) on serum components and reproduction in female Sprague-Dawley rats. In Exp. 1, 36 rats at d 5 (d 1) of pregnancy were offered SW extracts (ethanol and hexane) at 20% and 30% of diet (25g/rat). In Exp. 2, 36 rats at d 5 (d 1) of pregnancy were offered ruminally digested SW extracted (ethanol and hexane) at 20% and 30% of diet (25g/rat). Each rat was assigned a non-SW control rat fed 5001 Rat Chow. Rats were fed for 10 d and BW was recorded on d 1 and 11. Blood samples were collected via heart puncture and rats were euthanized on d 11. Experimental design was completely random with split-plot when appropriate. In Exp. 1, rats consuming 20% ethanol SW extract (20% ESW) had decreased ($P < 0.05$) feed intake on d 1 to 3 and increased ($P < 0.05$) intake on d 10, while those fed the 20% hexane SW extract (20% HSW) had increased ($P < 0.05$) feed intake from d 6 through d 10 compared with control rats. Rats consuming 30% ESW resulted in decreased ($P < 0.05$) feed intake on d 1 to 3 and increased ($P < 0.05$) intake on d 8 to 10. Rats consuming 30% HSW decreased intake on d 1, 2, 3, and 5 and increased intake ($P < 0.05$) on d 7, 9, and 10 compared with controls. Rats consuming 20 and 30% HSW had increased ($P < 0.05$) aspartate and alanine aminotransferase concentrations. Blood urea nitrogen, albumin, and creatinine increased ($P < 0.05$) in treated rats compared with controls. In Exp. 2, rats consuming 20% ethanol extract of digested SW (20% EDSW), 20% hexane extract of digested SW (20% HDSW), and 30% ethanol extract of digested SW (30% EDSW) increased ($P < 0.05$) feed intake compared with controls and 30% HDSW decreased ($P < 0.05$) feed intake on d 1, 2, and 7. Alkaline phosphatase, BUN, globulin and creatinine increased ($P < 0.05$) in rats consuming SW extracts compared with controls. In exp 1 and 2, Serum P4 and number of pups were similar ($P > 0.05$) among treatments. Results indicate that SW, both ruminally digested and undigested may contain potential chemical compounds that cause a mild toxicity and ruminal digestion altered SW hepatotoxicity.

Key Words: snakeweed, Sprague-Dawley rats, toxicity

W188 Effect of niacin on heat shock protein gene expression in transformed bovine mammary epithelial cells. S. Rungruang,* J. L. Collier, and R. J. Collier, *University of Arizona, Tucson.*

Recent studies have indicated a niacin receptor, GPR109A, was differentially distributed in bovine liver, muscle, brain and fat tissues. Objectives of this study were to confirm presence of a niacin receptor in bovine tissues and to examine the effect of niacin on heat shock protein (HSP) gene expression in transformed bovine mammary epithelial cells (MAC-T). In this study,GPR109A was detected by agarose gel electrophoresis and quantified using quantitative real-time reverse transcription-PCR (q-PCR) in tissue samples from 3 cows. Tissues examined were mammary, uterine, ovary, liver, skin, cultured MAC-T and primary bovine mammary epithelial cells (BMEC). Ribosomal protein subunit 9 (RPS9) was used as the reference gene. The receptor was present in all tissues and cells. Expression of the gene for the receptor was highest in skin, the next highest was mammary ($P < 0.01$) and no difference was detected between liver, uterine and ovary receptor gene expression. The receptor in skin and mammary was 26.41 and 4.37-fold higher than liver, respectively ($P < 0.01$). The MAC-T were treated with niacin in different doses (0, 0.01, 0.1 and 1.0 mM) and 2 incubation times (0 and 4 h) at 37 C before incubation in 42 C for 8 h. The expression of genes for HSP27 and HSP70 were analyzed by q-PCR. The expression of HSP27 and 70 genes was increased during heat stress ($P < 0.01$). The data indicated niacin had a dose effect on HSP27 ($P < 0.03$) and HSP70 ($P < 0.02$) expression. The analysis also identified a quadratic relationship in HSP27 ($P < 0.01$), and linear relationship in HSP70 ($P < 0.01$) gene expression. MAC-T supplemented with 0.1 mM niacin had the highest HSP27 and 70 gene expression during heat stress when compared with 0 mM (11.45 vs −2.41-fold, $P < 0.02$ and 77.73 vs 5.26-fold, $P < 0.01$, respectively).Longer incubation times with niacin increased HSP expression ($P < 0.01$). However, we did not detect an interaction between incubation time, dose and temperature. These data indicated that niacin increases HSP gene expression in bovine cells during heat stress.

Key Words: heat shock protein, bovine mammary epithelial cells, heat stress

W189 Effects of betaine on heat induced heat shock protein expression in primary bovine mammary epithelial cells. Y. Xiao*[1,2], J. L. Collier[1], S. Rungruang[1], L. W. Hall[1], F. R. Dunshea[3], and R. J. Collier[1], *[1]University of Arizona, Tucson, [2]Huazhong Agricultural University, Wuhan, Hubei, China, [3]The University of Melbourne, Parkville, Vic., Australia.*

Betaine, an organic osmolyte, is accumulated by cells and stabilizes protein structure and cellular metabolism during physiological stress. Decreased induction of heat shock protein-70 (HSP70) gene expression and anti-apoptotic effects were found in betaine-treated mammalian cell lines (Madin-Darby canine kidney and mouse embryonic fibroblast cells) exposed to a hypertonic environment. To evaluate effects of betaine on heat-shocked bovine mammary epithelial cells (BMEC), we isolated primary BMEC from mammary gland tissue of a pregnant Holstein cow, seeded in collagen for 6 d of culture then determined gene expression of HSP70 and HSP27 in cells treated with 0 mM or 25 mM betaine in thermoneutral (TN, 37°C) and heat stress (HS, 42°C) conditions at 0, 2, 4 and 8 h, using quantitative real-time PCR (qRT-PCR). Hypoxanthine phosphoribosyltransferase served as the reference gene. A one-way ANOVA was conducted on ΔC_t value with the PROC MIXED procedure of SAS. The fold change was calculated by the $2^{-\Delta\Delta C_t}$ method. After 8 h of HS exposure, morphology in 0 mM betaine-treated BMEC indicated distinct cell degradation, which was absent in 25 mM betaine-treated BMEC. The qRT-PCR indicated that, in TN conditions, expression of HSP70 was significantly ($P < 0.01$) decreased in 25 mM betaine-treated cells compared with 0 mM at 2 h and 4 h, and expression of HSP27 decreased significantly ($P < 0.01$) as well at 8 h. In HS condition, HSP70 expression peaked at 2 h in 25 mM betaine-treated BMEC and at 4 h in 0 mM. The expression of HSP70 in BMEC in control media was decreased significantly at 8 h compared with betaine-treated cells (20.80 ± 6.19 *vs.* 57.18 ± 6.19 fold, $P < 0.01$). A continuous increase of HSP27 expression was evident in all HS groups from 0 h to 8 h. Higher expression levels of HSP27 were detected in 25 mM betaine-treated BMEC than 0 mM at 4 h (21.93 ± 2.16 *vs.* 12.93 ± 2.16 fold, $P < 0.01$) and 8 h (61.55 ± 2.64 vs. 33.40 ± 2.64 fold, $P < 0.05$). Collectively, data indicated that betaine had a protective effect in heat-shocked BMEC by increasing expression of heat shock proteins during heat stress.

Key Words: mammary epithelial cells, betaine, heat shock protein

W190 Cloning and responsiveness of bovine glucose-6-phosphatase promoter to cyclic AMP and glucocorticoids.

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Gluconeogenesis is an essential process in ruminants. Glucose-6-phosphatase (G6Pase) is a rate-limiting and final step in gluconeogenesis and catalyzes the release of glucose from liver. The objective of this experiment was to clone bovine G6Pase promoter and determine the effects of cyclic AMP (cAMP) and dexamethasone (DEX), on G6Pase promoter activity. Bovine genomic DNA was extracted from liver and used as a template to clone the promoter sequence. A region from −1012 to −17 bp relative to the transcription start site (TSS) and truncated sequences within this region, from −801 to −17 bp, −530 to −17 bp and −312 to −17 bp relative to the TSS were generated by PCR. Amplicons were sequenced and cloned into a eukaryotic expression vector (pGL-3 basic) and linked to a luciferase reporter gene. Each promoter-luciferase construct was transiently transfected into rat hepatoma (H4IIE) cells. Cells were treated with either a combination of 0.70 mM cAMP and 0.10 mM DEX or vehicle. Cells were harvested after 23 h and luciferase activity was determined in the cell homogenate. Basal luciferase activities for all 4 promoter sequences were not different from pGL-3 basic luciferase activity ($P > 0.05$). The activities of all G6Pase promoter sequences were induced ($P < 0.05$) with exposure to cAMP and DEX. The data demonstrate the direct role of cAMP and glucocorticoids in regulating bovine G6Pase expression through promoter activation. Furthermore, the data indicate responsiveness to cAMP and dexamethasone that is within the −312 to −17 bp region of the bovine G6Pase promoter.

Key Words: bovine glucose-6-phosphatase, promoter activity, cAMP and glucocorticoids

W191 Effects of heat stress on insulin production in β-TC-6 pancreatic cells.

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Heat stress (HS) decreases feed intake but inexplicably increases plasma insulin and the insulin response to a glucose tolerance test in a variety of animal models. Whether HS directly or indirectly (via an altered hormonal or metabolic profile) alters insulin synthesis/secretion is not known. We utilized murine β-TC-6 pancreatic cells to directly evaluate the effects of HS on glucose stimulated insulin secretion (GSIS). Cells were exposed to 1 of 2 environments: 1) HS (41°C) or 2) thermo-neutral (TN; 37°C). After 2 h of environmental exposure, cells were incubated with 1 of 4 glucose concentrations: 1) 0 mM, 2) 2.5 mM, 3) 5 mM, and 4) 10 mM; and further exposed to their respective temperatures for an additional 2 h. Both HS and TN cells had a similar ($P > 0.10$) maximal GSIS at 2.5 mM glucose. To study the temporal pattern of HS effects on GSIS, β-cells were exposed to HS or TN environments for 0, 2, 6, 12, 24, 48 h; and incubated with either 0 or 2.5 mM glucose. HS decreased ($P < 0.01$) insulin production with time. By 48 h, HS β-cells had a 75% decrease ($P < 0.01$) in GSIS compared with TN cells. Taken together, our results demonstrate that HS decreases insulin secretion in β-TC-6 pancreatic cells. These data suggest that additional mechanisms participate to increase plasma insulin parameters during in vivo HS. This work was supported by USDA NIFA grant #2011–67003–30007.

Key Words: heat stress, insulin, pancreas

W192 Relationship of single nucleotide polymorphisms of the bovine NOS2 and NOS3 genes with disease resistance in feedlot steers.

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Nitric oxide synthase activity is a key element in the inflammatory process initiated by bovine respiratory disease (BRD). Single nucleotide polymorphisms (SNP) in the promoter region of the endothelial nitric oxide synthase (NOS3) and inducible nitric oxide synthase (NOS2) genes may be related to the etiology of BRD, as well as, the damage and pathology that occurs in the lungs as a result of the inflammatory process associated with BRD. Therefore the objective of this study was to characterize SNP in the promoter region of the NOS3 and NOS2 genes and to determine the relationship of SNP to disease resistance in feedlot calves. Steers were randomly selected from ongoing trials conducted at the University of Arkansas Stocker and Receiving Cattle Research Unit. Health and performance records were used to identify sick (n = 12) and healthy (n = 12) animals. Animals were defined as sick if pulled from their pen for treatment of respiratory disease or suspected respiratory disease. Healthy animals were defined as animals randomly selected from the same pen as the selected sick animals which did not display health related or performance related problems during the feeding period. Upon arrival to the facility, animals were weighed (avg BW = 256.583 ± 16.5 kg) and blood was collected via jugular venipuncture. DNA (n = 24) was extracted from EDTA treated whole blood and SNP identified by sequencing a 5′ region approximately 700 bp upstream from the start of exon 1 for the NOS2 and NOS3 gene promoter region. Eight SNP, 2 deletions, and 1 insertion were observed for NOS3 and 1 SNP for NOS2. Chi-squared analyses did not reveal interactions between SNP and sick feedlot calves ($P \geq 0.12$), although the number of animals used in this study was limited. Additional research is needed to determine the relationship of SNP of the bovine NOS2 and NOS3 genes with disease resistance.

Key Words: nitric oxide, single nucleotide polymorphism, bovine respiratory disease

W193 Hypothalamic and abomasal mRNA expression of regulatory feed intake genes in cows grazing different herbage allowances of native pastures.

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In extensive rangeland cow-calf systems, annual variability of herbage allowance affects cow energy balance through changes in feed intake. There is scarce information about gene expression of key factors involved in the central and peripheral regulation of energy intake. Thus, the aim of this study was to evaluate the effect of 2 different herbage allowances of native pastures on hypothalamic (NPY, AgRP, POMC, CCK A receptor) and abomasal (ghrelin, CCK) mRNA expression. Pure and crossbred adult beef cows were used in a complete randomized block design and were maintained in the same herbage allowance throughout the year (2.5 vs. 4 kgDM/kgBW; LO vs. HI; n = 8, n = 5 respectively) since May 2007. Cows used in this study gestated and lactated one calf every year from 2007 to 2009. At the end of the third year, all cows were slaughter at 190 ± 15 d postpartum. Samples of hypothalamus and abomasum were collected to measure gene expression by SYBR-Green real time PCR using *RSP9* and β-actin as endogenous control genes. Data were analyzed using a mixed model that include the effect of herbage allowance as a fixed effect and cow genotype as a random effect. Means were considered to differ when $P < 0.05$. Expression of NPY and POMC mRNA did not differ due to herbage allowance. However, hypothalamic expression of AgRP mRNA tended ($P = 0.077$) to be less in HI than LO cows (0.84 vs. 2.3 ± 0.48) and CCK A receptor mRNA was numerically ($P = 0.157$) greater in HI than LO cows (1.91 vs. 1.31 ± 0.26). Herbage allowance did neither affect abomasal expression of CCK mRNA nor ghrelin mRNA expression. Results suggest that rangeland beef cows are sensitive to different nutritional planes and may respond by changing the expression of genes that regulate feed intake in hypothalamus.

Key Words: nutrition, feed intake regulation, mRNA

W194 Identification of short-chain fatty acid (SCFA) receptor transcripts in ruminal papillae and responses to SCFA infusion.

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Large quantities of short-chain fatty acids (SCFA) are produced by microbial fermentation in the rumen, but little is known about the mechanisms underlying their regulatory effects in cattle. Recent studies identified SCFA, including acetate, propionate, and butyrate as ligands for G protein-coupled receptor 41 (GPR41) and 43 (GPR43); lactate as a ligand for GPR81; and β-hydroxybutyrate and possibly butyrate as the ligand(s) for GPR109A. The objective of this study was to evaluate the effects of SCFA infusions on the transcript abundance of GPR41, GPR43, GPR81, and GPR109A in ruminal papillae. Six ruminally cannulated lactating Holstein cows were randomly assigned to treatment sequence in replicated 3 × 3 Latin squares and fed a standard lactation diet. Initially, cows were infused with 10 mol/d sodium acetate, sodium propionate, or sodium butyrate for 2 d. However, during period (P) 1, both DMI and calculated energy intake were decreased by infusions ($P < 0.01$) relative to pre-treatment. Therefore, infusion rates were decreased to 5 mol/d for P 2 and P 3. Ruminal papillae were collected immediately after each infusion period, and the mRNA abundance of the GPRs were determined by quantitative RT-PCR relative to the internal control gene RPS9. Data were analyzed using the REML procedure of JMP. Results showed that GPR41, GPR43, GPR81 and GPR109A genes are expressed in ruminal papillae in dairy cows. Transcript abundance of GPR41, GPR43 and GPR109A were not altered by SCFA infusion types or rates ($P > 0.10$), but GPR81 expression was increased by 1.9 ± 0.28 fold ($P = 0.01$) following the 10 mol/d SCFA infusion rate compared with the 5 mol/d infusion (across infusates). Abundance of these transcripts were not correlated with DMI or total energy intake ($P > 0.10$). Interestingly, GPR41 mRNA was positively correlated with GPR43 ($P < 0.001$, $r^2 = 0.71$) and GPR81 ($P < 0.001$, $r^2 = 0.59$), and GPR43 was positively correlated with GPR81 ($P < 0.001$, $r^2 = 0.96$). This study verified the expression of these SCFA receptors in ruminal papillae and indicated possible co-regulation of gene expression across several GPRs. Further research is needed to examine the roles of these GPRs in mediating the regulatory effects of SCFA on rumen function in dairy cows.

Key Words: G protein coupled receptors, rumen, volatile fatty acid

W195 Calibration of a dynamic, mechanistic model of amino acid and insulin effects on protein synthesis in animal tissues to represent liver and skeletal muscle.

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The objective of the present study was to calibrate a dynamic, mechanistic model of nutritional control of protein synthesis in animal tissues to represent liver and muscle, respectively. The model predicts the fractional synthesis rate (FSR) of protein based on mass action kinetics of translation initiation and elongation, and insulin- and amino acid-mediated regulation of the concentration of bound eukaryotic initiation factor-4E (c4eBp) and the recycling of eukaryotic initiation factor 2 (UF2d, F2d→F2t). Sensitivities of model predictions to 50% changes in each of 16 kinetic parameters were determined. Exponents in the initiation equation and the first-order rate constant for elongation had the greatest effect on tissue FSR and UF2d, F2d→F2t. The steady-state value of c4eBp was highly sensitive to all 5 parameters of factor-4E association and dissociation and lacked sensitivity to any of the other parameters. The strategy for calibration of the model to liver and muscle data was to fit the top 5 parameters to which c4eBp was most sensitive first, followed by fits of the top 5 parameters to which FSR was most sensitive. More than 99% of this error was attributed to random disturbance, indicating a lack of either slope or mean bias. Mean square prediction errors for c4eBp and FSR in liver were 32.9 and 5.0% of their observed means, respectively, with 56 and 99% of the respective errors attributed to random disturbance. Bias in c4eBp prediction was attributed to technical errors in its measurement and did not affect the accuracy or precision of FSR prediction. Sensitivity analysis and accuracy testing suggested that modification of the model structure was not required. Two unique sets of parameters were obtained to describe protein synthesis in liver and muscle in terms of the regulation of c4eBp by insulin and leucine, and of UF2d, F2d→F2t by uncharged tRNA.

Key Words: mechanistic model, amino acid, insulin

W196 Expression of adiponectin and leptin receptors and angiopoietin-like protein 4 (ANGLP4) mRNA differed in the of pure and crossbred beef cows grazing different herbage allowances of native pastures.

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Leptin, adiponectin, and ANGLP4 play important roles in energy expenditure, insulin sensitivity, glucose homeostasis, and lipid metabolism but information in ruminants is scarce. Therefore, the objective of this study was to evaluate the effect of the herbage allowance of native pastures and cow genotype, on hepatic expression of receptors of leptin (LEPRb), adiponectin (ADIPOR1 and ADIPOR2) and insulin (INSR), and ANGLP4 mRNA. Adult cows (n = 24) in a factorial arrangement of herbage allowances (2.5 vs. 4 kgDM/kgBW in average throughout the year; LO vs. HI) and cow genotype (purebred: Aberdeen Angus and Hereford vs. their F1 crossbred; PB vs. CB) were used in a complete randomized block design. Cows were maintained in the herbage allowance treatment since May 2007 and gestated and lactated one calf every year from 2007 to 2009. At the end of the third year, cows were slaughter at 190 ± 15 d postpartum and liver samples were collected to measure gene expression by SYBR-Green real time PCR using hypoxanthine phosphoribosyltransferase and β-actin as endogenous control genes. Data were analyzed using a mixed model and means were considered to differ when $P < 0.05$. Cow body weight and body condition score were greater in HI than LO cows and in CB than PB cows through the gestation-lactation cycle. At slaughter, hepatic ADIPOR2 and INSR mRNA did not differ among groups but ADIPOR1 mRNA tended ($P = 0.09$) to be greater and ANGLP4 mRNA was greater in CB than PB cows (1.21 vs. 1.62 ± 0.26 and 0.54 vs. 1.05 ± 0.27, respectively) and these differences were mainly due to cows in low herbage allowance. In addition, expression of LEPRb mRNA was affected by the interaction between herbage allowance and cow genotype, as its expression was highest in HI-PB, lowest in HI-CB and LO-CB, and intermediate in LO-PB cows (3.58, 1.58, 0.73, and 0.77 ± 0.21, for HI-PB, LO-PB, HI-CR, and LO-CB, respectively). Hepatic LEPRb, ADIPOR1 and ANGLP4 mRNA could play a role in adaptation mechanisms to changes in energy balance through the production cycle of beef cows in rangeland conditions.

Key Words: adipokines, hepatic gene expression, beef cattle

W197 Gene expression analysis of glutathione peroxidase, catalase, and superoxide dismutase (Mn) in white blood cells from dairy cows receiving an apple base nutraceutic supplement. L. E. Escobedo-Morales, J. A. Grado-Ahuir,* C. Rodríguez-Muela, P. Hernández-Briano, and R. M. Villaseñor-González, *Facultad de Zootecnia y Ecología, Universidad Autónoma de Chihuahua, Chihuahua, Chihuahua, México.*

This work was carried out to analyze the gene expression of antioxidant enzymes in white blood cells of cows under a nutraceutical diet based on apple pomace. We studied 8 Holstein cows at fresh stage that were randomly assigned to one of 2 experimental groups, control (T) and supplemented with a nutraceutical feed (M), being both diets isolaloric. Blood samples were obtained from the caudal vein every 14 d for 2 mo. Ribonucleic acid from white blood cells was isolated and real time RT-PCR reactions were performed to measure expression levels of genes coding for superoxide dismutase (SOD2), catalase (CAT) and glutathione peroxidase (GPX) relative to Glyceraldehyde 3-phosphate dehydrogenase (GAPDH). Data were analyzed under a mixed model including treatment, period and their interaction as fixed effects and cow as a random effect. Expression level for CAT and SOD2 genes were higher ($P < 0.05$) in M than in T cows (1.40 and 1.43 times, respectively). There were no difference between groups ($P = 0.4893$) for the enzyme GPX. According to our results, it appears to be a relationship among the antioxidant effects of apple pomace with increased mRNA levels of 2 antioxidant enzymes CAT and SOD2 (mitochondrial), which may explain at the genetic level the synergy of its components to achieve the reduction of reactive oxygen species in dairy cows.

Table 1. Overall fold change in gene expression (least squares means ± standard errors) of genes for antioxidant enzymes

Gene	Apple pomace	Control
Catalase	2.17 ± 0.16^{a}	1.55 ± 0.16^{b}
Glutathione peroxidase	6.26 ± 0.43^{a}	5.83 ± 0.43^{a}
Superoxide dismutase 2	2.72 ± 0.19^{a}	1.90 ± 0.19^{b}

^{a,b}Means with the same letter within a row are statistically similar (P < 0.05).

Key Words: apple pomace, antioxidant enzymes, dairy cows

W198 Measurements of saliva secretion and salivary fluxes of metabolites from jugular–arterial concentration differences, hemoglobin concentration, and jugular blood flow. A. C. Storm*[1], M. Larsen[1], and N. B. Kristensen[1,2], [1]*Aarhus University, Department of Animal Science, Tjele, Denmark,* [2]*Syddanskkvæg, Vojens, Denmark.*

The objective was to assess saliva secretion in lactating dairy cows during resting and rumination by measuring blood flow in right and left jugular vein and the concentration difference of hemoglobin in arterial and jugular blood. Three lactating dairy cows were surgically implanted with permanent catheter inserted into *A. intercostales dorsales* with the tip of the catheter placed in *Aorta*. On sampling days, temporary catheters were inserted 20 cm into *V. auricularis intermedialis* or *V. auricularis lateralis*, for infusion of the blood flow marker *p*-aminohippuric acid (11.17 ± 0.44 mmol/h), initiated 1 h before first blood sampling. Temporary catheters were also placed in the right and left *V. jugularis externa* for sampling of blood. Simultaneous blood samples from the artery and jugular veins were obtained during resting and rumination in 2 subsequent periods. For rumination and resting activity 2–4 and 2–3 repeated samples, respectively, were obtained with 5–10 min frequency. Cows were feed a 50:50 forages to concentrate diet. The difference between periods were dietary Na and K, (period 1 Na = 1.23, K = 1.41; period 2 Na = 0.37, K = 2.81% DM). Means within resting and rumination periods for each cow were analyzed statistically by a mixed model including main effect of activity (rumination and resting), period, and their interaction, considering cow as a random effect. The summed jugular blood flow, saliva secretion, and salivary flux of HCO_3^-, urea, and P were higher during rumination as compared with rest (Table 1), and were not affected by dietary Na or K. In conclusion, the current method for measuring saliva secretion produced reasonable estimates for secretion of selected metabolites in saliva.

Table 1. Jugular blood flow, salivary flow, and salivary flux of P, urea, and bicarbonate in lactating dairy cows during resting and rumination periods

Item	Rest	Rumination	SEM[1]	ACT[2]	Period
Jug. blood flow, L/h	199	430	22.7	<0.001	0.76
Saliva flow, L/h	7.4	13.6	0.77	<0.001	0.14
HCO_3^- salivary flux, mmol/h	870	1879	72	<0.001	0.07
P salivary flux, mmol/h	81	126	8.7	0.003	0.99
Urea salivary flux, mmol/h	22.7	37.8	3.17	0.011	0.13

[1]n = 3.

[2]ACT = rest or rumination.

Key Words: saliva secretion, flux

W199 Is colostrum quality in dairy cows related to postpartum health, production, or fertility? A. R. Dresch*[1], A. H. Souza[1], P. D. Carvalho[1], L. M. Vieira[1,2], J. L. M. Vasconcelos[3], R. A. Cerri[4], M. C. Wiltbank[1], and R. D. Shaver[1], [1]*University of Wisconsin-Madison, Madison,* [2]*University of Sao Paulo-VRA, SP, Brazil,* [3]*Sao Paulo State University Botucatu, SP, Brazil,* [4]*University of British Columbia, BC, Canada.*

Two studies were performed to investigate the relationship between colostrum quality and postpartum health, production and fertility in Holstein cows. In Experiment 1, colostrum samples were from 66 cows housed in a WI tie-stall barn. The DMI and milk yield measurements were daily and milk samples were collected from both AM/PM milkings twice weekly for determination of milk composition from calving to 70DIM. In Experiment 2, colostrum samples (n = 989) were from 2 commercial free-stall/parlor herds in WI. Colostrum was collected from the 1st milking and frozen for later quality analysis (Brix refractometer, 0 to 53% scale). Only cows with at least 3 weeks of dry period were used in the analysis. Data were analyzed using Proc Mixed and Proc Glimmix of SAS. Viscosity (r = 0.75, $P < 0.01$) and color (r = 0.46, $P < 0.01$) were highly correlated to Brix readings. Interestingly, there was no difference ($P > 0.10$) in proportion of primiparous (85%, n = 353) or multiparous (87%, n = 636) cows with Brix > 22%, that was considered to be good quality colostrum. In Experiment 1, cows with lower colostrum quality (LC, n = 18) were not different from cows with greater colostrum quality (GC, n = 48) for DMI, milk yield, fat%, or MUN. In contrast, LC cows tended ($P = 0.07$) to have greater linear SCC score in the first 5 weeks postpartum, with reduced milk protein content (2.9% vs 2.7%; $P < 0.01$) through 70DIM. In Experiment 2, although cows having retained placenta tended ($P = 0.07$) to have lower colostrum quality, but the logistic regression model indicated that cows with LC had similar %RP than GC, respectively (7% vs 4%, $P = 0.13$). In addition, LC cows were more likely to have postpartum metritis (13% vs. 7%, $P = 0.02$). Despite some significant associations between colostrum quality and RP and/or metritis, conception rate to 1st postpartum AI was not related to colostrum quality (LC = 33.8%, n = 133 vs GC = 34.2%, n = 856; $P = 0.90$). In conclusion, measurement of colostrum quality at calving was associated with some important production and health parameters postpartum; whereas, fertility following 1st postpartum AI was independent of colostrum quality. Supported by USDA Grant 2010–85122–20612.

Key Words: colostrum quality, postpartum health, dairy cow

W200 Effect of 17β-estradiol on cGMP-PK1 expression in myometrial longitudinal muscles.

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The characteristics of spontaneous longitudinal myometrial contractility change due to direct actions of 17β-estradiol (ES) and nitric oxide (NO). NO inhibits the contractility of smooth muscles via guanylate cyclase (GC) where activated GC increases cGMP-PK1 expression and relaxes smooth muscles. Previous studies from our laboratories suggested that ES could inhibit the NO effect in myometrial longitudinal muscle via altering cGMP-PK1 expression. Thus, the aim of this study was to evaluate the effect of injecting different doses and time intervals of 17β-estradiol on cGMP-PK1 expression on myometrial longitudinal muscles of ovariectomized rats. Three to 6 mo old female Sprague Dawley rats (n = 71) were used in the current study. The ovariectomized rats (270 ± 20 g) were randomly assigned to one control (Ov) and 3 17β-estradiol injected groups of 18 rats each. Rats in the Ov group received daily sesame oil (0.2 mL, IM), whereas each rats in the 3 17β-estradiol injected groups were treated with daily 25, 50 and 100 µg estradiol in sesame oil (IM), respectively. Each group was further divided in 3 subgroups: 6 rats in each group were sacrificed by cervical dislocation at 18, 90 and 162 h. Uterus samples removed immediately after sacrifice for immunohistochemical evaluation (streptavidin-biotin-peroxidase method) to determine cGMP-PK1 expression in longitudinal muscles. For statistical evaluation of the data, one-way ANOVA was used. In myometrial longitudinal muscles, cGMP-PK1 scores (expression levels as mean ± SD) at 18, 90 and 162 h for Ov, 25, 50 and 100 µg estradiol groups were 7.33 ± 0.10, 7.41 ± 0.08, 7.00 ± 0.44, and 7.75 ± 0.11 ($P = 0.21$); 6.58 ± 0.53, 6.75 ± 0.11, 7.33 ± 0.27, and 6.50 ± 0.00 ($P = 0.24$); and 7.08 ± 0.08, 6.00 ± 0.89, 7.25 ± 0.11, and 6.16 ± 0.73 ($P = 0.34$), respectively. Our results indicated that effects of estrogen on cGMP-PK1 expression in uterine longitudinal smooth muscles were minimal. Thus, our data suggested that 17β-estradiol did not show its effect through cGMP-PK1 in uterine longitudinal muscles.

Key Words: ovariectomized rats, cGMP-PK1, estradiol

W201 Expression of sex steroid receptors in placental tissues during early pregnancy in sheep.

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Vascularization of the placenta during early pregnancy is critical for the successful establishment of pregnancy and also supports normal fetal growth and development. Sex steroids and their receptors are important regulators of angiogenesis and growth in reproductive tissues, including the placenta. However, little is known about the expression of sex steroid receptors in placental tissues during early pregnancy. To examine mRNA expression of sex steroid receptors, we collected maternal (caruncular, CAR) and fetal (fetal membranes, FM) placental tissues on d14, 16, 18, 20, 22, 24, 26, 28, and 30 of early pregnancy (n = 5–6/day) and on d9–11 after estrus (nonpregnant [NP] controls; n = 5). Placental tissues were snap-frozen, RNA was extracted, and mRNA expression was evaluated using quantitative, real-time PCR. For both CAR and FM, nuclear progesterone receptor (P4R) mRNA was greatest ($P < 0.03$) in NP controls and through d22 of early pregnancy then declined and remained low on d24–30. For CAR, nuclear estrogen receptor (ER) α mRNA was greatest ($P < 0.01$) in NP controls and on d14 but declined on d18 of early pregnancy and remained low thereafter; for FM nuclear ERalpha was greatest ($P < 0.02$) on d20 of early pregnancy. For CAR, nuclear ERbeta mRNA was greater ($P < 0.01$) in NP controls than on any day of early pregnancy; for FM it did not change ($P = 0.33$) across days of early pregnancy. For CAR, membrane P4Ralpha and β were greatest ($P < 0.01$–0.07) in NP controls compared with any day of early pregnancy, whereas membrane P4Rgamma was 2- to 8-fold greater ($P < 0.01$) on d18 and 22 compared with NP controls or any other day of early pregnancy. For FM, membrane P4Ralpha, β, and gamma were elevated ($P < 0.01$–0.10) on d18 or 20 compared with NP controls or other days of early pregnancy. Thus, sex steroid receptors showed distinct patterns of expression in placental tissues during early pregnancy in ewes. These data establish the normal pattern of sex steroid receptor mRNA expression in maternal (CAR) and fetal (FM) placental tissues during early pregnancy, thus providing a basis for understanding the mechanisms by which sex steroids regulate placental growth and vascular development in normal and compromised pregnancies. Supported by USDA-NRI grant 2007–01215 to LPR and ATGB.

Key Words: placental angiogenesis, early pregnancy, sex steroid receptors

W202 Carryover effects on progesterone concentrations and fetal numbers in ewes given human chorionic gonadotropin.

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Administration of hCG will increase serum progesterone (P4) and potentially increase number of lambs born. The objective of this study was to determine if a carryover effect of previous hCG administration would alter serum P4 concentrations and increase fetal number in ewes in subsequent years. A single dose of hCG was administered on d 4 post mating with the purpose to increase serum P4 concentrations in ewes and increase number of lambs born. Mixed aged Suffolk ewes (n = 40) received an intravaginal P4-containing insert (CIDR; 0.3 g P4) for 10 d to synchronize estrus. Ewes were mated with fertile rams on the first estrus after CIDR removal and were assigned to 1 of 3 treatments. Ewes that were treated with hCG (600 IU; i.m.) 1 year prior were divided into 2 groups; hCG/hCG and hCG/NO hCG. The hCG/hCG group received hCG (600 IU- i.m.) on d 4 post mating. Ewes that received hCG the year prior and were in the hCG/NO hCG group did not receive hCG and were administered a saline i.m. injection. Control ewes received saline both years. Jugular blood samples were taken from 7 ewes of each treatment group starting on d 1 through 21 d post mating to monitor serum P4. Ovulation rates were determined via laparoscopy on d 44. On approximately d 70, flank ultrasound was used to establish fetal numbers. A treatment x day interaction was observed for serum P4. Ewes in hCG/hCG group had greater ($P < 0.05$) P4 concentrations beginning on d 8 through d 15 than hCG/NO hCG and control treated ewes; whereas, treatments hCG/ NO hCG and controls had similar ($P > 0.05$) serum P4 concentrations. Ovulation rates, CL number ($P > 0.33$)

and fetal numbers ($P > 0.62$) did not differ among treatment groups. In conclusion, administration of hCG in subsequent years does not produce carryover effects allowing multiple year administrations of hCG.

Key Words: human chorionic gonadotropin, progesterone, fetal numbers

W203 Serum testosterone concentrations after feeding in rams treated with GnRH.

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Circulating testosterone (T) is highly variable due to alterations in testicular T production, driven by pulses of luteinizing hormone, and alterations in T metabolism, primarily in the liver. In this study we attempted to develop an experiment to better understand the pattern of T release in male ruminants treated or not with GnRH and after feeding. The hypotheses for this study were: 1) circulating T will rapidly increase in rams following an LH pulse induced by exogenous GnRH treatment, 2) circulating T will decrease following feeding. Eight pubertal Santa Inês rams, weighing 56.6 kg on average, were used in a crossover design to test the first hypothesis and to provide initial observations related to the second hypothesis. Jugular blood samples were collected just before i.v. treatments that were performed 3 times a day (7:00, 11:00, and 15:00 h) with saline (Control group, n = 8) or GnRH (50 µg Gonadorelin, Fertagyl, MSD Saúde Animal; GnRH group, n = 8) and 30, 60, and 120 min after treatments. Rams were fed 1 h after the first i.v. treatment. Serum T concentrations were measured by radioimmunoassay. Data were analyzed using a generalized linear mixed model, considering the first-order heterogeneous autoregressive covariance matrix, due to repeated measures on the same ram at different hours. The model included the fixed effects of treatments, time of blood collection (hour) and treatment × hour interaction. Period and error were included as random effects. There was an effect of treatment ($P < 0.001$), hour ($P = 0.0123$) and treatment by hour interaction ($P < 0.001$). After the first GnRH treatment, T concentrations increased by 30 min with peak concentrations attained by 2 h after GnRH (8.8 ± 1.3 and 2.3 ± 1.3 ng/mL, GnRH vs. Control respectively; $P = 0.004$). There were also increased T concentrations after the second (0.5, 1, and 2 h) and third (1 and 2 h) GnRH treatments, although the peak T concentrations were lower compared with the first GnRH treatment. In the Control group, there was an apparent decrease in circulating T at 3 h after feeding with a subsequent increase in circulating T at 7 h after feeding. Thus, the first hypothesis on GnRH-induced LH pulses driving testicular T production was supported and future studies are needed to validly test whether time of feeding regulates circulating T, possibly through increased T metabolism. Supported by MSD Saúde Animal, FAPESP and CNPq of Brazil.

Key Words: sheep, testosterone, GnRH

W204 The potential effects of dietary nitrate on pregnancy mechanisms in ewes.

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Subacute levels of dietary nitrate have been implicated in embryonic loss, abortion and infertility in ruminants. Previous studies have not shown differences in the levels of progesterone or the number of lambs born to nitrate treated ewes compared with control ewes when nitrate was administered for 2 estrus cycles before breeding. However, nitrate toxicity is highly variable in sheep, and tolerance to such toxicity has been observed especially in cases of subacute, chronic exposure. Therefore, we hypothesize that chronic exposure to subacute levels of dietary nitrate may alter pregnancy mechanisms not observed with short-term exposures. Purebred Suffolk ewes (n = 24) were randomly assigned to one of 2 treatment groups, 0 mg/kg KNO_3 /BW (control) or 175 mg/kg KNO_3/ BW (nitrate treated) for 26 d. Ewes were weighed weekly and levels of KNO_3 adjusted according to BW. Ewes were synchronized, monitored for heat, administered KNO_3 for 2 full cycles, and mated to one of 2 intact rams. Ewes were bled daily for 26 d post breeding, then weekly until parturition. Blood was analyzed for progesterone (d 12–14, 50 and 80), *ISG15* and *MX2* mRNA (d 12–14) and circulating levels of PSBP (d 50 and 80). Progesterone levels did not differ in nitrate treated ewes compared with controls on d 12–14 ($P > 0.30$), d 50 ($P = 0.51$) or d 80 ($P = 0.92$) of pregnancy. Message for *MX2* did not differ on d 12 and 13 ($P = 0.24$) but tended to be upregulated (2.6 FC, $P = 0.07$) on d 14 of gestation in nitrate treated ewes compared with controls. Message for *ISG15* tended to be decreased on d 12 (2.3 FC, $P = 0.09$) and 13 (1.6 FC, $P = 0.13$) and upregulated on d 14 (3.8 FC, $P = 0.09$) of gestation in nitrate -treated compared with control ewes. Levels of PSPB in blood tended to be upregulated (1.6 FC, $P = 0.10$) on d 50 but did not differ between control and nitrate treated ewes on d 80 of pregnancy($P = 0.24$). Results imply that although no effects of dietary nitrate were observed immediately following short-term treatment, there may be chronic effects of nitrate in the diet of sheep which may impair the ewe's ability to maintain pregnancy. Perhaps ISG15 and MX2 play some role in protecting pregnancy against this challenge.

Key Words: nitrate, ISG15, MX2

W205 Effects of intravenous glucose infusion and nutritional balance on expression of enzymes responsible for catabolism of progesterone in cattle.

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The objective of this study was to evaluate the effects of glucose infusion and energy balance on serum concentrations of glucose, insulin, IGF-1, progesterone (P4), as well as mRNA expression of hepatic GHR1A, IGF-1, CYP2C and CYP3A in nonlactating, ovariectomized cows inserted with an intravaginal device P4 (CIDR). Fifteen Gir × Holstein cows were stratified by BW and BCS on d −28 of the study, and randomly assigned to: 1) negative nutrient balance (NB) and 2) positive nutrient balance (PB). Cows assigned to PB were supplemented individually once a day. From d −28 to −15 of the study, cows received a previously used CIDR, which was replaced by a new CIDR on d −14 and remained until the end of the study (d 1). On d 0, cows within nutritional treatment were removed from pastures and randomly assigned to receive, in a crossover design containing 2 periods of 24 h each (d 0 and 1): 1) intravenous glucose infusion (GLUC; 0.5 g of glucose/kg of BW, over a 3 h period), or 2) intravenous saline infusion (SAL; 0.9% NaCl, over a 3 h period). Cows were fasted for 12 h before infusions, and remained fasted during infusion and sample collections. Blood samples were collected at −12 (beginning of fasting), 0 (before infusion), 3 and 6 h after beginning of infusions via the coccygeal vein. Liver biopsies were performed at 0 and 3 h relative to beginning of infusions. Compared with PB cows, NB cows lost ($P < 0.05$) more BW (−23.1 vs. 16.5 kg) and BCS (−0.20 vs. 0.07). Cows receiving GLUC had greater glucose ($P < 0.01$) concentrations at 3 h relative to infusion compared with SAL cohorts (148.04 vs. 65.5 mg/dL). Cows receiving GLUC infusion had greater ($P < 0.05$) insulin concentrations compared with cows receiving SAL at 3 h, although this glucose-stimulated increase in insulin was greater in NB compared with PB cows (nutritional status x infusion x h interaction; 136.71 vs. 51.3 µUI/mL; $P < 0.01$). In PB cows, glucose infusion reduced the expression of GHR1A and CYP3A, but did not impact serum P4 concentration. In NB cows, glucose infusion increased expression of GHR1A and CYP3A and decreased serum P4 concentration. In conclusion, the effects of glucose infusion on serum insulin, P4, GHR1A and CYP3A mRNA expression were dependent on the cow nutritional status.

Key Words: insulin, CYP3A, progesterone

W206 Ex vivo model for endotoxic laminitis in ruminants. S. Schaumberger,* N. Reisinger, and G. Schatzmayr, *Biomin Research Center, Tulln, Austria.*

It is well known that laminitis in ruminants has a multifactorial etiology. As a key factor feeding of increased fermentable carbohydrate has been identified. If animals are not adapted to these rations, this may lead to rumen acidosis. Coincident with the change in the rumen pH is the release of endotoxin from gram-negative bacteria. An enhanced absorption of bacteria, endotoxin, lactic acid and histamine through the rumen, leads to a direct or indirect disruption in the micro-circulation of the corium and later to the lesions observed in laminitis. Objective of our ex vivo study was to get a better understanding of the direct influence of endotoxins on the lamellar structure of the claw and the separation from the coffin bone. Four normal claws were collected from the slaughter housed. Claw explants consisted of 2 mm of the inner claw wall, 6 intact epidermal lamellae and 2 mm of connective tissue. Explants were cultured with 1 mL culture medium and in 0.9% sodium chloride solution at 37°C and 5% CO2. After 24 and 48 h, explants were studied for lamellar separation. In a second experiment, explants were cultured with different concentrations (200 to 5 µg/mL) of lipopolysaccharides (LPS) from *Escherichia coli* O55:B5 for 24 and 48 h. Explants cultured only in medium were used as a negative control, and those cultured in 0.9% sodium chloride solution as a positive control. After incubation explants were tested for their integrity. Viability was tested with the water soluble tetrazolium (WST)—1 assay. Explants were considered as viable if absorbance of the medium containing 1% WST reagent increased after 2 h of incubation. All explants cultured only in medium for 24 and 48 h remained intact, and all cultured in 0.9% sodium chloride solution separated. Down to 20 µg LPS/mL 100% of the explants seperated. From 10 µg to 5 µg LPS/mL, separation of 33% and 66% of the explants could be detected. Explants still were viable after 24 and 48 h of incubation. Endotoxins of *E. coli* showed a concentration dependent lamellar separation in claw explants. This model may be used to investigate substances which affect the development of bovine laminitis. Further experiments will be carried out to investigate supernatants and explants for their cytokine activity to explain the inflammation process induced by LPS.

Key Words: ruminants, laminitis, endotoxin

W207 Effect of different centrifugation protocols and comparison of four extenders for storage of cooled Caspian horse spermatozoa for 48 hours. H. Nouri[1], A. Towhidi*[1], and M. Bahreini[2], *[1]Department of Animal Science, Faculty College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran, [2]Animal Breeding Center of Iran (A.I. lab), Iran.*

The use of cooled transported equine semen continues to gain popularity among breeders as its acceptance increases among breed registries. Two experiments were conducted to evaluate the impact of 4 extenders and different centrifugation protocols on cooled preservation of Caspian horse semen. In experiment 1, extenders tested included EZ-mixin (Minitube, Germany), Kenney's (Minitube, Germany), INRA96 (IMV, France), and CPE (Caspian horse extender). Semen was collected from 4 adult Caspian horse with artificial vagina and each ejaculate was divided and extended in each of the aforementioned extenders and stored at 4ËšC. Motility measures were determined using computer-assisted sperm analysis at 0, 24, and 48, hours after collection. Samples were evaluated for total motility, progressive motility (PM), straight-line velocity, curvilinear velocity, straight-line distance. Total motility and PM decreased over time in storage ($P < 0.05$). Sperm stored in INRA 96, and CPE retained the most total motility and PM over the 48-h period ($P < 0.05$). CPE had the highest measurements for curvilinear velocity, straight line velocity, and curvilinear distance ($P < 0.05$). In experiment 2: The objectives of this experiment were to determine the effects of centrifugation on Caspian horse sperm progressive motility, viability, and plasma membrane integrity. Ejaculates from 4 Caspian horses were collected, extended (CPE) to a concentration of 50×10^6 cells/mL, and subjected for 4 and 7 min to: 1) no centrifugation (NC); 2) $500 \times g$ (500); 3) $1000 \times g$ (1000); and 4) $2000 \times g$ (2000). Before and after centrifugation (d 0), and after 24 and 48 h of cooling, sperm motility was assessed by computer assisted semen analysis, and samples were stained with Eozin negrosin for viability, and with Hypo-osmolarity swelling test (Host) for membrane integrity. Compared with the other treatment groups the 2000 treatment group showed reduced motility, viability, and membrane integrity ($P < 0.05$). The 500 and 1000 treatment groups centrifugation of semen Compared with uncentrifuged samples resulted in a better sperm quality after chilled storage. The 500 and 1000 treatment groups yielded lower recovery rates than the 2000 treatment group ($P < 0.05$). Centrifugation at $1000 \times g$ for 7 min did not damage Caspian horse sperm.

Key Words: Caspian horse, centrifuge, extenders

W208 Pigs fed camelina meal increases liver CYP8B1 expression. W. J. Meadus*[1], P. Duff[1], T. McDonald[2], and W. Caine[1], *[1]AAFC-Lacombe, Lacombe, AB, Canada, [2]Olds College, Olds, AB, Canada.*

Camelina, also known as false flax, has commercial potential, as an oil seed crop for biofuels and biolubricants grown on marginal lands. Camelina seed has an oil content of >40% and this oil is high in n-3 fatty acids and γ-tocopherol. The oil is not approved for human consumption because as a member of the mustard family (Brassicaceae) and is suspected to contain high levels of erucic acid (C22:1 n-9) and glucoinolates. Camelina meal is the by-product after the oil has been extracted. Pigs (n = 26) were fed 3.7% and 7.4% camelina meal for 20 d starting at weights of 12 kg and finished at 17kg. The livers of the pigs were obtained at slaughter and immediately extracted for total RNA. Total RNA was examined for gene expression changes by microarray analysis using the Rat drug metabolism: phase 1 array and the Human Drug Metabolism: phase 2 enzyme arrays, of SAbioscience. Expression analysis (ΔCt ref-sample) on the rat array identified the cytochrome P450 family 8b1 (Cyp8b1) and aldehyde dehydrogenase 2 (Aldh2); and on the human array, glutathione S-transferase mu 5 (GSTM5), and thiosulfate sulfurtransferase (TST), as being significantly upregulated, relative to the control livers. The porcine version of Cyp8b1 was cloned and confirmed, for significant ($P < 0.05$) upregulation of ~4-fold, by real-time PCR. The Cyp8b1 is associated with hyocholic bile acid formation. The camelina meal must be inducing bile acid formation, possibly due to erucic acids.

Key Words: camelina, gene expression, Cyp8b1

W209 Effect of exogenous testosterone on testes characteristics of large white pigs in a humid enviroment.

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A total of 24 pigs were used for the experiment to determine the effect of exogenous testosterone (testosterone enanthate) administered by intramuscular injection on testicular characteristics especially daily sperm production (DSP). Pigs were treated once weekly from birth until 24 weeks of age with vehicle or testosterone enanthate. Testosterone enanthate was given at the rate of 1.2mg/kg body weight. Corn oil was used as the vehicle. At the end of the 24 weeks, the pigs were slaughtered and their testes harvested. The parameters measured include seminiferous tubule diameter, paired testes weight (PTW), testis density, daily sperm production (DSP) from gonadal sperm reserves (GSR) and DSP from quantitative testicular histology (QTH). Data obtained were analyzed using Complete randomized design (one-way ANOVA) of Statistic Analytical System (SAS) package 2001. The results show that testosterone enanthate significantly ($P < 0.05$) increased the values of DSP from QTH (18.12 ± 3.00; 35.28 ± 4.11). The same trend was recorded for Seminiferous tubule diameter (117.73 ± 9.10µ and 148.29 ± 8.70µ respectively for control and testosterone). This present results show that exogenous administration of testosterone to large white male pigs, could be used to accelerate spermatogenesis and thus reproductive efficiency in swine herds especially for boars.

Table 1. Testicular characteristics of boars administered testosterone enanthate

Testicular characteristics	Control (blank injection)	Testosterone enanthate
Paired testes weight-PTW g	101.46^{b}	220.43^{a}
PTW per kg bodyweight	3.27^{b}	3.93^{a}
Testes density	1.10	1.06
DSP from GSR (x109)	4.37^{b}	8.56^{a}
DSP from QTH (x106)	18.12^{b}	35.28^{a}
Seminiferous tubule diameter (µ)	117.73^{b}	148.29^{a}
DSP per unit tubule diameter	28.12^{b}	50.16^{a}
Volume % of round spermatid nuclei	1.74^{b}	3.78^{a}

^{abc}Means in the same row with different superscripts differ significantly ($P < 0.05$).

Key Words: exogenous, testosterone, testes

W210 Effect of heat stress on phosphatidylinositol-3 kinase signaling in gilt ovaries.

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Heat stress (HS) negatively affects reproductive performance in swine, but the biological reasons responsible for this impaired fecundity are poorly understood. Paradoxically HS decreases feed intake but unexplainably increases plasma insulin in a variety of animal models including pigs. Insulin influences ovarian phosphatidylinositol-3 kinase (PI3K) signaling, which is important for follicle viability and regulating follicle activation and steroidogenesis. Two downstream mediators of PI3K action are Protein kinase B subunit 1 (*Akt1*), and the forkhead transcription factor subunit 3a (*Foxo3a*). This study investigated the effects of HS on PI3K signaling in the porcine ovary. Crossbred gilts (35 ± 4 kg) housed in constant climate controlled rooms in individual pens with ad libitum feed intake were exposed to thermal neutral (TN) conditions (20°C; 35–50% humidity; n = 3–6) or HS conditions (35°C; 20–35% humidity; n = 3–6) for 7 or 35 d to simulate acute and chronic HS, respectively. Gilts were euthanized, one ovary was stored at −80°C and the other ovary was fixed in 4% paraformaldehyde. Total RNA was isolated and levels of *Akt1* and *Foxo3a* mRNA were quantified by RT-PCR using *GAPDH*, as the internal control gene. The insulin receptor (IR) and phosphorylated (active) AKT (pAKT) proteins were localized by immunofluorescence staining. On d 7, HS decreased (12-fold; $P < 0.05$) mRNA encoding *Akt1*, but environment had no effect on *Foxo3a* mRNA abundance. After 35 d and relative to TN controls, HS increased ($P < 0.05$) *Akt1* (2.0-fold) and *Foxo3a* (2.1-fold) mRNA. Oocyte cytoplasm and cytoplasmic membrane of all stage follicles stained positive for the IR protein. pAKT protein was located in the oocyte cytoplasm of all stage follicles, with apparent greater expression in larger stage follicles. Additionally, theca and granulosa cells of preovulatory follicles were positive for pAKT protein. These data suggest HS leads to altered expression of PI3K signaling pathway members, which could alter dynamics of follicle activation, affect follicle viability and potentially alter ovarian steroid synthesis, thus leading to negative effects on fertility in swine.

Key Words: heat stress/hyperthermia, reproductive physiology, swine/porcine/pig

W211 Acute duration heat stress alters expression of cellular bioenergetic-associated genes in skeletal muscle of growing pigs.

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Heat stress (HS) causes significant losses to the US swine industry in several production and health areas including efficient lean tissue accretion. Perturbations in skeletal muscle metabolism may participate in this defect. The study objectives were to examine the expression of genes related to cellular bioenergetics in skeletal muscle of piglets subjected to thermal stress in utero and/or during postnatal life. To accomplish this, 48 offspring from 14 first parity gilts were prenatally exposed to 1 of 4 environmental treatments (TNTN, TNHS, HSTN, or HSHS). TNTN and HSHS sows were exposed to thermal neutral (TN, cyclical 18–22°C) or HS conditions (cyclical 28–34°C) for all of gestation, respectively. HSTN and TNHS treatments represent sows heat-stressed for the first or second half of gestation, respectively. At 12 weeks of age, offspring were exposed to one of 2 postnatal thermal environments for 24 h: constant TN (21°C) or HS (35°C). Gestational treatments were randomized across postnatal treatments, with each sow represented equally between the 2 postnatal treatments. Pigs were sacrificed after the 24-h TN or HS treatment and longissimus dorsi skeletal muscle samples collected for total RNA isolation. Real-time PCR was used to measure gene expression of pyruvate dehydrogenase kinase 4 (PDK4), hexokinase 2 (HK2), peroxisome proliferative activated receptor, gamma, coactivator 1 α (PGC-1α), mitochondrial transcription factor A (TFAM), succinate dehydrogenase complex (SDHA), cytochrome C oxidase (Cox5B), and Cytochrome *b* (Cyt B). Data was normalized using eukaryotic translation elongation factor 1 α 1 (EEF1A1) as a control gene and analyzed by the Proc Mixed procedure in SAS. Data analyses did not indicate interactions between gestational and postnatal treatments for the genes studied. Only Cyt B gene expression was altered by gestational HS exposure with HSHS increasing expression up to 2-fold over TNHS, HSTN and TNTN ($P < 0.01$). Neither in utero nor postnatal HS altered Cox5B or PGC-1α mRNA abundance. Postnatal HS significantly increased HK2 by 25%

($P < 0.05$) and tended to increase PDK4 8-fold ($P = 0.076$). In contrast, TFAM, SDHA, and Cyt B gene expression decreased significantly during postnatal HS ($P < 0.05$). These data indicate that acute postnatal HS alters skeletal muscle bioenergetic gene expression, which may favor enhanced glycolysis and a reduction in mitochondrial respiration. This work was supported by USDA NIFA grant #2011–67003–30007.

Key Words: heat stress, skeletal muscle, metabolism

W212 Effect of heat stress (HS) on thermal regulation during pregnancy in first parity sows.

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First parity sows suffer from seasonal infertility that is associated with HS. The objective was to test the effects of HS during gestation and assess carryover effects after farrowing in first parity sows. Nulliparous gilts (n = 23) were brought into environmental chambers, inseminated and assigned to one of 4 ambient temperature treatments [TRT; HS (28 to 34°C; relative humidity, RH 80 to 55%) or TN (18 to 22°C; RH 70 to 60%)] that were applied for either the entire gestation [HSHS (n = 4) and TNTN (n = 4)] or for the first (wk 2 to 8) or second (wk 9 to 15) half of gestation [TNHS (n = 4) or HSTN (n = 4)]. There were 3 HSTN and 4 TNHS gilts that were not pregnant after insemination. Rectal, ear and shoulder temperatures (RT, ET, and ST) and respiration rate [RR; breaths per minute (BPM)] were collected twice daily (0900 and 1500h). There was an effect of wk on RT because, regardless of TRT, the RT decreased ($P < 0.001$) in pregnant sows (38.5 ± 0.1 to 38.3 ± 0.1°C; wk 2 to 15). The decrease in RT was not observed in non-pregnant sows (38.4 ± 0.1 to 38.6 ± 0.1°C; wk 2 to 15). There was a TRT by wk interaction for RT because the effects of HS (HSHS, HSTN, TNHS, and TNTN, respectively) were greatest during early gestation (38.4 ± 0.1, 38.5 ± 0.1, 38.2 ± 0.1, 38.3 ± 0.1°C for wk 5), were less in mid-gestation (38.3 ± 0.1, 38.2 ± 0.1, 38.2 ± 0.1, and 38.3 ± 0.1 for wk 10) and increased in late gestation (38.4 ± 0.1, 38.2 ± 0.1, 38.3 ± 0.1, and 38.2 ± 0.1 for wk 15). Effects of HS on RR were greatest during late gestation (53 ± 3, 28 ± 3, 81 ± 3, and 23 ± 3 BPM for wk 15). Changes in ET and ST ($P < 0.001$) were associated with changes in room temperature. Sows moved to a farrowing room (22°C) during the last wk of gestation. The RT, ET, and ST (respectively) increased ($P < 0.001$; 38.3 ± 0.1 to 39.5 ± 0.1°C, 33.1 ± 0.2 to 36.6 ± 0.2°C, 32.1 ± 0.2 to 35.5 ± 0.2°C; d −5 to d 10) after farrowing (during lactation) but there were no carry-over effects of TRT. In summary, sows decreased RT during gestation. The ET, ST, and RR responded to HS. Changes in RT in response to HS were small during gestation. Lactation under non-HS conditions (22°C) was associated with large changes with RT, ET, and ST. This project was supported by USDA NIFA 2011–67003–30007.

Key Words: sow, heat stress

W213 Hair cortisol concentrations—Influence of color and location in Holstein cows.

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Cortisol is often used to measure stress. A change in blood cortisol after exposure to a stressor gives an estimate of an acute stress response. However, the episodic daily fluctuations make blood measures of cortisol unsuitable for measuring chronic stress. Cortisol levels within milk or feces reflect circulating levels of cortisol over a longer period than a single blood sample, but still is less than ideal for assessing chronic stress. Recent research in humans and wildlife has shown significant correlations between hair cortisol levels and ill health. Our objective was to determine the potential of extracting and measuring cortisol in hair from cattle and whether its location and color influence cortisol concentrations. We measured the level of cortisol in black and white hair of Holstein cows (n = 18). Cows had both black and white hair shaved from the shoulder, top line and hip; white hair was also harvested from the tip of the tail. The hair samples were cleaned of dirt and dander, washed in water then with isopropanol, dried and then ground in a ball mill or finely cut with scissors. Cortisol was extracted with methanol before being measured using an ELISA kit. Data was analyzed by ANOVA using SAS (significant if $P < 0.05$). Cortisol concentration was similar between locations; however, the white hair had higher ($P < 0.001$) levels than black hair 13.7 ± 1.01 vs. 6.8 ± 1.63 pg/mg, respectively. Primiparous cows had higher ($P < 0.001$) cortisol levels than older cows 21.9 ± 1.80 and 4.37 ± 1.48 pg/mg. Samples processed with a ball mill had higher ($P < 0.006$) cortisol levels than those cut up with scissors 12.6 ± 1.03 vs. 7.9 ± 1.61 pg/mg. Hair from the tail of the Holstein cow is always white and had numerically higher cortisol levels than hair from other locations. It also regrows more rapidly than other sites, allowing sampling as frequently as every 3 wk making it suitable for measuring chronic cortisol levels over extended periods of time. This approach is being used to monitor cortisol levels during lactation and its relationship to health and reproduction.

Key Words: cortisol, hair, cows

W214 Animal and ovarian parameters affect fertilization and embryo quality in high-producing lactating dairy cows.

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A total of 418 oocytes-embryos from single ovulating lactating Holstein cows were recovered 6 d after artificial insemination (AI). Cows were enrolled in a presynch-ovsynch program starting at 30 ± 3 d in milk. Ovarian responses were evaluated by ultrasonography and blood was analyzed for progesterone (P4) throughout the study. The body condition score (BCS) was measured at enrollment and uterine flush. Responses related to embryo quality were evaluated (tendency $P < 0.10$; significant $P < 0.05$) against parity (primiparous vs multiparous), cyclicity (until 44 ± 3 d in milk), BCS at enrollment (Low < 2.75 > Moderate), BCS change between measurements, ovulation to first GnRH of ovsynch, follicle size at AI (Small < 18mm > Large), and concentrations of progesterone (P4) at PGF (Low < 3 ng/mL > High), AI (Low < 0.2 ng/mL > High) and 6 d after AI (Low < 2 ng/mL > High). Moderate BCS tended to improve embryo quality by increasing proportion of grades 1–2 (73.1 vs 62.4%) and transferable embryos (84.6 vs 77.7%) and decreasing degenerated embryos (22.3 vs 15.4%). Ovulation to the first GnRH of the synchronization protocol improved proportion of embryos grades 1–2, transferable embryos, and live blastomeres, whereas decreased degenerated and unfertilized oocytes-embryos. Large follicles at AI increased fertilization rate (86.5 vs 78.2%) and the mean number of accessory sperm cells attached to the zona pellucida (28.1 ± 3.8 vs 17.8 ± 4.5). High P4 at PGF increased number of blastomeres in embryos (33.4 ± 2.6 vs 26.4 ± 2.3). Low P4 at AI tended to increase fertilization rate (88.0 vs 79.6%), oocyte-embryos grades 1–2 (60.9 vs 52.5%), mean number of cells (35.0 ± 2.3 vs 24.8 ± 2.5) and percentage of live cells (94.7 vs 88.9%), whereas it decreased degenerated and unfertilized oocytes-embryos (36.4 vs 27.1%). High P4 6d after AI significantly decreased proportion of transferable (76.9 vs 83.6%) and increased degenerated embryos (23.1 vs 16.4%). In conclusion, moderate BCS, large follicles with restricted length from emergence to ovulation, and very low P4 levels at AI are associated with greater fertilization rate and embryo quality.

Key Words: embryo quality, fertilization, ovarian dynamics

W215 Relationships between sperm motility and in vivo and in vitro fertility of Holstein and Jersey bulls.

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Sperm motility has been correlated to bull fertility in the past. Within the last 20 yr, computer-assisted sperm analysis (CASA) has provided a more detailed and objective evaluation of sperm motility. The objective of this experiment was to determine correlations of post-thaw CASA motility data to the following fertility estimates: sire conception rate (SCR; USDA, 2008), heterospermic in vivo (H-VIVO*) and in vitro (H-VITRO) competitive indices, and in vitro embryo cleavage rate (CLV). Extended semen from Holstein (H, n = 3) and Jersey (J, n = 3) bulls was either frozen homospermically or total sperm mixed 1:1 (H:J) to create 9 H/J heterospermic pairings that were later used for in vivo AI (H-VIVO*) or in vitro fertilization (H-VITRO). Frozen/thawed homospermic aliquots were used for determination of CLV or sperm motility parameters by CASA [n = 4 straws per bull; total motility (TM), progressive motility (PM), average path velocity (VAP), straight line velocity (VSL), amplitude of lateral head movement (ALH), tail beat frequency (BCF), and straightness (STR) and linearity of path (LIN)]. In vitro fertilization was performed on approximately 140 or 180 cumulus-oocyte complexes for each for each bull (CLV) or H/J pair (H-VITRO). Competitive indices were calculated for each bull based on mean proportion of calves or cleaved embryos sired by each bull across pairings (21 to 31 random parentage tests per pair; H-VIVO or H-VITRO). SCR data (0.0, 0.0, 0.0, +0.3, +2.0, +2.0) for the 6 bulls were not correlated to any sperm motility parameters. PM was correlated (r = 0.92; $P < 0.05$) only to H-VIVO. LIN, STR, and BCF were positively correlated to H-VIVO (r = 0.87, $P < 0.05$; r = 0.93, $P < 0.05$; and r = 0.78, $P < 0.10$, respectively) but negatively correlated to CLV (r = - 0.82, $P < 0.05$; r = - 0.83, $P < 0.05$; and r = - 0.75, $P < 0.10$, respectively). ALH was correlated to H-VITRO (r = 0.74, $P < 0.10$) and CLV (r = 0.73, $P < 0.10$) but not H-VIVO. In conclusion, correlations of CASA data to fertility differed between both heterospermic methods and between homo- and heterospermic methods in vitro. *Kasimanickam et al., 2006, 2007

Key Words: bull, fertility, sperm

W216 Placement of semen in uterine horns failed to improve fertilization rates in superovulated Holstein cows.

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This experiment was designed to test whether depositing the sperm in the uterine horns could improve fertilization rates in superovulated cows with synchronized ovulations. Holstein cows (n = 72), were milked twice daily and housed and fed individually in tie-stalls. Animals were blocked by parity and calving dates and randomly assigned to one of 2 treatments: 1) Semen placed in the uterine body (BAI); and 2) Semen placed in the greatest curvature of the uterine horns (HAI; semen dose split between the 2 horns). All cows had a synchronized superovulation using a modified 5-d Double Ovsynch protocol with 4 d of decreasing FSH (Folltropin, 400mg/cow) treatments. All animals were flushed between 65 to 75DIM, near peak production (39.6 kg/d). Non-sexed frozen semen (15x106 sperm/straw) were produced from single ejaculates of 2 high-fertility sires and cows were inseminated twice (12h and 24h after final GnRH treatment). To avoid variation, a single batch of FSH was used and 2 experienced AI technicians performed all breedings and flushings, which occurred 6d after synchronized ovulations. In addition, a single treatment-blinded technician graded all embryos. The proc GLIMMIX of SAS was used to compare embryo characteristics using cow as a random experimental unit. Site of semen deposit did not change fertilization rate (~78%) or any other measured embryo characteristic, as shown in the table below. In conclusion, placement of semen in uterine horns failed to improve fertilization rates or number of transferable embryos compared with standard body-AI in superovulated, high-producing dairy cows bred twice with high-fertility semen. Supported by Adisseo, Accelerated Genetics, USDA Grant 2010–85122–20612.

Table 1.

Item	Body AI	Horn AI	*P*-value
n	35	37	
CL number (ultrasound on the day of the flush)	17.1±1.5	17.6±1.3	0.58
Total ova/embryos recovered	7.1±1.0	8.7±1.4	0.33
% Ova/embryos per CL	40.4±5.1	44.4±4.5	0.75
Number of fertilized ova	5.3±0.9	6.6±1.1	0.33
% Fertilized ova	78.5±5.1	78.2±4.7	0.97
Number of transferable embryos	3.9±0.8	5.3±0.9	0.18
% Transferable embryos of fertilized	57.6±6.9	64.3±5.5	0.81
Number of degenerate embryos	1.4±0.4	1.3±0.4	0.90
% Degenerate of fertilized	32.2±6.7	20.7±4.9	0.39

Key Words: superovulation, AI technique, dairy cow

W217 Influence of sex and breed of the calf on synchronization and pregnancy rates in cows submitted to timed AI.

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Studies have shown that weight, sex, and breed of calves influence the productive status of cows. This study evaluated the influence of sex and breed of calves on the response of cows to a timed-AI (TAI) protocol. Primiparous and multiparous Nelore (*Bos indicus*) cows (n = 865; 44.3 ± 2.1 d postpartum[DPP]) were submitted to the following protocol: D0 - intravaginal progesterone (P4) device (DIB, Syntex S.A., Argentina), 2 mg estradiol benzoate (Gonadiol, i.m., Syntex S.A.) and 12.5 mg dinoprost tromethamine (Lutalyse, i.m., Pfizer Animal Health); D8 - 12.5 mg dinoprost, 0.8 mg estradiol cypionate (ECP, i.m., Pfizer Animal Health), withdrawal of DIB, and 300 IU eCG (Novormon 5000, i.m., Syntex S.A.) or saline; D10 - TAI using frozen/thawed semen from 3 bulls. Ovaries were evaluated by ultrasound (Mindray 2200 VET DP) 7 and 30 d after AI for presence or absence of CL and pregnancy diagnosis. Data were analyzed using PROC GLIMMIX of SAS and the use of eCG on Day 8, body condition score (BCS), DPP, sex (F: Female; M: Male), and breed (C: Crossbred Nelore × Angus; N: Nelore) of calves were included in the model. Results are presented as least squares means ± SE. Cows being suckled by F or M and C or N calves had similar synchronization rates (F: 86.2 ± 2.1% vs. M: 86.8 ± 2.1%; $P = 0.79$; C: 86.1 ± 2.3% vs N: 87.0 ± 2.1%, $P = 0.74$). Likewise, synchronized cows had no effect of calf sex or breed on conception rate (F: 46.8 ± 5.4% vs. M: 46.3 ± 5.3%; $P = 0.90$; C: 48.9 ± 5.5% vs. N: 44.2 ± 5.4%; $P = 0.33$). Cows with a better BCS had higher synchronization and pregnancy rates ($P < 0.001$). Interestingly, serum P4 concentrations of the synchronized cows were affected by the sex of the calf on d 7 (F: 4.9 ± 0.8 ng/mL vs. M: 4.0 ± 0.8 ng/mL, $P = 0.03$) and 14 (F: 8.1 ± 1.3 ng/mL vs. M: 6.2 ± 1.3 ng/mL, $P = 0.01$), and by calf breed (C: 4.9 ± 0.8 ng/mL vs. N: 4.0 ± 0.8 ng/mL, $P = 0.04$) on d 7 after AI. In conclusion, although there was a relationship between calf sex and breed on circulating P4 of the dam, these variables did not influence the reproductive efficiency of the cow bred by TAI early in postpartum. Supported by SYNTEX S.A. of Argentina, and Agropecuária Fazenda Brasil, CAPES, FAPESP, and CNPq of Brazil.

Key Words: calf, reproduction, artificial insemination

W218 The requirement of GnRH at the onset of the 5-d Select Synch + CIDR program in beef heifers. F. M. Abreu*[1], L. H. Cruppe[1], M. V. Biehl[3], A. D. P. Rodrigues[2], M. D. Utt[1], G. A. Bridges[4], J. L. M. Vasconcelos[2], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]Sao Paulo State University, Botucatu, SP, Brazil, [3]University of Sao Paulo, Pirassununga, SP, Brazil, [4]University of Minnesota, Grand Rapids.*

The objective of this study was to investigate whether or not the omission of the GnRH injection at CIDR insertion would affect luteolysis and pregnancy rates to AI in the 5-d Select Synch + CIDR program in beef heifers. Prepubertal (n = 27) and cyclic (n = 124) heifers from 3 locations were randomly assigned to receive either 100µg GnRH (n = 77) or 2 mL saline (SAL, n = 74) at CIDR insertion (d −5); followed by 25 mg PGF coincident with CIDR removal 5 d later (d 0). Blood samples were collected on d −15 and −5 to assess puberty status. Estrus detection was performed twice daily from 0 to 60 h after PGF and AI based on the AM/PM rule. Heifers not detected in estrus were timed AI followed by a GnRH injection 72 h after PGF. In 2 locations, blood samples from heifers with no visual signs of estrus were collected at 72 h to assess progesterone concentrations. Ovarian ultrasonography was performed on d 0 to determine ovulation response to the first GnRH (GnRH treatment) and presence of CL in all heifers. Pregnancy diagnosis was performed on d 35. At CIDR withdrawal, presence of a minimum of one CL in the ovaries tended ($P = 0.09$) to be greater in the GnRH (94%) than SAL (86%) treatment, and was greater ($P < 0.01$) in cyclic than prepubertal heifers (95 and 67%). Size of the largest ovarian follicle on d 0 was greater ($P < 0.01$) for heifers in the SAL (10.6 ± 0.4 mm) than GnRH (8.9 ± 0.3 mm) treatment. The proportion of heifers detected in estrus and time to estrus did not differ (72% and 48.2 ± 0.8 h). For the 2 locations in which blood samples were collected from heifers that did not exhibit estrus (n = 27), incidence of luteal regression was 85.2% and did not differ between treatments. All 4 heifers deemed to have not regressed their CL (not detected in estrus and progesterone concentrations >0.5 ng/ml) were in the GnRH treatment. Synchronization pregnancy rate did not differ between GnRH and SAL treatments (48 and 53%, respectively). In conclusion, administration of GnRH at the onset of the 5-d Select Synch + CIDR protocol did not influence the incidence of luteal regression or benefit pregnancy rates to AI in beef heifers.

Key Words: GnRH, beef heifers, pregnancy rate

W219 Efficacy of the "CoPGF" approach to induce luteolysis in the 5-d CO-Synch + CIDR program in lactating beef cows. M. V. Biehl*[1,3], L. H. Cruppe[1], F. M. Abreu[1], A. D. P. Rodrigues[4], M. L. Mussard[1], G. A. Bridges[2], A. V. Pires[3], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]University of Minnesota, Grand Rapids, [3]University of Sao Paulo, Piracicaba, SP, Brazil, [4]Sao Paulo State University, Botucatu, SP, Brazil.*

The objective of this study was to determine the efficacy of using 50 mg (2 25 mg doses; CoPGF) of PGF2α (PGF) administered coincident with CIDR removal in the 5-d CO-Synch + CIDR estrous synchronization program in postpartum beef cows. This approach was compared with treatment with 2 25 mg doses of PGF given at an 8 h interval (25 mg at CIDR removal and 25 mg 8 h later; 8hPGF). Lactating multiparous cows (n = 51) were randomly assigned by age and calving date to treatments (CoPGF, n = 27; 8hPGF, n = 24). Blood samples were collected on d −15 and −5 to assess reproductive status at the onset of the program. All cows received 100 µg GnRH (GnRH-1; Cystorelin) at CIDR insertion (d −5). On d 0, the CIDR was removed 2 h before (h −2) the CoPGF treatment or the initial PGF injection of the 8hPGF treatment was given (h 0). Blood samples were collected at h 0, 8, 16, 24, 36, 60, and 84 to assess circulating progesterone concentrations (P4) and luteal regression, and on d 13 to assess function of the subsequent CL. Ovarian ultrasonography was performed on d −5 and 0 to identify the presence of spontaneously formed and GnRH-induced CL, respectively. Estrus detection was performed twice daily from d 0 to 5. Ovulation to GnRH-1 tended to be greater ($P = 0.07$) for the 8hPGF (83.3%) than the CoPGF group (59.3%). Proportion of animals in anestrus at CIDR insertion (33.3%) and presence of at least one CL at CIDR removal (94.1%) did not differ between treatments. The proportion of cows detected in estrus and interval from CIDR removal to estrus did not differ between treatments (8hPGF, 66.7% and 67.0 ± 2.79 h; and CoPGF, 70.4% and 64.6 ± 2.03 h). The incidence of luteolysis did not differ between treatments (8hPGF, 95.2%; CoPGF, 95.7%) and was characterized by P4 below 1 ng/ml by h 36 and thereafter to h 84. Progesterone concentrations on d 13 did not differ (8hPGF, 2.65 ng/ml; CoPGF, 3.03 ng/ml). In conclusion, the CoPGF approach is a highly effective method to induce luteal regression with the 5-d CO-Synch + CIDR program.

Key Words: beef cows PGF, PGFα, 5-d program

W220 Effects of GnRH and administering number of PGF2α doses in the 5-d timed AI program on ovarian responses and fertility of dairy heifers. F. S. Lima*[1], E. S. Ribeiro[1], R. S. Bisinotto[1], N. Martinez[1], L. F. Greco[1], K. N. Galvão[1], C. A. Risco[1], W. W. Thatcher[1], M. Amstalden[2], and J. E. P. Santos[1], *[1]University of Florida, Gainesville, [2]Texas A&M University, College Station.*

Objectives were to determine if GnRH at the initiation of 5-d timed AI combined with 2 doses of PGF2α improve ovarian responses and pregnancy per AI (P/AI) of dairy heifers. Holstein heifers (n = 2,118) received an intravaginal insert (CIDR) containing progesterone (P4) on d0. Inserts were removed on d5 and heifers were treated with PGF2α (25 mg dinoprost). GnRH was administered on d8 concurrently with timed AI. Heifers were allocated randomly to receive no additional treatment (NG1P = 711), a second injection of PGF2α on d6 (NG2P = 696), or an injection of GnRH on d0 and a second injection of PGF2α on d6 (G2P = 711). Ovaries were scanned on d0 and 5. Blood was sampled at AI to measure P4 concentrations. Pregnancy was diagnosed on d 32 and 60 after AI. Data were analyzed using GLIMMIX of SAS. Administration of GnRH on d0 increased ovulation and the proportion of heifers with a new CL on d5 (Table). The proportion of heifers with a CL on d5 (86.8%) did not differ among treatments. The second injection of PGF2α improved luteolysis compared with a single PGF2α despite administration of GnRH on d0. Concentration of P4 at AI was greater for NG1P than NG2P or G2P (0.36 vs. 0.27 vs. 0.30 ng/mL). The P/AI on d 30 and 62 were greater for G2P than NG1P or NG2P, but pregnancy loss did not differ with treatment (NG1P = 7.4%, NG2P = 6.3% and G2P = 4.3%). Heifers with a new CL on d5 that received 2 PGF2α had greater P/AI than those with a new CL but that received a single PGF2α (62.8% vs. 45.7%). Combining GnRH with 2 doses of PGF2α in the 5-d timed AI protocol improved fertility because of greater ovulation associated with adequate luteolysis in dairy heifers.

Table 1. Effect of treatment on reproductive responses [% (no./no.)] of dairy heifers

	Treatment			
	NG1P	NG2P	G2P	*P*-value
Ovulation d0	13.2 (40/303)^{b}	12.8 (38/296)^{b}	27.6 (85/308)^{a}	0.01
New CL d5	20.5 (62/303)^{b}	19.6 (58/296)^{b}	33.8 (104/308)^{a}	0.01
Luteolysis				
P4<0.5 ng/mL	82.5 (151/183)^{b}	92.9 (169/182)^{a}	88.3 (158/179)^{ab}	0.01
P4<0.3 ng/mL	61.2 (112/183)^{b}	74.2 (135/182)^{a}	71.0 (127/179)^{a}	0.03
Pregnant				
d 32	52.9 (376/711)^{b}	55.0 (383/696)^{b}	61.7 (439/711)^{a}	0.01
d 60	49.0 (348/711)^{b}	51.6 (359/696)^{b}	59.1 (420/711)^{a}	0.01

$^{a,b,c}P < 0.05$.

Key Words: dairy heifer, luteolysis, fertility

W221 Comparison between the GGPG and two PGF2α based resynchronization programs on fertility in lactating dairy cows. R. G. S. Bruno*[1,2], A. M. Farias[1], K. J. Lager[1,2], D. E. Hawkins[2], and T. R. Bilby[1], [1]*Texas A&M University, College Station,* [2]*West Texas A&M University, Canyon.*

The objective was to compare the use of either GnRH or PGF as a presynchronization strategy before a resynchronization program on fertility in dairy cows. Lactating cows (n = 2327) from a dairy in TX were assigned to 1 of 3 resynchronization programs at 29 ± 3 and examined for pregnancy at 36 ± 3 d after AI. Resynchronization programs consisted of: GGPG (n = 458), an injection of GnRH at enrollment followed by the Ovsynch protocol initiated at the time of non-pregnancy diagnose (NPD); POV7 (n = 940) an injection of PGF at NPD followed by the Ovsynch protocol 7 d later; and POV11 (n = 929) injection of PGF 3 d after NPD followed by the Ovsynch protocol 11 d later. Cows were AI at any time during the program and, if AI, cows were removed from subsequent injections. Ovaries were scanned and blood sampled for progesterone (P4) levels on day of first GnRH and PGF of Ovsynch. Pregnancy per AI (P/AI) was diagnosed at 36 and 66 d after AI. Overall 64% of cows were diagnosed pregnant 7 d after enrollment. Among non-pregnant cows, GGPG reduced ($P < 0.01$) re-inseminations upon ED (GGPG = 23.3 vs. POV7 = 74.9 and POV11 = 79.6%). Treatment did not affect overall P/AI (35d, GGPG = 29.2, POV7 = 28.7 and POV11 = 31.9%; 66d, GGPG = 25.8, POV7 = 26.6 and POV11 = 30.2%) or pregnancy loss between 36 and 66 d after AI ($P > 0.41$). Cows AI upon ED had greater ($P = 0.02$) P/AI then cows TAI (ED = 32.3, TAI = 25.1%). However, treatment did not affect ($P > 0.31$) P/AI for cows AI upon ED (35d, GGPG = 29.6, POV7 = 29.4 and POV11 = 35.7%; 66d, GGPG = 27.3, POV7 = 28.1 and POV11 = 33.7%) or TAI (35d, GGPG = 29.1, POV7 = 25.0 and POV11 = 16.9%; 66d, GGPG = 25.3, POV7 = 22.1 and POV11 = 16.9%). Treatment affected ($P < 0.01$) the median days between NPD and re-breeding (GGPG = 10, POV7 = 4 and POV11 = 7 d). At beginning of Ovsynch, more GGPG cows had CL (GGPG = 86.8 vs. POV7 = 50.7 and POV11 = 60.0%, $P < 0.01$). However, treatment did not affect ($P = 0.42$) ovulation to the first GnRH of Ovsynch. In conclusion, GGPG reduced re-insemination during resynchronization. Reproductive program did not affect P/AI but starting the resynchronization with PGF at NPD shortened the interval between non-pregnancy diagnose and re-breeding.

Key Words: dairy cow, fertility, resynchronization

W406 See abstract #92

Production, Management and the Environment: Dairy II

W222 Evaluation of management, nutrient consistency and sanitation of automated calf feeders. K. L. Machado,* R. E. James, and M. L. McGilliard, *Deptartment of Dairy Science, Virginia Tech, Blacksburg.*

The objective of this study was to evaluate management, sanitation and consistency of liquid diets delivered to calves via autofeeders. Ten herds in Virginia and North Carolina with sophisticated (Förster-Technik, Germany) and basic (Biotic Industries, TN) machines were asked a 60-question survey concerning calf and autofeeder management. Duplicate milk replacer samples were obtained to measure standard plate count (SPC), Brix refractometer value and temperature of liquid diet delivered by the autofeeder at the time of the survey. Dairies were also categorized based upon management strategies for the autofeeders. Producers purchased autofeeders to manipulate feeding rate, refocus labor to improved sanitation, explore new feeding options and provide better care and well-being of calves. Six dairies were visited monthly for 3 mo for continued evaluation of milk replacer from the autofeeder. Survey questions did not reveal differences related to management strategy or autofeeder type as determined by Proc Freq. Variables, SPC, Brix and temperature were analyzed by Proc Glimmix with a fixed effect of management strategy, or autofeeder type, and random effect of dairy nested in management strategy or autofeeder type, and residual. Seven herds utilizing basic machines had milk replacer liquid with a mean SPC of $6.9 \times 10^6 \pm 7.3 \times 10^6$ cfu/mL. The mean Brix and temperature readings were 12.0 ± 2.1 Brix and 38.8 ± 6.7°C. Three dairies that used sophisticated autofeeders had milk replacer liquid with a mean SPC of $1.3 \times 10^6 \pm 2.2 \times 10^6$ cfu/mL. Mean Brix and temperature readings were 10.3 ± 1.7 Brix and 38.6 ± 6.7°C. Differences could not be attributed to either management strategy or autofeeder type. This study suggests that implementation of management protocols was more important than autofeeder type or management strategy category.

Key Words: calf, automated feeder, milk replacer

W223 Performance, health, behavior and respiratory antibody production of individually vs. grouped housed dairy calves. M. S. Calvo[1], C. J. Neumeier*[1], L. E. Hulbert[1], A. Louie[2], L. J. Gershwin[3], K. E. Pinkerton[4], C. B. Tucker[1], K. C. Klasing[1], and F. M. Mitloehner[1], [1]*Department of Animal Science, University of California, Davis,* [2]*School of Veterinary Medicine, University of California, Davis,* [3]*Department of Pathology, Microbiology and Immunology, School of Veterinary Medicine, University of California, Davis,* [4]*Department of Anatomy, Physiology, and Cell Biology, School of Veterinary Medicine, Center for Health and the Environment, University of California, Davis.*

Individual calf housing systems are widely used in the US to inhibit competition for food and reduce the transmission of disease between calves. Future legislation could mandate group housing for dairy calves without identifying suitable alternatives. Therefore, the objectives were to evaluate the effects of individual housing versus group housing in modified hutches on calf performance, resting behavior, health and respiratory antibody production. The 2 housing treatments were: 1) individual housing (INV; 1.23 m^2/head; n = 18) and 2) group housing (GRP; 3 calves per hutch; 1.23 m^2/head; n = 16). Milk and starter intake were recorded daily and BW measured on d 0, 20, 45, 73, and 87. Visual health assessment scores were recorded daily and behavior loggers utilized on d 21–23, 47–49, and 74–76. In a sub-experiment, healthy calves from each treatment (n = 6, SML; n = 7, GRP) were sensitized (subQ) and challenged (aerosolized) with Ovalbumin (OVA) at age 76 ± 0.5 d. Bronchoalveolar lavage fluid (BALF) was collected at age 80 ± 0.5 d and was analyzed for OVA-specific IgG, IgG1, IgA, and IgE. All calves had increased ADG at 45 d of age compared with 20 d (INV: 0.53 ± 0.05 kg/d; GRP: 0.61 ± 0.04 kg/d). In addition, at age 73 d, INV calves tended ($P = 0.09$) to be more efficient than GRP calves (INV: 7.97 ± 0.45 Mcal/BW gained; GRP: 8.64 ± 0.35 Mcal/BW gained). The INV calves spent more time in the resting-position than GRP calves ($P < 0.01$). The GRP calves had greater percent days of nasal discharge than INV calves ($P < 0.05$). A greater percentage of days of clean hide scores were observed in INV than GRP calves ($P < 0.05$). However, GRP calves had less BALF OVA-IgE compared with INV ($P = 0.03$). Although GRP calves appeared dirtier and had more days with nasal discharge, the decreased BALF OVA-IgE suggests that early life microbial exposure may be beneficial to the respiratory antibody milieu later on in life, which warrants more investigation.

Key Words: bovine, performance, behavior

W224 Performance and welfare of high-yielding dairy cows subjected to 5 or 8 cooling sessions daily in a hot and humid climate. U. Moallem,* J. Miron, H. Lehrer, M. Zachut, and H. Honig, *Volcani Center, Bet Dagan, Israel.*

The objectives were to determine the effects of cooling frequency of high-yielding dairy cows on intake, milk yield, rumination time, and welfare parameters. Forty-two multiparous dairy cows were divided into 2 treatment groups and were housed in an open barn divided into 2 pens. The groups were subjected to different cooling schedules, in a crossover design as follows: cows were exposed to 5 or 8 cooling sessions per day (5CS and 8CS, respectively), in the holding area of the milking parlor. Each period lasted 4 wk, and then treatments were switched for another 4-wk period. Each cooling session lasted 45 min, comprising cycles of 30 s of showering and 4.5 min of ventilation. Rectal temperature (RT) and respiration rate (RR) were recorded twice per week at 0630 and 1600. Rumination and lying times were recorded automatically. RT was 0.16 and 1.08°C lower in 8CS than in 5CS cows in the morning and afternoon, respectively ($P < 0.001$). RR was lower in 8CS than in 5CS cows in the morning (49.1 and 54.6 breaths/min, respectively; $P < 0.001$), and more so in the afternoon (50.0 and 83.0 breaths/min, respectively; $P < 0.001$). DMI and milk yields were 9.3 and 9.6% higher in the 8CS than in the 5CS cows (27.0 vs. 24.7 and 40.1 vs. 36.6 kg/d, respectively; $P < 0.001$), with no differences in milk fat and protein contents. Daily rumination time was 7.4% longer in the 8CS than in the 5CS (440.1 and 409.6 min/d, respectively; $P < 0.001$). Although the 8CS cows moved 3 times more to the milking area for extra cooling sessions than the 5CS ones, they spent 9.9 min/d more than the 5CS ones in lying down (484.4 and 474.5 min/d, respectively; $P < 0.004$), and used more of their free time in resting than the 5CS cows: 52.0 and 43.9%, respectively ($P < 0.001$). In conclusion, increasing the cooling frequency of cows under hot and humid conditions from 5 to 8 times a day increased their intake and milk yield, and lowered their RR and RT. Moreover, the 8CS cows spent more time resting and ruminating than 5CS cows, an indication that increasing cooling frequency improved animal welfare.

Key Words: cooling frequency, animal welfare

W225 Effects of presynchronization with GnRH or prostaglandin F2α before the start of a resynchronization protocol on reproductive performance of dairy cows.

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Objectives were to evaluate estrus expression, ovarian responses, and pregnancy outcomes of dairy cows submitted to different presynchronization protocols before the start of a resynchronization protocol. Cows from 2 herds (MN = 611 and WI = 307) were enrolled in the study 28 to 37 d after AI (d0). The GGPG treatment consisted of GnRH on d0 and start of the resynchronization protocol on d7. The PGPG treatment consisted of a prostaglandin (PG) F2α on d2 to 4 and start of the resynchronization protocol on d14. The resynchronization protocols were the Ovsynch56 and the Cosynch48 in the MN and WI herds, respectively. Cows submitted to the resynchronization protocol were randomly selected to receive or not a CIDR insert. Sub-sample of cows from the MN herd had ovaries scanned by ultrasound on the day of non-pregnancy diagnosis (n = 342) and on the days of the GnRH and PGF2α injections of the resynchronization protocol (n = 215). Diagnosis of pregnancy was done by ultrasound (MN herd) or by concentration of pregnancy-specific protein B (WI herd) at 33 ± 4 d after AI. Continuous data were analyzed by ANOVA, dichotomous data were analyzed by logistic regression, and time dependent dichotomous data were analyzed by Cox proportional hazard ratio. Mean and median intervals to re-insemination were ($P < 0.01$) greater for GGPG cows (14.8 ± 0.3 and 16 d) than PGPG cows (12.9 ± 0.3 and 8 d) as the former were ($P < 0.01$) less likely to be re-inseminated in estrus (16.2 vs. 61.4%). Percentage of cows with a CL on d0 was similar ($P = 0.24$) among treatments, but fewer ($P < 0.01$) PGPG cows had a CL at the start of the resynchronization (67.2 vs. 93.6%). Percentage of cows ovulating to the first GnRH ($P = 0.32$) and percentage of cows with a CL on the day of the PGF2α ($P = 0.19$) of the resynchronization were not different between treatments. Treatment ($P = 0.67$) and farm ($P = 0.38$) did not affect pregnancy outcome, but treatment by farm interaction tended ($P = 0.06$) to affect pregnancy outcome (MN–GGPG = 43.8 vs. PGPG = 36.2%; WI–GGPG = 39.9 vs. PGPG = 45.3%). Among cows re-inseminated at timed AI, pregnancy outcome did not differ between cows treated or not treated with a CIDR insert ($P = 1.0$). Presynchronization with PGF2α increased the number of cows re-inseminated in estrus and reduced AI interval, but pregnancy outcomes were dependent on farm.

Key Words: presynchronized-resynchronization, dairy cow

W226 Seasonal effect of a reduced dose of prostaglandin $F_{2\alpha}$ on estrus response in lactating dairy cows.

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We have previously shown that 15 mg of prostaglandin $F_{2\alpha}$ (PGF; Prostamate) injected in the ischiorectal fossa (IRF) is just as effective in inducing luteolysis in lactating dairy cows as the normally prescribed dose of 25 mg administered intramuscularly (IM). The objective of this study was to compare estrus response in lactating dairy cows treated with 15 mg PGF IRF versus 25 mg PGF IM during different seasons of the year under field conditions experienced in a single dairy herd located in Utah. The study began in February and concluded in February the following year. The study was divided into 3 seasons: Season 1-February–April; Season 2-May–August; Season 3-September–February. Five hundred seventy-seven lactating Holstein cows (lactation number 1–5) eligible for first breeding (days in milk ≥59) were selected for study based on the presence of a responsive corpus luteum as estimated by palpation performed by a field veterinarian. Selected cows were grouped each week of the study by lactation (lactation 1 versus lactation 2 versus lactation ≥ 3) and randomly assigned within group to treatment. Estrus was detected by pedometer. Overall, cows treated with 15 mg PGF IRF had an estrus response rate (161/285; 56%) lower than cows treated with 25 mg IM (200/292; 68%; $P < 0.01$). Response rate between treatments differed during Season 2 (IRF = 46/109;42% vs IM = 70/109;64%; $P < 0.01$) but did not differ ($P > 0.05$) during Season 1 (IRF = 68/107;64% vs IM = 77/111;69%) or Season 3 (IRF = 47/69;68% vs IM = 53/72;74%). Response within treatment was unaffected by season in cows given 25 mg PGF IM ($P > 0.05$) but did differ by season in cows given 15 mg IRF ($P < 0.01$). In summary, season did not affect estrus response when cows were administered 25 mg PGF IM. In contrast, lowering the dose to 15 mg injected by way of the IRF during the summer months did reduce estrus response as compared with administration during other seasons of the year and as compared with the response in cows receiving the full dose. We conclude that lactating dairy cows should not be administered a reduced dose of PGF by way of the IRF during the summer months.

Key Words: season, prostaglandin $F_{2\alpha}$, estrus

W227 Degree of agreement between the ration formulated and the ration fed on seven California dairies.

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Dairy nutritionists utilize computer models to formulate least cost rations that maximize feed to milk conversion efficiency. However, the nutrient composition of the fed ration often differs from the formulated ration as a result of errors associated with weighing ingredients into the mixer wagon, and uncertainties in dry matter content and nutrient composition of the ingredients. If large deviations exist between the formulated and the fed ration, important consequences on the environment and animal performance should be expected. The objective of this study was to evaluate the degree of agreement between the dairy cow ration formulated by the nutritionist and the ration fed at the feedbunk. A total of 7 dairies in Merced County, CA were enrolled in this study. Feedbunk samples of the total mixed ration were taken on 2 non-consecutive days from 4 (n = 1), 3 (n = 5) and 2 (n = 1) lactating groups, composited and assayed for CP, NDF, fat, Ca and P. Results are presented in Table 1. Dairies over or under fed more than 10% of CP (n = 4), NDF (n = 3), fat (n = 3), Ca (n = 6) and P (n = 2). Results from this study indicate that despite formulating rations to meet animal requirements, and implementing grouping strategies, we will not improve nutrient efficiency utilization unless best feeding management practices are implemented to minimize errors during the feeding process.

Table 1. Maximum and minimum percentage of nutrient under or over fed per dairy across the different total mixed rations (TMR)

Dairy	1	2	3	4	5	6	7
Milk (kg)	39	29	36	27	36	31	35
TMR #	3	2	3	3	3	3	4
CP max	21.3	14.9	14.4	−10.6	9.6	−6.1	−6.0
CP min	15.0	7.7	4.3	−4.6	1.7	−1.5	−5.3
NDF max	42.0	5.4	6.5	11.2	−5.0	17.1	18.1
NDF min	27.0	3.2	1.3	2.9	−2.2	0.1	9.6
Fat max	25.7	−5.9	15.4	−9.3	−8.5	−17.3	−13.8
Fat min	−1.3	3.8	5.5	−3.3	−4.1	−10.3	10.3
Ca max	−10.8	−7.9	−17.8	−28.6	−13.1	−17.2	−13.8
Ca min	6.7	0.3	−11.4	−22.1	−4.2	−3.6	−7.9
P max	14.7	9.7	7.2	−6.4	−5.0	14.7	6.4
P min	−4.9	−1.1	−1.0	−4.6	2.6	3.8	−2.4

Key Words: feeding management, TMR, dairy

W228 Nitrogen and phosphorus utilization by dairy cows on small and medium-sized farms.

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Small and medium-sized dairy farms (<700 cows) are exempted from EPA nutrient management regulations, but can account for a major proportion of animals in traditional agriculture regions. Reducing nutrient loading to sensitive water bodies is a challenge that needs to be shared by animal operations of all scales. Ten dairy farms with 50 to 250 cows (900 total) were randomly selected from the Chesapeake Bay watershed in Pennsylvania and monitored for nutrient utilization for 2 yr in comparison with baseline data collected during the first 3 mo of the project. Farms were evaluated regularly for nutrition and management practices and presented with recommendations for improvement, as appropriate. Diets and feces were sampled quarterly (fecal from 5 randomly selected cows per herd) and analyzed for nutrient content. DHIA reports were collected monthly. Most of the farms used dietary P appropriately, and half of the farms reduced dietary protein during monitoring, averaging 0.38% in P and 16.5% in CP, both consistent with current industry usages and NRC standards. However, variation existed in the diets as well as fecal analysis among farms and over time within farms. Analyzed dietary P exceeded formulated concentrations, whereas the trend was the opposite for protein. Pregnancy rate (21-d) increased during the monitoring period. While combined data across farms showed that there was little change in milk production or MUN during the monitoring period, half of the farms showed improvements. Although not mandated to implement nutrient management plans, producers of small and medium farms were conscientious about dietary CP and P content, and willing to adopt new technologies to reduce excretion. Extension services for reducing nutrient excretion on small and medium farms may use the approach of identifying vulnerable farms followed by close monitoring and evaluation. Partially supported by National Fish and Wildlife Foundation.

Table 1. Protein and phosphorus utilization on small and medium dairy farms during 2-yr monitoring

Item	Baseline	Monitoring	SEM	*P*
Dietary CP, %				
Formulated	17.0	16.8	0.1	0.24
Analyzed	16.3	16.1	0.2	0.44
Dietary P, %				
Formulated	0.37	0.36	0.01	0.13
Analyzed	0.39	0.40	0.01	0.45
Fecal CP, %	17.4	17.4	0.3	0.84
Fecal P, %	0.68	0.69	0.02	0.81
Milk, kg/d	33.4	33.7	0.3	0.41
MUN, mg/dL	12.5	12.4	0.3	0.79
Pregnancy rate, %	20.4	22.7	0.5	0.01

Key Words: dairy cows, nutrient management, environment

W229 Basic economic indexes on small and medium sized dairy farms.

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Ten dairy farms with 50 to 250 cows (averaging 87.7 cows/herd) were randomly selected from the Chesapeake Bay watershed in Pennsylvania and monitored for nutrient utilization and production efficiency for 2 yr in comparison with baseline data collected for the first 3 mo of project. Farms were evaluated regularly for nutrition and management practices and economic parameters were collected from herd accountants, tax reporting forms, and herd record systems. DHIA reports were collected monthly tracking production, herd demographics, culling, and reproductive performance. Farm wealth was hypothesized to be improved by selling products (milk, calves, and culls) as well as the accumulation of valued livestock over the course of the study. Nutrient efficiency was hypothesized to improve due to improved animal performance per unit of animal maintenance and replacement. Herds varied greatly in their nutritional, animal, and management practices and were offered evaluations and recommendations by participating study members. Herd parameters in yr 1 and 2 were compared with baseline values recorded in yr 1 as well as values reported for similar Pennsylvania herds at large. Basic economic metrics (milk price: \$0.352/kg milk; marginal feed cost: \$0.08/kg milk; cull values: \$600; cow value: \$1600) were set to average values observed over the study period so that changes in production efficiency could be observed. Milk production, estimated from changes in rolling herd average, improved by approximately 270 kg/cow over the 2-yr period with an estimated marginal value of \$71.35/cow. Herd value on 8 herds (cows and heifers valued at constant prices) increased by 3% in yr 1 and 5% in yr 2 compared with starting values. Estimated net income over feed cost increased by \$72.83/cow over the 2-yr period while a comparable estimate of herds with <100 cows in Pennsylvania increased by only \$4.39 over the same period. Seven of the 10 farms had increases in pregnancy rate from 20.4 to 22.7% with an estimated reproduction efficiency value of \$53.02 per cow per year (REPMON economic analysis). Improved nutrition by nutrient management strategies is synergistic with positive economic consequences on dairy herds. Partially supported by National Fish and Wildlife Foundation.

Key Words: dairy farm management, farm economic, dairy herd evaluation

W230 Technological level of Holstein cattle herds in the West and North of Mexico.

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The objective of this study was to classify family-based dairy enterprises considering their technological level (TL). Surveys following FAO´s guidelines were applied to 45 producers, located in the states of Chihuahua, Coahuila, Durango, Aguascalientes, Jalisco and Michoacán in México, to diagnose the type and use of technology. From outputs of the surveys, indexes for reproductive (RMI), health (HMI) and nutritional (NMI) management, genetic quality (GQI), and infrastructure and equipment (IEI) were calculated. Later, these indexes were combined to get the TL by weighing each index with their importance to differentiate the enterprises. FAO´s guidelines were modified getting the weights, proportional to the variation coefficients of the indexes (26.0, 19.6, 25.0, 3.6, and 25.8% for RMI, HMI, NMI, GQI and IEI, respectively). The enterprises were classified as subsistence, transition or business (transition enterprises are those moving from subsistence to business, the latter being the ones that market all their products), if the TL was ≤ 0.4, > and ≤ 0.8 or >0.8, respectively. Eighty 6 percent of enterprises were classified in transition and 14% in business. Transition enterprises averaged 7 years of school attendance, agricultural or grazing area of 26.9 ha, herd size of 98 animals, 53 cows in milk, 20.2 L of milk/cow per day, and a milk price of \$4.43/L, artificial insemination (AI) is used, 17% use bulls for mating repeated not pregnant cows, and cattle feeding is variable. Business enterprises averaged a 9 years of school attendance, agricultural or grazing area of 56.6 ha, herd size of 384 animals, 215 cows in milk, 26 L of milk/cow per day, and a milk price of \$4.68/L, AI is used, cattle are confined and the feeding is based on forage and concentrates. The TL is important to advise producers in a different manner, according to the strengths and weaknesses, to improve production efficiency of their enterprises.

Key Words: cattle, dairy enterprises, producer stratification

W231 Association of stocking density, production, and behavioral patterns of dairy cows milked in automatic milking systems.

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The objective of this cross-sectional study was to examine the associations between stocking density, production, and behavioral patterns of cows milked in automatic milking systems (AMS) under commercial management settings. Thirteen AMS farms were enrolled in the study. Average herd size was 71 ± 30 lactating cows. Farms either had 1 (n = 11) or 2 (n = 2) AMS units. All of the farms utilized free-stall barns, each set up for free cow traffic. Across farms there were, on average, 55 ± 10 cows/AMS, 0.9 ± 0.1 cows/free stall, and 0.66 ± 0.17 m/cow of feed bunk space. A random sample of 30 cows per herd was selected to monitor standing and lying behavior for 4 d using electronic data loggers. Times of feed delivery and feed push-up were recorded daily. Milking times and yield were automatically recorded by the AMS units. Data were analyzed in multivariable mixed-effect regression models. Cows were milked less frequently ($P < 0.05$) when they were further in lactation, were of higher parity, and as AMS stocking density (#cows/AMS) increased; milking frequency (#/d) = −0.003(SE = 0.0004) × DIM + −0.06(SE = 0.03) × parity + −0.02(SE = 0.009) × cows/AMS + 4.4(SE = 0.5). Milk yield increased with feed bunk space and parity ($P < 0.05$) and decreased ($P < 0.001$) with DIM; milk yield = 16.9(SE = 5.3) × bunk space (m/cow) + 1.9(SE = 0.03) × parity + −0.05(SE = 0.004) × DIM + 26.6(SE = 3.7). Lying bout lengths increased with DIM ($P = 0.02$) and tended ($P = 0.11$) to increase with more feed bunk space; bout length (min/bout) = 0.035(SE = 0.01) × DIM + 36.7(SE = 21.7) × bunk space (m/cow) + 49.0(SE = 14.8). Cows spent more time lying down ($P = 0.02$) the further along they were in lactation; lying time (h/d) = 0.004(SE = 0.001) × DIM + 7.5(SE = 0.7). Cows of higher parity stood longer after milking ($P = 0.003$); post-milking standing time (min) = 5.3(SE = 1.8) × parity + 63.2(SE = 6.7). The results suggest that within AMS herds, more milkings per cow may be achieved with having fewer cows per AMS unit. Further, in AMS herds, longer lying bouts and greater milk yield may be achieved with providing more feed bunk space per cow.

Key Words: automatic milking, behavioral pattern, stocking density

W232 Performance of dairy cows managed with automatic milking and three contrasting feeding systems.

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The effects of contrasting feeding systems (FS) on milk production and frequency of milkings in 2 separate herds of Holstein cows (n = 45 to 53 cows/herd) managed with automatic milking systems (AMS) was quantified in this pilot study. Feeding systems were: pasture grazing (GRASS); total mixed ration (TMR); and, pasture grazing plus supplemental TMR (pTMR) lasting 66, 51 and 96 d, respectively. Average DIM and parity of cows for the 3 FS were 169 ± 13(mean ± SE) and 2.3 ± 0.2, respectively. Cows received in addition to basal diets in the FS, 1 kg of concentrate per 4 kg of milk. Voluntary milking with one single-stall AMS per herd was applied at variable rates of 4 to 2 milkings/day based on DIM and daily milk yield. ANOVA for a completely randomized design (Proc Mixed, SAS) and path analysis (Proc Calis, SAS) of standardized regression coefficients (r) for the interrelationships among milk yield, milking frequency and concentrate intake was conducted using a total of 14,035 daily cow records. As expected, milk yield, milking frequency and body weight were greater ($P < 0.001$) for cows in TMR, intermediate for those in pTMR and lower for those in GRASS (Table 1). Conversely, cow activity in GRASS increased ($P < 0.001$) by 46% and 68% compared with pTMR and TMR, respectively (Table 1). Path analysis detected greater direct effects ($P < 0.05$) of concentrate intake on milk yield for GRASS (r = 0.52) compared with pTMR (r = 0.46) and TMR (r = 0.44) feeding systems. Conversely, the path analysis detected lower direct effects ($P < 0.10$) of milking frequency on milk yield for GRASS (r = 0.14) compared with the pTMR (r = 0.21) and TMR (r = 0.32) feeding systems. This analysis highlights the importance of proper concentrate feeding in FS, increasingly limited by low feed or energy intake, such as in GRASS, and the potential milk yield response to increased milking frequency in FS offering increasing amounts of feed or energy intake, such as pTMR and TMR.

Table 1. Cow performance in three feeding systems

Response	GRASS	pTMR	TMR
Milk yield, kg/d	23.0^{c}	27.0^{b}	30.1^{a}
Milking frequency, /d	2.4^{c}	2.7^{b}	3.1^{a}
Body weight, kg	566^{b}	574^{ab}	597^{a}
Activity, accelerometer counts	415^{a}	284^{b}	245^{c}

$^{a–c}$Means within a row with different superscripts differ ($P < 0.05$).

Key Words: automatic milking systems, feeding systems, pasture-based dairy

W233 Potential for a real-time location system for dynamic tracking of dairy cow location within dairy facilities.

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The objective of this study was to evaluate the potential accuracy of real time location systems (RTLS), commonly used to track assets or people, within a roofed dairy facility. AiRISTA (Sparks, MD) developed a leg-based RTLS tag incorporating Wi-Fi and RFID to locate tags through received signal strength indication (RSSI). The RTLS was installed in a newly constructed 120-cow compost bedded pack barn, measuring 59.1 long (X plane) by 39.6m wide (Y plane). Six locators, mounted around the perimeter of the barn to transmit a signal, and 6 access points, mounted throughout the barn interior to send and receive signals, were installed at 4.3m high. X and Y coordinates of 43 evenly distributed locations throughout the barn were obtained with a total surveying station (Trimble SPS390 Universal Total Station, Sunnyvale, CA). Calibration was achieved using AirCalibrator software and tags and 7 reference location (RL) poles. The total surveying station determined RL coordinates. To assess system accuracy, a tag was attached to the researcher's leg while the researcher rotated among each RL 5 times to obtain X and Y coordinates for 35 samples. The mean (±SD) difference from the RL for the X coordinate was −0.08 ± 0.85m, ranging from −1.49 to 1.12m, and 0.37 ± 0.55m for the Y-coordinate, ranging from −0.46 to 1.36m. The mean (±SD) root squared error of the mean (RSEM) was 0.91 ± 0.48m. The mean (±SD) of the X and Y coordinates and RSEM for each location are depicted in the table below. A RTLS system may be able to identify animal position within a few meters, although additional validation with multiple cows is needed.

Table 1. Mean (±SD) of X and Y coordinates (m) and RSEM (m) for each RL

Location	X-coordinate	Y-coordinate	RSEM
1	50.02 ± 2.12	9.49 ± 1.91	1.22
2	43.05 ± 0.87	8.56 ± 1.64	0.87
3	34.30 ± 1.53	9.01 ± 1.49	0.39
4	26.67 ± 0.68	8.80 ± 1.46	0.49
5	19.34 ± 1.50	7.78 ± 1.67	1.36
6	14.86 ± 1.68	8.70 ± 1.03	1.56
7	6.33 ± 1.53	8.85 ± 0.95	0.46

Key Words: real time location system, animal tracking, dairy

W234 Effects of prepartum dietary energy density and postpartum extruded full-fat soybean (ESB) supplementation on energy balance and productive performance of transition dairy cows. H. Su,* F. Wang, Z. Yang, Z. Cao, and S. Li, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The objective of this study was to determine the ideal energy density that could alleviate negative energy balance (NEB) without jeopardizing milk production of transition cows. Three prepartum diets of different energy levels (NEL = 5.25, 5.88 and 6.48 MJ/kg DM for L, M and H, respectively) and 2 postpartum diets (basal TMR or supplementing with 1.5 kg/d ESB in the first 30 d of lactation) were studied in a 3 × 2 factorial design experiment. Sixty multiparous dairy cows were blocked according to expected calving date, BW, BCS, parity and previous mature-equivalent milk into 6 groups, and each group was randomly allocated to one treatment. Individual feeding started 3 wk before the expected calving date and measurements were taken until 56 DIM. All data were analyzed using the PROC MIXED procedure of SAS (version 9.1). With the increase of prepartum dietary energy density, the birth weight of calves increased ($P < 0.05$), and prepartum DMI as well as energy balance of the transition cows improved ($P < 0.01$). However, compared with L and M groups, postpartum DMI of H group tended to decrease ($P < 0.079$), and postpartum BCS decreased significantly ($P = 0.007$). From 35 to 56 DIM, milk yield tended to decrease ($P = 0.061$) and milk fat and protein yields were lower ($P < 0.05$) for cows in the H group. Milk urea nitrogen (MUN) concentration ($P = 0.034$) and postpartum plasma nonesterified fatty acids (NEFA) concentration ($P < 0.10$) of M group were the lowest. By supplementing ESB during early lactation, the dairy cows had greatly improved energy balance ($P < 0.05$), less BW loss ($P = 0.09$), and a tendency for increased milk yield ($P < 0.10$). Taking all these results into account, feeding prepartum diets of low or medium energy and supplementing 1.5 kg/d ESB in the postpartum diet might be the best approach for alleviating NEB, improving productive performance and maintaining optimum health in transition dairy cows.

Key Words: transition cow, energy balance, productive performance

W235 Physiological and productive responses to seasonal variation in transition dairy cows. H. Su,* F. Wang, Z. Yang, Z. Cao, and S. Li, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The objective of this study was to investigate physiological and productive responses of cows calving in summer compared with cows calving in autumn. During each season, 20 multiparous Holstein dairy cows were selected and dried off 60 d before expected parturition, and balanced according to BW (699 ± 34 kg), BCS (3.57 ± 0.17), parity (2.14 ± 1.22) and previous mature-equivalent milk (7520 ± 858 kg). The cows were monitored from the last 3 wk of pregnancy until 21 DIM. All cows were fed a TMR formulated to meet or exceed NRC (2001) requirements. The average temperature-humidity index (THI) was 75.9 ± 3.1 in summer and 52.9 ± 7.1 in autumn. Results showed that cows were experiencing heat stress for nearly 96% of the test days during summer. In comparison with the autumn group, cows in summer had significantly increased rectal temperature and respiration rates ($P < 0.01$), decreased BW, BCS and DMI ($P < 0.05$), which induced more severe negative energy balance (NEB) ($P < 0.01$). Cows that experienced transition period during summer also had lower milk yield, percentages of milk fat, protein, solids-not-fat (SNF), and feed efficiency ($P < 0.01$), but higher concentration of milk urea nitrogen (MUN) ($P < 0.01$) and a tendency for higher somatic cell count (SCC) ($P = 0.054$). In addition, plasma concentrations of insulin, leptin, glucose, triiodothyronine (T3), thyroxine (T4) and cortisol of cows calving in summer were significantly lower ($P < 0.05$), whereas the concentrations of plasma glucagon, urea nitrogen, nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHBA) were significantly higher within 14 d postpartum ($P < 0.05$). In conclusion, compared with cows calving in autumn, cows calving in summer not only had more severe NEB and lower milk production, but also were at higher risk for health disorders. Based on our findings, we suggest producers avoid breeding dairy cows for calving during the hot season.

Key Words: transition cow, physiology, seasonal variation

Production, Management and the Environment: Environmental Quality

W236 Using dietary saponin extracts to reduce methane emissions from steers. W. Li* and W. Powers, *Michigan State University, East Lansing.*

A total of 3 experiments (Exp), in vitro and in vivo, were conducted to investigate the effects of saponin extracts from *Quillaja saponaria* (QS), *Yucca schidigera* (YS) and *Camellia sinensis* (TS) on CH_4 emissions from steers. The in vitro Exp was carried out to determine the effects of saponin inclusion on ruminal methanogenesis and fermentation parameters. Two doses (0.5% and 2.0% of substrate DM) of each saponin were added to the mixture of rumen fluid and buffer for 0, 4, 8, 12 and 24 h incubation. During the in vivo experiments (Exp 1 and 2), concentrations of saponin extracts added to the diets were determined based on the actual saponin content in the extract to provide 0.54 g/kg DM saponin in the diets. Exp 1 used a 3 × 3 Latin Square design with 4 replicates for each treatment, to compare the effects of saponin containing diets, QS (LQS, 1.5% DM) and YS (LYS, 0.64% DM), to a corn and corn silage based control (C1) treatment on enteric CH_4 emissions. Exp 2 used a 2 × 2 Latin Square design with 6 replicates to evaluate the effect of TS (LTS, 0.25%) on enteric CH_4 emissions, by comparing it to a corn and corn silage based control diet (C2). For each study, 12 Holstein steers were individually housed in environmental rooms for 14 d per period. Methane concentrations were monitored in room exhaust air. In the in vitro experiment, both inclusion rates reduced in vitro CH_4 production in all saponin treatments at 24 h incubation ($P < 0.01$), while gas production and pH were not affected ($P > 0.05$). Acetate concentration was reduced in all treatments except 0.5% QS and 0.5% YS ($P < 0.01$). With the exception of the QS 0.5% treatment, all saponin treatments reduced A:P ratio and the NH_4-N concentration compared with the control treatment, at 24hr time point ($P < 0.01$). During both in vivo Exp, feeding saponins to steers did not change ADG or manure excretion characteristics ($P > 0.05$), but decreased DMI with TS saponin supplementation ($P < 0.01$). Methane emission mass, emission factors and manure excretions were not affected by dietary saponin inclusion. Results indicated that dietary supplementation of 0.54 g/kg DM saponin did not decrease ruminal CH_4 emissions.

Key Words: saponin extracts, CH_4 emissions, Holstein steer

W237 Does total condensed tannin concentration predict rumen methane production in vitro? H. D. Naumann*[1], L. O. Tedeschi[1], J. P. Muir[2], B. D. Lambert[2,3], D. K. Andrade Silva[4], and M. A. Fonseca[5], [1]*Texas A&M University, College Station,* [2]*Texas AgriLife Research, Stephenville,* [3]*Tarleton State University, Stephenville, TX,* [4]*Federal Rural University of Pernambuco, Garanhuns, Pernambuco, Brazil,* [5]*Federal University of Viçosa, Viçosa, Minas Gerais, Brazil.*

The US EPA has indicated that 20% of total CH_4 emissions in the US are the result of enteric fermentation in domestic ruminants. Previous studies have indicated that forages containing biologically active condensed tannins (CT) may reduce the amount of CH_4 produced during rumen fermentation. The objective of this work was to verify if the concentration of total CT (TCT) from warm season perennial herbaceous legumes affects CH_4 production in vitro. Five forages commonly fed to ruminants were evaluated, including *Desmanthus illinoensis* (Illinois bundleflower), *Lespedeza cuneata* (sericea lespedeza), *Acacia angustissima* (prairie acacia), *Desmodium paniculatum* (panicled tickclover), and *Arachis glabrata* (rhizoma perennial peanut). Each of these forages was fermented for 48 h under anaerobic conditions. Perennial peanut had the least TCT at 5.69 g/kg DM and produced 110.62 mM CH_4/g DM, which was greater ($P < 0.05$) than the other species surveyed. There was no difference in CH_4 production between Illinois bundleflower and sericea lespedeza ($P > 0.05$), which produced 66.17 and 46.73 mM CH_4/g DM and had TCT concentrations of 81.49 and 82.95 g/kg DM, respectively. There was no difference in CH_4 production between sericea lespedeza and panicled tickclover ($P > 0.05$), which produced 46.73 and 23.26 mM CH_4/g DM, respectively, even though panicled tickclover had the greatest TCT concentration of all plants surveyed at 124.63 g/kg DM, suggesting the type, but not necessarily the amount, of CT might have affected CH_4 production. Prairie acacia had a TCT concentration of 84.66 g/kg DM and produced 6.93 mM CH_4/g DM. Prairie acacia suppressed CH_4 to a greater degree than sericea lespedeza, Illinois bundleflower, and perennial peanut but not panicled tickclover ($P < 0.05$). Results indicated that feeding native warm season perennial herbaceous legumes containing CT is a promising alternative to feeding introduced and potentially invasive species sericea lespedeza as it relates to reducing CH_4 production during fermentation in vitro. In addition, it appears that TCT concentration alone is not a reliable predictor of the CT biological activity relative to CH_4 production by rumen liquid in vitro.

Key Words: condensed tannins, legumes, greenhouse gas

W238 Methane production from novel oat varieties measured by gas production. J. M. Moorby,* A. A. Cowan, D. K. Leemans, and A. H. Marshall, *Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Aberystwyth, UK.*

Methane emissions from sheep fed naked oats has been shown previously to be lower than from sheep fed husked oats or barley, offering the potential of this crop as a potential mitigation option. However, the price of naked oats is significantly higher than that of husked oats, which limits their use. To improve the digestibility of husked oats, a breeding program aimed at producing low-lignin oats with a high oil content has generated several new breeding lines. The methane production potential of these lines was compared with commercial naked oat varieties using the gas production technique. Triplicate ground samples of 1 g DM of each oat whole grain (including the husk, if present) were incubated in dairy cow rumen fluid at 39°C in gas-tight bottles. Gas was removed from the bottles to equalize pressure at 3, 6, 10, 14, 20, 26, 31, 47, 71 and 81 h from the start of incubation, and the methane concentration in the recorded volume was measured. Dry matter residues were weighed to determine apparent digestion. Methane production varied from 28.3 to 46.1 (mean = 35.4, SD = 4.73) ml per g grain DM incubated, and 39.7 and 52.2 (mean = 46.3, SD = 3.68) ml per g of apparently digested DM (adDM). Methane production was negatively related to grain ADL content ($r = -0.86$; $P < 0.001$) but was positively related to DM loss ($r = 0.78$; $P < 0.001$). Methane production per g adDM was also negatively related to grain total fatty acid (FA) content ($r = -0.77$; $P < 0.001$). As the relative proportion (g FA/100g total FA) of some of the unsaturated FA increased, methane production per g adDM decreased (e.g., C18:1, $r = -0.76$; $P < 0.001$). However, because the relative proportions of individual FA did not vary greatly among the different oat lines, the relationships with methane emissions were similar to those of total FA, particularly for those FA in greatest abundance (C16:0, C18:1, C18:2 n-6). In conclusion, breeding husked oats for reduced lignin concentrations and increased FA concentrations to produce more digestible oat with a high oil content offers potential as a ruminant dietary ingredient that could help mitigate methane emissions.

Key Words: oats, methane, gas production

W239 Effect of crude glycerin on methane emissions of male beef calves finished in feedlot. J. F. Lage*[1], T. T. Berchielli[1], I. P. C. Carvalho[1], A. Berndt[2], R. T. S. Frighetto[3], E. San Vito[1], R. A. Silva[1], A. F. Ribeiro[1], L. M. Delevatti[1], E. E. Dallantonia[1], L. R. Simonetti[1], and R. A. Reis[1], [1]*Universidade Estadual Paulista, Jaboticabal, São Paulo, Brazil,* [2]*Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil,* [3]*Embrapa Meio Ambiente, Jaguariúna, São Paulo, Brazil.*

The objective of this study was to evaluate the effects of feeding crude glycerin (CG; 80% glycerol) included as 10% of diet DM to replace corn or soybean hulls in 2 concentrade:roughage ratios (60:40 or 40:60) on enteric methane (CH4) production of young bulls finished in feedlot. Thirty 6 young bulls (Nelore breed) with 374.11 ± 24.77 initial BW, were randomly assigned to 6 treatments, with 6 replicates. The diets were: 1- corn, no CG; 2- CG and corn, 3- CG and soybean hulls. These 3 diets were formulated with 2 concentrate:roughage ratios (60:40 or 40:60), resulting in 6 treatment diets in a 2 × 3 factorial arrangement. The diets were isonitrogenous. Animals were slaughtered at 495.50 kg BW. The CH4 emissions were evaluated using the SF6 tracer gas technique. Five consecutive gas samples were collected in 24-h intervals from each animal. Data were analyzed using the GLM procedure of SAS. Characteristics evaluated in the study were daily carcass gain (CrG, kg.d-1), and CH4 emission expressed in kg of CH4 emitted per year (kg CH4.yr-1), gram of CH4 emitted per day (g CH4.d-1), gram of CH4 emitted per day per kg of metabolic BW (g CH4.d.MBW-1) and kg of CH4 emitted per kg of carcass produced (kg CH4.kg CAR-1). The CrG was not different ($P > 0.05$) among the treatments, with mean values of 0.94 kg.d-1. The CH4 emission was also not different ($P > 0.05$) among the treatments in any unit expressed, with mean values of 62.5 kg.yr-1, 171.2 g.d-1, 1.62 g.d.MBW-1, 0.22 kg.kg CAR-1, respectively. Interaction between concentrate:roughage ratios and feeding regimens was not significant ($P > 0.05$). The evaluated variables did not change ($P > 0.05$) in response to the ratio of roughage utilized (60:40 or 40:60). Animals fed with CG in diet with low or high level of concentrate showed similar enteric methane production.

Key Words: beef cattle, greenhouse, glycerol

W240 Prediction of methane emission from enteric fermentation of growing-finishing Hanwoo steers using IPCC methodology. N. C. Jo*[1], S. Y. Jeong[1], K. H. Park[2], and S. Seo[1], [1]*Chungnam National University, Daejeon, Republic of Korea,* [2]*National Institute of Animal Science, R.D.A., Suwon, Republic of Korea.*

The objectives of this study were 1) to predict methane (CH_4) emissions from enteric fermentation of Hanwoo steers using the Intergovernmental Panel on Climate Change (IPCC) Tier 2 equations and 2) to evaluate and compare the adequacy of the use of the IPCC Tier 2 and the Japanese Tier 3 equations for predicting enteric methane emissions from Hanwoo steers. The values of animal and feed characteristics required for the equations (e.g., BW, ADG, and energy content of feeds) were obtained from Kim et al. (2005). CH_4 emission was calculated by multiplying gross energy (GE) intake with constant CH_4 conversion factor as suggested by IPCC. Methane emission from enteric fermentation of Hanwoo steers was estimated to be 116.3, 93.6, and 99.1 g CH_4 /head/day for the growing, finishing, and overall, respectively. These resulted in an estimated enteric methane emission factor of 36.2 kg CH_4 /head/year for growing-finishing Hanwoo operation. The value was lower than the one estimated using IPCC Tier 1 (53 kg CH_4 /head/year) which is being used for the national inventory report of Korea. When GE intakes were replaced by the values estimated from actual feed intake, estimated enteric methane emission was significantly lower ($P < 0.01$) in the finishing period (80.3 g CH_4 / head/day) and overall (91.7 g CH_4 /head/day). Consequently, enteric methane emission factor was estimated to be 33.5 kg CH_4 /head/year. This imply the IPCC Tier 2 method may overestimate enteric methane emission from Hanwoo especially during the finishing period, which is primarily due to overestimation of GE intake. On the contrary, the Japanese Tier 3 predicted DMI of Hanwoo steers surprisingly well ($R^2 = 0.88$, root mean squared prediction error = 0.4). However, it estimated enteric methane emission factor of 69.1 kg CH_4 /head/year, which is even larger than the default value based on IPCC Tier 1. The discrepancy was due to over-prediction of a percentage of feed energy converted to methane. We concluded that either the IPCC Tier 2 or the Japanese Tier 3 method overestimated methane emissions from enteric fermentation of growing-finishing Hanwoo steers and further research to develop Korean-specific equations and parameter estimates is warranted.

Key Words: Hanwoo steers, enteric fermentation, methane emission factor

W241 Enteric methane emissions by dairy cows grazing temperate pastures. N. Nelson*[1], K. Steensma[1], S. Utsumi[1], D. K. 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 grazing ryegrass (RG) or orchardgrass (OG) pasture on milk production, enteric methane (CH_4) flux and CH_4 per unit of milk by United States Holstein (USH; 552 ± 6 kg BW; n = 24) and New Zealand Friesian (NZF; 342 ± 11 kg BW; n = 6) cows managed with an automatic milking system (AMS) was quantified. Rotational grazing of RG and OR pastures was applied at conservative stocking rates (2.5 cow/ha) using pre- and post-grazing pasture biomass targets of 2400 ± 200 and 1500 ± 200 kg/ha, respectively. Voluntary milking with one single-stall AMS was applied at variable rates of 4 to 2 milkings/day based on DIM and milk yield (MY). In addition to pasture, cows received 1 kg of concentrate per 6 kg of MY. Concentrate was fed in the AMS unit. Mass flux of eructed and expired CH_4 during individual milkings (n = 1,151) was automatically recorded using nondispersive infrared sensors and tracer gas (Greenfeed system, C-Lock Technology Inc., Rapid City, SD). Repeated measures analysis of daily CH_4 fluxes and Pearson correlation of calculated CH_4 fluxes and milk production for a completely randomized design were conducted ($\alpha = 0.05$). Enteric CH_4 flux (g/d) was greater ($P < 0.001$) for USH (384 ± 8) than NZF (281 ± 22) cows, but CH_4 flux per unit of metabolic BW was not different ($P = 0.68$) between the 2 breeds (average: 3.43 ± 0.14 g/kg $BW^{0.75}$). Daily CH_4 flux was affected by a pasture by day interaction ($P = 0.002$), likely influenced by daily decreases in CH_4 flux in RG pastures. Milk yield was not different ($P = 0.84$) between RG and OG pastures (average: 20.5 ± 1.5 kg/cow per d), but MY was greater ($P < 0.001$) for USH (27.2 ± 1.0 kg) than NZF (14.1 ± 1.9 kg) cows. Differences in MY between breeds explained the diluted ($P = 0.05$) CH_4 per unit of milk in USH compared with NZF cows (15.8 ± 0.9 vs. 21.2 ± 2.5 g CH_4/kg milk). There was a positive correlation ($P < 0.001$) between MY and CH4 flux ($r = 0.20$) and a significant negative correlation ($P < 0.001$) between CH_4 emissions per unit of milk and MY ($r = -0.75$), highlighting the importance of high milk production levels as a management strategy to mitigate CH_4 emissions in pasture-based dairy systems.

Key Words: methane, pasture-based dairy, automatic milking

W242 Estimation of greenhouse gas emissions from beef cattle production systems using whole-farm models. A. W. Alemu*[1], K. H. Ominski[1], M. Tenuta[1], and E. Kebreab[2], [1]*University of Manitoba, Winnipeg, MB, Canada,* [2]*University of California, California, Davis.*

Measuring greenhouse gas (GHG) emissions from beef cattle operations is challenging as these are complex systems, composed of multiple interacting components. Whole-farm modeling integrates these components and can be used to determine the effects of change in management practices on net emissions and to develop cost-effective mitigation options. The objectives of this study were to: 1) integrate process-based models into a whole-farm GHG model and 2) compare the outputs from the integrated model with outputs from other whole-farm models under different management practices. Input data for the models were obtained from published literature including a 3-year study which examined GHG emissions associated with the following management practices: no application of liquid hog manure on pasture (baseline), application of manure in fall and spring (split) and single application of manure in spring only (single). An integrated whole-farm model (IM) was developed by integrating the process-based models, COWPOLL and manure-DNDC, as well as aspects of IPPC. Emission estimates from IM were examined along with those generated from HOLOS and the Integrated Farm System Model (IFSM). It was assumed that the simulated cow-calf operation was self-sufficient with regard to feed and bedding. Estimated whole-farm emissions were 13, 15 and 14 kg CO_2 eq/kg animal live weight for the baseline scenario using IM, HOLOS and IFSM, respectively. However, whole-farm emission estimates were higher for split (24 and 19 kg CO_2 eq/kg animal live weight) and single (29 and 19 kg CO_2 eq/kg animal live weight) application using IM and IFSM, respectively. Estimates from all models indicated enteric methane was the major contributor in the baseline scenario (68–74%) whereas enteric methane (36–54%) and soil nitrous oxide (34–51%) were the major contributors for the split and single application. In general, variation was observed among models, not only in estimating whole-farm emissions, but also in the proportion of methane and nitrous oxide produced from the different farm components.

Key Words: greenhouse gas emissions, whole-farm model, beef cattle production

W243 Isotope ratio mass spectrometry monitoring of nitrogen volatilization from cattle feces and ^{15}N-labeled synthetic urine.

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Losses in the nitrogen cycle from manure, to fertilizer, to crops fed to the animal and back to manure are losses of valuable nutrients to the environment in form of gaseous emission or runoff. To minimize these losses, we must first understand the nitrogen source. The objective of this study was to verify the ^{15}N-labeled urea tracer method to determine the fate and origin of nitrogen in manure. A bench-scale manure storage experiment with beef feces and synthetic urine was conducted to monitor the movement of nitrogen (N) via ^{15}N-labeled urea through the system. Isotope ratio mass spectrometry (IRMS) was used to determine the ratio of fecal material vs. urine contribution to loss of ^{15}N and total nitrogen from a manure mixture. Feces were collected from beef cattle and mixed in a 1:2.2 ratio with 10 atom % ^{15}N-labeled synthetic urine. Fresh urine and feces were added daily for 4 d to jars that were connected to a vacuum pump which pulled the exhaust through a sulfuric acid trap solution. Acid traps were exchanged daily and exhausted ammonia was collected for 15 d. All samples (initial urine and feces, acid trap, and final manure mixture) were analyzed for total N and ^{15}N using IRMS. Results showed that nitrogen loss of the manure mix was highest during the first 2 to 3 d of monitoring. The majority of N loss (92.2%, SE = 0.3) occurred from the urine portion of the manure mixture on d 2. On d 15 only 68.6% (SE = 1.1) of the volatilized N was derived from urine. The average N volatilization from urine from d 1 to 15 was 83.7% (SE = 0.1). Nitrogen losses from feces were more variable, being high on d 1 (24.5%, SE = 0.5), decreased to 9.0% (SE = 0.3) on d 5 and gradually increased to 31.4% (SE = 1.2) on the last day of sampling (d 15). This study verified the applicability of IRMS measurements for beef manure mixtures that has previously been verified for dairy systems. The results suggest that further research to explain and model the ammonia/nitrogen release from fecal material is warranted.

Key Words: ammonia volatilization, gas emission, beef cattle manure

W244 Identifying ammonia hotspots on a Colorado dairy using conditional passive samplers and inverse modeling.

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Increasing pressure is being placed on concentrated animal feeding operations to reduce NH_3 emissions as the public becomes more concerned over effects on environmental and human health. The purpose of this study was to identify and monitor strong NH_3 emission zones on a northern Colorado dairy farm using a newly developed conditional sampling system. Passive samplers can be used to measure spatial variations of NH_3 near livestock operations, but results are often confounded by changing weather conditions during extended deployment periods (e.g., 1 to 2 weeks). A new type of conditional sampler was developed that only exposes the passive samplers when a user-defined set of wind and weather conditions are met. Several sampling stations were deployed on a northern Colorado dairy for an 8-wk period during late summer. Stations were placed on the downwind side of potential NH_3 sources, including; the composting area (S1, S2, and S3), lagoon and open-sided freestall barns. Each station contained 2 passive samplers. One sampler deployed whenever weather conditions were met (Full-day), while the other deployed when weather conditions were met between 1000 and 1600 h (Mid-day). Passive samplers were exchanged every 2 wk during the sampling period. Background NH_3 concentrations averaged 19.9 ppb NH_3 over the course of the study. Full-day samplers averaged 430.9, 637.0, and 588.9 ppb NH_3 for S1, S2 and S3, respectively. The sampler downwind of the 4 open-sided freestall barns averaged 321.5 ppb, while the lagoon averaged 1126.5 ppb NH_3. Analysis of all 4 sampling periods yielded similar patterns, with the lagoon consistently producing the highest NH_3 concentrations of the sources measured ($P = 0.02$). An inverse dispersion model also was used to estimate NH_3 emissions from each zone where the samplers were deployed. Deployment of the conditional sampling system on dairies or other livestock operations will help producers identify hotspots of NH_3 emissions, as well as monitor any subsequent changes in emissions resulting from implementation of best management practices. Data will also help quantify farm-specific NH_3 losses for mandatory reporting requirements.

Key Words: environment, emissions, ammonia

W245 Effects of alum and aluminum chloride on volatile fatty acid concentration and pathogen populations in Hanwoo (Korean native cattle) manure.

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Several recent studies have shown that treating animal manure with alum (aluminum sulfate) and aluminum chloride is one of the most effective methods of reducing odor and inhibiting microbial growth.

Of all treatments tested, alum has been intensively used in the poultry industry, but there is little information available on the effects of alum and aluminum chloride on odor and pathogen populations from Hanwoo manure. The objective of this study was to evaluate the effect of applying alum and aluminum chloride on VFA concentration and pathogen populations of Hanwoo manure. A total of 36 steers (8 mo old and averaging 300 kg in weight) were used in this trial and allotted to 9 pens (3 replication pens per group with 4 steers per experimental unit, 5 × 8 m). Chemical additives were applied as a top dressing with garden rake to a depth of 1 cm of manure with wood shavings in each treatment. The treatments were control (without chemical amendments) or 50 g of alum and 50 g of aluminum chloride/kg of Hanwoo manure. The experiment was carried out for 6 weeks. The addition of alum and aluminum chloride reduced ($P < 0.05$) volatile fatty acid concentration (6.2 mM/100 g compared with 9.7 mM/100 g for control) during the 6-wk period. Manure pH was lower ($P < 0.05$) in alum and aluminum chloride treatments (7.5 to 8.4) compared with the controls (9.2 to 9.3) during the 6-wk period. Both levels of the alum and aluminum chloride treatments tested decreased ($P < 0.05$) *Escherichia coli* and *Salmonella enterica* populations (average 4~5.7 log 10 cfu/g manure compared with average 7~7.5 log 10 cfu/g manure in untreated controls) in Hanwoo manure during the 6-wk period. It appeared that the reduction in VFA concentration and pathogen populations was primarily associated with the lower manure pH. If more strict environmental regulations are put into effect regarding VFA concentration and pathogen populations from Hanwoo facilities, treating Hanwoo manure with alum and aluminum chloride may be a good management practice.

Key Words: alum, aluminum chloride, Hanwoo manure

W246 Whole-farm balances of phosphorus and potassium on dairy farms. D. Fulawka, T. L. Garner, K. H. Ominski, D. Flaten, and J. C. Plaizier,* *University of Manitoba, Winnipeg, MB, Canada.*

Imports and exports of phosphorus (P) and potassium (K) were monitored during a 12-mo period on 10 commercial dairy farms in Manitoba. Balances were expressed per kg of milk shipped, milking cow, and ha. The farms differed in housing, feeding, manure management systems, and in the production and purchase of feeds. Imports included feed, bedding, animals, inorganic fertilizer, and manure. Exports included milk, animals, feed, and manure. A farm included the milking herd, the replacement herd, and the fields used to produce feed for these herds. Two farms purchased all their feed and exported all their manure. Results show that P and K balances varied substantially among farms. Based on these balances, P accumulated on all farms and K accumulated all but one farm. On average, the imports of P through feed, inorganic fertilizer, animals, bedding, and manure were 47.8, 47.7, 2.6, 1.7, and 0.2% of total P imports, respectively. The imports of K through feed, inorganic fertilizer, animals, bedding, and manure were, on average, 78.4, 0, 1.4, 20.1, and 0.2% of total K imports, respectively. On average, the exports of P through feed, animals, and milk were 5.4, 9.1, and 85.5% of total P exports respectively. The exports of K through feed, animals, milk, and manure were, on average, 15.3, 3.5, 78.6, and 2.6% of total K exports, respectively. The coefficients of variation (CV) for the import of P through feed, inorganic fertilizer, animals, and manure were 28, 168, 97, and 101%, respectively. The CV for the export of P through feed, animals, milk, and manure were 170, 53, 3, and 262%, respectively. The CV for the import of K through feed, animals, bedding and manure were 74, 112, 128, and 217%, respectively. The CV for the export of K through feed, animals, milk, and manure were 165, 83, 10, and 265%, respectively. This shows that the greatest opportunity to reduce the P balance is through management of inorganic fertilizer and to reduce the K balance is through the reduction of the import of bedding and increasing the export of feed that is not needed. As the largest imports of P and K occur through feed, ensuring that dietary P and K do not exceed requirements is critical in avoiding whole farm surpluses of these minerals.

Table 1.

	Minimum	Median	Maximum	SD
Milking cows	46	82	634	237
Total cows, heifers and calves	64	213	1027	332
Landbase, ha[1]	65	432	1272	446
P balance, g/kg of milk	0.3	2.4	16.8	5.1
P balance, kg/cow yr	4.2	29.1	159.1	48.7
P balance, kg/ha year[1]	1.1	10.5	112.6	37.8
K balance, g/kg of milk	−1.3	3.6	17.6	5.3
K balance, kg/cow yr	−16.9	40.5	156.3	52.1
K balance, kg/ha yr[1]	−4.2	22.7	118.0	38.8

[1] Excluding 2 farms that purchased all feed.

Key Words: phosphorus, potassium, dairy

W247 Foliar uptake and utilization of phosphorus by grazing cattle as influenced by nitrogen fertilization regime. S. L. Dillard,* W. F. Owsley, C. W. Wood, B. H. Wood, and R. B. Muntifering, *Auburn University, Auburn, AL.*

Accumulation of soil nutrients potentially restricts production and land-use options available to resource managers. Efficiency of nutrient utilization may be increased by implementation of management practices that facilitate phytoextraction of nutrients from nutrient-enriched soils. An experiment was conducted to determine the effect of different N-fertilization regimens on foliar P uptake and P utilization by grazing cattle in plots with high soil-test P. In October 2010, 6 0.28-ha plots were overseeded with triticale (*Triticum secale*) and crimson clover (*Trifolium incarnatum*) into a tall fescue (*Lolium arundinacea*)/bermudagrass (*Cynodon dactylon*) sod and assigned randomly to 1 of 3 treatments (trts) (n = 2): 100% of N recommendation for tall fescue in a split application (100N), 50% of N recommendation (50N), and 0% of N recommendation (0N). In February 2011, 6 cattle (339 ± 11 kg; 4 steers, 2 heifers) were randomly assigned to plots (1 animal/plot) until May. In June, plots were overseeded with cowpea (*Vigna unguiculata*) and maintained on the same N-fertilizer regimens, based on N recommendation for bermudagrass. In August, 6 steers (361 ± 23 kg) were randomly assigned to plots (1 steer/plot) until September. Forages were sampled biweekly, and intake and fecal excretion of P was determined for each animal in mid- and late season using Cr dilution technique by reference to forage IVDMD. Data were analyzed as a completely randomized design using a mixed-model in which intake and fecal excretion of P were treated as repeated measures. Forage DM availability ($P = 0.002$) and uptake of P ($P = 0.01$) were greater for cool- than warm-season forage (4,441 vs. 2,311 kg/ha and 8.44 vs. 5.30 kg P/ha, respectively), but were not different among trts. Foliar P concentrations were not different among trts. Daily P intake and excretion were not different among trts (12.2, 11.3 and 13.3 g /d, and 14.8, 15.0 and 11.9 g /d for 0N, 50N and 100N, respectively). Results indicate manipulation of N-fertilization regimen did not affect P removal from plots with high soil P beyond that from overseeded small-grain and annual legumes, and seasonal differences in P removal were not reflected in patterns of P utilization by grazing cattle.

Key Words: phosphorus, cattle, nitrogen

W248 Soil CO_2 emission during the dry season under different grazing intensities in Southern Brazil. L. de Figueiredo Brito, M. Vieira Azenha,* A. R. Panosso, F. H. M. de Souza, A. A. Oliveira, S. S. Santana, R. A. Reis, N. La Scala, and A. C. Ruggieri, *Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil.*

Greenhouse gas emissions have been considered in sustainable livestock production, and the objective of this study was to monitor the soil CO_2 emission in Marandu-grass pasture submitted to continuous stocking with different grazing intensities during the drought period of the year. Three grazing intensities, defined by heights of 15, 25 and 35 cm, were studied in 6 plots (2 plots for each treatment) with 6 replications in each. Soil CO_2 emission and soil temperature were evaluated in 20 d between May 3rd and September 29th, 2011, in all plots, by using a LI-8100 portable Flux System. Data were submitted to variance analysis and Tukey test for mean comparison ($P < 0.05$). Daily soil CO_2 means varied from 0.90 to 5.58 μmol CO_2 m^{-2} s^{-1} with significant reductions probably due to reductions in soil moisture. Higher values were observed at the beginning of the dry season reflecting the importance of soil moisture to biological processes, such as biological activity and root respiration. In the last days of the study, soil respiration reached a minimum, similar to what was observed in relation to plant′s growth. Accumulated monthly precipitation along the wet period before these evaluations were 267, 202, 495 and 92 mm (January to April 2011), and in the drought period the total precipitation was 59 mm (May to September, 2011). On the other hand, while soil CO_2 emission and soil moisture declined, soil temperature increased (18.4°C in May to 22.1°C in September, 2011), indicating that soil moisture was a limiting factor to soil CO_2 production. Total mean values indicate higher grazing intensities (15 and 25 cm) resulted in higher CO_2 emissions, 2.64 and 2.59 μmol CO_2 m^{-2} s^{-1}, respectively, when compared with the lower grazing intensity (35 cm), 2.30 μmol CO_2 m^{-2} s^{-1} ($P < 0.001$). Total CO_2 emission for the period was estimated as being 4.10, 3.93 and 3.48 Mg C ha^{-1}, respectively, for heights of 15, 25 and 35 cm.

Key Words: *Brachiaria brizantha*, carbon cycle, greenhouse gases

W249 Using a batch culture system to measure volatile organic compounds as the primary substrates for methanogenesis in anaerobic digestion of dairy waste. C. L. Ross,* K. C. Das, and M. A. Froetschel, *University of Georgia, Athens.*

Cost effective anaerobic digestion of dairy excrement is limited by its relatively low energy content. As a result, anaerobic digestion of dairy waste requires a greater reactor volume and retention time for stable and efficient methane production. Processing dairy waste to concentrate its volatile organic compound (VOC) content as substrate for methanogenesis could improve digester efficiency and reduce costs associated with volume and retention time. Dairy excrement was processed using different methods to alter its concentration of VOC′s. Bio-conversion of processed dairy excrement into methane was studied in a one-way factorial designed experiment. Processing methods included: A) oven-dried (55°C for 72 h) and ground through a 1mm screen, B) freeze-dried, C) fresh whole manure in a 1:1 water dilution (with solids present), D) a water extract of fresh whole manure from a 1:1 dilution (without solids), or E) dairy excrement processed through an on-farm solid separator. All waste substrates were fermented in batch cultures for 48 h after being inoculated with a mixed culture of rumen microorganisms. Gas production was analyzed for volume and concentrations of methane (CH_4) and carbon dioxide, pH, volatile fatty acid concentration, in vitro dry matter digestion, and free-ammonia. All data were analyzed with SAS 9.2 using PROC GLM. Caloric values of volatile fatty acids and CH_4 were calculated. Process C produced the greatest volume of CH_4 gas, 33–179% more than the other methods ($P < 0.01$). Process C, D, and E had higher concentrations (mM) of acetate ($P < 0.01$) than A or B (C = 43.5, D = 22.3, E = 20.8 vs. A = 1, C = 3.5). C and D both contained more acetate calories (70% and 7%, respectively) than E ($P < 0.01$). Calories of CH_4 were also higher for the C (23.1) and D (17.1) than A (4.4), B (4.9), or E (0.8) ($P < 0.01$). Energetic data implies that substrate processed to contain more VOC′s increasingly fuels methanogenesis. The liquid fraction of dairy excrement contains the VOC′s that may be concentrated to enhance methane production during anaerobic digestion.

Key Words: volatile organic compounds, methanogenesis, anaerobic digestion

Ruminant Nutrition: Beef: Feed Additives

W250 Live yeast and adaptation protocols on finishing feedlot Nellore cattle fed high concentrate diets. P. L. Alvarez,* S. L. Silva, L. S. Martello, M. R. Mazon, L. S. Oliveira, P. H. Cancian, A. C. Ianni, L. Z. Zanoni, R. F. Carvalho, A. P. S. Silva, and P. R. Leme, *Universidade de São Paulo, Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, SP, Brazil.*

Adaptation period on feedlots is a critical step for rumen stability. Inclusion of live yeast on high concentrate diets has been reported to be an alternative to reduce nutritional disorders such as acidosis and ruminitis on beef cattle. The aim of this work was to evaluate the performance and carcass traits of finishing feedlot Nellore (*Bos indicus*) cattle fed high concentrate diets with (LY) or without (CON) live yeast under 2 different adaptation protocols. Fourty-8 Nellore bulls (24 intact and 24 castrated) (372 ± 22.5kg BW; 20-mo) were distributed in individual pens in a randomized block (initial BW) and fed LY or CON diets. Diets were composed by 85% of concentrate (corn grain, corn gluten, soybean meal, mineral salt and monensin) and 15% of sugarcane bagasse as roughage source. Animals were adapted to final diets using step-up (ST) or feed intake restriction (FR) methods. The ST group started with 30% of concentrate increasing 15% each 2 d until it reached 85% while the FR group started with 4.5kg of final diet increasing one kg each 2 d. Both groups achieved the final diets after 10 d. After that, animals were fed for 56 d with LY or CON diets. Feed and orts were registered daily for DMI and F:G determinations. Animals were weighed at the beginning and at the end of adaptation period and then every 28d. Ultrasound measurements of LM area (LMA) and backfat thickness (BFT) between 12th/13th ribs were collected every 28d intervals. Fixed effects of initial BW (block), adaptation protocol, treatment and adaptation protocol x treatment interaction were evaluated using GLM procedure of SAS system. No interactions were observed for any trait. There was no effect of treatment on ADG and DMI on adaptation period. Animals fed FR protocol had higher ADG (1.121 vs 0.580 kg/day; $P = 0.0417$) and F:G (0.158 vs 0.085 kg ADG / kg DMI; $P = 0.0599$) than those fed ST but they did not differ for BW (379 kg) and DMI (6.6 kg). After adaptation period final BW (497 kg), ADG (1.72 kg), DMI (12.2 kg), F:G (0.143 kg ADG/ kg DMI) LMA (76.1 cm2) and BFT (4.1 mm) were not affected by treatments or adaptation protocols. Use of FR protocol improves performance on adaptation period but has no effect on post-adaptation period. LY does not affect feedlot performance.

Key Words: beef cattle, performance, probiotics

W251 Effect of slow release urea supplementation during the dry season on Nellore cattle performance in Brazil. D. P. Pantoni*[1], D. S. Graça[1], M. H. Ramos[2], and P. C. Molina[1], [1]*Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil,* [2]*Research Institute Flávio Guarani - Rehagro, Belo Horizonte, Minas Gerais, Brazil.*

This study was developed to synchronize the release of nitrogen from supplement with carbohydrate from pasture. Forty Nellore bulls (average weight 446 kg ± 24,6) were allowed to graze pastures of *Brachiaria brizantha* 'Marandu' during the dry season (June to September of 2010). Pastures were divided into 3 paddocks of 10 ha each with water and mineral ad libitum and managed in a rotation system. Dry matter availability averaged 5,200 kg of DM/hectare. Forage quality average 6% for CP, 69% for NDF and 51% for IVDMD. Treatments were: only mineral (T1), supplement containing 6% Urea (T2), supplement containing 3% Urea and 3% of slow release Urea (T3), supplement containing 6% of slow release Urea (T4). All supplements contained 15% soybean meal, 67% ground corn and 12% mineral with 200 mg of monensin. Pasture intake was measured using lignin as an internal marker. Cattle was brought together every day, divided by their treatments into pens, and allowed to eat the supplement (average of 1 kg/animal). Statistical analysis was performed using PROC MIXED of SAS (SAS Institute, Cary, NC) with treatment as the experimental unit for performance and animal as the experimental unit for nitrogen variables. There was no difference ($P > 0.05$) in forage consumption expressed as a percentage of BW (2.3, 2.1, 2.2, and 2.1; respectively for T1, T2, T3, and T4). There was no difference ($P > 0.05$) in ADG (316, 327, and 286 kg/d for T2, T3, and T4, respectively) and total gain (22, 23, and 20 kg, for T2, T3, and T4 respectively) between the urea treatments. Blood urea nitrogen (mg/dL) was not different ($P > 0.05$) between T2, T3, and T4. Allantoin (microbial marker) was not different ($P > 0.05$) between treatments (250, 327, 349, and 351 mg/dL, respectively for T1, T2, T3, and T4). Internal rate of return was greater for T2 followed by T3, T4, and finally T1 (19, 17, 10, and −2%, respectively). We concluded that slow release urea did not provide any benefit over conventional urea when Nellore bulls were offered low quality pastures.

Key Words: urea, braquiaria, cattle

W252 Intake, digestibility and digestion kinetics of beef steers supplemented with slow-release urea in diets with two concentrate levels. P. D. B. Benedeti, P. V. R. Paulino,* T. S. Martins, E. F. Lisboa, L. H. P. Silva, C. R. V. Teixeira, L. C. Alves, M. S. Duarte, R. Mezzomo, J. C. M. Lima, J. P. I. S. Monnerat, M. I. Marcondes, and S. C. Valadares Filho, *Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

This study evaluated the effects of replacing soybean meal (SBM) by slow-release urea (SRU) in beef cattle diets containing 2 concentrate levels on intake, partial and total digestibility and digestion kinetics in finishing beef steers. Eight crossbred steers were used (average BW of 418 kg) fitted with ruminal and abomasal cannulas. Total fecal collections were performed to determine digestibility and rumen evacuation was used to determine passage and digestion rates. The animals were distributed in 2 groups of 4 steers, when each group received one of the 2 levels of concentrate (40 or 80% of the total DM). The experiment was designed as a Latin square in 2 × 4 factorial scheme, with 2 concentrate levels in the diet, and within each square, 4 levels of SBM protein replacement by SRU: 0, 33, 66 and 100%. The interaction of concentrate level x SRU levels was not significant ($P > 0.05$) for any variable measured. Dry matter (DM) intake, as well as organic matter (OM) intake and crude protein (CP) intake decreased linearly ($P < 0.05$) as SBM was replaced by SRU. For each percentage unit of SRU added to the diet there was a reduction of 5.80, 5.17 and 0.58 g in DMI, OMI and CPI, respectively. The intake of non-fiber carbohydrates (NFC) was higher ($P < 0.05$) in the diet containing 80% concentrate when compared with the 40% concentrate diet, whereas neutral detergent fiber (NDF) intake was greater ($P < 0.05$) on the low concentrate diet when compared with the high concentrate diet. Ruminal digestibility coefficient of OM tented to be greater ($P < 0.074$) for the 40% concentrate diet, whereas all other ruminal, intestinal and total digestibility parameters evaluated were not statistically different ($P > 0.05$) among treatments. DM and OM passage rates (Kp) were greater ($P < 0.05$) on the 80% concentrate diet than on the 40% concentrate diet. Replacing SBM by SRU up to 100% on the diet did not lead to any modification ($P > 0.05$) on DM, OM, CP and NDF passage rate. Digestion rates (K_d) were also not affected by either concentrate level or SRU level ($P > 0.05$). The average K_d for DM, OM, CP and NDF were 3.82, 4.21, 1.13, and 2.20%/h, respectively.

Key Words: soybean meal, nonprotein nitrogen, feedlot

W253 Dose response effects of laidlomycin propionate plus chlortetracycline or monensin plus tylosin on growth performance, carcass merit and health of growing-finishing beef steers.

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Doses of laidlomycin propionate plus chlortetracycline (LP/CTC) or monensin plus tylosin (M/T) were evaluated in an experiment with growing-finishing steers. No ionophore, low, moderate, and high levels of LP (50, 100 and 150 mg/animal per day) and M (150, 300 and 450 mg/animal per day), respectively were compared. Chlortetracycline (350 mg/animal per day) or T (90 mg/animal per day) were fed in combination with LP or M, respectively. Four-hundred 20 steers (average. initial wt. 357 kg) were randomized by initial BW to 6 blocks (7 pens/block). Steers were on feed for 153 d (3 heavy weight blocks) or 175 d (3 lightweight blocks) at a commercial feedlot facility before slaughter. Ionophores, CTC, and T were added to a non-medicated basal diet using a micro-ingredient allocation machine. Linear (L) and quadratic (Q) effects of ionophore dose were evaluated for growth performance and carcass measurements. Carcass-adjusted final BW, ADG, and hot carcass weights indicated a Q increase ($P \leq 0.05$) with dietary LP level. Dry matter intake and carcass-adjusted DM feed:gain ratio were not affected by LP dose. Neither L nor Q responses were observed for M level on DMI, carcass-adjusted BW, growth performance, or DM feed:gain ratio. Hot carcass weight was not affected by M level. Increasing M level increased number of Prime/Choice carcasses (L and Q); increased marbling score (L and Q); twelfth rib fat thickness (Q); and calculated yield grade (Q). Incidence and severity of liver abscesses were not affected by ionophore type or level. Morbidity and mortality rates from respiratory disease were minimal across treatments. Across dose levels, mean ionophore effects indicated LP increased ($P \leq 0.05$) carcass-adjusted final BW, ADG, DMI and hot carcass weight compared with M, with no difference between ionophores for carcass-adjusted DM feed:gain ratio. Growth performance responses of feedlot cattle may be modified by medicated feed additive program and dietary level of ionophore.

Key Words: ionophore level, laidlomycin propionate, monensin

W254 Adipose gene expression patterns in finishing steers fed steam-flaked corn diets supplemented with dietary *Aspergillus oryzae* extract containing α-amylase activity.

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We evaluated the effect of dietary *Aspergillus oryzae* extract on lipogenic gene expression in finishing beef cattle. Cross-bred yearling steers were randomly assigned to 2 groups (n = 135/treatment). From receiving until d21, starter and step-up diets were fed to acclimate steers to steam-flaked corn. Steers were then fed a finishing diet ad libitum until harvest that met or exceeded NRC requirements: basal diet with or without 5 g/hd/d A. oryzae extract (Amaize, Alltech Inc.) containing α-amylase (AMZ). On d70 and at harvest (d160), adipose tissue was sampled from one steer per pen (n = 15/treatment). Gene expression was profiled using the Affymetrix Bovine Genome Array. Of the 24,000 probe sets on the array, ~60% were expressed in subcutaneous adipose tissue. At d70, 270 genes were affected ($P \leq 0.05$, fold-change ≥ 1.1; 124 upregulated, 146 downregulated) and at d160, 399 genes were affected (176 upregulated, 223 downregulated) by AMZ. At both times the main functions affected were lipid metabolism, cellular development and cell-to-cell signaling/interaction. Gene classification based on gene ontology (GO) using the PANTHER database revealed the most affected GO term was metabolic processes (d70, 90 affected genes; d160, 149 affected genes). Analysis of individually affected genes showed a 1.42-fold ($P = 0.04$) increase in AMZ steers at d70 of peroxisome proliferator-activated receptor gamma coactivator 1 α mRNA, a key gene in fat and energy metabolism. Results suggest AMZ added to a steam-flaked corn finishing diet affects expression of genes involved in metabolism, growth and cellular development in steer adipose tissue. These results offer genomic support to previous findings that AMZ supplementation results in improved performance and carcass characteristics in finishing steers.

Key Words: amylase, beef, gene expression

W255 Effect of *Saccharomyces cerevisiae* CNCM I-1077 supplementation on zootechnical performances and feeding behavior of dairy bull calves during growing period.

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The aim of this study was to evaluate the effectiveness of supplementation with *Saccharomyces cerevisiae* CNCM I-1077 (SC) in the diet of the growing period of dairy bull calves. Sixteen Montbéliarde calves aged 6 mo and weighing on average 251 ± 22 kg at the beginning of the adaptation period were used. The trial was preceded by 28 d of adaptation during which the animals all received the same ration composed of corn silage and 2.5 to 3 kg of concentrate. During the trial′s experimental phase, the animals were fed either with control diet (C), or an experimental diet supplemented with SC (5×10^9 cfu/kg feed). Both groups received corn silage as forage. Animals were fed according to the following program: 1 kg concentrate /100 kg BW and 1 kg DM forage /100 kg BW. The animals were placed in a Roughage Intake Control system (RIC) (8 animals per box, 4 animals per trough), which allowed to record individual feed intake as well as feeding behavior. The experimental period lasted for 56 d. The animals were weighed every 28 d and individual consumption was recorded. The results show that the supplementation with live yeast SC positively influenced the animals ADG compared with C (2.05 ± 0.09 kg/d vs 1.80 ± 0.28 kg/d; $P \leq 0.05$). Moreover, the homogeneity of growth was increased in the SC group. Consumption of feed was higher in the SC group (8.01 ± 0.73 kg DM/head per day vs 7.48 ± 0.49 kg DM/head per day; $P \leq 0.1$). The feed conversion ratio was enhanced by the SC in the diet (3.92 ± 0.35 kg DM/kg live weight for SC vs 4.22 ± 0.43 kg DM/kg live weight for C; $P \leq 0.1$). The SC supplemented animals also showed a different feeding behavior (higher number of visits to the RIC, shorter feeding time per visit and lower quantity ingested per visit; $P \leq 0.05$). This trial shows that the incorporation of live yeast SC stimulates the consumption of dairy bull calves, involving thus a higher weight gain of these animals. The inclusion of SC also reduces the heterogeneity of growth of young bulls during the early stage of fattening.

Key Words: fattening beef, *Saccharomyces cerevisiae* CNCM I-1077

W256 Effects of medicinal feed additive (MFA) program fed with varying levels of wet distillers grains (WDGS) on growth performance, carcass characteristics and health of growing / finishing beef steers.

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Dose level effects of wet corn distillers grains (WDGS) and medicinal feed additive (MFA) program were evaluated. Three hundred twenty yearling steers (average initial weight 320 kg) were randomized in a 2 × 4 factorial arrangement (4 blocks / treatment) with main effects of MFA program consisting of laidlomycin propionate (LP; 11.1 g/DM ton) plus chlortetracycline (350 mg/animal per day; CTC) or monensin (M; 28 g/ton DM) plus tylosin (T; 90 mg/animal per day) and 0, 15, 30 and 45% dietary (DM basis) inclusion level of WDGS . A single source of WDGS was used throughout the study with cattle fed once daily. Cattle were on feed for a total of 179 d before being shipped to a commercial plant for slaughter where carcass and liver abscess data were collected. MFA × WDGS interactions were not observed for any growth, health, or carcass parameter. Growth rate between MFA programs did not differ ($P \geq 0.05$); however, DM intake tended to be greater ($P \leq 0.10$) for LP/CTC and feed efficiency improved ($P \leq 0.05$) by M/T. Carcass measurements and liver abscess incidence were not affected ($P \geq 0.05$) by MFA program. Linear ($P \leq 0.01$) and cubic effects ($P \leq 0.06$) of dietary WDGS were present for bodyweight, growth rate and carcass weight with 15% WDGS having greater response than the 0% diet and 30 and 45% WDGS. Feed efficiency and DM intake were not affected by WDGS level. Marbling score was linearly decreased with increased WDGS level. Overall health was not affected by MFA program; however, apparent morbidity from respiratory disease, while low, was increased ($P \leq 0.05$) with higher WDGS levels. Overall morbidity at the 30 and 45% WDGS levels was increased ($P \leq 0.01$) compared with 0 and 15% inclusion levels, with no differences among WDGS levels for mortality. Alternative MFA programs may have application in feedlot diets containing varying levels of WDGS

Key Words: Ionophore, laidlomycin propionate, wet distillers grains

W257 Basal diet affects ruminal in situ degradation rate of urea and Optigen II in steers.

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The objective of this study was to determine whether basal diet would have an effect on the ruminal degradation of urea and a slow release urea product (Optigen II). The basal diets were 30% vs. 100% forage. The 30% forage diet was offered at 2.4% of BW and was based on fescue hay, cracked corn, cottonseed hulls, soybean meal and urea. The 100% forage diet was offered ad libitum and consisted of fescue hay plus a vitamin and mineral supplement. Intake of the 100% forage diet was approximately 2.2% of BW. Steers were fed once daily at 7am. Four Angus steers (BW = 311 kg) were used in a crossover design with 3 weeks of adaptation to diets before each in situ experiment. Experiments were conducted independently for urea and Optigen II respectively. Triplicate 10-g samples of Optigen II and urea in 5 × 10 cm polyester bags were sequentially inserted into the rumen before simultaneous removal to achieve various incubation times. Incubation times were 0, 5, 10, 15, 20, 30, 40, 50 and 60 min for urea and 0, 1, 2, 6, 10 and 24 h for Optigen II. In situ residues were processed by flash freezing in liquid N then subsequently dissolving residues in a known amount of 1 M HCl. Resulting solutions were incubated at 100°C for 25 min to ensure total dissolution of urea. The determination of urea concentration of the solutions allowed direct quantification of urea disappearance from both sources. Urea disappearance reached a maximum (100%) by 10 min of incubation. Urea disappearance was higher on the 100% forage diet than the 30% forage diet at 5 min (95.3 vs. 77.5%, $P < 0.05$). Urea disappearance from Optigen II was higher on the 100% forage diet than the 30% forage diet for all time points from 2 h onwards ($P = 0.0005$) and the difference was maximum at 24 h (78 vs. 87%, $P < 0.05$). These data demonstrate that diet does affect the degradation characteristics of protected urea. Forage:concentrate affects ruminal pH, passage, viscosity, and lipase and urease activities all of which may contribute to the observed differences.

Key Words: forage:concentrate, NPN, ruminant

W258 Effect of feeding chelated forms of Zn, Cu, and Mn in combination with methionine on growth and reproductive development of heifers.

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Heifer production across most of the US is based upon forage-dominant diets. Methionine is typically the first-limiting amino acid in a forage-based diet. Forages can also vary widely in mineral composition, often being deficient relative to the animal's micromineral requirement. Therefore, the objective of this study was to determine the effect of 2-hydroxyl-4-methyl-thio butanoic acid (HMTBA; MFP) and/or organic trace mineral in the form of Zn, Cu, and Mn (HMTBA; Mintrex), Novus International) supplied to a forage-fed diet on growth and reproductive characteristics of developing heifers. The experiment was carried out in a 2 × 2 factorial design plus negative control. The treatments consist of Negative Control (NEG)- heifers were fed diet without additional Zn, Cu, Mn and MFP supplement; ITM- heifers were fed inorganic Zn, Cu, and Mn (30, 10, 20 mg/kg respectively); ITM + MFP- Supplemental MFP at 15 g/d with inorganic Zn, Cu, and Mn (30, 10, 20 mg/kg respectively); CTM- No MFP- Supplemental Mintrex to supply Zn, Cu, and Mn (30, 10, 20 mg/kg respectively); CTM + MFP- Supplemental Mintrex at levels delivered in Mintrex treatment, MFP was given at 15 g/d. Sixty purchased, weaned and prepubertal heifers were used in this experiment (252.3 ± 23.3 kg). Data were analyzed as a completely randomized design with repeated measurements using MIXED procedure of SAS. There was no significant treatment effect on DMI, ADG, and RTS ($P > 0.05$). Heifers fed MFP had a tendency for higher gain efficiency ($P = 0.10$), compared with no MFP^{TM} heifers. A trend for a mineral by MFP interaction was observed ($P = 0.06$) in serum antibody titer after 4 weeks of vaccination. The combination of CTM and MFP had the greatest serum antibody titers ($P < 0.05$), and CTM, and ITM+MFP treatments had the least. Therefore, supplementation of HMTBA and chelated minerals was effective at improving efficiency and health responsiveness of developing heifers.

Key Words: heifer development, methionine, microminerals

W259 The effect of combination of metal amino acid chelates, Se yeast, mannaoligosaccharides, and dietary antioxidants on the health and growth performance of high-risk calves.

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Calves that are new to the feedyard are often exposed to numerous stressors (weaning, transportation, commingling, dietary restriction, etc.) that cause oxidative stress and compromise health and performance. Cu, Mn and Zn play a role in superoxide dismutase activity and Se in

glutathione peroxidase activity. Dietary antioxidants have been shown to improve overall anti-oxidant status, and mannanoligosaccharides improve the body's natural defense mechanisms. Therefore, the objective of this study was to evaluate the effects of feeding the combination of trace minerals chelated to glycine (MAAC- Zn,- Cu and -Mn), Se yeast (Zorien) dietary antioxidant (Agrado Plus), and mananoligosacharide (Zorien MOS) on growth performance, feed efficiency, and health in receiving calves. The study utilized 955 calves (742 steers and 213 bulls) that were obtained from 2 order buyers through sale barns in SE OK and SE TX with an average initial body wt of 233.6 ± 0.4 kg. The dietary supplements (Control or Treatment) were formulated to contain the same amount of supplemental Zn (320 mg), Cu (120 mg), Mn (200 mg), and Se (0.6 mg) from either organic or inorganic sources. In addition, calves consuming the Treatment supplement were fed 2 g/hd/d Agrado Plus and 20 g/hd/day Zorien MOS. After initial processing, calves were blocked by truckload (1–12), origin (TX vs OK), sex (bull vs steer), and individual body wt (light to heavy). No differences ($P > 0.14$) in body wt, gain, intake, or feed conversion were detected during the 42 d receiving period between Control and Treatment supplement supplemented calves. Calves were highly stressed as evidenced by the high morbidity (68% treated at least once). No differences ($P > 0.27$) between treatments were detected for morbidity, days between re-pulls, medicine cost, realizers, or total out. However, approximately 50% less ($P = 0.05$) calves died when fed the Treatment (1.04%) compared with the Control (2.09%). Therefore, the combination of organic trace minerals, dietary antioxidants and mannanoligosacharides was an effective way to reduce death loss in highly stressed receiving cattle.

Key Words: health, oxidative balance, receiving calves

W260 Effect of addition of increasing doses of chitosan in diets of Nellore cattle on the intake and digestibility total nutrients. R. V. Barletta,* A. P. C. Araújo, R. Gardinal, R. D. Mingoti, B. C. Ventureli, J. E. Freitas Jr., T. H. A. Vendramine, J. R. Gandra, M. C. B. Santos, B. C. Benevento, V. G. C. Lacuna, and F. P. Rennó, *1University of Sao Paulo, Sao Paulo, 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 total apparent digestibility of nutrients. 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 an 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. The total apparent digestibility of nutrients, was determined by the concentration of indigestible acid detergent fiber (iADF). There was quadratic effect ($P < 0.05$) to the NDF intake with the inclusion of chitosan in the diets (2.99; 3.06; 3.09 and 2.91 to the doses CH0, CH50, CH100 and CH150 respectively). The inclusion of chitosan in the diets caused linear increase ($P < 0.05$) to the NDF digestibility (56.62, 60.19, 60.69 and 60.59% for the doses CH0, CH50, CH100 and CH150 respectively). There was increase ($P < 0.05$) to the crude protein digestibility with the inclusion of the chitosan in the diets (63.12, 64,92, 66,49 and 67,51 CH0, CH50, CH100 and CH150 respectively). The total carbohydrate digestibility was positively influenced by dose of the chitosan, probably by effects of the NDF digestibility. The inclusion of the chitosan increased ($P < 0.05$) the total nutrients digestibility, resulting in linear increase (68.07, 70.97, 71.59 and 72.10 to the doses CH0, CH50, CH100 and CH150 respectively). At the significance level of 5% in the analysis by SAS PROC MIXED the inclusion of chitosan in the diet did not affect dry matter intake and obtained positive effects on total apparent digestibility of nutrients.

Key Words: beef cattle, chitosan, metabolism

W261 Ruminal parameters, microbial protein production, protein efficiency and nitrogen balance on beef steers supplemented with slow-release urea in diets with two concentrate levels. P. D. B. Benedeti[1], P. V. R. Paulino*[1], T. S. Martins[1], E. F. Lisboa[1], L. H. P. Silva[1], C. R. V. Teixeira[1], L. C. Alves[1], M. S. Duarte[1], R. Mezzomo[1], J. C. M. Lima[1], J. P. I. S. Monnerat[1], M. I. Marcondes[1], S. C. Valadares Filho[1], and M. Manella[2], *[1]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]Alltech do Brasil, Curitiba, PR, Brazil.*

This study evaluated the effects of replacing soybean meal (SBM) by slow-release urea (SRU) in beef cattle diets containing 2 concentrate levels, on ruminal parameters, microbial protein production, protein efficiency and nitrogen balance in finishing beef steers. Eight crossbred steers (average BW of 418 kg) fitted with ruminal and abomasal cannulas were used. The animals were distributed into 2 groups of 4 steers each, and each group received one of the 2 levels of concentrate (40 or 80% of the total dry matter). The experiment was designed as a double Latin square in a 2 × 4 factorial scheme, with 2 concentrate levels in the diet, and within each square, 4 levels of replacement of soybean meal protein by slow-release urea: 0, 33, 66 and 100%. The diets with different levels of concentrate were applied independently in each Latin square and were fed once daily. Ruminal fluid samples were taken every 2 h after feeding throughout a 24 h period to determine pH and ammonia concentration. A cubic effect ($P < 0.05$) of SBM replacement by SRU on ruminal ammonia ($N\text{-}NH_3$) concentration in relation to the hours of collection was detected. A quadratic effect of replacing SBM by SRU was observed ($P < 0.05$) on pH and on the excretion of urea N in urine, expressed both as g/day or mg/kg of BW. The animals had higher ($P < 0.05$) total N excretion in urine, in g/day, as the slow-release urea levels were increased in the diet, but no significant effects were observed ($P > 0.05$) for total N in urine in mg/kg BW (average of 148.56 mg/kg BW) and for the concentration of urea N in the serum (average value of 11.53 mg/dL). Nitrogen intake, N excreted in feces, nitrogen balance and efficiency of nitrogen use decreased linearly ($P < 0.05$) as the levels of SRU increased in the diet, whereas the amount of nitrogen compounds excreted in urine increased linearly ($P < 0.05$) as SRU replaced SBM in the diet. The production of microbial nitrogen and microbial efficiency were not significantly affected by the experimental treatments ($P > 0.05$) obtaining average values of 173.75 g/day and 128.36 g/kg TDN ingested, respectively. Replacing SBM by SRU decreases nitrogen efficiency utilization in beef steers.

Key Words: feedlot diet, pH, ruminal ammonia

W262 Impact of an all-natural liquid fermentation prototype on performance of feedlot cattle. M. Scott*[1], J. Miles[2], H. Vermaak[3], and S. Schalk[3], *[1]Diamond V, Cedar Rapids, IA, [2]University of Pretoria, Pretoria, Gauteng, South Africa, [3]Essential Nutrient Systems, Pretoria, Gauteng, South Africa.*

As feed costs continue to rise, new technologies that will improve feed efficiency in a safe and consistent manner will become more critical for beef cattle production. With this in mind, a randomized complete block design study utilizing 144 bonsmara-type steers (233 ± 0.8 kg BW) was conducted to examine the effect of a liquid *Lactobacillus* fermentation prototype (LFP; Diamond V, Cedar Rapids, IA) on performance of feedlot cattle. The 134 d study was conducted on a commercial beef research facility in South Africa. Upon arrival, cattle received a feedlot ID tag, were vaccinated and treated for parasites, and were allocated to a free-range pasture for 8 d. On d 9, cattle received a trial ID tag and growth implant, and were re-vaccinated, castrated, and dehorned. Steers were then blocked by arrival body weight and randomly assigned to one of 3 treatments with 8 pens per treatment and 6 steers per pen. Dietary treatments included a control diet that contained 0, 5, or 10 g LFP per head daily. Treatments were provided in the starter (d 9 to 29) and grower diets (d 30 to 43), and in the finishing diet that contained 49% hominy chop, 23% maize, 20% maize plant, 3% soya oil cake, and 5% supplement (DM basis). Data were analyzed using Proc Mixed procedures of SAS with pen as the experimental unit. Data were considered significant at $P < 0.05$ and tendency at $0.05 < P < 0.10$. No differences were detected ($P > 0.10$) among treatments for BW, ADG, or DMI. From d 107 to 134, steers supplemented with 5 g LFP had numerically higher ADG ($P = 0.11$; 1.57 vs. 1.39 kg/d) and improved F:G ($P = 0.16$; 6.54 vs. 7.03) compared with 0 g LFP. Overall (d 9 to 134), F:G was improved ($P = 0.03$) for 5 g LFP supplemented steers compared with those receiving 0 or 10 g LFP (4.70 vs. 4.82, 4.86). Results from this study suggest that LFP does improve feed efficiency of beef cattle fed a typical South African feedlot diet and that the effect was dose dependent.

Key Words: beef cattle, feedlot, *Lactobacillus* fermentation prototype

W263 Effect of β-carotene supplementation on fatty acid profile and expression of genes involved in vitamin A metabolism in beef cattle.

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Thirty Angus-cross calves allotted to 5 treatments were used to examine the effects of dietary β-carotene (βC) or vitamin A (VA) on fatty acid profile and expression of genes involved in VA and lipid metabolism. Treatments consisted of retinyl palmitate (RP) supplemented at the NRC vitamin A requirement (2200 IU/kg), synthetic βC supplemented at 1×, 5×, and 10× the NRC VA requirement, and natural βC (50/50 mix of all-trans and 9-cis-βC) supplemented at 5× the NRC VA requirement. Longissimus muscle (LM), liver, and small intestinal (SI) tissues were collected immediately after slaughter, snap frozen in liquid nitrogen, and stored at −80°C for subsequent analysis of fatty acid profile and mRNA expression by quantitative PCR. β-Carotene monooxygenase 1 (βCMO1) and β-carotene oxygenase 2 (βCO2), the enzymes responsible for symmetrical and asymmetrical cleavage of βC, respectively, were both expressed in the SI. Liver and LM tissues did not express βCMO1, but did express βCO2. Natural βC tended ($P < 0.10$) to increase expression of βCMO in the SI relative to 5× synthetic βC. Expression of βCO2 was not different among treatments ($P > 0.54$) in the liver, but in LM βCO2 expression was increased ($P < 0.01$) in 1× βC compared with VA, tended to decrease ($P < 0.10$) in 5× βC vs natural βC, and decreased linearly ($P < 0.02$) as synthetic βC concentration increased. Expression of alcohol dehydrogenase (ADH1), an enzyme that converts retinol to retinaldehyde, tended ($P < 0.06$) to decrease in the SI as synthetic βC supplementation increased, but did not differ in the liver ($P > 0.36$). The polyunsaturated fatty acid (PUFA) to saturated fatty acid (SFA) ratio increased linearly ($P < 0.05$) as dietary synthetic βC increased because of a linear decrease in SFA concentration ($P < 0.08$), including C16:0, as well as a tendency ($P < 0.10$) for a linear increase in PUFA concentration, including C18:2, as synthetic βC supplementation increased. βC fed at 1× the NRC requirement decreased ($P < 0.04$) the concentration of CLA relative to VA supplemented at the NRC requirement. In conclusion, βC supplementation seems to inhibit expression of enzymes involved in metabolism of βC and VA, potentially allowing these metabolites to accumulate in muscle, thus altering fatty acid profile and fat deposition.

Key Words: beef cattle, β-carotene, gene expression

W407 Analysis of rumen methanogen diversity in cattle divergent for residual feed intake using next generation sequencing technology.

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Methane (CH_4), a potent green house gas, is an undesirable end product of fermentation activity of ruminal methanogens. Production of CH_4 in the rumen represents a significant source of energy loss in cattle, accounting for up to 15% of dietary gross energy intake. Improved residual feed intake (RFI), a measure of energetic efficiency, has been associated with reduced ruminal CH_4 emissions in cattle. However there is little published information on whether the ruminal methanogenic population varies between animals of different RFI phenotype and in particular across different dietary regimen. The aim of this study was to analyze the rumen methanogen community in cattle divergent for RFI using 454 pyrosequencing. Yearling Limousin sired heifers (n = 86) were ranked on the basis of phenotypic RFI over an 80 d period while consuming a 30:70 maize silage to concentrate diet. The 7 highest (HRFI; inefficient) and 7 lowest (LRFI; efficient) ranking animals were selected for use in this study. Both groups had similar mean bodyweight and ADG but HRFI had, on average, 20% higher DMI. Following ranking on RFI all animals were offered (i) a low energy, high forage grass silage diet, followed by (ii) a high energy, low forage, concentrate based diet. Both diets were offered ad libitum for a 6-wk period. Ruminal fluid was sampled at the end of both periods using a specialized trans-esophageal sampling device. Total microbial DNA was isolated from the rumen fluid and amplified using fusion primers, which included sequencing adaptors and a unique 8-base barcode designed to amplify ca. 550-bp region of the 16S rRNA gene. Across RFI phenotype and diet *Methanobrevibacter* spp. were found to dominate, with *Methanobrevibacter smithii* the most abundant species within this genus. Rare phylotypes contributing <5% of sequences were also detected, and were influenced by both host feed efficiency and diet. Thus the rumen microbiome appears to harbour a core group of methanogens and differences in ruminal methane emissions between efficient and inefficient cattle may be due to variation in the relative abundance of specific rare microbial phylotypes.

Key Words: bovine rumen methanogens, pyrosequencing, residual feed intake

Ruminant Nutrition: Co-Products

W264 In vitro intestinal amino acid digestibility of distillers grains varies with grain source and milling process.

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A study was conducted to evaluate the in vitro intestinal digestibility of amino acids (AA) in dried distillers grains with solubles (DDGS) originating from different grain sources (corn vs. wheat) and milling processes (conventional vs. fractional). The experimental feeds were: wheat grain, wheat DDGS (wDDGS), corn grain, corn DDGS (cDDGS) and corn fractional DDGS (fDDGS). Ruminal residues were produced by incubating the feeds in polyester bags for 16 h in the rumen of 3 ruminally cannulated beef heifers fed a diet containing 60% barley silage and 40% barley-based concentrate (DM basis). In vitro intestinal digestibilities of the rumen undegradable protein (RUP) and AA were determined on the residues using a modified 3-step method. In vitro intestinal digestibilities of individual AA were similar for wheat and wDDGS, except for His ($P < 0.05$; 65 vs. 83%) and Glu ($P < 0.05$; 95 vs. 90%). The digestibilities of most AA, especially the individual essential AA (EAA), were lower ($P < 0.05$) for cDDGS than for corn, and as a result, the digestibility of CP, total AA and EAA were lower ($P < 0.05$) for cDDGS (86, 86 and 87%, respectively) than for corn (92, 92 and 91%, respectively). Digestibilities of 3 EAA (His, Met and Thr) were lower ($P < 0.05$) for cDDGS (68, 81 and 83%, respectively) compared with wDDGS (83, 87 and 87%, respectively) with no differences in the digestibility of CP, total AA, and EAA. For fDDGS, 6 individual AA (4 EAA and 2 non EAA), total AA, non EAA and CP had lower ($P < 0.05$) digestibilities compared with cDDGS. The results suggest that the AA availability of DDGS varies with the grain source used to produce ethanol and with the milling process before ethanol fermentation. Information on the intestinal digestibility of individual AA can be used to improve accuracy of diet formulation.

Key Words: AA digestibility, DDGS, in vitro

W265 In vivo determination of undegradable intake protein (UIP) of dried distillers grains with solubles (DDGS) and comparing DAPA and DNA as bacterial markers.

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The objectives of this trial were to determine the undegradable intake protein (UIP) of dried distillers grains with solubles (DDGS) and to compare the estimates of duodenal bacterial crude protein (BCP) flow using either DAPA or DNA as bacterial markers. Three crossbred steers fitted with ruminal and double L-shaped duodenal cannulas (average BW 780 ± 137 kg) were used in a 3 treatment, 6 period crossover design. Animals were housed in individual free stalls and fed twice daily at 0700 and 1900. Diets (DM basis) were 1) CONTROL, 0% DDGS, but with 19.5% corn bran, 20% sorghum silage, 60% brome hay, 0.5% trace minerals and 0.25% urea; 2) LOW DDGS, inclusion of 9.75% DDGS replacing equal percentage of corn bran; 3) HIGH DDGS, inclusion of 19.5% DDGS completely replacing corn bran. On d 16 to 19 of each period, 200 mL of duodenal digesta were collected every 4 h from each animal, then composited by day, by animal within period, lyophilized and analyzed for CP. Duodenal BCP flow was estimated by 2 methods, using DAPA and DNA as bacterial markers. DNA marker was part of the 16S rRNA gene. The UIP of DDGS was determined by difference of residual duodenal CP flow between HIGH DDGS treatment and CONTROL. Data were analyzed using the MIXED procedure of SAS. Average DMI was 10.5kg/d across treatments. The average value of DDGS UIP as a percent of CP was determined to be 63.0 ± 0.64%. Average duodenal BCP flow across treatments was unaffected ($P = 0.71$) by marker type and were 404 and 417 ± 83 g/d for DAPA and DNA markers, respectively. Overall, the value of DDGS UIP determined in this study will contribute to better understand the effect of this byproduct in ruminant nutrition. Duodenal BCP flow tended to decrease with DDGS inclusion, but was not affected by marker type.

Key Words: dried distillers grains with solubles, duodenal bacterial crude protein flow, undegradable intake protein

W266 Urea treatment of different levels of pistachio hull and its relation to gas production in vitro.

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Tannins can inhibit enzymatic and microbial activity therefore affecting gas production. There is very limited information about effects of urea treatment on gas parameters in dietary of tannin. The objective of this study was to evaluate effects of processing of different levels of pistachio hull by urea on gas production in vitro. Experimental treatments were included: Control with 30% alfalfa, 20% straw and 50% concentration (0.42% tannin), T1) 15% alfalfa, 15% PH, 20% straw and 50% concentration (1.06% tannin) and T2) 30% PH, 20% straw and 50% concentration (1.83% tannin). The treatments were incubated with 0.5 and 1 percentage of urea. Gas production was measured (Theodorou et al., 1994; McDonald, 1979). The gas pressure and volume was recorded before incubation (0) and 2, 4, 6, 8, 12, 24, 36, 48, 72, 96 and 120 h after incubation. Gas production kinetics were estimated using the equation described by Ørskov and McDonald (1979), y = a + b (1-exp-ct). Statistical analysis was performed using the 3 × 2 factorial procedure of SAS ($P < 0.05$). Our data exhibited that extent of gas production in treatments incubated with 0.5% urea in T2 was significantly higher vs. T1 and control. Extent of gas production in treatments incubated with 1% urea was significantly affected i.e., the value of gas production in T1 + 1% urea was lower than T2 + 1% urea and control + 1% urea. Indeed, T2 + 1% urea was significantly higher than control + 1% urea. Rate of gas production was not affected when co-incubation was done by 0.5% urea in different treatments while by incubation with 1% urea, the rate of gas production was significantly higher in T1 than control and T2. The treatments were incubated with 0.5 vs. 1% of urea led to increase of extent and reduction of rate of gas production with the exception of T2 which extent and rate of gas production were stable. It seems that urea supplementation can eliminate the negative effects of tannins on gas production.

Table 1. Effect of urea treatment of different levels of pistachio hull gas production parameter

Gas production	Alfalfa		15% PH		30% PH			
parameters	0.5% urea	1% urea	0.5% urea	1% urea	0.5% urea	1% urea	SEM	*P*-value
Extent (ml/gDM)	199.194^{d}	204.128^{bc}	199.937^{cd}	196.598^{d}	205.317^{ab}	208.798^{a}	0.6182	0.0005
Rate (ml/h/g)	0.071^{ab}	0.056^{c}	0.078^{a}	0.079^{a}	0.072^{ab}	0.069^{b}	0.0011	0.0006

$^{a–d}$Means within same row with different superscripts differ ($P < 0.01$).

Key Words: urea, tannin, gas production

W267 Effect of different levels of pistachio hull on in vitro gas production.

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Tannins are a heterogeneous group of phenolic polymers of the plant origin that can be detrimental when consumed by herbivores. Pistachio hull (PH) is a by product that has a high tannin content. Tannins can also inhibit enzymatic and microbial activity and together with inhibition of gas production. The aim of this study was to evaluate effects of different levels of Pistachio Hull on in vitro extent and rate of gas production. The rumen fluid was obtained from 4 fistulated sheep which were fed twice daily with a diet containing alfalfa hay (60%) and concentrate (40%). Experimental treatments were included: Control consisted of 30% alfalfa, 20% straw and 50% concentration (0.42% tannin), T1) 15% alfalfa, 15% PH, 20% straw and 50% concentration (1.06% tannin) and T2) 30% PH, 20% straw and 50% concentration (1.83% tannin). Gas production was measured on procedure (Theodorou et al., 1994; McDonald, 1979). The pressure and volume of gas was recorded before incubation (0) and 2, 4, 6, 8, 12, 24, 36, 48, 72, 96 and 120 h after incubation. The linear regression equation between reading pressure and volume for determination of corrected volume of gas was estimated. Cumulative gas production data were fitted to the model of Ørskov and McDonald (1979), y = a + b (1-exp-ct). Statistical analysis was performed using the MIXED procedure of SAS (2000) using a completely randomized design. Extent of gas production decreased as the amount of tannin in the diet increased, but this decrease was significantly in treatment 2 (1.83% tannin) relative to T1 (1.06% tannin) and control (0.42% tannin; $P < 0.01$). Rate of gas production was not affected by the amount of tannin in experimental treatments. It seems that tannins could be inhibiting for microbial activity and thus reduced the amount of gas production.

Table 1.

Gas production parameters	Alfalfa	15% PH	30% PH	SEM	*P*-value
Extent (mL/g o DM)	212.754^{a}	204.799^{a}	196.334^{b}	0.692	0.003
Rate (mL/h/g)	0.086	0.082	0.084	0.0006	0.129

^{a,b}Means within same row with different superscripts differ ($P < 0.01$).

Key Words: gas production, pistachio hull, tannin

W268 Increased dietary tannin by addition of pistachio hull and its relation to fermentation parameters and protozoa content of rumen in Balochi male lambs.

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Tannins could affect rumen parameters such as pH, NH_3-N and microorganisms. The low rate and extent of protein degradation in the rumen by feeding tannin-rich feeds could lower rumen ammonia concentration. There are many reports indicating inhibitory effect of tannins on rumen protozoa. We aimed to determine the effects pistachio hull (PH) as a tannin source in the diet on rumen pH, N-NH_3 concentration, and protozoa content in Balochi male lambs. Three male lambs (35 ± 2 kg live weight) equipped with ruminal and abomasual cannula were randomly assigned into a changeover 3 × 3 design with 3 treatments: 1) control (alfalfa), 2) 15% alfalfa+15% PH and 3) 30% PH (DM basis). Rumen fluid pH was measured immediately before and every 30 min up to 8 h after the a.m. feeding. Also, rumen fluid was collected from the anterior dorsal, anterior ventral, medium ventral and posterior dorsal and posterior ventral locations within the rumen at 0, 1, 2, 4, 6 and 8 h after the 0800 h feeding for determination of NH_3-N concentration and protozoa count. Data were analyzed as a repeated measurement design using PROC MIXED of SAS ($P < 0.05$), assuming the model included treatment, time, and time × treatment as fixed effects and animal as random effect. Rumen fluid pH was not affected by PH content of diet, although tended to increase as the amount of dietary PH increased. Dietary PH content resulted in a decrease in the rumen N-NH_3 concentration. Protozoa content of rumen was not affected by the amount of PH in the diets, although a tendency to decrease was observed when dietary PH amount increased.

Table 1. Substitution of alfalfa with different levels of pistachio hull (PH) and its contribution to rumen pH, NH3-N and Protozoa count

					P-value		
Rumen parameters	Alfalfa	15% PH	30% PH	SEM	Treat	Time	Treat × Time
pH	6.41	6.48	6.48	0.017	0.331	<0.0001	0.977
NH_3-N (mg/dL)	15.42a	14.91 b	13.96 c	0.060	0.013	0.0003	0.055
Protozoa (Log10/mL)	3.06	3.00	2.99	0.062	0.935	<0.0001	0.540

$^{a-c}$Means within same row with different letter are significantly different ($P < 0.05$).

Key Words: pistachio hull, ammonia nitrogen, pH, protozoa

W269 Effects using of pistachio hull and polyethylene glycol supplementation on feed intake and apparent digestibility of nutrients in Saanen dairy goats.

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Tannins at low concentrations can confer nutritional advantages to ruminants by reducing protein degradation in the rumen and increasing the flow of protein and essential amino acids to the intestine. However, higher concentrations of condensed tannins have deleterious effects on animal performance, digestibility and voluntary intakes. Polyethylene glycol (PEG), react preferentially with condensed tannins and prevents the formation of tannin-protein complexes. The aim of this study was to evaluate the effects of feeding pistachio hull (PH, source of tannin) and PEG supplementation on feed intake and nutrients digestibility in Saanen dairy goats. Nine Saanen dairy goats were used in a 3 × 3 Latin square design with 21-d periods, including 14 d of adaptation followed by 7 d of sampling. Three treatments were formulated: T1) Control, without PH, T2) 30% PH (DM basis) that provided 18.1 g condense tannin per kg DM of diet and T3) 30% PH + 1% PEG (DM basis). In T2 and T3 PH was replaced with alfalfa hay. Statistical analysis was performed using the MIXED procedure of SAS ($P < 0.05$). Dry matter intake (DMI), DMI per body and metabolically weight were not affected in the experimental diets. Organic matter intake (OMI), OMI per body and metabolically weight, ADF, NDF and crude protein intake were significantly decreased in 30% PH (T2) and with the addition of PEG in T3 were significantly increased. Fat intake in T2 (168.40 g/d) and T3 (175.13 g/d) in comparison to Control (150.14 g/d) were significantly increased. DM, ADF and NDF apparent digestibility weren't significantly affected by the diets, but in T2 had a tendency to decrease and with the addition of PEG in T3 showed an increasing trend. OM and CP apparent digestibility were significantly decreased in T2 and with the addition of PEG in T3 were significantly increased. Fat apparent digestibility in T2 (84.95%) and T3 (85.98%) vs. Control (83.91%) was significantly increased. This study has shown that pistachio hull can replace alfalfa hay in diets for goats when PEG is given as a supplement.

Key Words: pistachio hull, feed intake, apparent digestibility

W270 Effects of feeding pistachio hull and polyethylene glycol (PEG) supplementation on milk fatty acids composition in Saanen dairy goats.

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Decreasing the level of saturated fatty acids (SFA) and increasing monounsaturated FA (MUFA) and polyunsaturated FA (PUFA) content in ruminant's milk would be beneficial for human health and would be of commercial interest. It is also recognized that tannins affect rumen biohydrogenation therefore increase the MUFA and PUFA content of milk and meat. We aimed to evaluate the effects of feeding pistachio hull (PH, source of tannin) and PEG supplementation on milk fatty acids composition in Saanen dairy goats. Nine Saanen dairy goats were used in a 3 × 3 Latin square design. Treatments were T1) Control, without PH, T2) 30% PH (DM basis) that provided 18.1 g tannin per kg DM of diet, and T3) 30% PH + 1% PEG (DM basis). In T2 and T3, PH replaced alfalfa hay. Milk fatty acids were analyzed on a Gas Chromatography with a flame-ionization detector and column. Statistical analysis was performed using the MIXED procedure of SAS ($P < 0.05$). Concentration of UFA, MUFA, and PUFA in treatments including of tannin (with PH) were significantly higher than control (without PH). Conversely, concentration of SFA and medium-chain FA (MCFA) in T2 were significantly lower than the control and with addition of PEG in T3 were significantly increased relative to T2. Concentration of short-chain FA (SCFA) in T2 and T3 was significantly lower than the control. Long-chain FA (LCFA) in T2 was significantly higher than the control and with addition of PEG in T3 was significantly decreased relative to T2. In conclusion, tannin has the ability to reduce SFA and to increase UFA. PEG will reverse this effect but not to the control levels.

Table 1. Effect of PH and PEG on milk fatty acids composition

Milk FA composition	Alfalfa	30% PH	30% PH+PEG	SEM	*P*-value
SFA	67.056^{a}	54.642^{c}	63.077^{b}	1.840	0.0001
UFA	32.940^{c}	46.746^{a}	37.910^{b}	2.023	0.0003
MUFA	28.018^{c}	40.666^{a}	31.527^{b}	1.888	0.0006
PUFA	4.922^{b}	6.080^{a}	6.383^{a}	0.223	0.0059
SCFA	5.408^{b}	3.295^{a}	3.967^{a}	0.312	0.0027
MCFA	26.706^{a}	14.996^{c}	21.981^{b}	1.702	0.0011
LCFA	67.882^{c}	81.697^{a}	74.039^{b}	2.013	0.0061

$^{a–c}$Means within the same row with different letters are significantly different ($P < 0.01$).

Key Words: fatty acids composition, tannin, goat

W271 Milk fatty acid profile of Saanen dairy goats fed diets containing pistachio hull tannin and polyethylene glycol supplementation.

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Tannins ability to modify the fatty acid composition of milk and meat has received great attention recently. There is limited information pertaining the effects of tannins on ruminal biohydrogenation process and content of C18:1, trans-11 (vaccenic acid) and C18:2, cis-9, trans-11 CLA (rumenic acid) in ruminants meat and milk. We aimed to evaluate the effects of feeding pistachio hull (PH, source of tannin) and polyethylene glycol (PEG) supplementation on milk fatty acid profile particularly vaccenic and rumenic acid in Saanen dairy goats. Nine Saanen dairy goats were used in a 3 × 3 Latin square design. Three treatments were formulated: T1) Control, without PH, T2) 30% PH (DM basis) that provided 18.1 g condense tannin per kg DM of diet and T3) 30% PH + 1% PEG (DM basis). In T2 and T3, PH replaced alfalfa hay. Statistical analysis was performed using the MIXED procedure of SAS ($P < 0.05$). Percentage of C18:1, trans-9, C18:1, cis-9 and C18:1, trans-11 (vaccenic acid), and C18:2, cis-9, trans-11 CLA (rumenic acid) significantly increased with addition of PH in T2. Blocking of PH with PEG significantly reduced the fatty acids but not to the same level as control group. Percentage of C18:0, C18:2, trans-9, 12, C18:2, cis-9, 12, and C18:3, cis-9, 12, 15 with increasing PH in T2 significantly increased and addition of PEG in T3 could not reduce them back to levels of control group. In conclusion, addition of PH could increase the level of polyunsaturated acids content of goat milk and PEG supplementation will conserve it while blocking PH tannin content.

Table 1.

Milk FA profile (%)	Alfalfa	30% PH	30% PH+PEG	SEM
C18:0	9.901^{b}	12.454^{a}	11.566^{a}	0.381
C18:1, trans-9	4.040^{c}	9.950^{a}	7.232^{b}	0.854
C18:1, cis-9	21.620^{c}	26.837^{a}	21.965^{b}	0.869
C18:1, trans-11	3.825^{c}	5.511^{a}	4.214^{b}	0.255
C18:2, cis-9,trans-11CLA	1.286^{b}	2.156^{a}	1.817^{c}	0.126
C18:2, trans-9,12	2.187^{b}	2.882^{a}	2.788^{a}	0.110
C18:2, cis-9,12	2.216^{b}	2.64^{a}	2.944^{a}	0.108
C18:3, cis-9,12,15	0.519^{b}	0.558^{a}	0.651^{a}	0.022

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

Key Words: Saanen goat, tannin, milk fatty acids

W272 Effects of pistachio hull and polyethylene glycol supplementation on milk yield and compositions in Saanen dairy goats.

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Evaluation of dietary containing tannin for animal performance was very varied. We aimed to investigate the effects of pistachio hull (PH, source of tannin) and polyethylene glycol (PEG) supplementation on milk production and milk composition in early lactation Saanen goats. Nine Saanen dairy goats (average DIM, 71.5 ± 6.5 d; milk production, 1.5 ± 0.25 kg; and live body weight, 45 ± 1.75 kg) were used in a 3 × 3 Latin square design with 21-d periods, including 14 d of adaptation followed by 7 d of sampling. Three treatments were formulated: T1) Control, without PH, T2) 30% PH (DM basis) that provided 18.1 g condense tannin per kg DM of diet and T3) 30% PH + 1% PEG (DM basis). In T2 and T3, PH replaced alfalfa hay. Goats were milked 2 times in day and milk yield was recorded. Milk samples were taken at the 3 last days of sampling. Statistical analysis was performed using the MIXED procedure of SAS ($P < 0.05$). Treatment means were compared using Duncan′s New Multiple Range test. The results showed that milk, fat corrected milk (FCM), and energy corrected milk (ECM) yields together with milk efficiency were not affected by experimental diets. Milk fat, lactose and solids not fat (SNF) percentage were not affected by addition of PH and PEG. Milk protein percentage in T2 in comparison to control was significantly decreased. Fat and protein yield (kg/d) were not affected by the experimental diets. In conclusion, use of tanniniferous sources had no negative effects on milk production and composition of goats except protein percentage that can be compensated partly by addition of PEG. However, goats are able to consume large amounts of tannin-rich plant material in comparison to other ruminant species.

Table 1.

Milk production and composition	Alfalfa	30% PH	30% PH+PEG	SEM
Milk yield (kg/d)	1.453	1.438	1.546	0.088
FCM 4% (kg/d)	1.288	1.281	1.355	0.075
ECM (kg/d)	1.438	1.356	1.451	0.083
Milk efficiency	0.622	0.628	0.659	0.037
Fat%	3.252	3.295	3.258	0.062
Protein%	3.085^{a}	2.881^{b}	2.910^{ab}	0.041
Lactose%	4.251	4.334	4.347	0.046
SNF (%)	8.460	8.245	8.102	0.092
Fat (kg/d)	0.047	0.047	0.049	0.015
Protein (kg/d)	0.044	0.041	0.044	0.002

[a,b]Means within same row with different superscripts differ ($P < 0.05$).

Key Words: Sannan goat, tannin, milk yield and composition

W273 Liver enzymes and immune system response of Saanen dairy goats supplemented with pistachio hull and polyethylene glycol.

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High tannin diets may increase the clinical symptoms of intoxication in ruminants. Toxic effects are reflected by damage in the liver, kidneys and the epithelium of the digestive tract. Polyethylene glycol (PEG) can neutralize the toxic effects of tannins. The aim of this study was to evaluate the effects of feeding pistachio hull (PH, source of tannin) and PEG supplementation on the liver enzymes i.e., alanine aminotransferase (ALT) and aspartate aminotransferase (AST) and blood factors such as packed cell volume (PCV), mean corpuscular hemoglobin concentration (MCHC), total white blood cells (TWBC), neutrophils, eosinophils, lymphocytes, monocytes, and hemoglobin in Saanen dairy goats. Nine Saanen dairy goats were used in a 3 × 3 Latin square design. Three treatments were formulated: T1) Control, without PH, T2) 30% PH (DM basis) that provided 18.1 g condense tannin per kg DM of diet and T3) 30% PH + 1% PEG (DM basis). In T2 and T3, PH replaced alfalfa hay. Statistical analysis was performed using the MIXED procedure of SAS ($P < 0.05$). Immune factors and liver enzymes were not significantly affected by the exprimental diets. But, plasma concentration of MCHC and hemoglobin and percentage of PCV in T2 had a tendency to decrease and was removed by PEG addition in T3 (with $P = 0.534$, $P = 0.735$ and $P = 0.732$ for MCHC, hemoglobin and PCV, respectively). Conversely, concentration of ALT and AST and number of TWBC, neutrophil, eosinophil, lymphocyte, and monocyte in T2 had a tendency to increase and was removed by PEG addition in T3 (with $P = 0.791$, $P = 0.931$, $P = 0.794$, $P = 0.399$, $P = 0.928$, $P = 0.659$, $P = 0.933$ and $P = 0.368$ for ALT, AST, TWBC, neutrophil, eosinophil, lymphocyte and monocyte, respectively).

Table 1.

Immune plasma factors	Alfalfa	30% PH	30% PH+PEG	SEM
AST (U/L)	86.44	100.44	98.66	2.621
ALT (U/L)	57.66	62.05	60.50	2.284
PCV (%)	28.55	28.11	28.44	0.343
MCHC (g/dL)	31.44	30.44	30.77	0.495
Hemoglobin (g/dL)	8.90	8.57	8.74	0.149
TWBC (cells/UL)	9566.67	10256.00	9922.22	508.690
Neutrophil: adult (cells /UL)	4832.44	5474.67	5371.33	275.555
Eosinophil (cells /UL)	140.89	178.33	145.56	19.819
Lymphocyte (cells /UL)	4288.56	4433.33	4377.33	228.582
Monocyte(/UL)	80.22	144.67	106.33	17.576

Key Words: tannin, immune system, goat

W274 Effects of pistachio tannins on nitrogen metabolism in Balochi male lambs.

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The decreased rate and extent of protein degradation in the rumen as observed due to feeding of tannin-rich feeds could lower ammonia concentrations in the rumen and hence urea N excretion in urine. The tannins shift the site of N metabolism from rumen to the lower digestive tract and large intestine. Shifting excretion pattern of nitrogen from urine to feces and formation of tannin—protein complex are beneficial environmentally. We aimed to evaluate if tannin rich diets (pistachio hull (PH) as a tannin source) manipulate intake, digestion, excretion and retention of nitrogen in Balochi male lambs. Three male lambs (35 ± 2 kg live weight) equipped with ruminal cannula were randomly assigned into a changeover 3 × 3 design. Treatments were: 1) control (alfalfa), 2) 15% alfalfa+15% PH that provided 10.59 g/kgDM tannin, and 3) 30% PH that provided 18.28 g/kgDM tannin. Statistical analysis was performed using the MIXED procedure of SAS ($P < 0.05$). As tannin was increased in the diets, the nitrogen intake linearly and quadratic was decreased, rumen N-NH3 concentration linearly was decreased, and nitrogen excretion from urine and digested nitrogen linearly were decreased. Nitrogen excretion from fecal linearly and quadratic and retained nitrogen linearly were increased, by increased of dietary tannin. Thus, effects of tannins to reduce the degradation of protein in the rumen and nitrogen excretion from urine and to increase the nitrogen excretion from fecal and retained nitrogen due to N metabolism in the large intestine could have important role to improve nitrogen efficiency in lambs.

Table 1.

	Alfalfa	15% PH	30% PH	SEM	*P*-value	
					Linear	Quadratic
Nitrogen intake (g/d)	14.70^a	14.05^b	13.92^c	0.121	0.0005	0.003
Rumen NH$_3$-N (mg/dL)	15.42^a	14.91^b	13.96^c	0.060	0.013	0.055
Nitrogen excretion from urine (g/d)	3.37^b	3.80^b	4.72^a	0.204	0.012	0.203
Nitrogen excretion from fecal (g/d)	7.12^a	4.25^b	2.15^c	0.720	0.0003	0.034
Digested nitrogen (g/d)	9.36^a	7.49^b	6.75^b	0.417	0.021	0.230
Retained nitrogen (g/d)	4.21^c	5.99^b	7.11^a	0.423	0.001	0.077

$^{a–c}$Means within same row with different letters are significantly different ($P < 0.05$).

Key Words: pistachio, nitrogen metabolism

W275 Different levels of tannin by dietary addition of pistachio hull and plasma metabolic profile in Balochi male lambs. A. Rahimi[1], A. A. Naserian[1], R. Valizadeh[1], A. Tahmasbi[1], and B. Saremi*[2], *[1]Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran, [2]Bonn University, Bonn, Germany.*

Pistachio hull (PH) is a byproduct that has high tannin concentration. Tannins can reduce the digestion of nutrients, especially proteins. We aimed to evaluate the effects of diets containing tannin on plasma metabolic profile of Balochi male lambs. Pistachio hull as a tannin source (with 6.68% tannin and 9.95% total phenol content) was used in diets of 3 male lambs (35 ± 2 kg live weight) which were randomly assigned into a changeover 3 × 3 design. Treatments were: 1) control (alfalfa), 2) 15% alfalfa+15% PH and 3) 30% PH (DM basis). Blood samples were taken from the jugular vein at 0, 2 and 4 h after the 0800 h feeding for measuring glucose, total protein, blood urea nitrogen (BUN), albumin, aspartate aminotransferase (AST), alanine aminotransferase (ALT), triglycerides and cholesterol. Data were analyzed as a repeated measurement design using PROC MIXED of SAS ($P < 0.05$), assuming the model included treatment, time, time × treatment as fixed effects and animal as random effect. Blood metabolites glucose, albumin, BUN, AST and ALT were not affected by the experimental diets ($P = 0.778$, $P = 0.264$, $P = 0.281$, $P = 0.538$ and $P = 0.899$ for glucose, albumin, BUN, AST and ALT, recpectively). Total protein was decreased as the dietary PH content (Tannin source) increased ($P = 0.003$). Plasma triglyceride concentration was significantly increased ($P = 0.0008$). The fat metabolite i.e., cholesterol ($P = 0.913$) was not influenced by PH content of diet.

Table 1. Effect of different levels of tannin by dietary addition of pistachio hull on plasma metabolic profile

Plasma metabolites	Alfalfa	15% PH	30% PH	SEM
Glucose (mg/dL)	57.22	58.44	57.33	0.947
Total protein (g/dL)	7.73^a	7.50^b	7.26^c	0.082
BUN (%)	10.95	10.64	10.01	0.161
Albumin (g/dL)	2.77	2.61	2.43	0.065
AST (U/L)	54.44	58.11	63.22	1.462
ALT (U/L)	28.11	29.44	30.21	1.053
Triglycerides (mg/dL)	3.89^c	4.27^b	5.36^a	0.126
Cholesterol (mol/L)	1.42	1.50	1.57	0.078

$^{a–c}$Means within same row with different superscripts differ ($P < 0.05$).

Key Words: metabolic profile, plasma, tannin

W276 Replacing alfalfa with different levels of pistachio hull and its effects on feed intake and digestibility of nutrients in total tract, rumen and post-rumen in Balochi male lambs. A. Rahimi[1], A. Ali Naserian[1], R. Valizadeh[1], A. Tahmasbi[1], A. R. Shahdadi[3], and B. Saremi*[2], *[1]Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran, [2]Institute of Animal Science, Physiology & Hygiene Unit, University of Bonn, Germany, [3]Agriculture Sciences and Natural Resources University of Gorgan, Gorgan, Iran.*

Dietary tannins can exert either positive or negative effects on ruminants' nutrition and performance. Pistachio hull (PH) is a by-product containing high amount of tannin. Herein we determined the effects of replacing different levels of alfalfa with PH on feed intake and digestibility of nutrients in total tract, rumen and post-rumen in Balochi male lambs. Three male lambs (35 ± 2 kg live weight) equipped with ruminal and abomasal cannula were randomly assigned into a changeover 3 × 3 design and fed the experimental diets for 35 d, 20 d adaptation, 5 d collection and 10 d break time between the 3 periods. Treatments were: 1) control (alfalfa), 2) 15% alfalfa+15% PH and 3) 30% PH (DM basis). Statistical analysis was performed using the MIXED procedure of SAS. Least squares means were separated using the LSD. Total dry matter intake (DMI), organic matter intake (OMI), DMI and OMI per kg of body and metabolic weight, CP, ADF, NDF and fat intake were not different between treatments. Total tract and ruminal digestibility for DM, OM, ADF and NDF was not significantly affected by the diets, but CP in total tract and its ruminal digestibility were linearly decreased with 66.03, 60.11 and 55.50% for total tract ($P = 0.011$ and SEM = 1.616) and 59.97, 53.67 and 49.17 for ruminal digestibility ($P = 0.022$ and SEM = 1.718) for 0, 15 and 30% PH respectively. Total tract and ruminal digestibility of fat were linearly increased with 78.97, 80.37 and 82.43% for total tract ($P = 0.025$ and SEM = 0.529) and 11.98, 17.47 and 21.98 for ruminal digestibility ($P = 0.027$ and SEM = 1.558) as the amount of PH in the diet increased. Post-ruminal digestibility of OM, Fat, ADF and NDF was not significantly affected by the diets while DM decreased ($P = 0.037$ and SEM = 0.419) from 29.03 to 28.64 and 27.31 and CP increased ($P = 0.049$ and SEM = 0.642) from 7.90 to 10.52 and 12.21 for 0, 15 and 30% PH respectively.

Key Words: pistachio hull, feed intake, digestibility

W277 Effect of increasing amounts of corn dried distillers grains with solubles in dairy cow diets on enteric methane emissions, digestibility, and milk production. C. Benchaar*[1], F. Hassanat[2], R. Gervais[2], P. Y. Chouinard[2], C. Julien[3], F. Tremblay[1], D. I. Massé[1], and H. V. Petit[1], *[1]Dairy and Swine Research and Development Centre-Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [2]Département des Sciences Animales-Université Laval, Québec, QC, Canada, [3]INRA-Université de Toulouse, Castanet-Tolosan, France.*

Twelve lactating Holstein cows (DIM = 99 ± 18; BW = 645 ± 49kg) were used in a triplcated 4 × 4 Latin square (35-d periods, 14-d adaptation) to examine the effect of including increasing amounts (0, 10, 20 and 30%, DM basis) of corn dried distillers grains with solubles (DDGS) in the diet on enteric CH$_4$ emissions, digestibility, and milk production. Diets were isonitrogenous (CP = 16.9%) and isocaloric (NE$_L$ = 1.64 Mcal/kg) and fed for ad libitum intake. Production of CH$_4$ was measured (3 consecutive days) using respiration chambers. Digestibility and milk performance were determined over 6 consecutive days. Linear and quadratic contrasts (Proc MIXED; SAS) were used to determine effects of dietary DDGS levels on variable responses. Significance was declared at $P \leq 0.05$. Dry matter (DM) intake increased linearly as DDGS proportion increased in the diet (23.4, 24.4, 24.8 and 25.2 kg/d for 0 to 30% DDGS, respectively). Digestibility of DM (70.7, 70.2, 69.6, and 68.1% for 0 to 30% DDGS, respectively), and energy (69.6, 69.2, 68.7, and 67.6% for 0 to 30% DDGS, respectively) declined linearly as DDGS level in the diet increased. Milk yield increased linearly (up to + 4 kg/d) with increasing levels of DDGS in the diet. Milk fat (3.93 to 3.47% for 0 to 30% DDGS, respectively) and milk protein (3.49 to 3.31% for 0 to 30% DDGS, respectively) contents decreased linearly with the addition of DDGS in the diet. There was a tendency ($P = 0.10$) for a quadratic increase in energy corrected milk (ECM) as the proportion of DDGS in the diet increased. Methane production decreased linearly with increasing levels of DDGS in the diet (495, 490, 477 and 475 g/d for 0 to 30% DDGS). When adjusted for gross energy intake, CH_4 losses also decreased linearly as DDGS proportion increased in the diet (5.53, 5.30, 5.14, 4.76% for 0 to 30% DDGS, respectively). When expressed relative to ECM, CH_4 production declined linearly as the amount of DDGS increased in the diet. Results from this study show that feeding DDGS to dairy cows can help to mitigate enteric CH_4 emissions without negatively affecting intake and milk production.

Key Words: corn DDGS, methane, dairy cows

W278 The effect of feeding canola meal on the performance of Chinese Holstein cows.

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The objective of this study was to evaluate the effects of canola meal (CM) on the lactational performance of Chinese Holstein cows. One hundred multiparous Chinese Holstein cows average 102 ± 38.13 d in milk were randomly assigned to one of 5 treatments. During the 8-wk periods, cows were fed total mixed diets containing 21.8% soybean meal (control), 16.4% soybean meal and 6.3% CM (CM1), 10.9% soybean meal and 12.6% CM (CM2), 5.5% soybean meal and 19% CM (CM3) or 25.3% CM (CM4) as the major protein source. All diets had a 60:40 forage-to-concentrate ratio, and were formulated to be isonitrogenous at 16.25% CP. Results showed that dry matter intake did not differ among control, CM1 and CM2 (17.54, 17.53 and 17.55 kg/d), but was lower for CM3 andCM4 (17.27 and 17.19 kg/d, $P = 0.03$). Milk yield (26.3, 26.4, 26. 5, 26.3 and 26.2 kg/d) was no different ($P = 0.11$) when CM replaced soybean meal and corn except when the percentage of CM reached 25.3% DM. Milk SNF, TS, fat and protein percentages decreased for CM4 compared with other groups, but only the percentage of milk SNF and protein reached a significant level ($P < 0.05$). Milk fat yield was higher for CM1 ($P = 0.02$) and CM2 ($P = 0.02$) compared with other groups. Milk protein yield was affected among CM1, CM2, CM3, CM4 and control (0.78, 0.74, 0.81, 0.71, 0.87 kg/d. for, CM1, CM2, CM3, CM4 and control respectively). The percentage of milk lactose was higher for control compared with the other four treatments, whereas the milk lactose yields of CM1 and CM2 were higher than control, CM3 and CM4. Results of this study showed that maximum economic payback could be obtained when the dairy ration was formulated to contain about 12.6% CM (DM basis).

Key Words: canola meal (CM), performance, Chinese Holstein cows

W279 Effects of limit-feeding dried distillers grains to ewes during mid- to late-gestation on ram progeny post-weaning performance and carcass composition.

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Mature Polypay and Hampshire ewes (n = 48; BW = 83.1 ± 2.7 kg) were used to evaluate the effects of maternal dietary energy source fed during mid- to late-gestation on postnatal progeny performance. Ewes were blocked by breed (n = 2) and BW (n = 3), stratified by age, sire, and fetal number, and randomly assigned to pens (n = 12). Pens were allocated to 1 of 2 treatments: ad libitum alfalfa hay (H) or limit-fed dried corn distillers grains plus solubles (D) as the primary dietary energy source from 63 to 130 ± 6 d of gestation then removed from experimental treatments and managed as 1 group until weaning (66 ± 9 d). All ram lambs (n = 25) were fed the same diet as 1 group: whole shelled corn (82.5%), commercial finishing pellet (12.5%, 150 g/t lasalocid), molasses (3.75%), calcium carbonate (0.75%) and ammonium chloride (0.5%) on DM basis. Rams were weighed bi-weekly until slaughter at 114 ± 9 d post-weaning. At slaughter, KPH was removed before collecting HCW. Carcass measurements were collected 24 h after slaughter. Ram lambs from Hampshire ewes fed D during gestation tended ($P = 0.08$) to be lighter at slaughter than lambs from Hampshire ewes fed H or Polypay ewes fed D or H, whereas ADG was similar ($P = 0.34$) for rams between treatments from weaning to slaughter. Hampshire ram progeny from ewes fed H had greater ($P = 0.05$) HCW than those from Hampshire ewes fed D and Polypay ewes fed H but not different than ram progeny from Polypay ewes fed D. Organ weights, KPH, and mesenteric fat as % HCW were similar ($P \geq 0.17$) among treatments. No differences ($P \geq 0.55$) were detected in 12th rib fat thickness, body wall thickness, intramuscular fat (% ether extract), or LM area, however, lambs from Hampshire ewes fed H had greater ($P = 0.05$) percentage of boneless trimmed retail cuts than lambs from Polypay ewes fed H. Measurements for USDA quality grade (leg score and conformation) were also similar ($P \geq 0.47$) among treatments. Feeding D versus H to ewes in mid to late gestation resulted in no difference in post-weaning growth performance but slight differences in ram progeny carcass weight.

Key Words: distillers grains, fetal programming, sheep

W280 Effect of dried distillers grains with solubles (DDGS) on duodenal microbial crude protein (MCP) flow in steers as determined with DNA microbial markers.

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The objectives of this trial were to evaluate the effect of dried distillers grains with solubles (DDGS) on duodenal flow of bacterial crude protein (BCP), protozoal crude protein (PCP) and yeast crude protein (YCP) in steers fed DDGS. Three crossbred steers fitted with ruminal and double L-shaped duodenal cannulas (average BW 780 ± 137 kg) were used in a 3 treatment, 6 period crossover design. Animals were housed in individual free stalls and fed twice daily at 0700 and 1900. Diets (DM basis) were 1) CONTROL, 0% DDGS, but with 19.5% corn bran, 20% sorghum silage, 60% brome hay, 0.5% trace minerals and 0.25% urea; 2) LOW DDGS, inclusion of 9.75% DDGS replacing equal percentage of corn bran; 3) HIGH DDGS, inclusion of 19.5% DDGS completely replacing corn bran. On d 16 to 19 of each period, 200 mL of duodenal digesta were collected every 4 h from each animal, then composited by day, by animal within period. Duodenal microbial crude protein (MCP) was estimated using DNA as microbial markers. For bacteria, marker was part of the 16S rRNA gene. For protozoa, marker was part of the 18S rRNA gene. For yeast, marker was part of the II chromosome of *Saccharomyces cerevisiae*. Data were analyzed using the MIXED procedure of SAS. Average DMI was 10.5 kg/d across treatments. Duodenal BCP flow tended ($P = 0.14$) to decrease with DDGS inclusion; estimates were 479, 397 and 368 ± 74 g/d for CONTROL, LOW DDGS and HIGH DDGS, respectively. However, duodenal PCP flow was unaffected ($P = 0.64$) and averaged 80 ± 12 g/d. Duodenal YCP flow increased ($P < 0.01$) with DDGS inclusion; estimates were 0.15, 1.94 and 4.80 ± 0.66 g/d for CONTROL, LOW DDGS and HIGH DDGS, respectively. Overall, when animals were fed DDGS, duodenal BCP flow tended to decrease, PCP flow was unaffected, YCP flow increased and total duodenal MCP flow tended to decrease.

Key Words: dried distillers grains with solubles, duodenal microbial crude protein flow

W281 Effect of canola meal on growth performance, carcass quality and meat fatty acid profiles of feedlot cattle.

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This study investigated the effect of substituting canola meal (CM) for barley grain on growth performance, carcass quality and meat fatty acid (FA) profiles of feedlot cattle. Cross bred calves (n = 140; 285 ± 27 kg) were individually fed diets comprised of a barley grain based concentrate (including 5% supplements) and barley silage in dry matter (DM) basis at ratios of 45:55 and 92:8 during growing and finishing periods, respectively. Solvent extracted and pressed CM derived from *Brassica napus* or solvent extracted CM from *Brassica juncea* canola was compared. Pressed CM contained 11.4% residual oil. CM was substituted for 0 (control), 15, or 30% barley grain (DM basis) in the diet. There was no difference ($P = 0.54$) in average daily gain among the treatments. The inclusion of 30% pressed CM increased ($P < 0.05$) feed intake compared with the control and those 15% CM groups, but reduced ($P < 0.05$) feed efficiency as compared with the control and 15% *Brassica juncea* or 15% pressed CM. Feed efficiency of cattle fed 15% CM did not differ from those fed the control diet. Carcass quality and incidence of liver abscesses were not affected ($P > 0.05$) by inclusion of CM. Inclusion of 30% pressed CM resulted in higher ($P < 0.05$) FA of total polyunsaturated, n-3, *trans*, non-conjugated dienes, α-linolenic acid and rumenic acid, and a decrease ($P < 0.05$) in n-6/n-3 ratio in the *pars costalis diaphragmatis* muscle as compared with the control diet. In conclusion, inclusion of 15% CM did not alter the growth performance or feed efficiency of beef cattle during the growing and finishing period. However, inclusion of 30% CM in the diet decreased feed efficiency, particularly during the finishing period. The inclusion of 15% or 30% solvent extracted CM did not alter carcass quality whereas that of 30% pressed CM increased functional fatty acids (i.e., n-3 and CLA) in beef.

Key Words: canola meal, beef cattle, growth performance

W282 Effects of roughage concentration in steam-flaked corn-based diets containing wet distillers grains with solubles on nutrient digestibility by feedlot cattle.

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Effects of concentrations of alfalfa hay (AH) and wet distillers grains with solubles (WDGS) on apparent total-tract digestibility of nutrients were evaluated with 56 beef steers (initial BW = 395.3 ± 6.9 kg) in a randomized complete block design. Treatments were arranged in a 2 × 3 + 1 factorial and consisted of steam-flaked corn-based diets with (DM basis) 6 or 12% AH and 15, 30, or 45% WDGS plus a control diet without WDGS that contained 9% AH. Diets were fed for 28 d, and 0.15% (DM) of Cr_2O_3 was included in the diet as an indigestible marker for measurement of nutrient digestibility from d 21 to 28. A WDGS × AH interaction (Linear and quadratic, $P \leq 0.02$) was detected for intake of starch. Intakes of DM, OM, NDF, ADF, and CP were greater ($P \leq 0.048$) for steers fed 12 vs. 6% AH. Increasing the dietary concentration of WDGS increased NDF, ADF, and CP intakes (quadratic, $P \leq 0.046$). Dry matter and OM digestibility were greater for the control steers vs. the average of the other treatments ($P < 0.01$). A WDGS × AH interaction was noted for apparent total tract digestibility of DM, OM, and starch ($P < 0.01$). Dry matter and OM digestibilities were decreased (AH × linear, $P < 0.03$) and increased (AH × quadratic, $P < 0.01$) with 6 and 12% AH; respectively, as WDGS increased in the diet, and starch digestibility increased (AH × quadratic $P < 0.01$) at 12% AH. Increasing WDGS in the diet resulted in a linear increase of NDF and CP digestibilities ($P < 0.01$). Results from this experiment suggest an interaction of WDGS and roughage concentrations in terms of total tract digestibility.

Key Words: alfalfa hay, digestibility, wet distillers grains with solubles

W283 Effect of sarsaponin supplementation on digestive function of steers fed a high grain distillers grain-feedlot diet.

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Six Holstein steers (132 ± 3 kg) with cannulas in rumen and duodenum were distributed in a 3 × 3 replicated Latin square design to evaluate the effect of supplementation of sarsaponin on a finishing diet with 40% of dried distillery grains plus soluble (DDGS) on the characteristics of digestion and rumen function. Treatments were a combination of an initial dose of SarStart (SarTec Corporation, Anoka, MN) via mouth on the d 1 of each experimental period plus a daily dose of SarStart DSC (SarTec Corporation) offered in the diet. Treatments were as follows: 1) 0cc of SarStart + 0 g/d of SarStart DSC; 2) SarStart 100cc + 2 g/d of SarStart DSC and 3) 200cc of SarStart + 4 g/d of SarStart DSC. Ruminal starch digestion was greater (79.6 vs 82.1%; $P < 0.05$), as well as its amount reaching duodenum (160 vs. 125 g/d; $P < 0.05$), in T2 compared with T3. There was no effect of treatment on ruminal, postruminal or total digestibility of the nitrogen components of diets, or microbial efficiency ($P > 0.05$). The treatments did not affect ($P > 0.05$) total volatile fatty acids, or its composition, or ruminal pH. It was concluded that the doses from sarsaponin used in this experiment did not significantly alter the digestive efficiency of the components of finishing diets with high levels of dried distillery grains plus soluble in cattle.

Key Words: distillery grains, sarsaponin, steers

W284 Effect of tannins extract supplementation on feedlot performance and plasma urea nitrogen of yearling bulls fed dry-ground corn-based diets containing corn-DDG and cane molasses.

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Thirty *Bos Taurus* × *Bos indicus* yearling bulls 365 ± SE 1.10 kg, were used in a 84 d experiment to determine the effect of tannins extract supplementation on feedlot performance and plasma urea nitrogen of yearling bulls fed dry-ground corn-based diets containing corn-DDG and cane molasses. Prior to the experiment, bulls were placed in experimental pens and fed a 15.4% CP, 70% roughage diet for 90 d to homogenize previous nutritional plane. Day-1 bulls were weighed and blocked by initial weight, and in groups of 5 were placed in 6 ground floor pen (6 × 12 m). In agreement with a complete randomized block design, in each block, bulls were randomly assigned to one of next treatments: 1) Feeding with a finishing diet containing ground corn 53.37%, corn dry distiller grain 13.51%, sugar-cane molasses 12.71%, tallow 2.35%, mineral premix 2.82%, and corn straw 14.23% (Control); or 2) Diet similar to Control, added with 0.3% (dry matter basis) of a tannins extract (TE). Tannins extract was supplied as ByPRO (Pronutrient Developers; Mexico), a premix that contains 72% of a condensed (Quebracho tree) and soluble (Chesnutt) tannins blend. Bulls were weighed in d 1 and 84. In d 1 and 28, blood samples were taken from jugular vein for plasma urea nitrogen (PUN) determination. Real mean daily tannins extract intake was 36 g by bull, equivalent to 0.33% of the dietary DMI. In d 28 TE decreased ($P = 0.08$) PUN concentration in 18%. At end of the experiment TE-fed bulls were 2.9% heavier ($P = 0.04$) than Control (498.25 vs. 512.98 kg, for Control and TE, respectively). TE supplementation increased ($P = 0.02$) average daily gain by 11.8% with mean values of 1.580 vs. 1.767 for Control and TE treatments, respectively. DMI was not affected by treatments ($P = 0.91$). TE improved ($P = 0.06$) the Gain:DMI ratio by 12% (0.149 vs. 0.167 kg/kg, for Control and TE, respectively). It is concluded, that tannins extract supplementation improves feedlot performance of yearling bulls fed dry-ground corn based-diets containing corn-DDG and cane molasses.

Key Words: feedlot performance, tannins, yearling bulls

W285 Inclusion of triticale dried distiller grains and flaxseed in feedlot cattle diets increases alpha-linolenic acid in beef without affecting carcass or meat quality traits.

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This study examined the effect of including triticale dried distillers grain (TDDG), with and without ground flaxseed (FS) or high oleic acid-sunflower seeds (SS), in feedlot finishing diets on carcass and meat quality and fatty acid profiles in beef. Steers (n = 90; 455 ± 31kg) were housed in individual pens and fed either: 1) control (CON) consisting of (dry matter basis) 90% barley concentrate (including 5% supplements) - 10% barley silage, or the following diets with barley grain substituted for 2) 30% TDDG; 3) 10% FS; 4) 30% TDDG – 8.5% FS (FS+DDG); 5) 10% SS; and 6) 30% TDDG – 8.5% SS (SS+DDG) over a 15 wk finishing period. Major carcass traits including grade fat depth, rib eye area and marbling (n = 15) as well as meat quality parameters including *longissiumus thoracis* (LT) pH, temperature, drip loss, shear force, cook loss and meat color (n = 8) were measured. Fatty acids in back fat, perirenal fat and LT muscle samples were analyzed (n = 8). Including TDDG, in combination with either oilseed did not affect ($P > 0.05$) carcass or meat quality except for: a higher ($P < 0.05$) post-slaughter temperature at 45 min, an increase ($P < 0.05$) in drip loss and chroma values after inclusion of TDDG; and a reduction ($P < 0.05$) in cook loss after inclusion of FS. Inclusion of TDDG decreased ($P < 0.05$) total *trans* fatty acids (excluding conjugated linoleic acids and vaccenic acid), whereas inclusion of FS increased ($P < 0.05$) α-linolenic acid (ALA) as well as associated biohydrogenation products (non-conjugated dienes (NCD)) in meat and adipose tissues. Inclusion of TDDG together with FS further increased ($P < 0.05$) ALA, but decreased ($P < 0.05$) NCD in the meat and adipose samples. Compared with inclusion of FS alone, addition of DDG+FS in feedlot diets increased n-3 fatty acid while reducing levels of *trans* fatty acids in fat and meat, without adversely impacting carcass or meat quality.

Key Words: carcass, flaxseed, triticale dried distillers grain with solubles

W286 Effects of increasing distillers grain and monensin on feed intake and ruminal fermentation in feedlot cattle diets.

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It has been reported that diets that contain corn distillers grain with solubles (DG) are less responsive to monensin (M) addition in feedlot cattle. A study was conducted to determine the effects of increasing M supplementation and inclusion rates of corn DG on DMI, sorting index and ruminal fermentation. Five ruminally and duodenally cannulated beef heifers were used in a 5 × 5 Latin square design with 2 × 2+1 factorial arrangement. Treatments were control (CON; 10% barley silage, 87% barley grain, 3% supplement, and 28 mg M/kg DM), and diets substituting 20% or 40% corn DG for grain combining with 28 or 48 mg M/kg diet DM, i.e., 20DG-28M, 20DG-48M, 40DG-28M and 40DG-48M. The CON is a standard feedlot diet in western Canada. Sorting index was calculated as the ratio of actual intake to expected intake for particles retained on 19- and 8-mm sieve of Penn State Particle Separator. DMI (kg/d) was lower ($P < 0.05$) for CON (7.2) than for DG (8.3) diets. There was no interaction between DG and M on DMI, which was not affected by the level of DG (8.3 kg/d), whereas DMI was higher ($P < 0.05$) with 28M (8.9) than with 48M (7.7). Sorting index was not affected by treatments but it was 109 for the particles retained on 19 mm sieve, indicating that animals were intentionally selected for the coarse particles. Total VFA concentrations (mM), molar proportions of acetate and propionate were not different between CON (128, 52 and 29, respectively) and DG (126, 50 and 32, respectively) diets. There was no interaction of DG with M on ruminal fermentation. Total VFA concentration was greater ($P < 0.06$) for 20DG (130) than for 40DG (122) with no difference in molar proportions of acetate and propionate. Increasing the level of M increased ($P < 0.04$) proportion of acetate from 48 to 51% but did not affect other fermentation variables. These results indicate that manipulating the levels of corn DG and M in feedlot diets can change DMI, whereas the effects on ruminal fermentation appear minimal.

Key Words: distillers grain, feedlot cattle, monensin

W287 Modeling nutrient supply from combined feeds of corn with wheat dried distillers grains with solubles at different ratios in ruminants.

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The objectives of this study were to use modeling approach to estimate nutrient supply from combined feeds of corn with wheat DDGS at 4 different ratios of corn to wheat dried distillers grains with solubles (DDGS): 100:0, 75:25, 50:50; 25:75. Each feed treatment had 2 different replicates using 2 different DDGS sources. The parameters for nutrient supply prediction that were accessed included: truly absorbed rumen synthesized microbial protein in the small intestine; truly absorbed rumen undegraded feed protein in the small intestine; endogeneous protein in the digestive tract; total truly absorbed protein in the small intestine and degraded protein balance. Two dry Holstein Friesian cows, fitted with a flexible rumen cannula were used for measuring rumen degradation kinetics of the 4 combined feeds. Based on lab chemical analysis, in situ degradation and in vitro intestinal digestion data, the nutrient supply to dairy cattle was predicted. The data were analysis by Mixed procedure of SAS with a CRD model. The results showed that with increasing inclusion rate of wheat DDGS to corn, it did not change the truly absorbed rumen synthesized microbial protein in the small intestine with an average of 54 g/kg DM and endogenous protein with an average of 7 g/kg DM, but changed the truly absorbed rumen undegraded feed protein in the small intestine from 50 to 108 g/kg DM, total truly absorbed protein in the small intestine from 95 to 154 g/kg DM and degraded protein balance from −54 to 102 g/kg DM. These results indicated that with the inclusion of bioethanol co-product, the nutrient supply from corn grain could be further improved.

Key Words: combined feeds, modeling, nutrient supply

W288 Effects of biodiesel by-products on in vitro fermentation, digestion kinetics and methane production. S. J. Meale*[1], S. M. Olivares-Palma[1], L. G. R. Pereira[2], F. S. Machado[2], H. Carneiro[2], F. C. F. Lopes[2], and A. V. Chaves[1], *[1]Faculty of Veterinary Science, University of Sydney, Sydney, NSW, Australia, [2]Embrapa Dairy Cattle, Juiz de Fora, MG, Brazil.*

Increasing interest in the biofuel industry has produced by-products which show promise as energy and protein feeds in the diets of ruminant livestock. The objective of this study was to determine the effects of biodiesel by-products, from a variety of oilseed sources on *in sacco* nutrient degradability, in vitro ruminal fermentation and CH_4 production. Beard grass (*Brachiaria brizantha*) was incubated alone (control) and in combination with 7 biodiesel by-products (i.e., moringa, castor, cotton, radish, palm kernel and sunflower press oil seeds and glycerine) at ratios of 900:100, 800:200 and 600:400 for each treatment, in a 48 h in vitro batch culture. Gas production (mL/g incubated DM) was measured at 6, 12, 24 and 48 h. Methane production (mg/g of DMD) was measured at 6 and 12 h. Data were analyzed using the MIXED procedure of SAS. After 48 h, culture pH and IVDMD were affected by level x supplement interaction ($P < 0.05$). Supplement type affected gas production, total VFA, proportions of individual VFA and CH_4 production ($P < 0.05$). Moringa produced the lowest amount of CH_4 (g/kg of DM) at 6 and 12 h of incubation, whereas glycerine had the highest CH_4 production ($P < 0.05$). The in sacco experiment examined ruminal degradation of CP and DM in moringa, castor, cotton, radish, palm kernel and sunflower press oil seeds and soybean meal (control). Three nylon bags, containing 5 g of sample, were placed into the rumen of each of the 3 lactating Holstein-Friesian dairy cows. Corresponding bags were removed at 0, 3, 6, 12, 24, 48 and 96 h (i.e., 3 replicates per cow, 9 replicates per time point) for determination of CP and DM disappearance. Moringa press oils seeds exhibited the greatest effective degradability of DM. Similarly, moringa and sunflower press oil seeds exhibited rapid degradation rates of both CP and DM and showed the greatest effective degradability of CP compared with other feed sources ($P < 0.05$). The findings suggest moringa press oils seeds may have the potential to be included in ruminant diets to reduce CH_4 production without adversely affecting nutrient degradability.

Key Words: methane, press oil seeds, ruminal fermentation

W289 Effect of replacing barley grain with glycerol in feedlot diets on nutrient digestibility, methane emissions, growth, fatty acid profiles and carcass traits of lambs. J. S. Avila[1,3], S. J. Meale*[1,2], T. A. McAllister[2], M. L. He[2], O. M. Harstad[4], K. A. Beauchemin[2], S. M. McGinn[2], and A. V. Chaves[1], *[1]Faculty of Veterinary Science, University of Sydney, Sydney, NSW, Australia, [2]Lethbridge Research Center, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada, [3]Facultad de Ciencias Veterinarias, Universidad de Concepción, Chillan, Chile, [4]Norwegian University of Life Sciences (UMB), Ås, Norway.*

The aim of the study was to assess the effects of replacing barley grain with increasing concentrations of glycerol on total tract nutrient digestibility, methane (CH_4) emissions, growth performance, and fatty acid (FA) profiles. The control diet (DM basis) contained 57% barley grain, 14.5% wheat dried distillers grain with solubles (WDDGS), 13% sunflower hulls, 6.5% beet pulp, 6.3% alfalfa and 3% mineral-vitamin mix. Increasing concentrations (7, 14 and 21% dietary DM) of glycerol in the diet DM were achieved by substituting it for barley grain. As glycerol was added alfalfa and WDDGS were increased to maintain similar concentrations of CP and NDF among diets. Nutrient digestibility and CH_4 emissions from 12 ram lambs were measured in a repeated 4 × 4 Latin square experiment. Additionally, 60 weaned lambs were blocked by weight and randomly assigned to one of the 4 dietary treatments and fed to slaughter weight. Data were analyzed using the mixed procedure of SAS. The model included the fixed effects of treatment (diet), day and treatment by day interactions and the random effects of period (n = 4), chamber (group) and lamb nested within treatment as random effects with day of sampling within each period treated as repeated measure. Nutrient intakes, digestibility and CH_4 emissions were not altered by inclusion of glycerol in the diets. In the growth trial, increasing glycerol in the diet linearly decreased DMI ($P < 0.01$) and linearly decreased final bodyweight ($P = 0.01$). The 7% glycerol group tended to have higher ADG ($P = 0.06$) compared with all other treatments. Feed efficiency, carcass traits and total SFA or MUFA proportions of subcutaneous fat were not affected by inclusion of glycerol, but PUFA were linearly decreased ($P < 0.01$). Proportions of 16:0, 10*t*-18:1, linoleic acid 18:2 (n-6) and the n-6/n-3 ratio were linearly reduced ($P < 0.01$) and those of 18:0 (stearic acid), 9*c*-18:1 (oleic acid) were linearly increased ($P < 0.01$) by glycerol inclusion in the diets. In conclusion, glycerol did not affect nutrient digestibility or CH_4 emissions of lambs fed barley-based finishing diets. Lamb growth performance was optimized at 7% glycerol inclusion in the diet and may improve back fat fatty acid profiles by increasing 18:0 and 9*c*-18:1, while reducing 10*t*-18:1 and the n-6/n-3 ratio.

Key Words: biofuel by-products, methane, *trans* fatty acids

W290 Crude glycerin decreases fiber digestibility in finishing Nellore bulls. E. H. C. B. van Cleef*[1], J. M. B. Ezequiel[1], J. B. D. Sancanari[1,2], A. P. D′Aurea[1], V. R. Fávaro[1], D. A. V. Silva[1], J. W. Catellan[1], and F. B. O. Scarpino[1], *[1]São Paulo State University, Jaboticabal, São Paulo, Brazil, [2]Uzinas Chimicas Brasileiras S.A., Jaboticabal, São Paulo, Brazil.*

Nellore bulls (n = 30, 277.7 ± 23.8 kg BW) were used to evaluate total tract digestibility when fed diets containing 0, 7.5, 15, 22.5, or 30% crude glycerin. Treatments (5 diets) consisted of a control diet containing 30% corn silage, 35% corn grain, 19.2% soybean hulls, 14.6% sunflower meal, and 1,2% supplement, and diets containing 7.5, 15, 22.5 or 30% glycerin (dry matter basis). In this study, glycerin replaced specifically corn grain. Bulls were vaccinated against common viral and clostridial diseases, stratified in a randomized block design, by initial BW, and assigned randomly to 30 individual feedlot pens (6/treatment). Over a period of 21 d, bulls were transitioned from diets containing 20% concentrate to their respective 70% concentrate finishing diets using 4 step-up diets that contained progressively greater proportions of concentrate. Final diets provided 12.2% CP and 2.5 MCal ME/kg. Data were analyzed using the General Linear Model procedure of SAS, with animal considered as experimental unit. Indigestible acid detergent fiber was used as internal marker to determine nutrient apparent digestibility. Five Nellore rumen-cannulated steers (approximately 400 kg BW) were adapted to experimental diets and incubated in situ with diets, orts and fecal samples from the 30 finishing study animals for 264 h. Feeding glycerin caused linear ($P \leq 0.01$) reductions in neutral detergent fiber and hemicellulose apparent digestibility, while simultaneously increased crude protein apparent digestibility ($P \leq 0.01$). Dry matter, ether extract and acid detergent fiber apparent digestibilities were unaffected ($P > 0.05$) by adding glycerin. The negative effect in digestibility was not reflected in changes in DMI ($P > 0.05$) nor ADG ($P > 0.05$). The inclusion of crude glycerin in finishing Nellore cattle diets cause significant decrease in digestibility of neutral detergent fiber and hemicellulose, suggesting caution to the level and type of roughage used. Further studies are needed to elucidate the effect of crude glycerin on mechanisms of action of fibrolytic microorganisms as well as the processes involved in the adhesion of these to fiber particles. Supported by FAPESP and CNPq.

Key Words: biodiesel, co-product, beef cattle

W291 Effect of replacing wheat offal with dried oil palm slurry on the performance and carcass traits of Ndama weaners. M. K. Adewumi* and J. A. Aderiye, *Department of Animal Science, University of Ibadan, Ibadan, Oyo State, Nigeria.*

The objective of this trial was to evaluate the effect of replacing wheat offal (WO) with dried oil palm slurry (DOPS) on performance and carcass traits of weanling Ndama calves. Sixteen calves weighing 60.00 ± 1.50 kg were used in a complete randomized design. Control (T1) diet consisted of 53.0% wheat offal (WO), 30.0% dried brewers grains (DBG), 15.0% palm kernel cake (PKC) and 2.0% of a ruminant premix on dry basis. In the test diets, wheat offal was replaced with dried oil palm slurry at 18.9% (T2), 37.7% (T3) and 56.6% (T4) on dry matter basis. The supplements were fed at the rate of 3 kg/100 kg of body weight. Animals, also had access to fresh *Panicum maximum*. The trial lasted 180 d with a 14 d adaptation. All animals were weighed at the start of the trial and subsequently every 14 d to obtain average daily gain (ADG). At the end of 180 d, 3 animals were slaughtered per treatment after fasting for 16 h and hot carcass weight (HCW) determined. Dressing percentage (DP) and rib eye area (REA) were measured after cooling the carcass. Data were analyzed using ANOVA. Dry matter intake (2.58 ± 0.04 kg/d) was similar for T1, T2 and T3 but higher ($P < 0.05$) than for T4 (2.17 ± 0.01 kg/d). Dry matter digestibility (69.88 ± 3.18%) was not different among treatments. Hot carcass weight (kg) and dressing percentage (%) were higher ($P < 0.05$) for T2 (74.20 ± 1.80 and 49.19 ± 0.76) and T3 (78.07 ± 1.76 and 50.99 ± 0.68) than T1 (52.00 ± 1.68 and 40.86 ± 0.74) and T4 (59.17 ± 1.80 and 43.45 ± 0.72) respectively. Rib eye area (cm^2) was higher ($P < 0.05$) for T3 (76.00 ± 1.78) than the average (52.33 ± 3.18) for the other 3 treatments respectively. Replacing wheat offal with not more than 37.7% dried oil palm slurry improved performance and carcass traits of Ndama weaners.

Key Words: dried oil palm slurry, Ndama, performance

W292 Glycerin from soybean biodiesel in diets with high levels of concentrate for sheep. R. L. Galati,* P. G. Paiva, L. S. Cabral, J. T. Zervoudakis, J. G. Abreu, R. S. Gomes, M. P. S. Fachin, and A. P. G. Baroni, *Universidade Federal do Mato Grosso, FAMEV/UFMT, Cuiabá, Brazil.*

The objectives of this study were to evaluate the effect of glycerin from soybean biodiesel in high-concentrate diets on intake, digestibility, rumen pH and glucose blood concentrations. Animals were housed in individual pens, randomly allocated in a 5x5 Latin square design, and the dietary treatments were: 0, 5, 10, 15 and 20% of glycerin on diet DM. The glycerin used was derived from soybean biodiesel (98% glycerol, 0.98% methanol, 0.18% ethanol, 101 mg KOH/g). Five male sheep, castrated and cannulated in the rumen, with initial body weight of 52.2 ± 5.5 kg were used in this study, and fed isoproteic diets (11.2% CP), containing 25% cotton boll and 75% concentrate, on DM basis. Water, feed, refusal and total fecal output were collected on 8 d through 13 d of each period. Rumen fluid was collected on 14 d to measure the pH values up to 8 h after feeding. The glucose blood concentrations were measured with AccuChek on 17 d of each period until 4 h after feeding. Quadratic responses ($P < 0.03$) were observed on DM (1631.16 g/d), OM (1515.69 g/d), CP (184.98 g/d), total digestible nutrients (TDN) intakes, with maximum inclusions of 12.95, 12.55, 13.01 and 15.75% glycerin, respectively. Linear response ($P < 0.01$) from 32.21 to 93.41 g/d was observed for ether extract (EE) intake, while non-fiber carbohydrate (NFC) linearly decreased from 761.79 to 501.69 g/d. Water intake was about 2.3 L/kg DM without glycerin effect ($P > 0.10$). For the most part of nutrients digestibility (DM, OM, CP, EE and NDF), a positive linear response ($P < 0.08$), without any effect on fiber carbohydrate ($P > 0.10$), were observed. Linear decreases ($P < 0.07$) were observed in NFC digestibility, and to the TDN, a positive response ($P < 0.01$) was obtained (71.55 to 75.24%). Quadratic response ($P < 0.03$) were observed on rumen pH values by glycerin and collection times, with the maximum of 5.57 for 8.63% glycerin, and minimum of 5.39 about 4.78 h after feeding The increase of glycerin did not affect ($P > 0.11$) the blood glucose concentration (63.66 mg/dL). The dry matter intake was not affected by the inclusion of 13% soybean glycerin in high-concentrate diets, and the linear digestibility response could compensate low intake, so that, 15% glycerin could be adequate without compromising nutritional parameters.

Key Words: digestibility, glycerol, soybean

W293 Nitrogen balance and microbial efficiency in sheep fed with diets containing glycerin. R. L. Galati,* P. G. Paiva, J. T. Zervoudakis, L. S. Cabral, J. G. Abreu, M. Zanchetin, L. R. Rebelo, and R. S. Fioravante Filho, *Universidade Federal do Mato Grosso, FAMEV/UFMT, Cuiabá, Brazil.*

The objective of this study was to evaluate the effect of glycerin inclusion in diets with high levels of concentrate on nitrogen balance (NB), excretion of purine derivatives, microbial production (Pmic) and efficiency (Efmic), and ruminal ammonia concentrations. The glycerin used was derived from soybean biodiesel production (98% glycerol, 19.2% fat, 0.98% methanol, 0.18% ethanol, 101 mg KOH/g). Five castrated male sheep, cannulated in the rumen, with initial body weight of 52.2 ± 5.5 kg were used in this study. Animals were housed in individual pens and fed isoproteic diets (11.2% CP), containing 25% cotton boll and 75% concentrate, on DM basis. Animals were randomly allocated in a 5 × 5 Latin square design, and treatments were 0, 5, 10, 15 and 20% of glycerin on diet DM. The total fecal collection was performed during 3 d, and urine for 24 h to enable quantification of nitrogen (N) intake, in feces, urine, and therefore the balance of this nutrient. Estimates of Pmic and Efmic were obtained from the total excretion of purine derivatives in urine. The inclusion of glycerol increased quadratically ($P < 0.08$) the intake, fecal, urinary and the uptake of nitrogen, with estimated values of 31.21, 11.71, 8.12 and 18.93 g/d for 14.22, 11.53, 11.86 and 15.52% glycerin, respectively. The nitrogen balance was not affected by glycerin ($P > 0.10$) with values of 57.97%, on average. Ammonia concentrations linearly decrease ($P = 0.01$) from 23.64 to 20.45, which corresponded to 0.16 mg/dL for each 1% of glycerin. The excretion of purine derivatives were not affected ($P > 0.10$), except for xanthine + hypoxathine which was linearly increased ($P < 0.01$), but without influences on total excretion of purine (9.85 mmol/d), which result in Pmic 55.03 g/d, and Efmic of 48.35 g CP/kg TDN. It was concluded that up to 20% of glycerin could be utilized. The nitrogen intake and losses could vary above 15% of glycerin, but without any damage in retention. Ammonia concentrations decreased with the inclusion of glycerin, but without disadvantage in microbial production and efficiency.

Key Words: ammonia concentration, glycerol, purine derivatives

W294 Blood parameters of Nelore steers fed with glycerin. V. R. Fávaro,* J. M. B. Ezequiel, A. P. D'Áurea, J. B. D. Sancanari, E. H. C. B.van Cleef, A. C. Homem Junior, and V. C. Santos, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Ruminants fed high concentrate diets frequently present metabolic disorders. Blood parameters have been used to assess the health status of animals. The viability of glycerin use in cattle diets may be indicated by the blood parameters of the animals. This study aimed to evaluate blood parameters indicators of metabolic disorders (glucose, triglycerides, cholesterol and urea). Five rumen cannulated Nelore steers (420 ± 20 kg BW) were used in a 5 × 5 Latin square design. Orthogonal contrasts were used to determine the linear, quadratic, and cubic effects of glycerin. Experimental diets (DM basis) consisted of 40% corn silage and 60% concentrate (corn grain, soybean hulls, sunflower meal, glycerin) with the following levels of glycerin 0, 5, 10, 15 and 20% of DM. Blood samples were taken on 25d of each experimental period through coccygeal vein puncture, 4h after morning feeding, using Vacutainer tubes. The samples were analyzed using commercial kits. There was no effect ($P > 0.05$) of treatment for serum triglycerides and urea. The average values (7.3 and 21.4 mg/dL, respectively) were in agreement with those suggested in the literature (0–14 mg/dL and 12–65 mg/dL). Diets promoted quadratic effect on plasma glucose concentration ($P = 0.0001$) which presented as maximum point 73.1 mg/dL (10% of glycerin) and minimum, 50.9 mg/dL (0% of glycerin), and promoted cubic effect on serum cholesterol ($P = 0.04$) which presented as maximum point 117.0 mg/dL (0% of glycerin) and minimum, 88.6 mg/dL (5% of glycerin). Although there was difference between treatments, these values were in according to those suggested in the literature (45–75 mg/dL, and 80–120 mg/L, respectively for glucose and cholesterol). The inclusion of glycerin in cattle diet affect blood concentrations of glucose and cholesterol, however, the values for all parameters obtained in this study are in agreement with the suggested in the literature.

Key Words: beef cattle, biodiesel, blood

W295 Levels of replacement of corn by glycerin in multiple supplements for Nelore steers grazing in dry season: Performance. J. T. Zervoudakis,* R. P. da Silva, L. C. R. P. Silva, A. J. Neto, J. F. W. Koscheck, R. G. F. da Silva, T. P. Trindade, A. O. Zanette, and E. R. Donida, *Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil.*

The objective of this study was to evaluate the productive performance of Nelore steers in growing on *Brachiaria brizantha* cv. Marandu during dry season and receiving supplements with partial replacement of corn by glycerin. Forty Nelore steers with initial body weight of 203. 12 ± 20.10 kg and average initial age of 12 months, divided into eight paddocks of 1.6 ha each, were used. The design was completely randomized with five replicates and eight supplements. The supplements were formulated with levels of partial replacement of corn by glycerin: 0% (G0), 10% (G10), 20% (G20), 30% (G30), 40% (G40), 50% (G50) and 60% (G60). The supplements were supplied to the animals in the level of 1 kg/animal/day. A group of animals was allotted to untreated control treatment (MM) and received exclusively mineral mix. Average daily gain (ADG) was higher ($P < 0.10$) for animals receiving supplements G30 (0.568 kg/d), G 40 (0.548 kg/d) and G60 (0.570 kg/d) in relation to supplements G0 (0.510 kg/d), G10 (0.475 kg/d), G50 (0.523 kg/d) and MM (0.208 kg/d). Significant differences ($P < 0.10$) in ADG were observed for supplemented animals as compared MM. It is concluded that supply of supplements using partial replacement for corn by glycerin in levels of 30, 40 and 60%, results in higher performance of cattle grazing in dry season.

Key Words: beef cattle, in growing, supplementation

Ruminant Nutrition: Dairy: Feeds and Co-Products

W296 Productive response of lactating cows fed low-fat dried distillers grains with solubles in combination with rumen-inert fat. H. A. Ramirez Ramirez*[1], P. J. Kononoff[1], and K. Karges[2], *[1]Department of Animal Science, University of Nebraska, Lincoln, [2]Dakota Gold Research Association, Sioux Falls, SD.*

Twenty Holstein cows, 12 primiparous and 8 multiparous, with (mean ± SD) 91 ± 19 DIM and 594 ± 81 kg were used in replicated 4 × 4 Latin squares to compare the effects of feeding conventional dried distillers grains with solubles (DDGS) and low-fat DDGS (LF-DDGS) in combination with rumen-inert fat (RIF, as calcium salts of long chain fatty acids). In each 21-d period cows were randomly assigned to one of 4 dietary treatments (values expressed on a DM basis): control diet (CONT) that contained 0% DDGS; a second diet (DG) that contained 30% DDGS; a third diet (LF-DG) that contained 30% LF-DDGS in substitution of DDGS; and a fourth diet (COMBO) that was similar to LF-DG with the addition of 1.9% RIF. Dry matter intake was similar across treatments containing any form of DDGS, 26.0 ± 0.6 kg/d, and greater ($P < 0.01$) than CONT, 21.6 ± 0.6 kg/d. Milk yield was similar across treatments averaging 33.4 ± 0.94 kg/d. The COMBO treatment resulted in the greatest ($P = 0.05$) fat corrected milk (3.5% FCM), 35.0 ± 0.98 kg/d, and no differences were observed among the remaining treatments averaging 33.4 ± 0.98 kg/d. A reduction in milk fat percentage and yield was observed ($P < 0.01$) when cows consumed the DG diet, 3.27 ± 0.10% and 1.11 ± 0.04 kg/d, whereas these parameters were similar among CONT, LF-DG and COMBO which averaged 3.68 ± 0.10% and 1.22 ± 0.04 kg/d. Concentration of milk protein was highest ($P < 0.01$) for the DG and LF-DG treatments, intermediate for the COMBO treatment and lowest for the CONT diet, namely 3.21, 3.12 and 3.07 ± 0.05%. Milk protein yield for the CONT diet was 1.0 ± 0.03 kg/d and was lower ($P < 0.01$) compared with DG, LF-DG and COMBO which averaged 1.08 ± 0.03 kg/d. These results demonstrate that compared with typical dairy diets, feeding high proportions of LF-DDGS to lactating dairy cows results in greater DMI with no risk for milk fat depression and that the addition of RIF supports greater yield of fat corrected milk.

Key Words: milk fat depression, corn milling

W297 Production performance and ruminal fermentation of dairy cows fed diets replacing starch from corn with non-forage fiber from distillers grains. S. D. Ranathunga,* M. M. Abdelqader, K. F. Kalscheur, A. R. Hippen, D. J. Schingoethe, and D. P. Casper, *Dairy Science Department, South Dakota State University, Brookings.*

The objective was to evaluate replacing starch from corn with non-forage fiber from dried distillers grains with solubles (DG) on the intake, lactation performance, and ruminal fermentation of lactating dairy cows. Six Holstein cows with ruminal fistula were assigned to a multiple 3 × 3 Latin square design. Three diets were formulated: 1) high starch (33% starch, 0% DG), 2) medium starch (25% starch, 12% DG), and 3) low starch (17% starch, 24% DG). Ground corn, soybean feeds were replaced by DG at 2 inclusion amounts to formulate diets containing medium and low starch concentrations. Diets contained 27.5% corn silage, and 22.5% alfalfa hay, and were formulated to contain 17% CP, 4.4% fat, and 21% forage NDF. Intake of DM was not affected by the diets. As dietary starch concentrations were decreased across diets, milk yield ($P = 0.04$), milk fat percentages ($P = 0.04$), milk fat yield ($P = 0.03$), total solids (TS) yield ($P = 0.03$), and energy-corrected milk ($P = 0.02$) were increased linearly, whereas protein percentages ($P = 0.01$) were decreased linearly. Diets were similar for milk lactose, and TS percentages, protein yield, and feed efficiency. Ruminal pH (6.23) and total VFA concentrations (102 mM/L) were similar for all diets. Quadratic responses were observed for the concentrations of acetate and propionate when starch concentrates were decreased across diets. Decreasing starch concentrations in the diet by replacing corn with DG increased milk production and milk fat percentages, while altering ruminal VFA concentrations.

Table 1.

Item	High Starch	Medium Starch	Low Starch	SEM	*P*-value[1]
DMI, kg/d	22.3	21.9	22.9	1.50	NS
Milk, kg/d	30.7	31.2	32.4	2.75	L
Fat, %	3.03	3.37	3.40	0.30	L
Protein, %	3.10	3.05	3.00	0.15	L
Total VFA, mM/L	103	101	101	3.33	NS
VFA, mol/100 mol					
Acetate	61.5	63.3	62.5	1.63	L,Q
Propionate	24.5	22.6	23.3	1.71	L,Q
Butyrate	10.1	10.9	10.9	0.41	L
A:P ratio	2.74	2.83	2.75	0.24	NS

[1]L= linear effect ($P < 0.05$); Q = quadratic effect ($P < 0.05$); NS = nonsignificant.

Key Words: distillers grains, starch, non-forage fiber

W298 Effect of supplementing dairy cow diets with different forms of palm oil-based supplements on the fatty acid profile of milk fat. P. C. Aikman[1], K. E. Kliem[1], R. M. Kirkland*[2], A. K. Jones[1], S. L. Potterton[1], and C. K. Reynolds[1], *[1]University of Reading, Reading, UK, [2]Volac International Ltd., Royston, UK.*

Calcium salts of palm fatty acids (FA) and high palmitic acid-based products, are commonly used as rumen-protected energy supplements for high yielding dairy cows. The objective of this study was to determine the effects of including these 2 types of palm oil-based fat supplement in dairy cow diets on milk FA profile, particularly total saturated FA (SFA) and C16:0, given current interest in the effects of these on long-term human health. Forty-two cows were randomly allocated to diets from calving until wk 12 of lactation, in a completely randomized block design. Diets were total mixed rations with a forage:concentrate ratio of 50:50, with the forage portion comprising 50:50 corn silage:grass silage, wt/wt (DM). A control diet (Control) contained 32 g/kg DM molasses in the concentrate portion, and this was replaced by either calcium salts of palm FA distillate (Megalac; CPO) or a high-C16:0 (>85%) product (H16), each contributing 19 g lipid per kg ration DM. All diets were isonitrogenous. Milk FA profile (g/100 g total FA) was analyzed during wk 6 and 12. Data were analyzed as repeated measures using mixed model procedures of SAS (see Table 1). It is concluded that CPO supplementation had no effect on 16:0 but reduced total SFA concentration in milk fat, while H16 increased milk 16:0 but had no effect on SFA when compared with the Control diet.

Table 1.

g/100 g fatty acids	Control	CPO[1]	H16[1]	SEM	Diet effect (*P*)
4:0-10:0	9.29^{a}	7.91^{b}	7.68^{b}	0.171	0.001
12:0-14:0	17.5^{a}	14.2^{b}	13.6^{b}	0.38	0.001
16:0	38.1^{b}	37.4^{b}	43.5^{a}	0.66	0.001
18:1 cis-9	17.9^{b}	21.6^{a}	19.3^{b}	0.72	0.004
Total SFA[2]	75.3^{a}	70.9^{b}	73.8^{a}	0.80	0.002
Total cis-MUFA[2]	21.4^{b}	25.2^{a}	23.1^{b}	0.71	0.003

^{a,b}Means within rows with different superscripts are significantly different ($P < 0.05$).

[1] CPO = calcium salts of palm fatty acid distillate; H16 = High C16 supplement.

[2] SFA = saturated fatty acids; MUFA = monounsaturated fatty acids.

Key Words: milk fatty acids, palm oil, saturated fatty acids

W299 Influence of corn silage hybrid on lactation performance by dairy cows. M. S. Akins* and R. D. Shaver, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

The objective of this study was to determine lactation performance by dairy cows fed diets containing different corn silage hybrids; dual-purpose (DP; Pioneer 34A89), brown midrib (BMR; Mycogen F2F665) or NutriDense (ND; NutriDense 905823). One hundred and 28 Holstein and Holstein × Jersey cows were stratified by breed and parity and randomly assigned to 1 of 16 pens, each with 8 cows. Pens were randomly assigned 1 of 4 TMR treatments containing DP, BMR, or ND. Three treatments (DP40, BMR40 and ND40) contained 60% forage DM with 2/3rd (40% of TMR DM) from the respective corn silage and 1/3rd alfalfa silage on DM basis. The fourth treatment contained 65% forage DM entirely from ND corn silage (ND65). All diets were formulated to be isonitrogenous. A 2-wk covariate period with all pens receiving a TMR containing equal DM proportions of DP40, BMR40 and ND40 was followed by an 11-wk treatment period with pens fed their assigned treatment TMR. Contrasts were used to compare ND40 vs. DP40, ND40 vs. BMR40, and ND40 vs. ND65. Data are presented in Table 1. Dry matter intake, actual milk and 3.5% fat-corrected milk (FCM) yields, milk fat%, and yields of protein and lactose were greater ($P < 0.05$) for cows fed ND40 compared with ND65. Cows fed ND40 tended ($P = 0.08$) to produce more milk and had greater ($P < 0.05$) protein and lactose yields than DP40. Cows fed ND40 and BMR40 had similar ($P > 0.10$) actual milk and FCM yields, FCM/DMI, and milk fat% and component yields, with reduced ($P = 0.04$) MUN for BMR40. Overall, cows fed ND40 had improved lactation performance compared with DP40 and ND65, and similar performance to BMR40.

Table 1.

Item	DP40	BMR40	ND40	ND65	SEM
DMI, kg/d	23.9	24.4	24.5	22.7	0.3
Milk, kg/d	38.8	40.7	40.2	38.0	0.5
3.5% FCM, kg/d	42.0	42.5	43.6	37.1	0.9
FCM/DMI, kg/kg	1.73	1.74	1.74	1.65	0.03
Fat, %	3.91	3.76	3.78	3.33	0.11
Protein, kg/d	1.23	1.28	1.29	1.20	0.01
Lactose, kg/d	1.94	2.05	2.03	1.92	0.02
MUN, mg/dL	14.6	13.0	14.0	15.7	0.3

Key Words: corn hybrid, corn silage, lactating cow

W300 Sugar cane silage for lactating dairy cows. M. I. Marcondes*[1], F. L. Andrade[1], R. A. V. Vergara[1], A. S. Trece[1], T. E. Silva[1], W. L. Cardoso[1], and A. B. Fonseca[2], *[1]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]University of New Hampshire, Durham.*

Sugar cane has strong potential to replace corn as a silage source due to its higher productivity (80–120 tons/ha), lower costs, and maintenance of nutritive value during the dry season in tropical conditions. However, previous research showed that sugar cane silage has high concentration of ethanol and significant DM losses when ensiled. This study was conducted to evaluate the effects of sugar cane silage alone or ensiled with different additives on milk production and performance of lactating Holstein cows. Thirty 5 cows averaging 110 DIM were blocked by milk production and, within each block (n = 5), randomly assigned to one of 7 treatments: 1) corn silage (CS), 2) chopped sugar cane (SC), 3) sugar cane silage (SCS), 4) SCS + 0.5% of CaO (SCCaO), 5) SCS + *Lactobacillus buchneri* (2.5×10^{10} cfu/g; SCLB), 6) SCS + *Lactobacillus plantarum* (2.5×10^{10} cfu/g) and *Pediococcus pentosaceus* (2.5×10^{10} cfu/g; SCLPPP), or 7) SCS + *Propionibacterium acidipropionici* (5×10^{9} cfu/g; SCPA). Data was analyzed as completely randomized block design using a mixed model with repeated measures over time where block and treatment were considered as fixed variables and period and animal as random variables; each experimental period (n = 5) lasted 21 d. Diets were formulated to be isonitrogenous and isocaloric with a 60:40 (CS diet) or 40:60 (sugar cane silage-based diets) forage to concentrate ratios, There were no differences ($P > 0.05$) among treatments for milk production (18.5, 22.4, 19.4, 19.7, 18.8, 19.5, and 19.5 kg/d, respectively) and milk lactose content (4.16, 4.11, 4.08, 4.18, 4.03, 4.19, and 4.18%, respectively), FCM (4% fat) (20.0, 23.0, 21.4, 21.1, 20.2, 18.7, and 20.8, respectively), DMI (16.7, 19.3, 18.1, 17.2, 17.1, 17.4, and 20.2 kg/d, respectively), feed efficiency (1.12, 1.15, 1.05, 1.11, 1.09, 1.12, and 0.97 kg of milk/kg of DMI, respectively), and average daily weight gain (0.64, 0.81, 0.55, 0.56, 0.23, 0.37, and 0.77 kg/d, respectively). Cows fed CS (4.02%), SC (4.50%), SCCAO (3.99%), and SCPA (3.92%) had the highest ($P < 0.05$) concentration of milk fat, whereas those fed CS (3.16%), SC (3.19%), SCS (3.30%), SCLB (3.28%), and SCPA (3.32%) showed the greatest ($P < 0.05$) milk protein content. Cows receiving sugar cane silage-based diets produced 20 kg/d of milk and maintained body condition throughout the study, thus suggesting that nutrient requirements were met for this low milk output. Further research is needed to investigate the effect of sugar cane silage-based diets on milk production of high-producing dairy cows. Because ensiling sugar cane with additives did not improve milk yield when compared with the SCS diet, it can be concluded that silage made from sugar cane alone can maintain reasonable milk outputs in tropical conditions. Supported by INCT-CA/FUNARBE/CNPq.

Key Words: dairy cattle, lactobacilli, sugar cane

W301 Influence of dietary starch and forage NDF concentrations on digestion and lactation performance by dairy cows. L. F. Ferraretto* and R. D. Shaver, *University of Wisconsin-Madison, Madison.*

A meta-analysis was performed to evaluate the effect of starch and forage NDF concentrations in corn grain based diets on intake, digestion and milk production by dairy cows, and assess site of starch digestion using a data set comprised of 414 treatment means from 100 peer-review articles published during 2000 - 2011. Categories for dietary starch and forage NDF concentrations were: ≤18% (VLS), >18% to 24% (LS), >24% to 27% (MS), >27% to 30% (MHS), >30% to 33% (HS), and >33% (VHS) starch (DM basis); ≤17% (LFNDF), >17% to 20% (MFNDF), and >20% (HFNDF) forage NDF (DM basis). Data were analyzed using Proc Mixed of SAS with treatment as Fixed and trial as Random effects. Digestibility of dietary starch was greater ($P = 0.03$) ruminally, but not ($P = 0.61$) total tract (TT), for HS and VHS compared with VLS, LS and MS. Conversely, increased dietary starch concentration decreased ruminal ($P = 0.02$) and TT ($P = 0.001$) dietary NDF digestibilities. The TT digestibilities of dietary DM and OM were greatest ($P = 0.001$) for VHS and lowest for VLS. A quadratic effect ($P = 0.001$) was observed for DMI, which was lowest for VLS and VHS. Actual milk yield and protein content were unaffected by dietary starch concentration ($P > 0.10$). Fat-corrected milk (FCM) yield was 2.0 kg/d lower ($P = 0.01$) for VHS than the other dietary starch concentrations. A similar response was observed for milk fat content ($P = 0.001$). Ruminal and TT nutrient digestibilities were unaffected ($P > 0.10$) by dietary forage NDF concentration. Milk fat, protein and urea-nitrogen concentrations did not differ ($P > 0.10$) either. The DMI was 0.8 kg/d greater ($P = 0.01$) and milk yield tended ($P = 0.09$) to be 2.1 kg/d greater for LFNDF. Ruminal and TT starch digestibilities were positively related (R2 = 0.84), with an increase of 0.23%-units TT per %-unit increase ruminally. Digestibility of dietary NDF decreased 0.60% units ruminally (R2 = 0.58) and 0.52% units TT (R2 = 0.45) per unit increase in dietary starch concentration.

Key Words: dairy cow, milk production, starch digestibility

W302 Processed corn stover as a corn silage replacement feed for lactating dairy cattle.

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Corn silage represents almost half of the forage used in rations for dairy cattle in the Midwest region and increased value for corn grain has increased the costs of corn silage production. Our overall goal is to determine the potential for treated corn crop residues as replacement feeds for corn silage and corn grain. The objective of this initial study was to determine the short-term impact of feeding increasing amounts of processed and chemically treated corn stover on feed intake, milk production and milk composition. Baled stover was tub-ground, hydrated to approximately 50% moisture and treated with either 5% CaO or a mixture of 3% CaO and 2% NaOH (DM basis) in a twin-screw extruder. Separately, baled stover from the same lot, was chopped through a 10.2 cm screen using a HayBuster, mixed with water to 50% moisture and CaO to 5% of DM. All stovers were stored in AgBags. Fifty-six Holstein cows were assigned to 1 of 7diets in which corn silage was replaced by treated stover. Diets were: CaOH extruded stover at 12.5 and 25% of ration DM, CaOH +NaOH extruded stover at 12.5 and 25% of ration DM, on-farm prepared stover containing 5% CaOH and fed at 12.5 or 25% of ration DM and a control diet consisting of 37.5% corn silage. Cows were fed diets for 21 d to assess initial acceptance of treated stover and impact on production parameters. Milk production averaged 28.9 ± 2.22 kg/d and DM intake was 22.3 ± 1.26 kg/d and did not differ ($P > 0.05$) between treatments. There were no differences ($P > 0.05$) in milk composition, body weight changes during the 21-d feeding period. There were treatment × day of experiment effects ($P < 0.05$) for feed intake and milk production with the greatest difference with day observed for extruded stover containing NaOH. The data indicate that chemically treated corn stover can replace corn silage in diets for lactating dairy cows to at least 25% of the ration DM and potentially more for some compositions.

Key Words: biofuels, stover, corn replacement

W303 Effects of feeding camelina meal on milk production and composition in lactating Holstein cows.

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Meal from *Camelina sativa* is potentially available from the biofuel industry as a protein source rich in α linolenic acid for the dairy cow. The objective of this work was to determine the effects of feeding camelina meal to Holstein cows on milk production and composition. Cows (n = 15) were randomly assigned to diet after blocking for parity and milk production. Camelina meal replaced canola meal at 0, 50, and 100% so rations contained 0, 7 and 14% of the diet DM as camelina meal. Total mixed rations were formulated to meet NRC requirements for cows producing 35 kg of milk per day. Cows were fed individually in tie stalls for 6 wk. Milk production was recorded daily and composition was tested on d 41 and 42 of feeding. Results were compared using Tukey's test. Milk production (30.4, 32.0 and 29.3 kg/d for 0, 7 and 14% camelina, respectively; SEM = 1.6) for d 35–42 and milk protein percentage (3.2, 3.0 and 2.8% for 0, 7 and 14% camelina, respectively; SEM = 0.07) from d 41 and 42 were unaffected ($P > 0.05$) by diet. Milk fat percent was lower ($P < 0.05$) in milk from cows on 14% camelina meal compared with the other diets (3.8, 3.6 and 3.3% for 0, 7, and 14% camelina, respectively; SEM = 0.09). Camelina meal at 14% of diet DM reduced ($P < 0.05$) milk fat concentrations of 18:0 (10.8, 12.0 and 7.9% total fatty acids for 0, 7 and 14% camelina, respectively; SEM = 1.6), but increased ($P < 0.05$) α linolenic acid (0.1, 0.5 and 0.8% total fatty acids for 0, 7 and 14% camelina, respectively; SEM = 0.01), 18:1 trans isomers (2.6, 3.5 and 6.8% total fatty acids for 0, 7 and 14% camelina, respectively; SEM = 1.3) and c9t11 CLA (0.9, 1.1 and 2.3% total fatty acids for 0, 7 and 14% camelina, respectively; SEM = 0.18), relative to other diets. Camelina meal had no effect ($P > 0.05$) on 12:0, 14:0, 18:1c9 and linoleic acid concentrations in milk fat. In conclusion, camelina meal supported milk production similar to canola meal and enhanced the unsaturated portion of the fatty acid profile.

Key Words: camelina, milk fat, milk yield

W304 Comparison of the NRC (2001) model and the DVE/OEB system in the prediction of protein supply to dairy cows from hulless barley (*Hordeum vulgare* L.) with altered carbohydrate traits.

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The objective of this study was to predict protein supply to dairy cows from 4 hulless barley varieties (zero-amylose waxy, CDC Fibar; waxy, CDC Rattan; normal-amylose, CDC McGwire and high-amylose, HB08302) by using NRC 2001 model and DVE/OEB system. CDC Copeland was induced as a hulled control. The hulless barley breeding lines differed ($P < 0.05$) in amylose (1 to 20%DM), amylopectin (34 to 51%DM), amylose to amylopectin ratio (Ay:Ap) (0.02 to 0.59) and β-glucan contents (5 to 10% DM). In DVE/OEB system, CDC McGwire was higher ($P < 0.05$) in rumen fermented organic matter (FOM: 683 vs. 545 g/kg DM), metabolizable protein (MP: 102 vs. 82 g/kg DM), truly absorbed microbial protein in the small intestine (AMCP: 65 vs. 52 g/kg DM) and digested organic matter (DOM: 921 vs. 871g/kg DM) but lower ($P < 0.05$) in endogenous protein in the small intestine (ENDP: 5 vs. 9 g/kg DM), truly absorbed bypass protein in the small intestine (ABCP: 48 vs. 61 g/kg DM) and degraded protein balance (OEB: −35 vs. −24 g/kg DM) compared with HB08302. Highest OEB among all barley varieties was found in CDC Fibar (−14 g/kg DM, $P < 0.01$). Hulled barley was lower ($P < 0.01$) in true protein supplied to the small intestine (TPSI: 127

g/kg DM) and truly digested protein in the small intestine (DVE: 95 g/kg DM) than hulless barley lines but higher ($P < 0.01$) in undigested inorganic matter (9 g/kg DM). From NRC Dairy 2001 model, CDC Fibar was higher ($P < 0.05$) in OEB (−30 g/kg DM), microbial protein synthesized in the rumen (MCP: 76 g/kg DM), AMCP (49 g/kg DM) than the other hulless barley lines. Compared with hulless barley, hulled control was relatively lower ($P < 0.01$) in truly absorbed rumen undegraded protein in the small intestine (44 g/kg DM) and total MP (83 g/kg DM). In conclusion, altered carbohydrate traits in hulless barley varieties significantly improved the truly absorbed protein supply to dairy cattle compared with hulled barley.

Key Words: NRC dairy 2001 model, DVE/OEB system, amylose to amylopectin ratio

W305 Effect of different forage and dried distillers grains with solubles concentrations on sorting behavior of lactating dairy cows.

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The objective was to evaluate the effect of different forage and dried distillers grains with solubles concentrations on sorting behavior of lactating dairy cows. Four Holstein cows were assigned to a 4 × 4 Latin square in a 2 × 2 factorial arrangement of treatments with 4-week periods. 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. Ground corn and soybean feeds were partially replaced by DG from 0% DG diets to formulate 18% DG diets. Fresh TMR and orts were sampled for particle size analysis on the first 3 d of wk 3 and 4 of each period. Particle size distribution of samples of TMR and orts were determined using the 4-box Penn State particle size separator. The particle size separator had 3 screens (19, 8, and 1.18 mm) and a bottom pan, resulting in 4 fractions (long, medium, short, and fine). Feed sorting was calculated as the actual intake of each particle size fraction expressed as a percentage of the predicted intake of that fraction. Average DMI was similar ($P > 0.05$) across diets (23.8 kg/d). Cows fed HF diets sorted against long (91.2 vs. 97.6%) and medium (96.6 vs. 97.8%) particles compared with LF diets. Feeding HF diets increased selective consumption of short (103 vs. 101%) and fine (104 vs. 100%) particles compared with the LF diets. These results suggest that, despite geometric mean diameter of the diet being affected by forage (LF vs. HF: 1.55 vs. 1.95 mm) and DG (0DG vs. 18DG: 1.81 vs. 1.69) concentrations, only forage concentration affected the sorting behavior of lactating dairy cows.

Table 1. Effect of forage and DDGS concentration on sorting (%)

	LF	LF	HF	HF		
Item	0DG	18DG	0DG	18DG	SEM	*P*-value[1]
Particles						
Long	96.8	98.4	91.3	91.1	1.93	F
Medium	96.9	98.7	97.1	96.1	0.54	F
Short	102	101	103	104	0.59	F
Fine	101	99.5	104	104	0.43	F
Geometric mean diameter (mm)						
TMR	1.58	1.52	2.04	1.87	0.02	F, D, F×D
Orts	2.12	1.63	2.70	2.99	0.04	F, F×D
Geometric SD (mm)						
TMR	1.56	1.51	2.16	2.00	0.03	F, D
Orts	2.37	1.74	3.05	3.31	0.18	F, F×D

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

Key Words: distillers grains, forage, sorting behavior

W306 Effects of sudden additions of condensed distillers solubles to diets of lactating dairy cows on milk production and milk components.

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Variability in the fat content of dried distillers grains with solubles (DDGS) in dairy diets make dairy producers hesitant to utilize this coproduct. The objective of this study was to determine the effect of sudden additions of condensed distillers solubles (CDS) on milk production, milk components and rumen parameters. Eight ruminally cannulated Holstein cows (166 ± 12 DIM) were randomly assigned to treatments in a replicated 4 × 4 Latin square design with 21-d periods. The dietary treatments, on a DM basis, were CON (10% DDGS); DDGS (20% DDGS); CDS2.5 (17.5% DDGS plus 2.5% CDS); and CDS5 (15% DDGS plus 5% CDS). Cows were fed CON diets for a 14-d adaptation period and treatments diets for a 7-d treatment period with the last 3 d used for data collection. Milk samples were collected daily to determine milk components. Rumen samples were collected via rumen cannula for determination of pH, volatile fatty acids (VFA) and NH$_3$. Data were analyzed using PROC MIXED of SAS. Milk yield and fat percentage were similar between treatments ($P = 0.66$ and 0.82, respectively). Cows fed CON had greater ($P < 0.01$) and DDGS tended ($P = 0.06$) to have greater milk protein concentrations than CDS2.5 and CDS5 (2.89, 2.83, 2.77, 2.81%, respectively). Dry matter intake was greater ($P < 0.05$) for CON than CDS2.5 or CDS5 (21.6, 20.1, 20.5 kg/d, respectively), but was similar ($P = 0.11$) to DDGS (20.7 kg/d). Rumen pH was lesser for CON than CDS5 (6.05 and 6.13, respectively; $P = 0.03$) and lesser for DDGS than for CDS2.5 and CDS5 (6.03, 6.10, 6.13, respectively; $P \leq 0.05$). Total VFA concentrations were similar among treatments ($P = 0.84$); however, CDS5 had greater butyrate concentrations than CON (11.1 and 9.7 μmol/mL; $P = 0.05$) and tended to have greater concentrations than DDGS (9.7 μmol/ml; $P = 0.08$). Rumen NH$_3$ was greater for CON and DDGS ($P < 0.03$) and tended ($P = 0.08$) to be greater for CDS2.5 than for CDS5 (18.4, 17.5, 17.1, 15.0 mg/dL, respectively). Sudden additions of up to 5% added CDS in dairy cow diets decreased milk protein concentration and DMI without affecting milk yield or milk fat.

Key Words: condensed distillers solubles, dairy cow, milk fat

W307 Occurrence and concentration of mycotoxins, molds and yeasts on corn co-products from South Dakota and Minnesota dairy farms.

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Twenty-nine large dairies in SD and MN were visited during summer and fall 2011 to provide a comprehensive assessment of the prevalence of mycotoxins, molds, and yeasts on corn co-products. Samples were collected from every corn co-product used on these farms. Feed samples analyzed included: distillers grains (n = 13 wet, 6 dried), wet corn gluten feed (n = 11), high moisture corn (n = 2) and germ meal (n = 1). Ten subsamples (0.5 kg each) were taken from each corn co-product, pooled together and composited. This composite was split in two 0.8- to 1.0-kg samples. After vacuum sealing, one sample was stored at −20 °C for later mycotoxin analyses and the second was stored at 4 °C for mold and yeasts analyses. A total of 32 different mycotoxins were analyzed by triplicate using UPLC-MS/MS (tandem mass spectrometer coupled to liquid chromatography). Molds and yeasts counts were determined by direct plate dilution. In addition, mold isolates were identified in samples with mold growth equal to or greater than 1,000 cfu/g using the conventional microscopic tape method. Two distillers dried grains samples contained aflatoxin B2 levels (32.0 and 36.7 ppb) greater that the U. S. Food and Drug Administration (FDA) guidelines for use in feeds for dairy cows or immature animals (20 ppb). But these samples contained aflatoxin levels lower than the FDA recommendation for feeding mature beef cattle (300 ppb), swine (200 ppb) and poultry (100 ppb). The rest of the samples contained aflatoxins, deoxynivalenol, and fumonisins levels lower than the detection limit or the FDA guidelines for use in animal feeds. Mold growth was lower than 1,000 cfu/g in 25 corn co-product samples (75.7%) and greater than 2,000 cfu/g in 4 samples (12.1%). *Aspergillus* and *Mucor* were the fungi genera most frequently isolated. There were only 7 corn co-products (21.2%) with yeast counts lower than 1,000 cfu/g, with most of them containing levels greater than 105 cfu/g (63.6%). The majority of the samples analyzed in this experiment had high yeast counts not associated with the presence of detrimental mycotoxin concentration.

Key Words: corn co-products, dairy cows, mycotoxins

W308 Surveying the constraints of ethanol co-products utilization on dairy farms. F. Diaz-Royon*[1], A. Garcia[1], K. F. Kalscheur[1], K. A. Rosentrater[2], J. S. Jennings[3], and K. Mjoun[3], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Department of Agricultural and Biosystems Engineering, Iowa State University, Ames, [3]Alltech South Dakota, Brookings.*

Distillers grains (DG) originating from the corn-based fuel ethanol industry are an excellent source of energy and rumen undegradable protein, which complement well with other feedstuffs used in dairy cattle diets. However, despite the competitive pricing when compared with other protein sources and their availability in the market, DG are not always sought as dietary ingredient by nutritionists and dairy producers. A survey was mailed to every South Dakota grade A dairy farm (303) to determine current use and constraints to ethanol co-products usage in dairy cattle diets and whether dairy producers found the different co-products available in the market useful. The self-administered survey with an original cover letter and self-addressed stamped envelope were delivered to dairy farms though the US Postal Service in April of 2011. Forty-nine dairy producers (16.2%) filled out and returned the survey. The average number of years producers had been feeding corn co-products was 8, with a range between 0.5 and 21.Thirty-six producers (73% of respondents) were using ethanol co-products in their rations. Among those that did not feed them, the primary reason was price (31%). Modified distillers grains (MDG) was the ethanol co-product included at the highest percentage in lactating dairy cows and heifer rations (13.8 and 10.7% on a dry matter basis, respectively); however, distillers dried grains with solubles were mostly used in dry cow rations. In addition, MDG was the corn co-product most frequently fed in farms during 2010, with an average use of 1,048 ton/yr (as-fed basis). Outside piles were the most common storage method for wet or modified distillers grains while commodity sheds for distillers dried grains. When dairy producers were asked to rank the degree of importance of several DG issues (1 = none; 2 = low; 3 = average; and 4 = high), the majority (73%) ranked ″variability between batches″ highest, followed by price (60%), and mycotoxin content (58%). These results provide a snapshot of percent inclusion, storage methods, major concerns, amount fed and type of corn co-products used on South Dakota dairy farms.

Key Words: dairy farms, ethanol co-products, survey

W309 Effects of molasses products on productivity and milk fatty acid profile of cows fed high-DDGS diets. A. V. Siverson* and B. J. Bradford, *Kansas State University, Manhattan.*

Previous research has shown that replacing up to 5% corn with cane molasses can partially alleviate milk fat depression when cows are fed high-concentrate, low-fiber rations containing distillers grains with solubles (DGS). Our objective was to determine whether dietary molasses would alter milk fatty acid profile or improve solids-corrected milk yield in the context of a more typical lactation diet. Our secondary objective was to assess production responses to increasing RDP supply when molasses was fed. Twelve primiparous and 28 multiparous Holstein cows (196 ± 39 DIM) were randomly assigned to 8 pens. Pens were randomly allocated to treatment sequence in a 4 × 4 Latin square design balanced for carryover effects. Treatments were a control diet including 20% dried DGS, 35% NDF, 30% starch, and 5% EE (CON), a diet with 5% cane molasses (DM basis) replacing a portion of the corn grain (MOL), a diet with 3.25% (DM basis) QLF (Quality Liquid Feeds) 20% CP supplement (QLF3), and a diet with ~6.5% (DM basis) QLF 20% CP supplement (QLF6). Data were analyzed using mixed models including the fixed effects of treatment and the random effects of period, pen, period × pen interaction, and cow within pen. Diets had no significant effects on dry matter intake, milk production, milk component concentration or yield, crude feed efficiency, BW change, or somatic cell count in milk (all $P > 0.12$).Milk stearic acid content was increased by QLF6 compared with CON and QLF3 ($P < 0.05$), but the magnitude of the effect was small (12.27, 11.75 and 11.69 ± 0.29 g/100 g fatty acids). Production data revealed a dramatic effect of period on milk fat content and yield. Milk fat content dropped during the course of the experiment (3.16, 2.81, 2.93, and 2.64 ± 0.09% for periods 1–4, respectively) as did milk fat yield (1.20, 1.03, 0.98, and 0.79 ± 0.05 kg/d). Exchanging molasses-based products for corn at 3 to 6% of dietary DM did not influence productivity and had minute effects on milk fatty acid profile. The limited responses in this study may have been influenced by dietary unsaturated fatty acid content or advancing DIM of cows on the study.

Key Words: biohydrogenation, milk fat depression, sugar

W310 Effects of feeding brown midrib corn silage with a high dietary concentration of alfalfa hay during early and mid lactation on milk production of Holstein dairy cows. M. S. Holt*[1], A. J. Young[1], X. Dai[2], K. E. Nestor[3], and J.-S. Eun[1], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Utah Agricultural Experiment Station, Utah State University, Logan, [3]Mycogen Seeds, Indianapolis, IN.*

This experiment was conducted to determine the long-term effects of feeding brown midrib corn silage (BMRCS) fed with a high dietary concentration (25% DM) of good quality alfalfa hay in high-forage lactation diets on productive performance of dairy cows. Twenty 4 multiparous Holstein cows were used starting at the onset of lactation through 200 d-in-milk (DIM). Two dietary treatments were tested in a completely randomized design: TMR based on conventional corn silage (CCST) and TMR based on BMRCS (BMRCST). Intake of DM was not affected by dietary treatments throughout the experiment. During early lactation (0–60 DIM), milk yield was not different between dietary treatments, whereas milk yield during mid lactation (61–200 DIM) increased by feeding the BMRCST compared with the CCST (39.8 vs. 36.2 kg/d; $P = 0.05$), resulting in increased overall milk yield by feeding the BMRCST throughout the experiment (40.9 vs. 37.6 kg/d; $P = 0.05$). While milk fat concentration did not differ during early lactation, it tended to decrease by feeding the BMRCST compared with the CCST during mid lactation (3.51 vs. 3.82%; $P = 0.08$). During mid lactation, yield of 3.5% fat-corrected milk tended to increase for cows fed the BMRCST compared with those fed the CCST (42.5 vs. 39.3 kg/d; $P = 0.10$), but it remained similar during 200 DIM. Overall milk protein concentration was similar between dietary treatments throughout the experiment

(2.95% on average), but overall milk protein yield was higher for the BMRCST than the CCST (1.27 vs.1.14 kg/d; $P = 0.01$). Milk protein concentration and yield were similar between dietary treatments during early lactation; however, during mid lactation, milk protein yield was greater for cows fed the BMRCST than those fed the CCST (1.27 vs. 1.10 kg/d; $P < 0.01$). Feeding BMRCS with a high dietary concentration of alfalfa hay did not affect milk production during early lactation; however, cows fed the BMRCST maintained longer peak milk yield, which resulted in increased milk production during mid lactation, leading to greater overall milk production and milk protein yield.

Key Words: brown midrib corn silage, alfalfa hay, early and mid lactation

W311 Effects of harvest date and a BMR hybrid on yield and nutrient composition of corn plants harvested for silage.

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Maturity at harvest and the brown midrib (BMR) trait influence concentration and availability of nutrients from plants harvested for corn silage. To quantify these effects, 9 commercial elite Pioneer corn silage hybrids were planted in 12-row plots in a field near Lexington, IL on May 9, 2010 at 69K and 84K/hectare. Duplicate sets of 5 plants each were harvested 10 times (at 3 to 6 d intervals) spanning the silage harvest window (28 to 42% DM). Nutrient content and availability were estimated by calibrated NIR procedures. Averaged across hybrids, yield of DM reached a plateau at 33% plant DM, but starch content (% of DM and g/plant) continued to increase to over 40% plant DM. NDF digestibility was not altered by DM content. Per plant, grams of starch increased while grams of NDF, ADF, and sugars decreased as plant DM increased. Nutrient values for the Pioneer BMR hybrid (P1376XR) were compared with those from the non-BMR hybrids. Differences were not significant ($P > 0.05$) for starch, total sugars, hemicellulose, ash, dry matter yield per hectare (18.9 for BMR vs. 19.0 t/ha), or kg of grain per hectare estimated from starch content (8.1 vs. 7.8 t/ha). At equal moisture contents, the BMR hybrid had less ($P < 0.01$) NDF (41.4 vs. 43.7%) and ADF (23.8 vs. 25.9%) but more ($P < 0.01$) crude protein (7.9 vs. 7.4%) and greater ($P < 0.01$) digestion of NDF at 24 h (50.5 vs. 46.7%). Although it did not alter grain yield, the 21% higher planting density increased yield of DM per hectare only by 5% ($P < 0.01$) because individual plants weighed 13% less. When adjusted for DM content, the higher plant density decreased the percentage of starch and digestion of NDF at 24 h ($P < 0.05$). Harvest of modern corn hybrids below 33% DM sacrifices DM yield while harvest below 40% sacrifices yield of starch. The BMR tested had grain and NDF yields equal to elite non-BMR hybrids but greater NDF digestibility at 24 h.

Key Words: corn silage, harvest maturity, BMR

W312 Chemical and nutrient availability of hulless barley (*Hordeum vulgare* L.) with altered carbohydrate characteristics.

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Four hulless barley varieties and breeding lines with altered carbohydrate composition were developed at the Crop Development Centre, University of Saskatchewan based on amylose (1 to 20% DM), amylopectin (34 to 51% DM), amylose to amylopectin ratio (0.02 to 0.59) and β-glucan (5 to 10% DM) content. The objective of this study was to compare differences in chemical and nutrient profiles among the 4 newly developed hulless barley lines (zero-amylose waxy, CDC Fibar; 5%-amylose waxy, CDC Rattan; normal-amylose, CDC McGwire and high-amylose, HB08302). CDC Copeland hulled barley was included as a hulled control. Among the hulless barley lines, CDC Fibar showed greater ($P < 0.01$) crude protein (16.2% DM), soluble crude protein (7.8% of DM) and β-glucan (10.0% DM) but reduced ($P < 0.01$) amylose (1.3% DM), intermediately degradable CHO (51.9% CHO) and slowly degradable CHO (9.9% CHO). CDC McGwire had greater ($P < 0.01$) starch (61.5% DM) but reduced β-glucan (4.7% DM) while HB08302 had greater neutral detergent fiber (13.8% DM, $P < 0.01$) than the other hulless barley lines, but reduced intermediately degradable protein than CDC Fibar (30.5 vs. 40.9% CP, $P < 0.05$). The hulled control showed greater CHO ($P < 0.01$) but a reduced rapidly degradable CHO content and Mcal/kg of NEL (1.68 vs. 1.74, $P < 0.01$) versus the hulless barley lines. Altered carbohydrate composition improved chemical, protein and carbohydrate subfractions and energy values which affected nutrient availability for ruminants.

Key Words: amylose to amylopectin ratio, β-glucan, hulless barley

W313 Effects of dietary protein content and source of grain on milk production and nitrogen efficiency in early lactating primiparous Holstein cows.

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Nitrogen excretion from dairy farming systems is a major environmental challenge and formulating dairy ration to decreasing nitrogen excretion without compromising milk production and composition can be one of strategies. An experiment was conducted to determine the effects of dietary crude protein (CP) levels, source of grain and their interactions on performance and nitrogen efficiency of early lactating Holstein cows. Eight primiparous cows (BW = 560 ± 65 kg and DIM = 50 ± 15 d) were allocated to one of 4 diets in replicated 4 × 4 Latin square design. The diets containing: 1) 20% CP and barley grains as a cereal grain source (HPB), 2) 20% CP and a 50:50 ratio of barley and corn grain (HPBC), 3) 16% CP and barley grain (LPB), and 4) 16% CP and a 50:50 ratio barley and corn grain (LPBC). In 21 d periods, data collection was conducted in second and third weeks. Data were analyzed as repeated measure by using proc mixed of SAS software. The results showed that cows fed with LPBC diet had higher Dry matter intake ($P < 0.01$), dry matter digestibility ($P < 0.05$), organic matter digestibility ($P < 0.05$) and neutral detergent fiber digestibility ($P < 0.01$). Rumen fluid concentrations of total volatile fatty acids ($P < 0.05$), acetate ($P < 0.01$), propionate ($P < 0.05$), and rumen pH ($P < 0.01$) of cows fed with different source of grain was significant. Cows fed higher level of CP had greater ($P < 0.05$) urine and rumen ammonia nitrogen, blood and milk urea nitrogen, and lower nitrogen efficiency than those fed lower level of CP. There were no differences between milk production and contents. In conclusion, the results from this study showed lowered dietary nitrogen content and using a mix of barley and corn grain in dairy ration can improve nitrogen efficiency.

Key Words: cereal grains, crude protein, Holstein cow

W314 Lactational performance, chewing behavior, and ruminal fermentation of dairy cows fed diets differing in amount and digestibility of NDF from two sources of corn silage.

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Ruminally cannulated Holstein cows (n = 8, 91 ± 11 d in milk) were used in a replicated 4 × 4 Latin square design study with 21-d periods

(8-d collection periods) to evaluate intake, milk yield and components, chewing behavior, and ruminal fermentation in response to diets differing in amount and 24-h digestibility of aNDF ($NDFD_{24h}$) from 2 sources of corn silage. Treatments were 1) 53% forage, conventional corn silage (CCS)-based diet with 32% aNDF, 28% starch, 56% $NDFD_{24h}$ (Low CCS); 2) 68% forage, CCS-based diet with 36% aNDF, 21% starch, 54% $NDFD_{24h}$ (High CCS); 3) 50% forage, BMR-corn silage-based (BMR) diet with 32% aNDF, 28% starch, 62% $NDFD_{24h}$ (Low BMR); and 4) 64% forage, BMR-based diet with 35% aNDF; 24% starch; 60% $NDFD_{24h}$ (High BMR). Data were analyzed as a replicated Latin square with the MIXED procedure of SAS with fixed effects of diet, period, and replicate. Cow within square was the random effect. Intake, milk yield, and solids corrected milk (SCM) were lower on the High CCS diet. Efficiency of milk production (milk/DMI, 1.63 ± 0.04; SCM/DMI, 1.57 ± 0.03) was not affected ($P > 0.1$) by treatment. Differences in milk composition and chewing behavior reflected dietary inclusion of NDF. Chewing time per kg of NDF intake was greater for CCS diets. Mean ruminal pH was lower on the Low BMR diet, though time (min/d) below a pH of 5.8 (328 ± 89) or 5.5 (98 ± 43) did not differ ($P > 0.1$) among diets. Greater inclusion of highly digestible NDF forage promoted DMI and milk yield without compromising the ruminal environment.

Table 1.

Item	Low CCS	High CCS	Low BMR	High BMR	SE
DMI, kg/d	29.0^{a}	26.5^{b}	29.3^{a}	29.2^{a}	0.7
Milk, kg/d	47.0^{a}	43.1^{b}	48.6^{a}	47.2^{a}	1.6
SCM, kg/d	45.2^{ab}	41.8^{b}	46.4^{a}	45.7^{a}	1.2
Fat, %	3.82^{ab}	4.02^{a}	3.76^{b}	3.94^{ab}	0.14
Fat, kg/d	1.83	1.71	1.87	1.85	0.05
True protein, %	3.06^{ab}	2.92^{c}	3.10^{a}	3.02^{b}	0.05
True protein, kg/d	1.48^{ab}	1.25^{c}	1.55^{a}	1.43^{b}	0.04
Ruminating, min/d	514^{ab}	543^{a}	463^{b}	536^{a}	17
Chewing, min/kg NDF	84.6^{ab}	88.7^{a}	77.9^{b}	80.5^{b}	3.6
Rumen pH	6.09^{ab}	6.17^{a}	6.00^{b}	6.07^{ab}	0.08
Rumen NH3-N, mg/dL	10.49	11.60	9.88	10.42	0.79
Rumen VFA, mM	105^{ab}	102^{b}	110^{a}	111^{a}	8

$^{abc}P \leq 0.05$.

Key Words: BMR corn silage, chewing behavior, NDF digestibility

W315 Reduced protein for late-lactation dairy cows fed ryegrass haylage-based diets.

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Ryegrass is a reliable high-quality forage resource in Southeast Louisiana. In this study, 2 protein levels were compared in ryegrass-based diets fed to late lactation dairy cows. Twenty 4 lactating Holstein cows (244 ± 55 DIM and 30.7 ± 4.81 kg milk yield) were randomly distributed among 4 pens in a freestall barn equipped with Calan gates for individual TMR feeding. Higher protein TMR (HP) contained 15.4 ± 0.20% CP using soybean meal as the main protein supplement and rumen-protected Met (Metasmart, Adisseo; 0.10% DM basis). Lower protein TMR (LP) contained 13.8 ± 0.4% CP and was prepared using dry distillers' grains plus solubles (DDGS), soybean hulls, and rumen protected Lys (AminoShure-L, Balchem, 0.25% DM basis) and Met (0.18% DM basis) to offset dietary AA deficiencies. Cottonseed, corn, and minerals remained similar in both rations. Forage (ryegrass haylage) represented 41% of the rations (DM basis). Metabolizable protein (MP) balance (NRC, 2001) was estimated to be marginal (30 g/cow/d for HP) or deficient (−180 g/cow/d for LP). The experiment was analyzed as a crossover design using SAS MIXED procedure with pen as experimental unit. Cows in both treatments had similar intake (21.4 kg/cow/d for HP and 20.9 kg/cow/d for LP; $P = 0.51$) and maintained body condition score (0.03 unit/period for HP and 0.04 unit/period for LP; $P = 0.77$), but most lost weight (−18.1 kg/cow/period for HP and −14.0 kg/cow/period for LP; $P = 0.71$) mainly in the second period. Milk yield (27.5 kg/cow/d for HP and 25.9 kg/cow/d for LP; $P = 0.36$) and water intake (118 kg/cow/d for HP and 112 kg/cow/d for LP; $P = 0.47$) did not differ statistically. Cows ingested 4.3 kg of water per kg of milk output in both treatments. Milk components averaged 3.48%, 3.30%, and 4.71% respectively for fat, protein and lactose ($P = 0.12$). Milk urea nitrogen decreased ($P = 0.01$) from 9.85 mg/dL with HP to 6.40 mg/dL with LP. Results suggest late-lactation dairy cow performance can be maintained, at least in the short term (21 d-period), when fed an MP deficient diet based on ryegrass haylage and supplemented with DDGS and soybean hulls, adjusted with rumen-protected Met and Lys.

Key Words: dairy cows, protein, dry distillers grains plus solubles

W316 Energy intake of dairy cows grazing native rangeland in México.

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Energy requirements of cows for grazing on native rangeland are high; therefore determination of energy intake from grazed herbage (EIGH) is important. The aim was to estimate EIGH of dairy cows grazing native rangeland at Marcos Castellanos, Michoacán (19°59′ N, 103°01′ W, 2000 masl). The experiment took place in the dry (DS) and rainy (RS) seasons; DS measurements were taken in 2 farms and during the RS a third farm was added. Intake was measured on 6 cows during 2 (DS) and 3 (RS) cycles of 24 h. Offered and residual amounts of supplementary feed were measured and samples were taken to estimate the content of net energy of lactation (NEL) based on Acid Detergent Fiber contents. Hand-plucked samples of grazed herbage were taken for estimation of NEL content. Herbage dry matter intake (DMI) was estimated by means of fecal output (chromium oxide and acid insoluble ash). Calculation of EIGH was based on DMI and NEL content. A mixed model was used, with fixed effects of season, farm nested within season, cycle nested within farm and season, lactation stage and their interactions; the random effect of cows nested within farm was included. In Table 1 is shown that mean total energy intake was lower in DS than in RS due to lower EIGH. Total energy intake and EIGH in DS did not differ among farms and neither did EIGH in RS. Differences in RS were due to supplementary feeding. It is concluded that due to very low EIGH, accurate use of supplementary feeding is crucial in the dry season.

Table 1. Energy intake (Mcal NE_L) of dairy cows grazing native rangeland

Season	Farm			Mean
	A	B	C	
Total				
Dry		$18.5^{x,b}$	$19.5^{x,a}$	19.0^{B}
Rainy	26.4^{x}	$23.2^{xy,a}$	$19.3^{y,a}$	23.0^{A}
Herbage				
Dry		$5.1^{x,b}$	$4.3^{x,b}$	4.7^{B}
Rainy	10.8^{x}	$10.8^{x,a}$	$11.0^{x,a}$	10.8^{A}

^{x,y}Means not sharing letters within rows and within each variable are different ($P \leq 0.05$).

^{a,b}Means not sharing letters within columns and within each variable are different ($P \leq 0$ .05).

^{A,B}Means not sharing letters within columns and within each variable are different ($P \leq 0.05$).

Key Words: dry and rainy seasons, grazed herbage, net energy of lactation

W317 Feeding canola meal to dairy cows: A meta-analysis on lactational responses suggests underestimation of metabolizable protein supply by NRC (2001). R. Martineau, D. R. Ouellet, and H. Lapierre,* *Dairy and Swine R&D Centre Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada.*

The objective of this meta-analysis was to determine the effects of the substitution of a protein source by canola meal (CM) on lactational responses (Δ = CM minus control) in dairy cows. The study included 83 comparisons of isoproteic (±1.5% CP) treatments published since 1975 (42 experiments). The CM intake ranged from 0.9 to 4.0 kg/d (SD 0.75). The level of inclusion of CM (ΔCM) was expressed as 100 g/kg of diet (DM basis); therefore, the coefficient associated with ΔCM represents the response observed with a 10% increment in the dietary proportion of CM (e.g., 2 kg of CM for 20 kg DMI = ΔCM of 10%). Dietary composition was estimated using NRC (2001). Regressions were forced through the origin, weighted by sample size and controlled for differences in DMI and diet concentrations of NDF, CP and ether extract. Milk yield (MY, kg/d) and milk protein yield (MPY, g/d) responded linearly to increasing ΔCM: $\Delta MY = 0.4^{***} (\pm 0.08) \times \Delta CM$, $R^2adj = 0.55$, n = 80; and $\Delta MPY = 25^{***} (\pm 2.6) \times \Delta CM$, $R^2adj = 0.53$, n = 80. The MPY response was different ($P = 0.04$) depending on the type of protein source that was substituted. The ΔCM coefficients were 14*** (±3.8) and 26*** (±3.5) with substitutions involving only soybean meal ($R^2adj = 0.44$; n = 37) or other protein sources ($R^2adj = 0.61$; n = 35), respectively. The greater effect with other protein sources was due to an additional positive effect of ΔCM on milk protein percentage. The efficiency of N utilization (milk N yield/N intake; g/kg) also responded linearly to increasing ΔCM: $7.5^{***} (\pm 0.96) \times \Delta CM$, $R^2adj = 0.48$, n = 82. The estimated supply of metabolizable protein (MP) was examined to explain the responses to ΔCM. Surprisingly, there was a negative effect of CM inclusion on ΔMP: $-85^{***} (\pm 9.2) \times \Delta CM$, $R^2adj = 0.53$, n = 80, contrarily to the usual positive relationship between MP supply and MY or MPY. In conclusion, current results suggest that a protein supplement can be substituted by CM with positive effects on lactational performances. It also appears that there is a systematic underestimation of MP supply associated with CM inclusion in dairy rations using the NRC (2001) model.

Key Words: canola meal, meta-analysis, metabolizable protein

W318 Milk production, milk composition and blood parameters of cows fed whole flaxseed or whole linola. H. V. Petit*[1], R. N. do Prado[1,2], M. F. Palin[1], and C. Benchaar[1], *[1]Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada, [2]Universidade Estadual de Maringa, Maringa, PR, Brazil.*

A total of 28 Holstein cows were stratified by groups of 3 within parity for similar expected calving dates, and cows within group were randomly assigned to one of 3 isonitrogenous and isoenergetic diets to determine the effects of feeding different sources of fatty acids (FA) on milk production, milk composition, and blood parameters related to fatty liver. The 3 TMR contained either calcium salts of palm oil (MEG), unsaturated lipids supplied as 4.8% whole linola (WLO) rich in *n*-6 FA, or unsaturated lipids supplied as 4.8% whole flaxseed (WFL) rich in *n*-3 FA. The experiment was carried out from wk 4 before parturition to wk 12 of lactation. All cows were fed for ad libitum intake. Milk production and DMI were recorded at every milking and daily, respectively. Cows were weighed weekly and body score was recorded at the same time. Milk composition was determined on wk 1, 2, 3, 4, 6, 10 and 12. Blood was collected on wk 1 and 2 prepartum and on wk 1, 2, 4, 6 and 8 postpartum to determine NEFA, glucose and β-hydroxybutyrate. Data were analyzed as repeated measures using the PROC MIXED procedure of SAS (SAS Institute, 2000).There was an interaction ($P = 0.01$) between wk and treatment as a result of a greater increase over time in DMI, expressed as a percentage of BW, for cows fed WFL compared with those fed MEG. Cows fed MEG tended ($P = 0.07$) to produce more milk (41.7 kg/d) than those fed WLF and WLO (38.3 and 38.2 kg/d, respectively). Concentrations of protein, fat and lactose in milk were similar among diets. Treatment had no effect on BW, body condition score, blood concentration of NEFA and β-hydroxybutyrate. Cows fed WFL tended ($P = 0.09$) to maintain higher blood concentrations of glucose than those fed WLO and MEG as shown by the interaction between treatment and wk. These data suggest that feeding oilseeds that differ only for their type of FA (*n*-6 in linola and *n*-3 in flaxseed) result in similar productivity of early-lactating dairy cows.

Key Words: dairy cattle, flaxseed, linola

Ruminant Nutrition: Dairy: Rumen function and digestion

W319 In situ ruminal degradability of soybean meal (SBM), canola meal (CM), and corn or wheat dried distillers grains (DDG).

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Different protein sources, as CM or by-products of ethanol production, are currently used in dairy rations to replace SBM. There is little data available on rumen degradation of these protein sources in a single study. Therefore, the objective of this study was to compare the dry matter (DM) and crude protein (CP) ruminal degradability of SBM, CM, high protein corn DDG with solubles (HPDDG) and wheat DDG with solubles (WDDG). In situ studies were conducted with 4 rumen-fistulated lactating Holstein cows fed a diet containing 38% grass hay and 62% corn-based concentrate. Each protein source was incubated in the rumen in nylon bags for 0, 2, 4, 8, 16, 24 and 48h according to NRC (2001) guidelines. DM and CP ruminal degradabilities were calculated from rumen-undegraded residues corrected or not for small particle loss according to Hvelplung and Weisbjerg (2000). Data were fitted to an exponential model to estimate degradation parameters and effective degradability (ED) was calculated with a passage rate of 7%/h. DM and CP contents for SBM, CM, HPDDG and WDDG were 88.7, 89.7, 92.2, 89.7% and 53.6, 40.0, 40.3, 37.2%. WDDG and SBM had higher uncorrected ED ($P < 0.05$, DM: 75.0 and 72.6%, CP: 84.8 and 66.0%) than CM and HPDDG (DM: 57.2 and 55.5%, CP: 59.3 and 48.2%). This was attributed to a higher soluble fraction in WDDG and a higher potentially degradable fraction and rate of degradation in SBM (9.0 vs. 5.8%/h for the other feeds). Small particle loss from the bags contributed to the DM and CP disappearance, being higher for WDDG (31.6% of DM, 45.7% of CP feed) than for the other feeds (11.2, 14.7, 17.3% of DM and 16.3, 19.7, 19% of CP for SBM, CM and HPDDG). Therefore, the corrected ED was lower than the uncorrected ED for all feeds, especially for WDDG where ED decreased to 53.2% (DM) and 60.8% (CP). However, this correction did not alter feed ranking, with SBM and WDDG being more degradable than CM and HPDDG. The results suggest that small particle loss correction is relevant for this type of feed ingredients and that higher RUP supply would result with CM and HPDDG substituting SBM, assuming similar intestinal digestibility.

Key Words: rumen degradation, protein

W320 Effect of carbohydrate source on performance and ruminal responses of dairy cows fed low-starch diets.

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Fifteen multiparous Holstein cows (6 ruminally cannulated) were used in a replicated 3 × 3 Latin square design with 21-d periods (7-d collection periods) to measure the effect of forage or nonforage sources of fiber on lactational and ruminal responses when fed to cows in lower-starch diets compared with a higher-starch control diet. Treatments were: 1) control diet (CON) containing 50% forage [20% conventional corn silage (CS), 20% brown midrib CS, and 10% haycrop silage (HCS)], 2) high-forage diet (FOR) containing 63% forage (53% brown midrib CS and 10% HCS), and 3) nonforage fiber source diet (NFFS) containing 50% forage similar to CON and partial replacement of corn meal and soybean meal with beet pulp, wheat middlings, and distillers grains. CON contained 35% neutral detergent fiber (NDF) and 26% starch, FOR contained 38% NDF and 21% starch, and NFFS contained 38% NDF and 21% starch. Data were analyzed as a Latin square by ANOVA with the MIXED procedure of SAS using cow as the experimental unit, treatment, period within square, and square as fixed effects, and cow within square as a random effect. Dry matter intake (DMI), NDF intake, milk yield, and milk composition differed among treatments, which reflected the dietary NDF content. There was no treatment effect ($P > 0.10$) on solids-corrected milk (SCM), efficiency of milk production, ruminal total volatile fatty acid concentration (126 ± 4 m*M*), ammonia concentration (6.7 ± 0.7 mg/dL), or microbial N yield (594 ± 28 g/d). CON was associated with compromised ruminal pH compared with FOR and NFFS. This study demonstrates the value of both a higher forage and a NFFS strategy compared with a higher starch feeding approach.

Table 1.

Item	CON	FOR	NFFS	SE
DMI, kg/d	28.2^{x}	27.2^{y}	27.7^{xy}	0.8
NDF intake, kg/d	9.1^{b}	10.0^{a}	9.9^{a}	0.3
Milk, kg/d	51.6^{ax}	48.4^{by}	50.5^{abx}	2.3
SCM, kg/d	49.0	47.3	48.5	1.9
Fat, %	3.66^{y}	3.98^{x}	3.76^{xy}	0.17
Fat, kg/d	1.86	1.88	1.86	0.08
True protein, %	3.10	3.07	3.08	0.06
True protein, kg/d	1.58^{ax}	1.45^{by}	1.54^{abx}	0.05
SCM/DMI	1.73	1.74	1.75	0.04
Rumen pH	6.09	6.16	6.11	0.04
Rumen pH range	1.17^{x}	0.99^{xy}	0.92^{y}	0.08
Rumen pH < 5.5, min/d	85^{x}	11^{y}	30^{xy}	22
Ruminating, min/d	530	554	541	12
Ruminating, min/kg NDF	58.3^{a}	56.1^{ab}	54.8^{b}	1.7

$^{ab}P \le 0.05$, $^{xy}P \le 0.10$.

Key Words: nonforage fiber source, low-starch, NDF

W321 Duodenal bioavailability of quercetin and rutin in German Holstein cows.

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Flavonoids were shown to have health promoting effects in vitro but evidence for in vivo efficacy is scarce. Whether they are effective depends on their bioavailability and metabolism. Since flavonoids are thought to be degraded by the rumenal microbiota we studied the bioavailability of the flavonol quercetin after duodenal administration of the aglycone and its glucorhamnosid rutin. Six German Holstein cows (>10,000 kg milk 305 d; 2nd lactation; 87 DIM) were fitted with duodenal cannulas. Bioavailability was tested at 4 different doses of each flavonoid (0 (NaCl only), 30, 60 and 90 μmol/kg BW). Before and after duodenal short-term infusion (10 min) at 0700 h, timed blood samples were taken until 24 h post-administration. Levels of plasma quercetin (Q), and its methylated (isorhamnetin, tamarixetin; I, T) and dehydroxylated (kaempferol; K) derivatives were measured after treatment with β-glucuronidase and sulfatase by HPLC with fluorescence detection. Data evaluation was performed using PROC MIXED of SAS. After rutin administration levels of plasma Q, I, T, and K did not increase above baseline. Administration of quercetin aglycone resulted in increased plasma concentrations of Q, I, T and K within 1 h ($P \le 0.05$). Although maximal plasma

Q concentrations showed high interindividual variability (331.9–842.8 nmol/L at 90 µmol/kg) peak time (115 min) did not differ ($P > 0.9$) among cows. With quercetin aglycone, Q was the main metabolite in plasma followed by I, K and T (81.5, 8.8, 5.8, 3.8% of total flavonol plasma area under curve). Flavonoids did not change DMI and plasma glucose levels but increased daily milk yield by 8% as compared with NaCl administration ($P \leq 0.05$). In contrast to findings in monogastric animals quercetin from rutin seems not to be available in cows when administered duodenally. Different intestinal microbiota composition in ruminants and monogastrics as well as differences in passage time could explain these findings. The increased milk yield upon flavonoid administration needs verification. Supported by BMBF, Germany.

Key Words: bioavailability, dairy cows, flavonoids

W322 Differences in rate of ruminal hydrogenation of C18 fatty acids in clover and ryegrass. J. Lejonklev*[1], A. C. Storm[2], M. K. Larsen[1], G. Mortensen[1], and M. R. Weisbjerg[2], *[1]Aarhus University, Department of Food Science, Tjele, Denmark, [2]Aarhus University, Department of Animal Science, Tjele, Denmark.*

The effect of forage type on ruminal hydrogenation was investigated by in vitro incubation of feed samples in rumen fluid from 2 rumen fistulated Holstein cows. Silages of red clover (RC), white clover (WC) and perennial ryegrass (PR) were produced in laboratory scale using forage harvested in primary growth and in third regrowth, resulting in 6 silages. Fatty acid content was analyzed after 0, 2, 4, 6, 8 and 24 h of incubation in triplicates to study the rate of hydrogenation of unsaturated C18 fatty acids. Initial composition of C18 fatty acids in dry matter varied between the different forages and growths. The amount of polyunsaturated fatty acids decreased with increased incubation time, whereas the amounts of monounsaturated vaccenic acid and saturated stearic acid increased. A dynamic mechanistic model was constructed assuming mass action driven fluxes between the following pools of C18 fatty acids: C18:3 (linolenic acid), C18:2 (linoleic acid), C18:1 (vaccenic acid, oleic acid, petroselidic acid) and C18:0 (stearic acid) as the end point. Longitudinal data from each single in vitro run was fitted to the final model and the rate constants (/h) of the hydrogenation were estimated using a Nelder-Mead optimization algorithm while maximizing the log-likelihood function. The estimated rate constants of hydrogenation were 0.069 (RC), 0.071 (WC) and 0.087 (PR) for $k_{C18:2->C18:1}$. 0.081 (RC), 0.077 (WC) and 0.102 (PR) for $k_{C18:3->C18:1}$. 0.046 (RC), 0.055 (WC) and 0.050 (PR) for $k_{C18:1->C18:0}$. Type of forage had a significant effect on $k_{C18:2->C18:1}$ ($P = 0.005$) and a tendency to influence $k_{C18:3->C18:1}$ ($P = 0.062$). The growth (primary or regrowth) had no effect on $k_{C18:2->C18:1}$ ($P = 0.42$) or $k_{C18:3->C18:1}$ ($P = 0.14$). Neither forage nor growth significantly affected $k_{C18:1->C18:0}$ ($P > 0.5$). Both RC and WC resulted in lower rates of hydrogenation of polyunsaturated fatty acids to monounsaturated than did PR, whereas the hydrogenation of monounsaturated to saturated fatty acids was similar between forages. This effect is present irrespective of the cutting time, i.e., primary growth or regrowth, despite large variations in fatty acid content between the cuts.

Key Words: clover, hydrogenation, rumen

W323 Corn source and dietary protein degradability: effects on ruminal measures and proposed mechanism for degradable protein effects. M. B. Hall,* *U. S. Dairy Forage Research Center, USDA-ARS, Madison, WI.*

Effects of corn source and ruminal degradability of dietary protein (RDP) on ruminal measures was evaluated in a partially balanced, incomplete Latin square design with 3 21-d periods, 8 ruminally cannulated lactating dairy cows, and a 2 × 2 factorial arrangement of treatments (trt). Trt were corn source (corn; DG: dry ground corn, HM: high moisture corn) and RDP (+RDP: added protein from soybean meal; -RDP: heat-treated expeller soybean product partially substituted for soybean meal). Diets were formulated to be isonitrogenous and similar in starch and NDF. Data were analyzed with mixed models with cow (a random variable), period, corn, RDP, and corn x RDP as factors. Rumen concentrations over time were analyzed as repeated measures. Significance was declared at $P < 0.05$, and tendency $0.05 \leq P < 0.15$. DMI was 1 kg less on -RDP as compared with +RDP diets. Weights of total digesta and liquid tended to be greater with +RDP than with -RDP at 2 h post-feeding, with digesta DM% greater with -RDP than with +RDP (DM%: 14.6, 15.7, 14.9, and 15.3% for DG+RDP, DG-RDP, HM+RDP, and HM-RDP, respectively, SED = 0.44). Differences in the digesta DM:liquid ratio could introduce dilution effects on pH and organic acid concentrations (OA), hence, 2 h post-feeding digesta DM% for each cow in each period were used as covariates for analysis of ruminal pH and OA. *P*-values of the covariate were < 0.04. pH was greater for DG (6.27) than for HM (6.09; SED = 0.12), and tended to be affected by RDP x time with HM+RDP numerically lower than other trt after 1 h post-feeding. Corn x RDP tended to affect mean OA with +RDP 4% lower than -RDP with DG, but 9% greater with HM. Interaction of time and RDP affected OA with +RDP (155 mM) greater than -RDP (141 mM; SED = 5.9) at 2 h post-feeding and with more similar values for trt at all other times. Average lactate concentration was greater and maxima tended to be greater for +RDP than for –RDP. +RDP effects on OA and pH may be due to more immediate fermentation of starch instead of storage as microbial glycogen, but presence of dietary starch precludes measurement of glycogen. The basis for RDP effects needs further exploration.

Key Words: corn, protein degradability, rumen fermentation

W324 A meta-analysis of continuous culture rumen fermentation and digestibility data. A. N. Hristov*[1], C. Lee[1], R. A. Hristova[1], P. Huhtanen[2], and J. L. Firkins[3], *[1]The Pennsylvania State University, University Park, [2]Swedish University of Agricultural Sciences, Umeå, Sweden, [3]The Ohio State University, Columbus.*

A meta-analysis was conducted to investigate variability in ruminal fermentation and nutrient digestibility in continuous culture (CC) experiments in comparison with in vivo data. One hundred and 80 CC studies representing 1,074 individual treatments were used in the analysis. Studies were classified into 2 groups based on the type of CC used: CC system specified as RUSITEC (Rumen Simulation Technique) and non-RUSITEC CC systems. The CC data were compared with a data set of in vivo trials (INVIVO) with ruminally-cannulated lactating dairy cows (a total of 366 individual cow data). Data were analyzed using the MIXED procedure of SAS with study as random effect. Average total VFA concentration for RUSITEC and non-RUSITEC was 68 and 80% ($P < 0.001$) of INVIVO concentrations: 79.0 (SD = 30.9), 93.8 (36.3), and 116.9 (19.8) m*M*, respectively. Average concentration of acetate was also lower ($P < 0.001$) for the CC data sets compared with INVIVO and that of propionate was considerably lower for RUSITEC compared with INVIVO ($P < 0.001$), but butyrate concentrations were similar between CC and INVIVO. Average acetate:propionate ratios were lower ($P < 0.001$) for the CC data sets compared with INVIVO (2.69, 2.61, and 2.94, respectively). Variability in the VFA data was generally the highest for non-RUSITEC (higher CV and variance; $P < 0.001$), followed by RUSITEC, and was the lowest for INVIVO. Digestibilities of neutral-detergent fiber (NDF) and particularly organic matter (OM) were lower ($P < 0.001$) in the CC data sets compared with INVIVO; average NDF digestibility was 34.2 (15.9), 45.5 (17.2), and

53.0 (11.6) % for RUSITEC, non-RUSITEC, and INVIVO. A possible explanation for the considerably lower NDF digestibility with RUSITEC vs. non-RUSITEC could be the lower microbial enzymatic activities within the nylon bag vs. the surrounding rumen reported for the in situ procedure. This analysis demonstrated that in CC, total VFA and acetate concentrations were lower, protozoa were low or absent, and OM and NDF digestibilities were lower than in vivo. Overall, variability was much greater for CC vs. in vivo experimental data.

Key Words: continuous culture, rumen fermentation, meta-analysis

W325 Amount and digestibility of NDF affects rumen nutrient pool sizes and passage kinetics of dairy cows. K. W. Cotanch,* C. Kokko, H. M. Dann, J. W. Darrah, and R. J. Grant, *William H. Miner Agricultural Research Institute, Chazy, NY.*

Ruminally cannulated Holstein cows (n = 8, 91 ± 11 d in milk) were used in a replicated 4 × 4 Latin square design study with 21-d periods to evaluate rumen pool size and turnover of organic matter (OM) and neutral detergent fiber (aNDF) of cows fed different sources and amounts of corn silage using a rumen evacuation technique. Conventional corn silage (CCS) and BMR corn silage (BMRCS) contained 37 and 39% aNDF with a 24-h aNDF digestibility (NDFD) of 38 and 51%, respectively. Treatments were 1) LCCS: 53% forage, 39% CCS, 32% aNDF, and 56% NDFD; 2) HCCS: 68% forage, 55% CCS, 36% aNDF, and 54% NDFD; 3) LBMR: 50% forage, 36% BMRCS, 32% aNDF, and 62% NDFD; and 4) HBMR: 64% forage, 50% BMRCS, 35% aNDF, and 60% NDFD. Intake was measured during d 14 to 21. Ruminal contents were evacuated manually 4 h after and before feeding on d 20 and 21, respectively. Total rumen contents were weighed and volume determined. Ten percent of rumen contents were collected, subsampled, and analyzed for OM and aNDF content. Data were analyzed as a replicated Latin square with the MIXED procedure of SAS with fixed effects of diet, period, and replicate. Cow within square was the random effect. Intake of dry matter (DMI) and aNDF were affected by treatment. Ruminal digest volume and mass were greatest for HCCS and lowest for LBMR. Pool size of OM did not differ among treatments but turnover time of OM was greater for HCCS than LBMR and HBMR. Pool size of aNDF was greater for HCCS than LBMR; LCCS and HBMR were intermediate. Turnover time of aNDF was greater for LCCS and HCCS than HBMR. The amount and digestibility of forage aNDF from corn silage affect nutrient pool size and passage kinetics of dairy cows.

Table 1.

Item	LCCS	HCCS	LBMR	HBMR	SE
DMI, kg/d	29.0^{a}	26.5^{b}	29.3^{a}	29.2^{a}	0.7
aNDF intake, kg/d	9.4^{b}	9.5^{b}	9.3^{b}	10.3^{a}	0.2
Ruminal digesta, L	123^{ab}	128^{a}	113^{b}	119^{ab}	3
Ruminal digesta, kg	106^{ab}	112^{a}	98^{b}	105^{ab}	3
Ruminal pool size, kg					
OM	13.00	12.49	12.14	12.64	0.59
aNDF	8.32^{ab}	8.45^{a}	7.64^{b}	8.36^{ab}	0.41
Ruminal turnover rate, %/h					
OM	8.95^{ab}	8.31^{b}	9.44^{a}	9.57^{a}	0.51
aNDF	4.84^{b}	4.76^{b}	5.12^{ab}	5.52^{a}	0.30
Ruminal turnover time, h					
OM	11.4^{ab}	12.2^{a}	11.0^{b}	10.9^{b}	0.5
aNDF	21.1^{a}	21.4^{a}	20.3^{ab}	19.0^{b}	1.1

$^{ab}P \leq 0.05$.

Key Words: corn silage, NDF digestibility, passage

W326 Orchard grass forage effects on bacterial communities and long-chain fatty acid profiles in the rumen of Holstein heifers. R. Mohammed[1,2], G. E. Brink[1], D. M. Stevenson[1], K. A. Beauchemin[2], and P. J. Weimer*[1], *[1]USDA-ARS, US Dairy Forage Research Center, Madison, WI, [2]AAFC, Lethbridge Research Center, Lethbridge, AB, Canada.*

The aim of this study was to determine if ruminal bacterial community composition (BCC) and long chain fatty acid (FA) profiles differed in heifers grazing orchardgrass pasture (OP) versus those fed hay (OH) harvested from the same field at the same stage of maturity. Five ruminally cannulated Holstein heifers were allotted to OP or OH with three 28-d periods. Three of these heifers were offered OP, OH and OP successively in the 3 periods while the other 2 heifers remained on OP for all periods. Ruminal digesta were collected on 3 consecutive days near the end of each period. Microbial DNA was extracted from solid and liquid phases of digesta, amplified by PCR using domain-level bacterial primers, and subjected to automated ribosomal intergenic spacer analysis (ARISA). Total ruminal volatile fatty acids (m*M*) and acetate (mol/100 mol) were greater for OH than for OP, while butyrate was less. The ARISA profiles for the OP and OH diets formed distinct clusters, indicating that ruminal BCC was affected by diet. Branched-chain FA (% total FA methyl esters) in rumen digesta (13:0 *anteiso*, 14:0 *iso*, 15:0 *iso*, 15:0 *anteiso* and 18:0 *iso* were greater for OH than OP. Total *trans* (*t*)-18:1, *t*11- and *t*10-18:1 were greater for OP than OH. Conjugated linoleic acid (CLA) isomers (*c*9, *t*11-CLA and *t*10, *c*12-CLA) were not influenced by the diets. Relative population size (RPS) of *Butyrivibrio fibrisolvens* and *Megasphaera elsdenii* in the liquid phase of rumen digesta (fraction of total 16S rRNA gene copy number), were not affected by diet. Regression analysis of ruminal *t*10-18:1 and RPS of *M. elsdenii* was not significant ($P = 0.59$; n = 8). Unexpectedly, the relationship between ruminal *t*11-18:1 and RPS of *B. fibrisolvens* was negative ($r^2 = 0.52$; $P = 0.04$; n = 8) suggesting that there are likely yet unidentified polyunsaturated FA biohydrogenating rumen bacteria. The difference in ruminal chemistry and BCC in heifers fed OP and OH reflects possible alterations in substrate availability to the rumen microflora due to differences in the form of diet (fresh vs. conserved forage).

Key Words: conjugated linoleic acid, orchardgrass, rumen bacterial communities

W327 Silicone plastination of rumen models: A room temperature technique. H. C. Puch,* K. B. Cunningham, and D. C. Brown, *LongView Animal Nutrition Center, Land O'Lakes Purina Feeds, Gray Summit, MO.*

The objective of this work was to create demonstration models of rumen tissues that are preserved and realistic compared with fresh tissues. Silicone plastination is a process that replaces tissue and cellular fluids with silicone polymers. Using this method, rumen tissue specimens can be preserved that are lightweight, flexible and anatomically correct. Random Holstein calves at 12, 20, or 24 weeks of age were euthanized and the reticulo-rumens collected for preservation. The full reticulo-rumen was placed on its right side, and an incision made around the outer circumference. The reticular fold, cranial and caudal pillars are cut at their mid points so that the reticulo-rumen can lay flat creating a symmetrical left and right side. The left side portion of the rumen was first dehydrated in cold 100% acetone at −24 C. Each rumen is stretched and attached to a customized polypropylene frame and placed into the vacuum chamber filled with silicone (NCS10 and NCS6, supplied by R.W. Henry, DVM, 1455 A. R. Davis Road, Seymour, TN. 37865). The lab made welded vacuum chamber is made from 6.5 mm steel with a chamber 810 mm long × 460 mm wide × 150 mm deep and has 170 mm

× 130 mm × 12 mm thick acrylic window in the top. Silicone replacement of tissue acetone occurs slowly in the vacuum chamber by decreasing pressure. Vacuum is controlled by adjusting inlet needle valve. Visually, the acetone will start to boil/vaporize at 22 cm Hg. Vacuum is held 22 cm Hg for 24 h. Each day the vacuum pressure is decreased by 1/2 for 3 d and the vacuum is 2 cm Hg. On d 4 the needle valve is completely closed and the vacuum held for 24 h or until acetone stops vaporizing. The rumen is removed from the silicone, allowed to drain, air dry for 24 h and removed from stretching frame. Final end chain polymerization is done by spraying tissue with the polymerizing catalyst (NCS3) and held in a closed plastic bag for 24 h. Visual differences can be observed in the plastinated rumens at different weeks of age in, papillae size, shape, color appearance and any abnormalities. This method creates preserved tissues that are ideal for teaching and demonstrations.

Key Words: model, plastination, rumen

W328 Techniques for sampling and measuring total two-dimensional surface area of rumen papillae. H. C. Puch*[1], K. M. O'Diam[2], and K. M. Daniels[2], [1]*LongView Animal Nutrition Center, Land O' Lakes Purina Feeds, Gray Summit MO,* [2]*Ohio Agricultural Research and Development Center, The Ohio State University, Wooster.*

The aim was to develop an objective method for determining total 2-dimensional (T2D) surface area of rumen papillae which can effectively be used to study rumen development. Eight Holstein steers were fed defined amounts of texturized grower concentrate with ad libitum access to alfalfa hay from 12 to 24 wk of age. Steers were euthanized at 24 wk to evaluate rumen development. The full reticulo-rumen was placed on its right side and an incision made around the outer circumference. The reticular fold, cranial and caudal pillars were cut at their mid points, so that it could be laid out flat creating a symmetrical left and right side. The right side was sampled to measure papillae development. Tissue sections (2x12 cm) were cut from 4 regions (caudal dorsal blind sac, caudal ventral blind sac, cranial dorsal and cranial ventral) and individually stapled to labeled 15 cm wooden tongue depressors and preserved in fixative for later histological analyses (data not shown). Ten representative papillae were dissected from each rumen tissue section and adhered to millimeter graph paper to determine length (L) and width (W). T2D surface area was calculated for each papilla, using an oval equation [2*(L/2*W/2 * 3.14)]. For comparison, T2D surface area of the same papillae was also determined via a digital image analysis program (CellSens Imaging; Olympus Corp.). In this method, papillae images were traced and the 2D area x2 determined. Both measurement techniques were not different (pooled across region: 32.2 vs. 31.6 mm2, SE 5.3). However, the 4 regions of caudal dorsal blind sac, caudal ventral blind sac, cranial dorsal and cranial ventral had different papillae surface area of 28.4, 30.9, 26.5, and 42.0 mm2, SE 5.4, respectively ($P < 0.001$). Both methods are effective in quantifying T2D surface area of rumen papillae; the digital method has an advantage in that it does not assume the shape of each papilla to be an oval. Both methods are helpful in evaluating dietary influences on rumen papillae size. Due to regional differences in papillae area, each region must be examined in future studies to fully characterize papillae surface area response to dietary changes.

Key Words: papilla, rumen, dairy steer

W329 Changes in rumen bacterial communities and rumen chemistry in primiparous Holstein cows during the periparturient period. R. Mohammed[1,2], D. M. Stevenson[2], P. J. Weimer[2], G. B. Penner*[3], and K. A. Beauchemin[1], [1]*AAFC, Lethbridge Research Center, Lethbridge, AB, Canada,* [2]*USDA-ARS, US Dairy Forage Research Center, Madison, WI,* [3]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

The objectives were to study the changes in: 1) rumen bacterial community composition (BCC) and fermentation as influenced by feeding regimen and period; and 2) pH and VFA profiles among selected cows with minimum (stable) and maximum variation (unstable) between pre- and post-parturient periods. Fourteen Holstein heifers paired by expected calving date and BCS were allotted to 1 of 2 prepartum feeding regimens: low concentrate regimen (2 diets ranging from forage:concentrate, F:C = 80:20 to 54:46); or a high-concentrate regimen (4 diets ranging from F:C = 68:32 to 46:54). All cows received the same lactation diet postpartum. Microbial DNA extracted from 58 rumen digesta samples collected prepartum (d −50, −31, −14) and postpartum (d +14, +52) and amplified by PCR were subjected to automated ribosomal intergenic spacer analysis (ARISA). Changes in rumen chemistry (pH, VFA, and acidosis indicators at d −54, −35, −14, −3, +3, +17, +37, +58) were analyzed using principal component analysis (PCA). The ARISA profiles did not show a diet effect; however, 4 out of 14 cows showed a shift in BCC from the prepartum to the postpartum period. The PCA profiles did not show a diet effect for rumen fermentation variables. However, 4 cows (stable) showed minimal changes while 4 other cows (unstable) had greater changes in rumen fermentation when PCA profiles of individual cows were examined. The remaining cows had a PCA profile intermediate between the stable and the unstable fermentation profiles. Cows with a stable profile had greater minimum rumen pH, mean pH, less bouts under pH 5.5 and 5.2, and less duration and area of moderate (pH <5.5) and acute ruminal acidosis (pH <5.2) compared with cows with an unstable profile. Milk fat content tended to be greater for cows with a stable profile than for those with an unstable profile, with no difference in milk yield or FCM. Substantial changes in rumen chemistry occurred before and after calving with only small changes in BCC. Rumen chemistry during the periparturient period was not affected by feeding regimen but varied considerably among cows.

Key Words: ruminal acidosis, ruminal bacterial communities, periparturient period

W330 Detection of the methanol dehydrogenase structural gene *mxaF* in rumen fluid by PCR. E. T. Kim*[1], C. S. McSweeney[2], S. S. Lee[1], S. C. Kim[1], and S. H. Kang[2], [1]*Division of Applied Life Science (BK21 Program), Gyeongsang National University, Jinju, Gyeongnam, Republic of Korea,* [2]*CSIRO Livestock Industries, Queensland Bioscience Precinct, St Lucia, Qld, Australia.*

This study was conducted to demonstrate the potential possibility of methane oxidation in rumen by the *mxaF* gene, a functional gene (methanol dehydrogenase (MDH)), involved in methane oxidation pathway. The rumen fluid was collected before morning feeding from fistulated Holstein cows maintained on Leucaena and Rhodes grass diets, and on Lucerne diet. The DNA sample was amplified by PCR with the *mxaF* target primers. The expected DNA size band from PCR products was observed, and then cut for sequencing analysis. The PCR products of gDNA were ligated into the pGEM®-T Easy Vector according to the protocol of the TA Cloning Kit. Briefly, after the transformed cells had been incubated with isopropylthiogalactoside (IPTG), 192 random clones of white colonies were sequenced by an ABI 3130xl Genetic Analyzer. The amplicon sequences were compared with sequences of reference organisms from Greengenes and NCBI. The result from sequencing analysis matched *Methylobacterium sp.* which is extremely important because they can use methanol and methylamine as well as acetate, propionate and butyrate compounds to grow. *Methylobacterium* *sp.* is common in soil and on surfaces of leaves and other plant parts, and has the ability to utilize methane and other more complex organic compounds as carbon and energy sources. *Methylobacterium sp.* is known as a facultative methylotroph. *MxaF* gene, one of functional genes involved in methane oxidation pathway, was detected in rumen fluid in present study

Table 1. The result of sequencing analysis of mxaF-target from the rumen fluid

Classification	Identity (%)	
Methanol dehydrogenase alpha subunit (mxaF) gene (Methylobacterium brachiatum)	99	(527/533)
Methanol dehydrogenase alpha subunit (mxaF) gene (Methylobacterium platani strain KCTC12901)	98	(533/544)
Methanol dehydrogenase alpha subunit-like (mxaF) gene (Methylobacterium aquaticum strain DSM 16371)	98	(545/558)
Methanol dehydrogenase alpha subunit (mxaF) gene (Methylobacterium hispanicum strain DSM 16372)	97	(516/532)

Key Words: methane oxidation, methanol dehydrogenase, MxaF gene

W331 Evaluation of DM, NDF, and starch ruminal degradabilities of corn silage hybrids: A three-year study.

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This experiment evaluated the DM, NDF, and starch ruminal degradabilities of 6 corn silage hybrids (Garst 8707 MP, Maizex leafy 2, Mycogen TMF 94, Novartis G 4106, Pickseed Exel, Pioneer 38T27) seeded at 5 different locations in Ontario, Canada, and in 3 consecutive years. Each year, corn hybrids were ensiled in duplicate in 20-L mini-silos which were sampled after more than 100 d of fermentation. All frozen silage samples were placed in nylon bags and incubated for 0 (wash only) or 16 h into the rumen of 2 fistulated cows to determine the ruminal degradation characteristics using double-point estimation (Vanzant et al. 1996 JAS 74:2773). Effective ruminal degradabilities (ED) of nutrients were estimated assuming a fractional rate of passage of 0.06 h^{-1}. There was no interaction between hybrids and production years for all parameters. Silage DM concentration varied between 32 and 36% and was affected by hybrids and years (32.4^{a}, 32.7^{a}, and 34.1^{b} % for year 1, 2, and 3, respectively). Silage NDF and starch concentrations were also affected ($P < 0.05$) by hybrids (46.2 to 49.2 and 26 to 32% of DM, respectively) and years. Degradation rates of the potentially degradable DM, NDF, and starch were not affected by hybrids averaging 1.7, 1.1, and 8.8% h^{-1}, respectively. Degradation rate of DM was affected by the production year (1.5^{a}, 2.2^{b}, and 1.3^{c} % $h^{-1}$for year 1, 2, and 3, respectively); NDF degradation rate was affected by year in the same manner. The ED of DM was affected by hybrids (53.1^{a}, 53.8^{ab}, 54.3^{ab}, 54.9^{ab}, 55.3^{b}, and 56.9^{c} for Garst 8707 MP, Pickseed Exel, Novartis G 4106, Pioneer 38T27, Maizex leafy 2, Mycogen TMF 94, respectively). The ED of NDF and starch were similar among hybrids averaging, 23.0% (SE = 1.4) and 90.1% (SE = 0.7), respectively. Years affected ED of DM (51.7^{a}, 57.1^{b}, and 55.5^{c}% for 1, 2, and 3, respectively), NDF (24.5^{a}, 25.9^{a}, and 18.6^{b}% for year 1, 2, and 3, respectively) and starch (90.6^{a}, 89.0^{b}, and 90.6^{a}% for year 1, 2 and 3, respectively). Results indicates that the production year have a significant effect on DM, NDF, and starch concentrations of silage, which in turn affected degradation rate and ED of these parameters except for degradation rate of starch. Degradation rates and ED of NDF and starch were not affected by hybrids, but the hybrid Mycogen TMF 94 had the greatest ED of DM.

Key Words: corn silages, forage degradation

W332 Rumen microorganisms growth as a function of the concentration of corn silage and soybean meal in culture medium.

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The objective was to assess the effect of levels of corn silage and soybean meal on the ruminal microbial growth. Vials containing 6 mL of artificial saliva, 24 mL of inoculum and substrate (half corn silage, half soybean meal) in weights of 1.2; 0.6; 0.3; 0.1; 0.05 and 0 g were incubated in triplicate at 39°C for 72 h. Optical density (OD-600nm) and pH were measured at 0, 6, 12, 18, 24, 48 and 72 h of incubation. The experiment was analyzed as completely randomized design as a function of substrate concentration, time of incubation and the respective interaction. Microbial growth has reached the maximum value ($P < 0.01$) in the highest concentration of substrate, where it was also noted the lowest pH value (6.75). Regardless of level of substrate, the largest optical density was observed within 24 h incubation ($P < 0.01$) showing that the limiting factor was the substrate, as the pH was always above 6.9. After the time of maximum growth the microbial growth curve followed the hyperbolic model, assimptotic, being analyzed by saturation kinetics model of Lineweaver-Burk, as follows: $1/OD = y = 0.0869 + 0.5573\ (1/\text{concentration of substrate})$, $r^2 = 0.90$. The theoretical maximum growth rate was 1.79 and the substrate concentration required to achieve half of the maximum response was 0.160 g. The pH values were 6.75; 7.48; 7.93; 8.06 and 8.16 for 1.2; 0.6; 0.3; 0.1 and 0.05 g of substrate, respectively, and 7.70; 7.98; 7.80; 8.07; 7.74; 7.09; 7.36 in times of 0, 6, 12, 18, 24, 42 and 72 h of incubation, respectively. The growth of microbial population in rumen depends not only on the availability and substrate concentration, but also on fermentation products accumulation. Under the terms of this work the limiting factor was the availability of the substrate, leading to saturation of microbial growth, following the hyperbolic model. Supported by FAPEMIG (Fundação de Amparo à Pesquisa do Estado de Minas Gerais).

Key Words: fermentation kinetics of saturation, microbial growth, substrate

W333 Passage of liquid and fiber particles in dairy cows fed diets differing in NDF from conventional and bmr corn silages.

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Ruminally cannulated Holstein cows (n = 8, 91 ± 11 d in milk) were used in a replicated 4 × 4 Latin square design with 21-d periods to evaluate mean retention time (MRT) of liquid and fiber particles in cows fed diets varying in aNDF and 24-h NDF digestibility (NDFD) from conventional corn silage (CCS) and bmr corn silage (BMRCS). Treatments were 1) LCCS: 53% forage, 39% CCS, 32% aNDF, and 56% NDFD; 2) HCCS: 68% forage, 55% CCS, 36% aNDF, and 54% NDFD; 3) LBMR: 50% forage, 36% BMRCS, 32% aNDF, and 62% NDFD; and 4) HBMR: 64% forage, 50% BMRCS, 35% aNDF, and 60% NDFD. Samples of feces, haylage, CCS, and BMRCS were extracted in neutral detergent and sieved to obtain fiber particles of defined sizes. Fine fecal particles (1.59 - 4.75 mm), medium haylage particles (1.18 - 4.75 mm), and small (0.30 - 1.18 mm), medium (1.18 - 4.75 mm), and large (>4.75 mm) particles of CCS and BMRCS were labeled with Cr, La, Sm, Yb, Pr, respectively. Cows were dosed ruminally with a liquid marker (Co-EDTA) and marked particles on d 14 before feeding. Fecal samples were collected from 0 to 168 h after dosing and analyzed for marker by ICP. The MRT were calculated from areas under marker excretion curves, and included ruminal residence time plus post-ruminal transit time, which varied from 6 to 9 h based on first excretion of markers. Data were analyzed as a replicated Latin square with the MIXED procedure of SAS with fixed effects of diet, period, and replicate. Cow within square was the random effect. DMI (kg/d) was lower ($P \leq 0.05$) for HCCS (26.5) than LCCS (29.0), LBMR (29.3), and HBMR (29.2). Small corn silage particles of LCCS had shorter MRT than HCCS, but were not different between LBMR and HBMR. Conversely, medium corn silage particles of HBMR had shorter MRT than these particles in LCCS and HCCS. The lower DMI of HCCS does not appear to be related to marker MRT.

Table 1.

Mean retention time, h	LCCS	HCCS	LBMR	HBMR	SE
Liquid	20.5	20.9	20.7	19.4	0.6
Fine feces	29.5	30.7	31.2	32.2	0.8
Medium haylage	41.8	43.3	42.7	41.9	1.6
Small corn silage	36.1^{y}	39.8^{x}	37.5^{xy}	36.5^{xy}	1.3
Medium corn silage	44.9^{axy}	46.0^{ax}	43.7^{abyz}	42.1^{bz}	1.5
Large corn silage	47.5	48.8	47.9	46.8	1.6

$^{ab}P \leq 0.05$; $^{xyz}P \leq 0.10$.

Key Words: corn silage, NDF, retention time

W334 Effect of silica levels, and its location in the detergent fiber matrix, on in vitro gas production of rice straw. G. S. Cun*[1], G. A. Nader[2], and P. H. Robinson[1], [1]*University of California, Davis,* [2]*University of California Cooperative Extension, Yuba City.*

Rice straw can be used as a forage for cattle but, due to its very low net energy (NE) value, its use is generally limited to cattle whose intake potential substantially exceeds their energy need. This low NE value, driven by a low digestibility of organic matter (OM), has often been attributed to the high silica (Si) level of rice straw. This series of experiments evaluated how simulated field drying of rice straw, its Si level and location in the detergent fiber matrix, affects in vitro gas production. We also determined how in vitro gas production at 4, 24 and 72h are affected by removing Si from rice straw entirely by growing it in a Si-free hydroponic solution. In Expt. 1, rice plants grown in controlled conditions were analyzed fresh (i.e., within 60 min of harvest), and when fully dried (i.e., 25°C for 7 d), for dry matter, ash, acid detergent fiber (ADF) and acid detergent extracted neutral detergent fiber (ND/ADF) by ND extracting ADF, Si in ADF (ADF-Si) and Si in ND/ADF (ND/ADF-Si), as well as in vitro gas production. Fresh straw had a higher proportion of ADF-Si (539 versus 485 mg/g total Si; $P < 0.01$) and less Si in ND extracted ADF (196 versus 340 mg/g total Si; $P < 0.01$), than the same plants after drying, which may have caused the higher in vitro gas production of fresh straw at all times. However this was not confirmed in Expt. Two where ADF-Si, ND/ADF-Si and total Si were not predictive of any in vitro gas production in 39 field samples of rice straws collected in the Sacramento Valley (CA), possibly due to the relatively narrow range of 3.5 to 6% Si in the samples, or because the location of the Si in the fiber matrix, or Si itself, is simply not predictive of the digestibility of its OM. Indeed, in Expt. 3, rice grown under controlled conditions in Si free or Si containing hydroponic media, in 2 sub-experiments, had similar gas production unit OM. The general lack of impact of rice straw Si levels, either in total or relative to its location in the detergent fiber matrix, on in vitro gas production seems to demonstrate that Si is not causative to the low fermentability of rice straw OM.

Key Words: in vitro, silica, hydroponic

Ruminant Nutrition: General III

W335 Variation in chemical composition among breeding lines of novel oat varieties as ruminant feeds. J. M. Moorby,* A. A. Cowan, and A. H. Marshall, *Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Aberystwyth, UK.*

Previous work has shown the nutritional benefits of naked oat varieties compared with husked oats, particularly for pigs and poultry, but also for ruminants. However, crop yields of naked oats are significantly lower than those of husked oats, leading to a more expensive crop which has limited its appeal to feed compounders in least-cost ration formulations. To improve the digestibility of husked oats, a breeding program aimed at producing low-lignin oats with a high oil content has generated several new breeding lines. The chemical composition of modern oat varieties is likely to be different from previous varieties, and therefore standard 'book' values. Samples of the whole grain (including husk if present) of 4 commercial varieties of winter naked (WN) oats, together with several novel low-lignin breeding lines of spring husked (SLLH; n = 5) and winter husked (WLLH; n = 8) oats, were analyzed for standard chemical composition. Data were analyzed by ANOVA, with multiple comparisons when the effect of treatment (SN, SLLH and WLLH) was significant ($P < 0.05$). Grain oil and CP concentrations were significantly lower in the novel husked oats than the conventional naked oat varieties (Table 1), while fiber concentrations were higher, leading to lower ME densities in the husked oats than the naked oats, as expected. In conclusion, although the apparent feeding value of the novel husked oats was not as good as naked oats in some areas, some values of novel spring varieties in particular were similar to naked oats and show promise as ruminant feeds. Oat breeding work is ongoing, and these results highlight breeding targets for future lines of high yielding husked oats.

Table 1. Mean chemical composition of oat varieties; values in % DM unless otherwise indicated

	WN	WLLH	SLLH	SEM	*P*-value
DM, %	89.4	90.9	90.9	0.49	0.053
OM	97.7^{a}	97.4^{a}	97.0^{b}	0.09	<0.001
Oil	13.8^{a}	7.5^{b}	6.3^{b}	0.74	<0.001
CP	12.7^{a}	8.3^{b}	11.1^{a}	0.49	<0.001
ADF	3.8^{a}	16.0^{b}	13.3^{b}	1.06	<0.001
NDF	8.2^{a}	29.7^{b}	27.5^{b}	1.30	<0.001
ME, MJ/kg DM	16.7^{a}	12.4^{b}	13.0^{b}	0.30	<0.001
Starch	54.6^{a}	47.7^{b}	48.4^{b}	1.40	0.004
ADL	1.2^{a}	2.9^{b}	1.8^{ab}	0.49	0.027

^{a,b}Values in rows with different letters indicate significant differences ($P < 0.05$).

Key Words: chemical composition, oats, plant breeding

W336 Ruminal metabolism in continuous culture fermentation when administrating high concentration of inorganic selenium in mixed cultures of ruminal microorganisms. J. M. Vera[1], T. Z. Davis[2], D. N. Miller[3], K. E. Panter[2], D. R. ZoBell[1], and J.-S. Eun*[1], [1]*Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan,* [2]*Poisonous Plant Research Laboratory, USDA-ARS, Logan, UT,* [3]*Agroecosystem Management Research Unit, USDA-ARS, Lincoln, NE.*

The current literature lacks information on ruminal microbial metabolism in response to high selenium (Se) concentration in the diet. We investigated changes in ruminal fermentation when high concentration of Se was administered in mixed ruminal cultures in fermentors. Two mature beef cows, fitted with a ruminal cannula, grazed on tall fescue pasture and were used as donor animals for ruminal contents. Filtered ruminal contents were allowed 11 d of adaptation to diets followed by 3 d of data collection. A dual-flow continuous culture system was used in a completely randomized design (n = 4) to test 2 dietary treatments: control (no Se addition) and 50 ppm Se addition. Grass hay (20 g DM/d) containing 0.12 ppm Se was added to the fermentors in 2 equal portions at 0800 and 1700 h. Selenium (sodium selenate) was added to the Se addition treatment by gradually increasing the concentration from 2 to 50 ppm over the 11 d in adaptation period. Culture pH averaged 6.04 and was not affected by treatment. Total volatile fatty acid (VFA) concentration averaged 52.2 and 55.5 m*M* in the control and Se treatment, respectively, and addition of Se did not affect the VFA concentration. Molar proportions of acetate and propionate did not differ due to Se addition, resulting in a similar acetate-to-propionate ratio. However, addition of Se tended to increase ($P = 0.09$) ammonia-N concentration. Additionally, Se addition increased methane production ($P = 0.01$). Selenate-respiring microorganisms were detected by the most probable number enumeration technique in 3 of the 4 replications receiving Se. Addition of 50 ppm Se in grass hay diet had no negative effects on ruminal fermentation, as was observed in similar culture pH and VFA concentration. However, addition of Se affected microbial N metabolism by increasing ammonia-N concentration. Overall data in this study suggest that the addition of Se up to 50 ppm would not interfere with in vitro ruminal metabolism by microbiota.

Key Words: continuous cultures, ruminal metabolism, selenium

W337 Effects of algae on ruminal fermentation and digestion in continuous culture fermenters. A. M. Gehman,* G. A. Harrison, and B. Jacobs, *Alltech Biotechnology Inc, Nicholasville, KY.*

The objectives of this experiment were to observe the effects on ruminal fermentation and digestibility when algae were included in a total mixed ration fed to continuous culture fermenters. Algae were *Schizochytrium* sp. and had a composition of 15.2% crude protein, 1.5% neutral detergent fiber (NDF), 3.9% ash, 30.9% non-structural carbohydrate, and 41.9% total fatty acids. Twelve single-flow continuous culture fermenters were used in a single-factor design with 6 dietary treatments with 2 replications per treatment. Diets were formulated to be isonitrogenous (17% crude protein) and to include algae at 0, 1, 2, 3, 4, and 5% dry matter (DM) or 0, 232, 465, 697, 930, and 1162 g equivalent for 22.7 kg DM intake. Diets were primarily comprised of corn silage, alfalfa hay, and corn grain. Cultures were fed 25 g twice daily for 6 d. Rates of flow and dilution were kept constant at 44 mL/h and 0.04/h for the duration of the study. Fermentation samples were collected from cultures before morning feeding during the last 3 d of the experiment to measure pH, ammonia, and volatile fatty acids (VFA). Composite effluent samples from each fermenter were used for DM and NDF digestibility. Data were analyzed for effects of treatment using PROC GLM of SAS. Culture pH and ammonia before morning feeding did not differ among treatments, averaging 6.21 ± 0.42 and 7.93 ± 0.32 mg/dL respectively. Molar proportions of acetate increased ($P < 0.01$) and propionate decreased ($P < 0.01$) similarly in all treatments containing algae compared with control (48.5 vs. 46.5 ± 0.5 and 26.0 vs. 29.4 ± 0.8 mol/100 mol). Butyrate, isobutyrate, isovalerate, valerate, and total VFA were not affected by treatment, averaging 18.2 ± 0.9, 1.81 ± 0.04, 1.73 ± 0.07, 2.32 ± 0.08, and 46.5 ± 2.1 mol/100 mol, respectively. Dry matter and NDF digestibility were not affected by treatment, averaging 43.4 ± 2.6 and 38.4 ± 6.4% respectively. Inclusion of algae affected the VFA profile but did not affect DM or NDF digestibility, indicating that algae modifies rumen fermentation in a manner that may not affect forage utilization.

Key Words: algae, continuous culture fermenter, rumen fermentation

W338 Digestion response of dairy heifers to the supplementation of autolyzed yeast.

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Response to autolyzed *S. cerevisiae* supplementation (Levabon Rumen, Biomin) was evaluated. Nine ruminally cannulated heifers (510kg) received a sequence of treatments in 35-d period, 3x3 Latin Squares. Treatments were 0, 10 or 30g/d, given twice daily via cannula. A TMR was individually fed twice a day: 51.8% corn silage, 48.2% concentrate, 15% CP, 34% NDF, 39% NFC. Low ruminal pH was induced by feed removal at 12h post-morning feeding on d 34 and ad libitum feeding on d 35. Ruminal pH was evaluated on d 28 and 35 at 0, 3, 6, 9, 12, 18 and 24h post-feeding, and ruminal ammonia and PUN simultaneously on d 28. Tifton was incubated in situ over time on d 30 to 33. Total tract digestibility of DM was done by total collection of feces on d 31 to 33, simultaneously to urine sampling to estimate the relative rumen microbial yield by allantoin excretion. Statistical models had the effects of heifer, period and treatment; some had time and time by treatment interaction. Preplanned contrasts were: T0 vs. T10 and T0 vs. T30. Ruminal pH did not respond to treatments ($P > 0.20$), neither protozoa count ($P > 0.24$). Mean and minimum pH were 6.45 and 6.01 on d 28, and 6.16 and 5.38 on d 35, respectively, nadir was at 12h post-feeding. Urinary allantoin excretion was (mmoles/d): 53.3 on T0, 60.5 on T10 ($P = 0.50$), 77.6 on T30 ($P = 0.04$). There were trends for increased kd of Tifton B fraction on T30 for DM ($P = 0.07$) and NDF ($P = 0.06$). Total tract DM digestibility was (% of intake): 67.3 on T0, 68.4 on T10, 69.5 on T30 ($P > 0.28$). Days 28 to 33 DMI was increased from 11.7kg/d to 12.5 on T10 ($P = 0.04$), but T30 induced no response ($P = 0.88$). Day 35 DMI was: 17.0 on T0, 17.2 on T10, 16.4 on T30 ($P > 0.43$). Ruminal ammonia concentration did not differ ($P > 0.58$), but PUN was (mg/dL): 17.5 on T0, 18.5 on T10 ($P = 0.14$), 19.1 on T30 ($P = 0.03$). T10 induced a flattened PUN curve along the day. Ruminal ammonia peaks posterior to the morning feeding induced PUN peaks, while the evening ammonia peak was associated to decreasing PUN concentration. Autolyzed yeast supplementation induced positive dose dependent responses in rumen microbial yield, digestion and DMI. Ruminal pH regulation by yeast was not a plausible mechanism for the response.

Key Words: rumen microbial yield, *Saccharomyces cerevisiae*, yeast

W339 The effect of several sodium and potassium salts on rumen pH.

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”Buffers” are broadly used in practice to counteract low rumen pH, but their mode of action is still open to question. Our work aimed to examine the rumen pH response to several Na and K salts, supplied at equivalent amounts of the cation. Two separate experiments (exp.) were conducted with Na and K salts, respectively. Each exp. was designed as a Latin square involving 5 rumen-fistulated cows in 5 periods of 2 d each. The cows were housed in a tie-stall barn, submitted to a fixed daily management schedule and fed a customary diet, but free of any mineral supplement, offered in 2 daily meals. The first day of each period, 1 of 5 possible treatments was supplied directly in the rumen, 2 h after the morning meal. Treatments were, for the Na exp.: $NaHCO_3$, Na_2CO_3, Na_2HPO_4, NaCl and none (control); and for the K exp.: $KHCO_3$, K_2HPO_4, K_2HPO_4 at double dose, KCl and none. Salts were supplied to provide 2 mol of the corresponding cation. Cows were fitted with indwelling rumen pH loggers set to record pH every 2 min for the whole duration of the exp. Every exp. was separately analyzed. First, pH data was averaged (avg.) for 3 time intervals post-administration of treatments, namely: 0 to 1 h, 1 to 3 h, and 3 to 6 h. Avg. pH were then analyzed with the mixed procedure of SAS, according to a model that included treatment, time (repeated measure), their interaction, and the pH at time 0 (covariable) as fixed effects; and cow and period as random effects. Any effects ($P < 0.05$) of these salts on pH were noticeable in the first 3 h, mostly in the first 1 h. In the Na experiment, NaCl did not cause any change in pH whereas all the other salts raised the pH. Similarly, in the K experiment KCl failed to cause any change in pH, while $KHCO_3$ rose, and the double dose of K_2HPO_4 tended to raise, pH. These results support that a positive strong cation to anion difference may be a determining factor for the salts tested to increase rumen pH.

Key Words: rumen pH, sodium, potassium

W340 Effect of polyethylene glycol on in vitro fermentation kinetics and digestibility of native tree fruits.

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This study evaluated the effect of polyethylene glycol on in vitro ruminal fermentation kinetics, in vitro organic matter digestibility (IVOMD), in vitro neutral detergent fiber digestibility (IVNDFD) and metabolizable energy (ME) in the fruit of native trees *Quercus hintonii* and *Quercus glaucoides* from the Mexican Central Plateau. Samples were collected in 4 sites where 3 trees were randomly selected. Three subsamples of 200g of ripe fruit were taken from each tree. They were dried at 40°C, ground in a Wiley mill with a 1mm sieve, and analyzed in triplicate. Fermentation kinetics, IVOMD and IVNDFD were evaluated with the in vitro gas production technique (GP) with and without polyethylene glycol (PEG 6000). In the former, 500 mg of substrate were added to each glass syringe plus 50 mL of buffered ruminal fluid (10 mL of ruminal fluid from forage-fed cattle: with a concentration of 80:20) and 40 mL of culture media. The syringes with PEG contained 500 mg of substrate, 1000 mg of PEG, plus 50 mL of ruminal fluid and 40 mL of culture media. All syringes were incubated at 39°C for 96 h. Gas volume was recorded from 1 to 8,12,16,20,24,36,48,72, and 96 h and was adjusted to mathematical model $Y = b(1\text{-}\exp\text{-}^{c(t\text{-}lag)})$. IVOMD and ME were determined with equations: IVOMD = 16.49+0.9042*GP+0.0492*RP+0.0587*EE, ME = 3.16+0.0695*GP+0.000730 *GP2 +0.00732*RP+0.02052*EE [RP = raw protein; EE = ether extract]. A completely randomized design was used with a 2x2 factorial arrangement. *Q. glaucoides* presented higher IVNDFD (52.7%) ($P < 0.001$), IVOMD (68.8%)($P < 0.001$) and ME (10.4 MJ/kgMS)($P < 0.010$). PEG addition between the species had a positive effect on IVNDFD, IVOMD and ME ($P < 0.02$). *Q. glaucoides* with PEG presented higher GP (200.1 mL/200mg) compared with *Q. glaucoides* without PEG (176.8 mL/200 mg)($P < 0.0001$). *Q. hintonii* presented a similar behavior with PEG (150.1mL/200mg) and without PEG (126.4mL/200mg) ($P < 0.018$). Adding PEG to the fruit had a positive effect, improving nutritional value. *Q. glaucoides* presented higher digestibility and better fermentation parameters.

Key Words: in vitro digestibility, native trees, polyethylene glycol

W341 Chemical composition and in vitro digestibility of foliage trees, and their use in feeding lambs in the dry tropics of central highlands of Mexico.

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The objective of this study was to evaluate the chemical composition and in vitro digestibility of *C. alata* and *G. ulmifolia*, and the productive response of lambs fed diets with different levels of foliage included, in terms of dry matter intake (DMI), total weight gain (TWG), daily weight gain (DWG), feed conversion (FC) and feed efficiency (FE). Twenty lambs at 3.5 mo of age and 22.9 ± 0.88kg were randomly distributed (n = 4) in 5 treatments: T0 = control diet, T1 = diet with 15% *C. alata*, T2 = diet with 30% *C. alata*, T3 = diet with 15% *G. ulmifolia*, and T4 = diet with 30% *G. ulmifolia*. A totally random design was used, the Tukey test was applied ($P < 005$). The *G. ulmifolia* foliage had greater crude protein, IVDOM, total phenols and condensed tannins content ($P < 0.01$), with 167.2, 491.0, 41.5, and 38.2 g/kg DM, respectively, and 2.08 Mcal/kg DM of metabolizable energy. The *C. alata* foliage had greater neutral detergent fiber and acid detergent fiber content ($P < 0.001$), with 502.0 and 315.0 g/kg DM, respectively; the *C. alata* foliage, at 24, 48 and 96 h of incubation, had greater gas production ($P < 0.001$) with 66.1, 170.9 and 210.6 mL/g DM, respectively. Asymptotic gas production (b) was greater ($P < 0.05$) in T0 (293 mL g^{-1} DM). DMI was less in lambs in T0 (1061.4 g/animal/day) ($P < 0.025$). The DWG of the control diet was similar to that of diets with the different levels of inclusion of each species ($P > 0.05$), however the DWG of the diet with 15% *C. alata* (T1) was greater (295.6 g/d) ($P < 0.05$) than that of the diet with 30% *G. ulmifolia* (T4) (227.8 g/day) and was similar to T2 (30% *C. alata*) (286.7 g/d) and T3 (15% *G. ulmifolia*) (267.8 g/d). The native, non-leguminous tree foliages, *C. alata* and *G. ulmifolia*, have potential as forage for lamb production in the dry tropics. Including foliage from these species may substitute 15 and 30% of the conventional ingredients in lambs diets, since they improve dry matter intake and productive response.

Key Words: kinetics of degradation, lambs, non-leguminous tree

W342 Effect of replacing barley grain with wheat dry distillers grains with solubles on *in situ* degradation kinetics, growth, and fatty acid profiles of lambs.

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The aim of the study was to assess the effects of replacing barley grain with increasing concentrations of wheat dry distillers grains with solubles (WDDGS) in lambs diets. The control diet contained (DM basis) 62.9% barley grain, 30% alfalfa hay, 2.5% molasses, 1% canola oil and 3.6% mineral-vitamin mix. Increasing concentrations (20, 40% of DM) of WDDGS was achieved by replacing barley grain with WDDGS. Digestion kinetics of DM, CP, and NDF of diets were measured by in situ incubations using 2 rumen cannulated cows. Additionally, 39 weaned Dorper/Merino lambs were used in a trial to determine the effects of WDDGS on growth performance, feeding behavior, subcutaneous fat fatty acid (FA) profiles and wool growth. Lambs were blocked by weight and randomly assigned to one of the 3 dietary treatments (Control, 20% WDDGS and 40%WDDGS). Lambs were fed ad libitum using 3 automatic feeders per treatment and had free access to water. Lambs were slaughtered at a BW of ≈44 kg. Data were analyzed using the mixed model procedure of SAS. In the in situ study, WDDGS did not affect ($P = 0.61$) DM or NDF degradation rates (k, h^{-1}), but reduced CP degradation rate ($P = 0.02$). Effective rumen degradable protein and ruminal undegradable protein (g/kg DM) were higher ($P < 0.001$) in the WDDGS diets compared with control. In the growth trial, increasing WDDGS in the diet did not affect ($P = 0.48$) eating time (min/d), but quadratically increased ($P = 0.02$) eating rate (g/min), intake ($P = 0.02$) and daily gain ($P = 0.05$). Final bodyweights were linearly increased ($P = 0.02$) by WDDGS addition and hot carcass weight was higher ($P = 0.04$) in the 40% WDDGS group compared with other treatments. Inclusion of WDDGS did not affect feed efficiency ($P = 0.62$), wool staple length ($P = 0.32$), total SFA ($P = 0.29$), MUFA ($P = 0.32$) or PUFA ($P = 0.11$) profiles of subcutaneous fat, but increased C18:3 ($P = 0.02$). This study suggested that WDDGS included up to 40% of dietary DM as replacement of barley grain increases RDP, RUP, and lamb growth performance.

Key Words: digestion kinetics, ethanol by-products, wool yield

W343 Could essential oils of thyme (*Zataria multiflora*) and peppermint (*Mentha piperita*) improve calf growth performance?

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This experiment was conducted to investigate the effect of feeding thyme and peppermint essence to calf starter on preweaning and postweaning calf growth performance, feed intake and blood metabolites. Following 3 d of colostrum and transition milk feeding 36 Holstein calves were assigned in a completely randomized block design with 3 dietary treatment with 12 calves (6 females and 6 males) per treatment including: 1) starter without essence (Control), 2) starter including 0.2% peppermint essence, and 3) starter including 0.2% thyme essence. Calves were housed in individual hutches, and fed whole milk at 10% of the initial body weight daily and had free access to starter and water. The weaning process defined when the calves had consumed 1 kg of starter for 2 d, consecutively. The experiment was ended 2 weeks after weaning the calves. Feed intake was measured daily. Body weight was measured at birth, at monthly throughout the study, at weaning and at the end of study. Blood samples were obtained 2 d before weaning and at the end of study. Plasma samples analyzed for glucose, urea nitrogen and β-hydroxybutyrate (BHBA) determination. Average daily feed intake and body weight gain was greater for calves fed peppermint compared with other calves (624.3 ± 43.5 vs. 526.2 ± 42.4 and 432.7 ± 44.7 g daily feed intake and 0.94 ± 0.03 vs. 0.88 ± 0.02 and 0.82 ± 0.04 g daily gain respectively for treatments 2, 3 and 1, $P < 0.05$). There were no differences between treatments for postweaning gain and feed consumption after weaning ($P > 0.05$). Plasma urea nitrogen and BHBA concentration decreased in calves fed thyme compared with other calves ($P < 0.5$). No significant difference showed in blood metabolites between calves after weaning ($P > 0.05$).The results of this study demonstrated that supplementation of peppermint essence to calf starter increased feed intake and body weight during suckling period,

but after weaning the supplementing of essence had no effect on calf growth performance. Also we concluded that supplementing of thyme essence to starter causes a decrease in blood urea nitrogen and BHBA concentrations in suckling calves.

Key Words: calf performance, essential oil, starter

W344 In vitro investigation of various adsorbents to adsorb aflatoxin B1.

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Aflatoxin B1 (AfB1) is the most important of a group of naturally occurring secondary metabolites produced mainly by *Aspergillus parasiticus* and *Aspergillus flavus* primarily in agricultural products from tropical and subtropical regions. A common way to counteract aflatoxicosis is the utilization of adsorbents added to AfB1 contaminated feed to bind the toxin in the gastro-intestinal tract before its resorption. Therefore, the aim of this study was to comparison of various adsorbents including bentonite (natural mineral), zeolite (synthetic mineral), Mycosorb (organic) and Biotox (mineral - organic) on their ability to adsorb aflatoxin B1. Hence, AFB1-contaminated rice was obtained after inoculation with the *Aspergillus parasiticus* type strain PTTC 5286 (Iranian Research Organization for Science and Technology). AFB1 was produced in 6 d at 28°C. Amounts of aflatoxin present in the contaminated rice were determined by HPLC. The result showed that the product obtained was containing aflatoxins in the following concentrations (μg/g of substrate): B1-B2-G1-G2, 13.5:0.5:0:0. AFB1 was extracted 3 times with chloroform by soaking rice in chloroform over night at room temperature and stirring rice. Adsorbents were individually mixed at 3 different ratios with AFB1 (1:1000, 1:5000 and 1:15000, w/w) in the McDougall buffer at pH 6.8 and shaken for 16 h at 39°C, centrifuged (at 3500 × g for 15min) and the supernatant evaluated for amount of aflatoxin B1 by aflatoxin B1 ELISA kit and then obtained data were analyzed using the general linear model procedure of the SAS in a 4 × 3 × 3 factorial arrangement of a completely randomized design. At the 1:15000 aflatoxin: adsorbent ratio, zeolite, Mycosorb and Biotox sequestered (adsorbed) over 0.8, 0.81 and 0.83 of the AFB1. This efficacy decreased when the amount of adsorbents was reduced. Bentonite had a lower sequestering efficacy in all of cases, with 0.38 being the maximum value obtained in the 1:15,000 aflatoxin: adsorbent ratio ($P > 0.05$). We concluded that there were significant differences between 3 ratios of aflatoxin: adsorbent and also between adsorbents for percentage of adsorption.

Key Words: aflatoxin B1, adsorbents, *Aspergillus parasiticus*

W345 Influence of *Yucca schidigera* on in vitro gas production and fermentation of rumen fluid.

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Several factors, including excessive foam production, may inhibit eructation and contribute to bloat in cattle. We hypothesized that saponins of *Yucca schidigera* in a commercially available feed supplement (Ruma-Just, Nova Microbial Technologies) will alter anaerobic microbial fermentation and decrease both foam and gas production in vitro. Rumen fluid was collected from 2 ruminally cannulated cows fed an 83% dry-rolled corn-based diet. Anaerobic fermentations were conducted at 39°C in 250-mL Erlenmeyer flasks containing 40 mL rumen fluid, 60 mL McDougal's buffer, and 1 g ground corn grain with treatments. Treatments were 0.00 (control), 0.01, or 0.02% Ruma-Just mixed with the ground corn grain. Gas production was recorded from 7 flasks per treatment at 0, 2, 4, 6, 8, 10, 12, 18, and 24 h. Foam height, viscosity, pH, VFA, and NH_3 were measured in 6 flasks per treatment that were incubated for 0, 6, 12, or 24 h. Results showed that gas production, VFA, and NH_3 concentrations increased ($P < 0.05$), and pH decreased ($P < 0.05$) from 0 to 24 h regardless of treatment. Rumen fluid pH tended to be greater (quadratic, $P = 0.06$) for 0.01% Ruma-Just (6.18 ± 0.10) than control (6.03 ± 0.10) and intermediate for 0.02% Ruma-Just (6.13 ± 0.10). Gas production was lower (quadratic, $P < 0.05$) for 0.01% Ruma-Just (102 ± 3.8 mL) than control (116 ± 4.5 mL) and 0.02% Ruma-Just (121 ± 3.8 mL). Similarly, foam height was lower (quadratic, $P < 0.05$) for 0.01% Ruma-Just (4.63 ± 2.85 mL) than control (8.25 ± 2.85 mL) and 0.02% Ruma-Just (8.75 ± 2.85 mL). Viscosity was lower (quadratic, $P < 0.05$) for 0.01% Ruma-Just (2.13 ± 0.06 cP) and 0.02% Ruma-Just (2.18 ± 0.06 cP) than control (2.30 ± 0.06 cP). Treatments did not affect ($P > 0.10$) VFA and NH_3 concentrations. In summary, Yucca Schidigera altered gas and foam production, rumen fluid viscosity, and pH, but did not affect VFA and NH_3 concentrations in vitro. Decreasing gas production, foam production, and rumen fluid viscosity could reduce ruminal bloat. Authors acknowledge R. Goodall, Nova Microbial Technologies and MBRS RISE Program (grant # R25GM061222).

Key Words: *Yucca schidigera*, gas production, rumen

W346 Effects of inclusion of bioethanol co-product on changes in the metabolic characteristics of the proteins in oat grain in ruminants.

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This research program aims to develop a strategy to more efficiently utilize oat grain by integration with bioethanol co-products (wheat dried distillers grains with solubles) in sustainable beef and dairy production and to assist the beef and dairy industry to develop low-cost and more efficiently feeding strategies by utilizing alternative feed resources. In this study, the objectives were to investigate the effects of inclusion of bioethanol co-product of wheat dried distillers grains with solubles into oat grain on changes in the metabolic characteristics of the proteins, total truly digested and absorbed protein supply and degraded protein balance, determined with the DVE/OEB system (non-TDN based model) and NRC-2001 model (TDN-based model). Oat grains with the co-products were mixed manually to combine in ratios of 4:0, 3:1, 2:2 and 1:3. Each combined feed had 2 replications with 2 sources of the co-products. The rumen degradation kinetics and intestinal digestion were determined using 2 Holstein Friesian dairy cows. The data were analyzed by mixed model procedure of SAS with a CRD model. A significant level was declared at $P < 0.05$ and a tendency was declared at $P < 0.10$. The results showed that by using the DVE/OEB system, when the co-products was included at the different ratios into oat grain, the total truly digested and absorbed protein supply tended to be linearly increased from 76 to 137 g/kg DM ($P = 0.06$) and degraded protein balance linearly increased from 6 to 133 g/kg DM ($P < 0.01$). By using the NRC-2001 model, when the co-product was included at the different ratios into oat grain, the metabolizable protein supply was numerically increased from 100 to 154 g/kg DM ($P = 0.20$) and degraded protein balance increased from −33 to 119 g/kg DM ($P < 0.01$). In conclusion, the inclusion of bioethanol co-product changed the metabolic characteristics of the proteins and improved nutrient supply from oat grain to cattle.

Key Words: metabolic characteristics of the protein, combined oat with bio-ethanol co-products, nutrient modeling

W347 Evaluation of forage indigestible NDF and relations with analytical parameters by principal component analysis.

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The estimation of indigestible NDF (iNDF) is considered as an important parameter in dynamic nutritional models to predict energy and protein values of forages. Currently, the iNDF is predicted as 2.4 times ADL. However, recent observations suggested the use of a constant coefficient provides inaccurate estimations of the iNDF across forages. The aim of this experiment was to evaluate the iNDF of different forages and to study its relationships with chemical parameters. A set of 35 forages (10 alfalfa hays or AH, 10 grass hays or GH and 15 corn silages or CS; respectively) was randomly collected from the Po Valley of the Northern Italy. Forages were characterized for chemical composition and iNDF, the latter evaluated after 288h of in situ rumen incubation. Then, a principal component analysis (PCA) was used to study relationships between original variables and extracted principal components. Overall, the nutritive value of forages was in the ranges of those reported by the National Research Council database. The iNDF was lower in CS than GH and AH (13.4 versus 25.1 and 26.8 g/100 g DM, $P < 0.05$; respectively). The iNDF/ADL ratio was higher than 2.4 for all forage classes, being 6.2, 3.5 and 4.7 in GH, AH and CS, respectively. As a result of PCA, the first 3 principal components explained more than 85% of total variation (eigenvalues of 6.13, 3.30 and 0.78). The loading plot from PCA showed iNDF clustered with different chemical parameters. Particularly, iNDF was positively correlated ($P < 0.05$) to CP ($r = 0.41$), ash ($r = 0.59$), ADICP ($r = 0.60$), NDICP ($r = 0.72$), ADL ($r = 0.73$) and ADF ($r = 0.81$). Furthermore, ether extract and NSC clustered and were oriented in an inverse direction to iNDF. The iNDF/ADL ratio clustered with ether extract and NDF ($r = 0.53$ and $r = 0.45$, $P < 0.05$; respectively) and was negatively related ($P < 0.05$) to NSC ($r = -0.72$) and soluble CP ($r = -0.55$). Our data suggested the iNDF was related to different chemical parameters and the use of simply regression seems to be inadequate to universally predict iNDF across forages.

Key Words: indigestible NDF, forage, principal component analysis

W348 Utilization of *Yucca schidigera* to alter hydrogen sulfide gas production from rumen fluid in vitro.

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This study evaluated the effects of an additive from *Yucca schidigera* (Ruma-Just, Nova Microbial Technologies) on in vitro fermentation of ground corn grain, total gas and H_2S production, and rumen fluid viscosity. Rumen fluid was collected from a ruminally-cannulated cow fed a corn-based diet. Anaerobic fermentations were conducted in 250-mL serum bottles containing 50 mL rumen fluid, 50 mL McDougal's buffer, and 1 g of ground corn grain that was thoroughly mixed with one of 6 treatments. Treatments, in a 3 × 2 factorial arrangement, were ground corn grain substrate mixed with 0%, 0.01%, or 0.02% Ruma-Just and 0% added sulfur, or 0%, 0.01%, or 0.02% Ruma-Just with 0.6% added sulfur as sodium sulfate. Total gas production was recorded, and a sample of gas for H_2S analysis was collected after incubating 9 replicate bottles per treatment for 24 h at 39°C. Contents from in vitro fermentations were frozen at −20°C, and later filtered for IVDMD and rumen fluid viscosity measurements. Gas production decreased in response to 0.01% Ruma-Just when no sulfur was added, and gas production decreased in response to 0.02% Ruma-Just when 0.6% sulfur was added (Ruma-Just × S interaction, $P < 0.01$). Ruma-Just at both 0.01% and 0.02% increased IVDMD when no sulfur was added, but Ruma-Just did not affect IVDMD when 0.6% sulfur was added (Ruma-Just × S interaction, $P = 0.07$). Production of H_2S per gram of substrate was not affected by Ruma-Just when 0% sulfur was added, but H_2S production decreased in response to 0.02% Ruma-Just with 0.6% added sulfur (Ruma-Just × S interaction, $P = 0.01$). By design, addition of 0.6% sulfur increased ($P < 0.01$) H_2S production. Rumen fluid viscosity tended to be lower ($P = 0.10$) for 0.02% Ruma-Just than 0% and 0.01% Ruma-Just. In conclusion, *Yucca schidigera* may decrease total gas and H_2S production in ruminants consuming diets high in sulfur. Authors acknowledge R. Goodall and Nova Microbial Technologies.

Key Words: *Yucca schidigera*, hydrogen sulfide, rumen

W349 Effect of monensin and bismuth subsalicylate on hydrogen sulfide in continuous culture fermenters.

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In ruminants, excess dietary S is associated with several conditions including a reduction in DM intake, negative effects on feedlot performance and carcass characteristics, and sulfur-associated polioencephalomalacia. Therefore, ruminant nutritionists are interested in methods to reduce negative effects of high S diets. Bismuth subsalicylate (BSS) has been shown to decrease fecal H_2S production in humans, while there are conflicting results about the effect of monensin (MON) on H_2S production in ruminants. Therefore, the objective of this experiment was to evaluate effects of these compounds on H_2S production by rumen microbes. Eight dual flow continuous culture fermenters were used during 2 consecutive 10-d periods with the first 7 d for stabilization followed by 3 d of sampling. The experimental design was a 2 × 2 factorial arrangement of treatments, with 2 levels of BSS (0 and 1% of DM) and 2 levels of MON (0 and 5 ppm in incubation fluid). Fermentation substrate consisted of 46% distillers dried grains, 41% ground corn, 8% hay, 2.5% $CaCO_3$, 1.5% molasses and 1% mineral premix and was provided at 75 g/fermenter/d. Addition of BSS to the diet increased ($P < 0.05$) digestion of OM, NDF and ADF but decreased ($P < 0.05$) NFC digestion and total VFA concentrations. Molar proportions of acetic and propionic acid increased ($P < 0.05$) with BSS, while butyric acid decreased ($P < 0.05$). Monensin decreased ($P < 0.05$) ADF digestion and A:P ratio, without affecting ($P > 0.05$) molar proportions of acetic, propionic and butyric acids. In regards to nitrogen metabolism, MON increased ($P < 0.05$) non NH_3-N outflow without affecting ($P > 0.05$) other parameters. BSS increased ($P < 0.05$) NH_3-N concentration, NH_3-N flow and tended to increase ($P < 0.1$) dietary-N flow, and decreased ($P < 0.05$) microbial-N outflow, CP digestion and efficiency of microbial protein synthesis. Headspace concentration of H_2S was reduced 99% ($P < 0.05$) with BSS. Conversely, a trend ($P < 0.1$) to increase H_2S headspace concentration was found following addition of MON. Only minor changes in fermentation pH were found with MON, but increases ($P < 0.05$) in mean, minimum and maximum fermentation pH were observed with addition of BSS. Results indicate that BSS can markedly decrease H_2S production in long-term in vitro rumen incubations.

Key Words: bismuth subsalicylate, hydrogen sulfide, rumen

W350 Alteration of fasting heat production during fescue toxicosis in Holstein steers.

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This study was designed to examine alteration of fasting heat production (FHP) during fescue toxicosis. Six ruminally cannulated Holstein

steers (BW = 348 ± 26 kg) were weight-matched into pairs and utilized in a 2-period crossover design experiment. Each period consisted of 2 temperature segments, one each at 22°C and 32°C. During each period, one steer per pair was ruminally dosed twice daily with 0.5 kg of ground endophyte-infected fescue seed (E+), the other with ground endophyte-free fescue seed (E-) for 7 d. Animals were pair-fed with E+ animals offered alfalfa cubes at 1.5 × NE_m. On d 8 of each segment, animals were moved to individual metabolism stalls fitted with indirect calorimetry head-boxes. Rumen contents were removed, weighed and subsampled for DM determinations. The reticulorumen was then washed and filled with a buffer ($NaCl$ = 96; $NaHCO_3$ = 24; $KHCO_3$ = 30; K_2HPO_4 = 2; $CaCl_2$ = 1.5; $MgCl_2$ = 1.5 mmol/kg buffer) that was gassed with a 75% N_2 and 25% CO_2 mixture before rumen incubation. During buffer incubation, an E+ or E-fescue seed extract was added at 12 h intervals to maintain treatment presentation to the animal. After a 12-h wait, heart rate (HR), core temperature (CT), O_2 consumed, and CO_2 produced were recorded for 16 h. There was no difference ($P > 0.9$) in DMI or DMI/kg $BW^{0.75}$ between endophyte treatments by design; however, intake decreased ($P < 0.01$) at 32°C. CT was unaffected by fescue treatment or temperature. Rumen contents weight (kg/ kg $BW^{0.75}$) tended to be increased ($P < 0.15$) and DM of rumen contents as well as total rumen DM/kg $BW^{0.75}$ was increased ($P < 0.0001$) in E+ animals. Increased temperature had no effect on measurements with the exception of HR and respiratory quotient (RQ). HR increased ($P = 0.05$) at 32°C, but was unaltered by fescue treatment. RQ was elevated ($P = 0.02$) in E+ animals and tended to increase ($P = 0.1$) at 32°C. O_2 consumption decreased ($P = 0.04$) and CO_2 production tended to be reduced ($P = 0.07$) in E+ animals. FHP (kcal/kg $BW^{.75}$) was reduced ($P = 0.04$) in E+ animals. These data suggest that consumption of E+ tall fescue by cattle results in a reduction in basal metabolic rate.

Key Words: cattle, fescue, fasting heat production

W351 Influence of maternal nutrition and prenatal adenovirus-VEGF gene therapy on fetal visceral tissues and crypt cell proliferation at d 130 of gestation.

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Adenovirus VEGF (Ad.VEGF) gene therapy has been shown to increase pre- and early post-natal growth velocity in an ovine model of fetal growth restriction. Our objectives were to investigate the effects of Ad.VEGF on fetal visceral tissues and crypt cell proliferation at d 130 of gestation in this paradigm. First parity ewe lamb recipients were initially allocated to a control (CON; n = 12) or high (H; n = 45) quantity of the same diet at singleton embryo transfer. Control diets provided met requirements for specific age and stage of gestation and H ewes received approximately twice the dietary intake of CON. At 89 ± 1.5 d of gestation H ewes were randomly allocated to receive 1 of 3 injections into both uterine arteries: a) Ad.VEGF (5×10^{11} particles) gene; (n = 18), b) control Ad containing the β-galactosidase reporter gene, Ad.LacZ, same dose; (n = 14), and c) saline (n = 13). On d 130 of gestation ewes and fetuses were necropsied. Fetal visceral tissues were harvested, weighed, and perfusion fixed. At necropsy, H ewes had increased ($P \leq 0.001$) BW, condition, and perirenal fat compared with CON (81.0 vs. 65.7 ± 1.2 kg; 2.9 vs. 2.4 ± 0.03; 1,334 vs. 543 ± 91 g, respectively). Maternal measurements were not altered by any injection treatment. Fetal BW was lower ($P < 0.001$) in H compared with CON (4,186 vs. 5,084 ± 214 g). Total fetal stomach, small intestine, and large intestine weights tended ($P \leq 0.07$) to be lower in H compared with CON. Fetal liver weight was less ($P \leq 0.01$) in H compared with CON. Fetal stomach (g/kg BW) was greater ($P < 0.01$) in H compared with CON. Fetal small intestine (g/kg BW) was less ($P = 0.016$) in Ad.VEGF vs. Ad.LacZ + saline. Small intestinal crypt cell proliferation was not altered by maternal nutrition or adenovirus-VEGF gene therapy. Adenovirus-VEGF gene therapy, while having some effects on proportional fetal visceral tissue mass, does not appear to alter intestinal crypt cell proliferation at d 130 of gestation. However, intestinal vascular responses to gene therapy treatment are unknown at this time.

Key Words: intestine, maternal nutrition, VEGF

W352 Effect of dried fermentation biomass on microbial fermentation in continuous culture.

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Fermentation biomass (FB) is a dried bacterial co-product derived from lysine production (Ajinomoto Heartland Inc.). The objective of this study was to determine if FB can be used as a protein source in ruminant diets. The study consisted of one experimental period where 8 dual-flow continuous culture fermenters were inoculated with rumen fluid. The experimental period consisted of a 7-d adaptation followed by 3 sampling days. Substrate for the microbes was provided by one of 2 isonitrogenous diets, CON or DFB. In CON diet, soybean meal (SBM) provided 55% of total CP, and in DFB diet, SBM and FB provided 12 and 45% of total CP, respectively. CON contained 3% molasses, 16% ground corn, 13% grass hay, 48% corn silage, and 20% SBM on a DM basis. DFB contained 3% molasses, 18.4% ground corn, 13% grass hay, 50% corn silage, 8.5% SBM, and 6.7% FB. Fermenters were fed 75 g/d of DM divided into 8 equal portions. Anaerobic conditions were maintained by infusion of N_2; pH was maintained between 5.8 and 6.8; and temperature was set at 38.6°C. On sampling days, liquid and solid effluent outflows were collected, combined, and homogenized to be used for chemical analysis. Both treatments had an average pH of 5.9. There was no effect ($P > 0.1$) of treatment on apparent or true OM digestibility (%). Nitrogen source had no effect ($P > 0.1$) on total-N, dietary-N, and bacterial-N flows. Addition of FB decreased ($P < 0.05$) ammonia-N flow from 0.41 to 0.23 g/d and tended to decrease ($P = 0.06$) effluent ammonia concentration from 17.1 to 9.7 mg/100 mL. Histidine and methionine flows increased ($P < 0.05$) from 0.48 to 0.53 and 0.18 to 0.20 g/d, respectively, when FB partially replaced SBM in the diet, but there were no effects ($P > 0.1$) on other AA or total AA. There was a trend ($P = 0.08$) in percent change from essential AA input (CON = 68.9% versus DFB = 63.74%) and from non-essential AA input (CON = 73.62% versus DFB = 82.22%); however, there was no effect ($P > 0.1$) on percent change of total AA. Results indicate that FB elicited a similar response in N metabolism and AA flows to SBM and may be used as a protein source in ruminant diets.

Key Words: continuous culture, fermentation biomass, protein

W353 Plasma metabolites and rumen ammonia concentration in steers fed high-forage diets and supplemented non-protein nitrogen.

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The objectives were to determine if Optigen, a slow-release NPN source, has a slower N release than urea and whether pelleting affects Optigen

N release. Treatments (TRT) were 1) control non-urea pellet, 11.0% CP; 2) ruminally pulse dosed Optigen, 12.4% CP; 3) Optigen incorporated into a pellet, 11.3% CP or 4) urea ruminally pulse dosed, 12.8% CP. Diets were 50% forage (oat hay; 5.5% CP, 66% NDF) and 50% pelleted feed (beet pulp, corn, soybean meal). NPN as a percent of dietary CP (36 ± 0.5%) did not vary among TRT 2, 3, and 4. Diets were fed to 4 ruminally fistulated steers (BW 387 ± 28.9 kg), fitted with indwelling jugular catheters, in a 4x4 Latin square designed experiment. Pellet was fed at 0800 (t 0) and consumed within 20 min. Pulse doses of Optigen or Urea occurred at t 0. Blood samples were collected in 10 min intervals (0800 to 1130), 1 h intervals (1300 to 1600), and 2 h intervals (1600 to 2000). Rumen fluid samples were taken at 1 h pre-feeding and at 0, 1, 4, 8, 12 and 16 h post feeding. TRT 2 and 4 resulted in higher dietary CP than TRT 1 and 3 (12.6 v 11.2%; $P < 0.01$).Diet did not affect DMI (6.5 ± 0.2 kg). At t 0, rumen ammonia-N (RAN; 4.4 ± 5.8 mg/dl), plasma urea-N (PUN; 10.0 ± 0.9 mg/dl) and blood ammonia-N (BAN; 0.8 ± 0.03 mg/dl) were similar across TRT. RAN was greatest for TRT 4 (28.1 ± 4.6 mg/dl) and similar between TRT 1, 2, and 3 (6.4 ± 5.3, 10.8 ± 4.6, 8.5 ± 5.3, respectively; $P < 0.05$). A TRT by time interaction occurred because of 60 min post feeding RAN concentrations of 8.6 ± 12.4, 34.6 ± 10.7, 25.3 ± 12.4 and 138.9 ± 10.7 mg/dl, for TRT 1 through 4, respectively ($P < 0.001$). PUN concentrations of 11.6, 11.5, 10.9 and 14.58 mg/dl, respectively, were not affected ($P > 0.05$) by time or TRT. BAN concentrations were highest for TRT 4 ($P < 0.05$) and peaked during 50 to 80 min post feeding. TRT 3 caused lower BAN concentrations compared with TRT 2 ($P < 0.05$) which was consistent with decrease in RAN at 60 min post feeding. Optigen had a slower rate of N release than urea, and was not adversely affected by pelleting.

Key Words: beef cattle, blood ammonia, non-protein nitrogen

W354 Gossypol and total phenols of eleven varieties of whole cottonseed (*Gossypium hirsutum*) in the north of Argentina.

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Whole cottonseed (WCS, *Gossypium hirsutum*) is a feedstuff usually fed in beef and dairy cattle rations. Gossypol is a polyphenol pigment in WCS and cotton byproducts, and its concentrations depend on several factors such as genotype, temperature, and rainfall. This pigment is considered as an antiquality factor that might affect animal performance and ruminal metabolism. The objective of this study was to quantify gossypol concentration and nutritional profile of WCS from 11 varieties cultivated in Northern Argentina, and usually fed to cattle. Varieties studied were: Guazuncho 3, Pora, Poraite, New opal BT, Guazuncho 2000 RR, BT604, BT404, Cacique, Chaco 530, Oro blanco, and an experimental cultvirar. Samples were collected in 2004, 2006, 2007, 2008, 2009 and 2011 were analyzed for total soluble protein, ash, total fat, total phenolic compounds (TF; Folin-Ciocalteu), and free gossypol. Gossypol was analyzed by HPLC-DAS with external standard using a purified gossypol. Total phenolic compounds concentration in the varieties oscillates from 0.54 to 1.16% (Tannic acid equivalent). Gossypol content in WCS was 0.06–1.36%. Soluble protein varied from 0.53 to 2.24%. Total fat was 17.59–25.65%. Results from this preliminary study indicate small variation in gossypol and TF levels among 11 varieties grown in the north of Argentina.

Key Words: antiquality, cotton varieties, gossypol

W355 Influence of nitrogen fertilization and fibrolytic enzymes on digestibility and utilization of the nutrients of ryegrass (*Lolium multiflorum* var. Jumbo) hay fed to Holstein steers.

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To evaluate the influence of fibrolytic enzyme addition × N fertilization (100, 200 or 300 kg of N/ha) on digestive function of ryegrass hay offered as basal diet, 6 Holstein steers (143 ± 5 kg LBW) equipped with cannulas in rumen and duodenum proximal were distributed in a split plot design. Orthogonal contrasts were used to test for linear, quadratic, and cubic effects of increasing N fertilization. Daily enzyme levels tested were 0 vs. 15 g/d and N fertilization levels applied to ryegrass were 100, 200, and 300 kg N/ha. Chromic oxide (0.3% as daily DMI basis) was added as digestive internal marker to basal diet. There was no interaction ($P \geq 0.05$) between enzyme and N fertilization. Enzyme addition increased N ($P \leq 0.05$; 76.6 vs. 77.4 g/d ±5.7) and microbial N flow ($P \leq 0.05$; 54.5 vs. 57.9 g/d ± 5.0) to the duodenum, N efficiency ($P \leq 0.05$; 1.34 vs. 1.42 ±0.1), microbial efficiency ($P \leq 0.01$; 24.6 vs. 26.5 ± 2.7) and postruminal OM digestion ($P \leq 0.10$; 42.1 vs. 45.5± 5.1). Nitrogen fertilization increased (linear component, $P \leq 0.01$) feed N leaving the abomasum and the OM rumen digestion ($P \leq 0.05$). Passage and digestion rates were not influenced ($P \geq 0.05$) by treatments. Fibrolytic enzymes had more influence on N metabolism in the rumen and total tract than for N fertilization.

Key Words: fibrolytic enzyme, N fertilization, rye grass

Ruminant Nutrition: Other Ruminants

W356 Diurnal pH of the first compartment stomach of alpacas fed alfalfa or grass hay supplemented with oats, corn, and corn/oats/barley.

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The purpose of this study was to determine the diurnal pH variation of the first compartment stomach (C1) of alpacas (vicugna pacos) fed grass hay (G) or alfalfa hay (A) and acute addition of grain supplements; oats (O), ground corn (C) or corn/oats/barley (COB). Three male (+3 yrs, 65 kg BW) were fitted with a C1 fistula, housed in metabolism crates and fed ad libitum grass hay or alfalfa hay and water. The treatments (TRT) included the addition of 454 g of O, C or COB to G (GO, GC, GCOB) or to A (AO, AC, ACOB). The alpacas were acclimated to A and each grain TRT was randomly administered followed by a 30 d acclimation period to G followed by the random administration of each grain so that each grain TRT was represented during each 3-d collection period. A pH probe was calibrated, fitted through the fistula plug and positioned at the anterior, ventral portion of C1 one day prior to beginning of data collection. Treatment periods included d1 to d7 diurnal pH collection of A or G. Grain TRT pH data were collected during d8-10, d 15 to 17 and d 22 to 24. Diurnal patterns for a 24-hour period are an average of the 3-d collection period. Dry matter intake (DMI) was 1415, 1142, 1146, and 1192 g for A, AO, AC and ACOB; and 1331, 1207, 1206, and 1260 for G, GO, GC and GCOB. Only A DMI was different from the alfalfa + grain treatments ($P < 0.05$). Overall pH was 6.87, 6.78, 6.78 and 6.56 for A, AO, AC and ACOB; and 6.95, 6.89, 6.76 and 6.83 for G, GO, GC and GCOB. Alfalfa pH was more acidic than G ($P < 0.05$) and was more basic than AO and AC which are more basic than ACOB ($P < 0.05$). All G TRT were different from each other ($P<0.05$). Diurnal pH patterns for each TRT showed a decrease in pH followed by a return. As indicated by overall pH, the COB pattern decreased the lowest before return. The alpaca C1 has a very effective buffering system, but acute intake of highly fermentable feeds does have a dramatic effect on pH. Support was provided by Brigham Young University and The Camelid Center.

Key Words: alpaca, compartment 1, pH

W357 Effect of castration on performance and carcass traits of crossbreed lamb on different time on feed.

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The use of non-castrated (NC) males for meat production has been an increased practice because they grow fast, utilize feed more efficiently and show high-yielding and leaner carcasses than castrated males (CM). To evaluate the performance and carcass traits of CM or NC crossbreed lambs slaughtered after different time on feed, 48 Dorper × Santa Ines males (32 ± 5.04 kg BW, 90 d old) were individually allotted in pens according to initial BW (block) and fed a diet with 75% whole corn grain, 20% of pelleted protein and mineral mix and 5% of coast cross hay. After 14 d of adaptation period 24 animals were Burdizzo castrated. Feed and orts were registered daily for DMI and feed efficiency (FE) determinations. Animals were weighed at the beginning of the trial and every 14 d. Two CM died during the trial due to urolithiasis problems. Animals were slaughtered after 36 or 78 d of feeding (half of each sex) for hot carcass weight (HCW) and *Longissimus* muscle area (LMA) and backfat thickness (BFT) at 12th rib level determinations. There was no significant sex x age interaction for any trait. BW at slaughter was greater for NC (52.2kg) than CM (46.8kg; $P = 0.005$). Non-castrated also had greater ADG (0.34 vs 0.27 kg/day; $P = 0.001$), DMI (1.2 vs 1.1 kg;$P = 0.007$) and FE (0.30 vs 0.25 kg ADG/kg DMI;$P < 0.006$), HCW (24.8 vs 22.7; $P = 0.030$), LMA (18.0 vs 16.1cm ^{2}; $P = 0.018$) with no difference in BFT (3.4 mm). Animals fed for 36 d had smaller HCW (21.2 vs 26.3 kg; $P < 0.001$), LMA (16.0 vs 18.2 cm ^{2}; $P = 0.005$) and BFT (2.9 vs 4.0 mm; $P = 0.030$) than those fed 78 d, as expected. Animals slaughtered after 78 d of feeding were heavier (54.2 vs 44.9 kg; $P < 0.001$) and had smaller ADG (0.33 vs 0.28 kg/day; $P = 0.019$) than those slaughtered at 36 d. DMI (mean = 1.15 kg DM/day) did not differ between time on feed but animals fed for 78 d had higher FE than those fed for 36 d (0.25 vs 0.29 kg ADG/kg DMI; $P = 0.020$. Non-castrated crossbreed lambs could be finished with a better performance and appropriate degree of fatness when fed high concentrate diets for short periods.

Key Words: feedlot, high concentrate, sheep

W358 Efficacy of novel feed products to reduce locoweed toxicity in wether lambs.

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Locoweed may result in impaired performance and possibly death when consumed by livestock. Novel products are needed that increase the tolerance of livestock to swainsonine, the toxicant in locoweed. The objective was to determine the efficacy of proprietary feed products to reduce locoweed toxicity in sheep. Wether lambs (n = 40; 39 ± 0.4 kg BW) were housed individually and fed 620 g/d of alfalfa hay and 100 g/d of corn-based feed in equal portions twice daily for 20 d. Lambs were equally divided into 4 BW blocks, and within block were randomly assigned to 1 of 5 treatments (randomized complete block design). Treatments were: no locoweed or feed products (CON); 20 g/d of locoweed (LOCO); 20 g/d of locoweed and 50 g/d of feed product 1 (AK1); 20 g/d of locoweed and 50 g/d of feed product 2 (AK2); 20 g/d of locoweed and 50 g/d of feed product 3 (AK3). Locoweed and feed products replaced alfalfa hay in the basal diet. Serum (from venous blood) was collected on d 0, 3, 6, 9, 12, 15, 18, and 20, and rumen fluid samples were collected on d 9 and 20. Swainsonine was detected in serum and rumen fluid of lambs fed LOCO, AK1, AK2, and AK3, but was not detected in lambs fed CON. Serum swainsonine of lambs fed LOCO, AK1, AK2, and AK3 increased ($P < 0.05$) from d 0 to d 3, and remained elevated for the remainder of the study. Serum alkaline phosphatase was greater ($P < 0.05$) in lambs fed treatments with locoweed than CON, and was less ($P < 0.05$) in lambs fed AK3 than LOCO. Serum thyroid hormones (T3 and T4), serum total iron, and serum transferrin saturation were lower ($P < 0.05$) in lambs fed treatments with locoweed than CON. Serum thyroid hormones (T3 and T4) were also lower in lambs fed AK1 than CON. Serum insulin was lower ($P < 0.05$) in lambs fed AK2 than LOCO. Serum total iron binding capacity, urea N, NEFA, and rumen fluid pH, ammonia, and total VFA were not different ($P \geq 0.10$) among treatments. In locoweed-fed treatments, rumen fluid swainsonine was not different ($P \geq 0.10$) for lambs fed AK1, AK2, or AK3 than LOCO. The results suggest that the novel feed products evaluated in the current study did not reduce symptoms of subclinical toxicity in wether lambs consuming locoweed. Authors acknowledge A. Temple and Agri-King, Inc.

Key Words: locoweed, serum, sheep

W359 Swainsonine excretion, nutrient digestibility, and nitrogen retention of lambs fed alfalfa hay, locoweed, and novel feed additives. F. A. Allataifeh,* C. A. Loest, M. N. Sawalhah, F. Castillo, A. F. Cibils, and E. J. Scholljegerdes, *New Mexico State University, Las Cruces.*

Novel products are needed that could reduce locoweed toxicity, alleviate impaired performance, and prevent possible death when consumed by livestock. This study evaluated the effect of 3 feed additives (Agri-King) on swainsonine intake and excretion, nutrient digestibility, and N retention of 40 wether lambs (39.2 ± 0.38 kg initial BW). Lambs were blocked by initial BW and assigned to 5 dietary treatments in a randomized complete block design (4 blocks). Treatments were a control diet (86% alfalfa hay and 14% corn-based supplement) fed to lambs at 1.8% of BW (as fed) for 20 d (CON), CON with 20 g/d locoweed replacing alfalfa hay (LOCO), LOCO with 50 g/d of feed additive 1 replacing alfalfa hay (AK1), LOCO with 50 g/d of feed additive 2 replacing alfalfa hay (AK2), and LOCO with 50 g/d of feed additive 3 replacing alfalfa hay (AK3). Lambs were housed individually for 14 d in pens and then for 6 d in metabolism crates for total fecal and urine collections. Statistical analysis used the mixed procedure of SAS with lamb as the experimental unit. Intake, fecal, and urinary swainsonine were greater ($P < 0.05$) for LOCO, AK1, AK2, and AK3 than CON. Intake of swainsonine was lower ($P < 0.05$) for AK3 than LOCO, fecal swainsonine was lower ($P < 0.05$) for AK1 than LOCO, and urinary swainsonine was lower ($P < 0.05$) for AK1 and AK2 than LOCO. Treatments did not affect ($P \geq 0.20$) DM intake, fecal DM, or DM digestibility. Nitrogen intake was lower ($P < 0.05$) for AK1, AK2, and AK3 than for CON and LOCO, but fecal N and urine N was not affected ($P \geq 0.11$) by treatments. Nitrogen digestibility was not different ($P = 0.26$) among treatments, but N retention was lower ($P < 0.05$) for AK1 and AK3 than CON. In summary, lamb consumption of locoweed with the feed additives evaluated in the current study does not significantly affect DM and N digestibility. Lower fecal and urinary swainsonine in lambs receiving AK1 indicated that it may affect metabolism of swainsonine in sheep. Authors acknowledge A. Temple and Agri-King Inc.

Key Words: swainsonine, nitrogen retention, sheep

W360 The serosal-to-mucosal urea flux across the cervine ruminal epithelium is not affected by mucosal ammonia or phloretin. M. E. Walpole*[1], G. B. Penner[1], M. Woodbury[2], and T. Mutsvangwa[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Saskatchewan, Canada,* [2]*Department of Large Animal Clinical Services, University of Saskatchewan, Saskatoon, Saskatchewan, Canada.*

Urea transporter (UT) proteins are involved in the movement of urea across the gastrointestinal tract in ruminants. Few studies with domesticated ruminants indicates that increasing ruminal ammonia concentration has inhibitory effects on urea transfer from blood into the rumen, but the exact mechanisms involved have not been elucidated. The effect of mucosal ammonia concentration on the serosal-to-mucosal flux of urea ($J_{sm\text{-}urea}$) was examined. Five white-tail deer (*Odocoileus virginianus*) bucks were killed and ruminal epithelial tissue was collected and mounted in Ussing chambers under short-circuit conditions. To simulate in vivo physiological conditions, the serosal buffer contained 1 m*M* of urea and was adjusted to a pH of 7.4, while the mucosal buffer lacked urea and pH was adjusted to 6.2. Treatments were control (no ammonia), 6.65 m*M* ammonia (as $[NH_4]_2CO_3$), and ammonia with phloretin (1 m*M*; a UT inhibitor). Fluxes of urea ($J_{sm\text{-}urea}$) and mannitol ($J_{sm\text{-}mannitol}$) were measured in parallel using ^{14}C-labelled urea (26 kBq/mL) and ^{3}H- labelled mannitol (74 kBq/mL), respectively, with $J_{sm\text{-}mannitol}$ being used as an indicator of paracellular transport. Ruminal ammonia and blood urea nitrogen concentrations averaged 12.3 and 34.4 mg/dL, respectively. The additions of ammonia or phloretin had no effect on tissue conductance (G_t) or short-circuit current (I_{sc}). Both $J_{sm\text{-}urea}$ and $J_{sm\text{-}mannitol}$ were not inhibited ($P > 0.05$) by mucosal ammonia or the serosal addition of phloretin. The $J_{sm\text{-}urea}$ and $J_{sm\text{-}mannitol}$ were highly correlated ($R^2 = 0.88$; $P < 0.001$), thus suggesting that $J_{sm\text{-}urea}$ was mediated via para-cellular pathways. Ruminal ammonia concentration was not correlated with $J_{sm\text{-}urea}$; however, blood urea nitrogen concentration was negatively correlated with $J_{sm\text{-}urea}$ ($R^2 = 0.81$; $P = 0.038$). We conclude that, because of the significant correlation between $J_{sm\text{-}urea}$ and $J_{sm\text{-}mannitol}$ and the lack of inhibitory action for phloretin, a known inhibitor of UT, urea flux across the ruminal epithelium in white-tail deer is likely via para-cellular routes.

Key Words: ammonia, rumen, urea transporter

Ruminant Nutrition: Feed Additives

W361 Effects of different feed additives on performance and carcass traits of feedlot cattle. C. A. Zotti, S. da Luz e Silva,* L. S. Martello, R. L. Meirelles, A. P. dos Santos Silva, P. L. Alvarez, P. H. Cancian, A. C. Ianni, L. E. Zanoni, and P. R. Leme, *Faculdade de Zootecnia e Engenharia de Alimentos, Universidade de São Paulo, Pirassununga, SP, Brazil.*

Feed additives are largely used in beef cattle diets to improve performance and reduce risks of nutritional disorder diseases like acidosis and timpanism. However, some countries tend to ban the use of ionophore in animal nutrition due to the risk of resistance of some microorganisms. Therefore, alternatives to non-antibiotic additives must be studied. The objective of this work was to investigate the effects of different feed additives on performance and carcass traits of beef cattle. Twenty 2 Nellore bulls (initial BW 353 ± 20.9 kg) and 22 steers (initial BW 320 ± 1.5 kg; 21mo old) were fed high concentrate diet (85% of concentrate and 15% of sugarcane bagasse as roughage source). The animals were allotted in 4 pens equipped with calan gate system and randomly assigned within sex (block) to one of the 4 treatments: Monensin at 30 mg/kg DM (MON); Virginiamycin at 30 mg/kg DM (VIR); combination to MON (15 mg/kg DM) plus VIR (15 mg/kg DM) (MPV); Blend of Castor Oil Acid and Cashew Oil fed at 500 mg/kg DM (COC). Feed and orts were computed daily for each animal for DMI and feed efficiency calculations. Animals were weighed (BW) and ultrasound scanned at the first day of the feedlot and each 28 d. Ultrasound measurements taken were Longissimus muscle area (ULMA) and backfat thickness (UBFT) between 12th and 13th ribs. After 112 d on feed, cattle were slaughtered and hot carcass weight (HCW), kidney, pelvic and inguinal fat (KPIF) and dressing percentage (DP) calculated. Dry matter intake for treatment MON was smaller (9.7kg/day; $P = 0.04$) when compared with COC (11.1kg/day) with no differences of VIRG and MPV (10.1 and 10.4kg/day, respectively). There was no effect of treatments on ADG (1.60 ± 0.26 kg), feed efficiency (0.156 ± 0.02 kg ADG/kg DMI), final BW (510 ± 47 kg), HCW (307 ± 27.2 kg), dressing percentage (60.0 ± 1.78%), UBFT (5.9 ± 2.1 mm) and KPIF (3.12 ± 1.62%) at slaughter. Longissimus muscle area was higher for MPV (80.9cm^2; $P = 0.008$) than COC (74.4cm^2) and VIR (74.4cm^2). The additives studied can replace ionophores to beef cattle fed high concentrate diet, without affecting animal performance and most of carcass traits.

Key Words: additives, feedlot, Nellore

W362 Effect of *Propionibacterium freudenreichii* supplementation in diets containing canola or flaxseed oils on in vitro methanogenesis and lipid biohydrogenation. S. Ding[1,2], S. J. Meale*[1,2], M. L. He[2], J. Long[3], A. Y. Alazzeh[2], T. A. McAllister[2], and A. V. Chaves[1], *[1]Faculty of Veterinary Science, University of Sydney, Sydney, NSW, Australia, [2]Lethbridge Research Center, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada, [3]Department of Animal Science, Northeast Agricultural University, Haerbin, Heilongjiang, China.*

The addition of propionibacterium as a direct fed microbial may provide a competitive pathway to methanogenesis for H_2 disposal in ruminants. Additionally, it has the potential to inhibit the biohydrogenation of polyunsaturated fatty acids (PUFA). Flaxseed and canola oils have been shown to reduce methane formation and rumen biohydrogenation due to the dominant levels of linolenic acid (C18:3) and linoleic acid (C 18:2), respectively. However, to-date, no studies have been undertaken regarding the ability of propionibacterium to mitigate methane from diets supplemented with plant oils or its effects on PUFA biohydrogenation. Thus, a 48 h, in vitro batch culture was conducted to determine the effects of *Propionibacterium freudenreichii* (PFB) on (1) in vitro VFA production and methane and (2) fatty acid biohydrogenation, in a backgrounding diet supplemented with 2 plant oils. Treatments were: backgrounding diet (CON); CON + PFB (CPB) (4x109 cfu propionibacteria/40 mL inoculum); CON + canola oil (6% DM; CCO); CCO + PFB (CCPB), CON + flaxseed oil (6% DM; FLO) and FLO + PFB (CFPB). Methane and gas production was measured at 3, 6, 12, 24, 48 h, whereas, total ruminal VFA were determined at 0, 6, 24 and 48 h of incubation. In vitro incubations were repeated twice with 3 replicates per treatment in each run. Data were analyzed using the MIXED procedure of SAS with treatments as fixed effect, and incubation run and interaction incubation run × treatments as random effects. Cumulative gas production (mL), CH_4 production (mL/g DM) and total ruminal VFA concentration (mM) were not affected by treatment ($P \geq 0.10$). However, there was a tendency ($P = 0.07$) for both oil-based diets, with or without PFB, to reduce CH_4 production (mL/g DM) at 24 and 48 h. Additionally, oil increased ($P \leq 0.002$) the percentage of CLA+VA at 24 and 48 h. Propionibacterium did not affect ($P > 0.05$) biohydrogenation. However, flaxseed and canola oil increased ($P < 0.001$) the proportion of unsaturated fatty acids and decreased ($P < 0.001$) the proportion of saturated fatty acids in the total incubation period, thus inhibiting biohydrogenation based on oil diets. Canola oil based treatments had the highest ($P \leq 0.003$) proportion of C18:1 (cis-9) across all time points, whereas flaxseed oil groups had the greatest ($P \leq 0.04$) percentages of PUFA including C18:3, C18:1 (cis-15), biohydrogenation intermediates from C18:3 at 6, 24, 48h, and CLA (cis-9,trans-11) at 6, 24h, indicating the capability of flaxseed oil to alter biohydrogenation in favor of desirable PUFA production. In conclusion, propionibacterium did not significantly affect methanogenesis and lipid biohydrogenation based on either flaxseed or canola oil diets on current in vitro study.

Key Words: biohydrogenation, methane, lipids

W363 Efficacy of an autolysed yeast product (Levabon Rumen) for ruminants versus live yeast and yeast culture in vitro. A. Ganner*[1], C. Stoiber[1], I. Dohnal[1], K. Deckardt[2], F. Klevenhusen[2], G. Schatzmayr[1], and Q. Zebeli[2], *[1]Biomin Research Center, Tulln, Lower Austria, Austria, [2]University of Veterinary Medicine, Vienna, Austria.*

Various yeast products for ruminants have been reported to improve rumen microbial activity, feed utilization and cow performance. Increasingly, literature reports about the benefits of live yeast and yeast culture. However, little has been reported about the effect of autolysed yeasts for ruminants. Moreover, the mode of action of different yeasts, with respect to improving animal performance, is still not completely understood. Target of the present study was to evaluate the efficacy of a novel yeast derivative (Levabon Rumen) on anaerobic bacterial count (batch culture); on crude fiber, dry matter and crude protein digestibility (RUSITEC) versus yeast culture and live yeast, which are used for animal feeding. In a first in vitro batch culture study, rumen simulation reactors were filled with rumen fluid, mixed with saliva and incubated under anaerobic conditions for 24 h. The yeasts (in mg yeast/flask: Levabon Rumen 40–300; yeast culture1 300, 600; yeast culture2 200, 400; live yeast 0.5, 5) were mixed into the ration (50% hay and 50% concentrate). Total viable anaerobic bacteria (batch culture) were counted (cfu/g). In a second experiment with the rumen simulation technique (RUSITEC), different levels of the yeast products (in mg yeast/12 g dry matter: Levabon Rumen 3, 6, 12, 18, 24;

yeast culture1 12, 36; yeast culture2 6, 12; live yeast1 2.4; live yeast2 0.3) were fed daily for 14 d. The samples were mixed into a ration consisting of 50% hay and 50% concentrate. The parameters measured include nutrient digestibility (Weender analysis), pH, redox potential and volatile fatty acids. Results indicate improved digestibility in RUSITEC and increased amount of anaerobic bacteria in batch culture by the autolysed yeast as well as by the probiotic yeast and the yeast culture. Volatile fatty acids also increased. None of the yeast showed an effect on either pH or redox potential, perhaps due to continuously buffering the system and strictly anaerobic conditions. Based on these findings, Levabon Rumen represents a promising feed additive to improve cattle health and performance.

Key Words: autolysed yeast, prebiotic, ruminants

W364 Effect of monensin on methane emissions in dairy cattle can be explained by level of dry matter intake and fat content of the diet.

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Methane (CH_4) is an important greenhouse gas that contributes to climate change. Cattle produce the majority of CH_4 emissions from ruminants accounting for about 30% of the global emissions. Monensin improves feed conversion efficiency and increases propionic acid molar proportion in the rumen. Several studies have investigated the effects of monensin on CH_4 emission from dairy cows and the results vary widely. The objectives of the present study were to conduct a meta-analysis to infer about the overall effect of monensin feeding on CH_4 emission from dairy cows and to quantify factors explaining between-study variability of the monensin effect. Data of mean and SD of CH_4 emission (g/d) in monensin and control groups, sample size (N), treatment duration (T, d), DMI (kg/d), monensin dose (mg/kg of DMI), and basal diet nutrient contents (g/kg of DM) from 11 controlled-trials were included. The Metafor package in R was used to conduct the meta-analysis. Effect size (ES, g/d) was calculated as difference between the means of monensin feeding and control groups. A model accounting for random study effects revealed significant ES heterogeneity between trials (98%, $P < 0.001$) suggesting T, DMI, monensin dose and nutrient contents as potential covariates for explaining between-study variability. The final model including potentially significant covariates were selected using Likelihood-ratio tests. Feeding monensin was shown to have a non-significant effect (ES = −2.88 ± 3.28 g/d, $P = 0.380$) on CH_4 emission from dairy cows. Effect size was positively (covariate coefficient = 1.35 ± 0.56, $P = 0.016$) and negatively (covariate coefficient = −5.15 ± 1.51, $P = 0.001$) associated with DMI and crude fat content, respectively. Monensin dose and T did not significantly affect ES. Inclusion of DMI and fat content into the model reduced total heterogeneity of ES (τ^2) by about 70% ($\tau^2 = 322$ vs. 100). Dry matter intake and crude fat content were significant and could explain between-study variability of the monensin effect on CH_4 emission from dairy cows.

Key Words: dairy cows, methane, monensin

W365 Effects of dietary supplementation of a yeast product on performance and morbidity of newly received beef heifers.

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Two truckloads of beef heifers (n = 237; average initial BW = 191 kg ± 1.17) were used to evaluate the effects of a yeast culture/enzymatically hydrolyzed yeast product (Celmanax; Varied Industries Corp. Inc., Mason City, IA) included in a 65% concentrate receiving diet on performance and percentage of bovine respiratory disease (BRD) morbidity during a 35-d receiving period. Treatments included: 1) the 65% concentrate receiving diet with the addition of Celmanax; 14 g/heifer/d; mixed in a carrier; or 2) the 65% concentrate receiving diet without Celmanax (Control; 14 g/heifer/d of carrier only). No load × treatment interactions ($P > 0.157$) were detected for any measures of performance or BRD morbidity. Initial BW did not differ ($P > 0.537$) between treatments nor did d-35 BW ($P = 0.332$). Average daily gain for d 0 to 14 ($P = 0.052$) and for the overall 35-d ($P = 0.078$) period tended to be greater for Celmanax heifers than for controls. Intake of receiving diet DM was greater ($P \leq 0.025$) by the Celmanax heifers than by Control heifers at all the measurement periods during the experiment, but G:F did not differ ($P > 0.175$) between treatments. The proportion of heifers treated once for BRD tended ($P = 0.094$) to be less with the Celmanax treatment (4.1 for Control vs. 10.5% for Celmanax). Results indicate that heifers fed Celmanax ate more receiving diet DM and tended to gain more than Control heifers, with a tendency for decreased BRD morbidity during a 35-d receiving period.

Key Words: newly received beef cattle, feedlot performance, yeast product

W366 Effect of oregano, ginger and thyme oils on in vitro rumen fermentation and methane emission.

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In vitro semi automated gas production technique has been used to evaluate the effects of essential oils at different levels (0, 15, 30, 45 and 60 μ/ml) on ruminal fermentation and methane production. The investigated essential oils were *Origanum vulgare* (OV_{15}, OV_{30}, OV_{45}, OV_{60}, *Zingiber officinale* (ZO_{15}, ZO_{30}, ZO_{45}, ZO_{60}) and *Thymus vulgaris* (TV_{15},TV_{30}, TV_{45}, TV_{60}). The analysis of the essential oils by gas chromatography - mass spectrometry demonstrated that the principal components were carvacrol (70%) and thymol (11%) in OV, zingiberene (33%) and zingerone (17%) in ZO, thymol (40%) and carvacrol (13%) in TV. A total mixed ration (50% roughage: 50% concentrate) was incubated with buffered rumen fluid. Data were analyzed using PROC MIXED of SAS 9.1. The inclusion of OV, TV, ZO_{15} and ZO_{30} did not affect significantly on true digestibility of dry matter and organic matter, while ZO_{45} and ZO_{60} decreased significantly ($P \leq 0.05$). The efficiency of microbial protein was estimated by partitioning factor (PF, estimated as ratio of truly organic matter degradation and gas volume produced in 24 h of incubation). There was no significant effect of investigated essential oils on PF except OV_{45}, TV_{45} and TV_{60} which improved significantly ($P \leq 0.05$) the PF. There was no significant effect of essential oils on the production methane except OV_{45} and TV_{60} which decreased significantly ($P \leq 0.05$) the methane production. The NH_3-N concentration was not altered with inclusion of essential oils at different doses. The short chain fatty acids concentration was not altered with inclusion of essential oils except OV_{30}, $TV_{45}$and TV_{60}which increased significantly ($P \leq 0.05$) the propionate concentration. This study suggested that essential oils have the potential to affect rumen fermentation and OV_{45} and TV_{60} could be a promising methane mitigating agent.

Key Words: essential oils, gas production, rumen fermentation

W367 Effect of some essential oils on rumen fermentation and methane emission in vitro. F. G. Vilela,* I. C. S. Bueno, A. S. Netto, J. E. Freitas Junior, B. C. Venturelli, T. S. Canaes, and F. P. Rennó, *University of São Paulo, Pirassununga, SP, Brazil.*

The objective of this study was to evaluate in vitro the effects of essential oils at different levels (0, 15, 30, 45 and 60 µL/100 mL buffered rumen fluid) on ruminal fermentation by semi automatic gas production technique. The selected essential oils were *Rosmarinus officinalis* (RO_{15}, RO_{30}, RO_{45}, RO_{60}), *Syzygium aromaticum* (SA_{15}, SA_{30}, SA_{45}, SA_{60}) and *Pimpinella anisum* (PA_{15}, PA_{30}, PA_{45}, PA_{60}). The analysis of the essential oils by gas chromatography-mass spectrometry demonstrated that the principal components were 1.8 cineol (28%) and p-cimeno (13%) in RO, eugenol (40%) in SA and anethol (45%) in PA. The trial was conducted in duplicates making a total of 12 bottles for each treatment. The substrate used was the basal diet consisting of corn silage and concentrate (71.66% corn, 12.12% soybean meal and 10% soybean), in ratio 50:50. Ground samples (1 g) were incubated in 100 mL of diluted rumen fluid (10 mL mixed rumen fluid + 90 mL of buffer solution mineralized) in 160 mL serum bottles. Data were analyzed using PROC MIXED of SAS 9.1. There was no significant effect of essential oils on the production methane except PA_{45} and PA_{60} which decreased significantly ($P \leq 0.05$) the methane production. The inclusion of RO_{45}, RO_{60}, SA_{15}, SA_{30} and PA did not affect on true digestibility of dry matter and organic matter, while RO_{15}, RO_{30}, SA_{45} and SA_{60} decreased significantly. The efficiency of microbial protein was estimated by partitioning factor (PF, estimated as ratio of truly organic matter degradation and gas volume produced in 24 h of incubation). There was no effect of investigated essential oils on PF except SA_{45} and SA_{60} which improved significantly the PF. The short chain fatty acids concentration was not altered with inclusion of essential oils except PA_{30}, PA_{45} which increased significantly the propionate concentration. This study suggested that essential oils could modify the rumen fermentation and have a potential in methane mitigation, which may be beneficial for animal growth.

Key Words: essential oils, methane, degradation

W368 Effect of abomasal inorganic phosphorus infusion on phosphorus absorption in lactating dairy cows. X. Feng,* J. P. Jarrett, P. P. Ray, L. Karpinski, B. F. Willing, and K. F. Knowlton, *Virginia Polytechnic Institute and State University, Blacksburg.*

The objective of the study was to evaluate the effect of inorganic P (Pi) supply on P disappearance from the intestinal tract of lactating dairy cows. Four ruminally and ileally cannulated crossbred cows were used in a 4 × 4 Latin square with 21-d periods. Cows were fed a total mixed ration containing 0.21% P, providing 50% of the cows' P requirement. Ytterbium (Yb) labeled corn silage and Co-EDTA were used as particulate and liquid phase markers, respectively, to measure digesta flow. Omasal samples were collected every 9 h from d 10 to 13 to measure omasal P flow from the basal diet. On d 13 to 21 of each period, each cow was infused daily with 0, 20.1, 40.2, or 60.3 g Pi into the abomasum and total collection was conducted on d 18 to 21. Ileal samples were collected every 9 h on d 18 to d 21. Feed, digesta, and fecal samples were analyzed for total P and Pi using the molybdovanadate yellow method and blue method, respectively. All data were analyzed using PROC GLIMMIX in SAS 9.2 using contrasts to evaluate linear and quadratic effects of Pi infusion dose. Dry matter (DM) intake, apparent DM digestibility, milk yield and milk total P were unaffected by Pi infusion ($P > 0.05$). Ileal flow and fecal excretion of total P and Pi increased linearly ($P < 0.05$) with increasing infused Pi. In the small intestine, net disappearance of total P and absorption of Pi decreased ($P < 0.05$; 67.7 to 37.4% and 83.2 to 52.8%, respectively) with increased Pi infusion. Similarly, total tract disappearance of total P and Pi decreased with increasing Pi infusion ($P < 0.05$; 74.3 to 54.3% and 81.1 to 66.6%, respectively). In the large intestine, net Pi absorption was unaffected but increasing Pi infusion increased disappearance of total P ($P < 0.05$). Results of this study suggest limits to Pi absorption in the small intestine.

Key Words: dairy cows, phosphorus absorption, phosphorus excretion

W369 Effects of essential oils on in vitro ruminal fermentation and methane production of a mixed diet. I. Mateos[1], A. Díez[1], C. Saro[1], D. Yáñez-Ruiz[3], M. D. Carro[1,2], and M. J. Ranilla*[1,2], [1]*Dpto. Producción Animal, Universidad de León, Campus de Vegazana, León, Spain,* [2]*Instituto de Ganadería de montaña (CSIC-ULE), Finca Marzanas, Grulleros, León, Spain,* [3]*Estación Experimental del Zaidín (CSIC), Camino del Jueves, Armilla, Granada, Spain.*

The effects of 6 doses (0 (control), 40, 80, 160, 320 and 640 mg/L incubation medium) of carvacrol (CAR), thymol (TYM), eugenol (EUG) and garlic oil (GO) on in vitro fermentation of a mixed diet (65:35 alfalfa hay:concentrate) were evaluated in batch cultures of mixed rumen microorganisms from the rumen of sheep fed the same diet. Previous in vitro studies have shown the ability of these compounds to modify ruminal fermentation, but the effects could be dose and diet dependent. After 24 h of incubation, the main fermentation variables were determined. Differences among treatments were declared at $P < 0.05$. Dose 640 mg/L of all additives tested inhibited almost completely rumen microbial fermentation, confirming their antimicrobial activity at high concentrations, and therefore the values were withdrawn from the statistical analysis. GO and EUG did not modify ($P > 0.05$) rumen fermentation at any other dose. TYM at 320 mg/L decreased ($P < 0.05$) total VFA, acetate, propionate and methane production, and increased ($P < 0.05$) acetate:propionate ratio compared with control. CAR has similar effects on VFA and propionate production at dose 160 mg/L, and tended ($P = 0.08$) to reduce methane production. At 320 mg/L, CAR also increased ($P < 0.05$) acetate:propionate ratio and decreased ($P < 0.05$) ammonia-N concentrations, compared with the control. These results confirm that essential oils supplementation shows different effects on ruminal fermentation depending on the administered dose and the nature of the compound. Under the conditions of this study the doses of essential oil that modified VFA profile and reduced methane production also resulted in a reduction in VFA production, which would indicate a decrease in feed digestibility and have negative consequences on animal productivity.

Key Words: essential oils, in vitro ruminal fermentation, methane

W370 Effect of feeding *Bacillus subtilis* and *Bacillus licheniformis* on dry matter and nutrient intake and digestibility by lambs fed a low quality roughage diet. E. Martínez-Loarte,* A. A. Rodríguez, and L. C. Solórzano, *University of Puerto Rico, Mayaguez, PR.*

The objective of this experiment was to evaluate the addition of *Bacillus subtilis* and *Bacillus licheniformis* (BSL) to the diet on DM, CP, and NDF intake and digestibility in growing lambs fed a diet consisting of 50% commercial tropical grass hay (mixtures of *Panicum maximum*, *Sorghum halapense*, and *Digitaria decumbens*, 71.7% NDF, 4.9% CP;) and 50% hay of the invasive weed *Hyparrhenia rufa* (78.8% NDF, 3.5% CP). Ten crossbred lambs (11.2 kg) were randomly assigned to one of 2 dietary treatments, with or without daily addition of BSL in the diet. The daily offering of hay was at the rate of 4% of body weight on a dry basis and water was available ad libitum. The bacterial strains were mixed with calcium carbonate carrier, and were included in the additive to provide

1.33×10^9 cfu/g supplying 1.33×10^8cfu/head/d. The additive was mixed with 225 g of a commercial concentrate (15.67% CP) and fed daily to the lambs during a 49 d period. Nutrient intake and digestibility (DM, CP, and NDF) were determined from d 42 to 49. Data was analyzed using the PROC MIXED procedure of SAS using the initial lamb body weight as covariance and Tukey′s test was used for mean separation. Total DM intake and tropical grass hay intake was higher ($P < 0.05$) in lambs consuming the additive containing BSL than control animals (484.26 vs 445.23 g/d and 236 vs 218 g/d, respectively), but intake of *Hyparrhenia rufa* hay was similar (32.18 vs 52.43 g/d). Total forage intake as percentage of total DM intake, and DM intake as percentage of lamb body weight was also higher ($P < 0.05$) in lambs consuming BSL than control (59.08 vs 55.09% and 2.36 vs 2.03%, respectively). Feeding the *Bacillus* strains to lambs also improved NDF digestibility (62.48 vs 58.71%), however, the experimental treatment did not affect DM and CP digestibility. In summary, addition of BSL improved total intake by lambs fed a diet containing commercial concentrate and low quality roughage as well as the individual tropical grass hay component. Addition of BSL to the diet also improved cell-wall digestibility of low quality forage by lambs.

Key Words: *Bacillus* spp., Tropical grass hay, *Hyparrhenia rufa*

W371 Efficacy of live yeast *Saccharomyces cerevisiae* (strain Sc 47) and/or yeast cell wall on rumen fermentation and digestive utilization of corn silage-based diet in mid-lactating dairy cows.

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Four ruminally cannulated Holstein cows in mid-lactating (DIM = 185 d) were assigned in a 4 × 4 Latin square design. They were fed a TMR composed of 78.8% corn silage, 9.8% soybean meal, 10.9% ground corn and 0.5% minerals at 23 kg DM daily during 10 d either supplemented with 5 g of live yeast (LY) at 10^{10} cfu/g (L1), or 5 g LY + 5 g yeast cell wall (YCW; L2), or 5 g LY + 10 g YCW (L3), or not supplemented (CTRL). Ruminal fluid was withdrawn from donor cows and mixed with 100 mL artificial saliva (1:1) and 3 g TMR for 8 h-anaerobic batch incubations to determine pH, E_h, rH index, total and individual VFA, and ammonia. The same donor cows were given chromic oxide (10 g before each daily meal) as indigestible flow marker to assess the fecal excretion of the cows and thus DM, OM, NDF and ADF digestibility. In vitro results showed that pH, E_h and total VFA were significantly modified (respectively +0.12 pH unit, −24 mV and +0.97 m*M*/L/h on average when compared with CTRL) with L1, L2 and L3. Ruminal reducing power (rH) was further improved with L2. Acetate contents of L2 and L3 differed significantly with CTRL (in average +0.52 m*M*/L/h). A 36% mean decrease in rumen ammonia was observed with L3 in comparison to other treatments. Propionate and butyrate contents tended to increase ($P < 0.1$) for L2 and L1 respectively. In vivo NDF and ADF digestibility tended to increase (+8 and +9 points respectively) with L3 compared with other treatments, while DM, OM and starch digestibility showed no significant difference. Combining LY and YCW resulted in improving ruminal conditions followed by better fiber utilization in mid-lactating dairy cows.

Key Words: live yeast, mid lactation cow, yeast cell wall

W372 Effect of live yeast *Saccharomyces cerevisiae* (strain Sc 47) on nutrient digestion and ruminal fermentation in relation with rumen degradable protein content of the diet.

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Four ruminally cannulated early lactating Holstein were involved in a cross over design. Cows were fed for a 33-d period a TMR containing an adequate level of RDP (HL) or was 30% below HL (LL), by using soybean meal or tanned soybean meal, respectively: for 21 d with no live yeast (LY) addition (14 d of adaptation and 7 d of sampling) followed by 12 d when LY (5 g at 10^{10} cfu/g /cow/d) was added to the diet (5 d adaptation and 7 d sampling). The pH and redox potential (E_h) were recorded over 3 consecutive days (d 15 to 17 and d 27 to 29) using the ex vivo method (Julien et al., 2010). Ruminal fluid samples were collected on the same days, before the morning meal then 1, 2, 4, 6 and 8 h post-feeding. Feces were collected individually and quantitatively over 48h (d 20 to d22 and d 32 to d 34) and individual DMI were measured for determining apparent nutrient digestibility. Nutrients daily intake did not differ between diets. Fecal excretion of OM was greater in LL (6.7 kg/d) compared with HL (5.6 kg/d). For LL diet, LY decreased ($P < 0.05$) fecal flows of OM (−19%), ADF (−17%), and N (−20%). Fecal N amount was lower ($P < 0.0001$) for HL than for LL: 128.5 vs. 232.9 g/d. Digestibility of CP was lower ($P < 0.0001$) for LL than for HL while that of ADF was higher ($P = 0.033$). With LY, digestibility of CP and ADF were increased ($P < 0.05$): respectively +0.8 and +4.8 points for HL, and +5.9 and +6.4 points for LL. Ruminal pH and E_h were lower ($P < 0.0001$) with HL compared with LL: 5.95 and −167 mV vs. 6.13 and −144 mV. Live yeast increased ruminal total VFA (+8.6%; $P < 0.05$), C2 (+10%; $P < 0.05$), and C4 (+35%; $P < 0.05$) contents for LL and decreased that of C3 (−9.8%; $P < 0.05$) for HL. Those results suggested a specific interest in using LY in RDP deficient diets for early lactating cows.

Key Words: digestion, live yeast, rumen degradable protein

W373 Effects of difructose anhydride III supplementation on serum calcium, dry matter intake and energy status in periparturient dairy cows.

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Difructose anhydride (DFA) III is an indigestible oligosaccharide. It has been shown that DFA III promotes intestinal Ca absorption in rats and reaches the duodenum without being degraded by rumen bacteria when ingested by dairy cows. The purpose of this study was to investigate the effects of DFA III supplementation on serum Ca, dry matter intake (DMI) and energy status in periparturient dairy cows. Twenty-two multiparous Holstein cows were divided into DFA and control group, which were balanced for parity and BW. DFA group was fed 40 g/d of DFA III from 2 wk before expected calving to 1 wk postpartum (pp) and control group was received no DFA III. DMI (−2 to 3 wk pp) and milk yield (0 to 3 wk pp) were recorded daily. BW was measured weekly during the study period (−3 to 6 wk pp). Blood samples were taken weekly throughout the study period as well as on the day before calving and at 0, 6, 12, 24, 48 and 72 h pp for serum Ca, glucose, NEFA and BHBA. Rumen contractions were also counted at blood sampling (5 cows in each group). All data was compared by repeated measures ANOVA. Changes in serum Ca were compared by Tukey-Kramer method for each group. The incidence of subclinical ketosis (SCK; BHBA ≥1400 μmol/L) was compared by Fisher′s exact test. Pretreatment blood parameter levels were similar between the groups. Hypocalcemia (≤7.4 mg Ca/dL) were observed at pp period in 2 DFA and 4 control cows. Serum Ca recovered to the prepartum level in 12 h pp in DFA cows and 48 h pp in control cows. The number of rumen contractions and DMI were higher in DFA cows than control cows during the first 3 wk pp ($P < 0.05$). Milk yield and BW were not affected by the treatment. DFA cows had lower NEFA at 1 ($P < 0.05$) and 7 ($P < 0.10$) d pp with a lower incidence of SCK during the 6 wk pp (9% vs. 45%; $P = 0.07$). These results suggest that periparturient DFA III supplementation encourages DMI by assisting recovery from hypocalcemia thereby maintaining gastrointestinal motility. Increased DMI by supplement of DFA III might reduce negative energy balance and prevent SCK in early lactation.

Key Words: DFA III, DMI, hypocalcemia

W374 Effects of monensin and extracts of hops and *Yucca schidigera* applied alone or in combination on rumen fermentation in vitro.

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There is increasing interest in using plant bioactive as alternative to in-feed antibiotics due to the public concerns over the possible contribution to the emergence of antibiotic resistant bacteria. One possible strategy to increase the efficacy of in-feed antibiotics and possibly circumvent the development of antibiotic resistance is to feed them in combination with plant bioactives. The objective of this study was to assess the effects of monensin (MON), and plant bioactives alone and in combination with MON on in vitro ruminal fermentation. Ethanol extracts of hops (HE; α- and β-acids) and *Y. schidigera* (YE; steroidal saponin) were used as sources of plant bioactives. Treatments were Control (no additive), MON alone (2.5, 5 and 10 µg/ml) and HE (600 µg/ml) or YE (650 µg/ml) alone or combined with the first 2 concentrations of MON. Total gas and CH_4 production were measured at 4, 8, 12, 24 and 48 h of incubation, whereas VFA, NH_3-N concentration, microbial protein (MP), true DM disappearance and ruminal bacteria were determined after 48h. All treatments decreased ($P < 0.05$) gas and CH_4 production, MP, and NH_3-N accumulation. VFA production decreased ($P < 0.05$) with addition of MON alone (10 µg/ml) or in combination with YE. Molar proportion of butyrate were reduced ($P < 0.01$) and that of propionate increased ($P < 0.01$) by all treatments. MON reduced ($P < 0.001$) the relative proportions of 16S *rRNA* copies associated with *Ruminococcus flavefaciens*, but increased those of *Selenomonas ruminantium* ($P < 0.01$) and *Ruminobacter amylophilus* ($P < 0.05$). All treatments reduced ($P < 0.01$) the relative abundance of methanogens. HE alone or in combination with MON reduced ($P < 0.01$) proportions of *R. flavefaciens*, but increased ($P < 0.05$) those of *S. ruminantium* when combined with MON. YE alone and in combination with MON increased ($P < 0.01$) *R. flavefaciens* and *S. ruminantium*. HE and YE altered rumen microbes and fermentation in a manner similar to MON with many responses being additive when applied in combination.

Key Words: monensin, plant bioactives, rumen fermentation

W375 Concentrate level and combined use of ionophore and virginiamycin on feeding behavior of Nelore steers fed high grain diets.

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The objective in this study was to evaluate feeding behavior of Zebu cattle fed 2 concentrate levels and 2 virginiamycin (VM) levels in diets containing salinomycin (SL). Eight ruminally cannulated Nelore steers (434 ± 35 kg initial BW) were randomly allocated to a 4x4 replicated Latin square design (21-d periods). Two concentrate levels (70C and 90C diets had 70 and 90% concentrate on DM basis, respectively) and 2 VM levels (0 and 15 ppm) were tested in a 2x2 factorial arrangement of treatments. Animals were housed in individual pens and fed once daily at 0800 h. The forage source was sugarcane silage (72.4% NDF on DM basis), and all diets included the ionophore SL (13 ppm). During a 24-h period, eating and ruminating activities were visually monitored every 5 min and assumed to persist for the entire 5-min interval. Total chewing time (TCT; min/d) was calculated as the sum of total time spent eating (TTSE; min/d) and ruminating (TTSR; min/d). Rate of intake (RI; g/min) was determined by dividing DM intake in the evaluation day by TTSE, and rate of rumination (RR; min/kg) was calculated by dividing TTSR by DM intake. Statistical analyses were conducted using the GLM procedure of SAS. There was an interaction ($P = 0.02$) between concentrate and VM levels only for TTSE. Within the VM treated group, steers receiving 70C spent 71.9 min/d more eating compared with 90C (234.4 ± 7.9 vs. 162.5 ± 11.7 min/d, respectively; $P < 0.01$). Due to higher NDF content of the diet, TTSR was higher for the 70C compared with the 90C treatment (427.8 ± 23.1 vs. 301.6 ± 18.9 min/d, respectively; $P < 0.01$). As a consequence, TCT increased as concentrate level decreased (643.7 ± 29.6 vs. 481.2 ± 21.3 min/d for 70C and 90C, respectively; $P < 0.01$). Because of the higher NDF content of the diet, the 70C group also showed lower RI (37.9 ± 1.7 vs. 49.7 ± 3.8 g/min for 70C and 90C, respectively; $P < 0.01$) and higher RR (53.6 ± 2.6 vs. 35.9 ± 1.7 min/kg for 70C and 90C, respectively; $P < 0.01$). In summary, feeding behavior of Nelore steers is more influenced by concentrate level than by VM supplementation in diets containing SL.

Key Words: antibiotics, beef cattle, salinomycin

W376 The effect of different doses of exogenous enzymes preparation on in vitro gas production and ruminal fermentation activities of some fibrous feeds in cows.

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This study was conducted to investigate effects of different doses of exogenous enzyme preparation (ENZ- 0, 0.06, 0.12 and 0.24 g/g DM) on in vitro gas production and some ruminal fermentation patterns such as truly degraded substrate (TDS), short chain fatty acids (SCFA), and microbial protein production (MP) of 4 fibrous feeds (FF - Sugarcane leaves, taiwan grass, sorghum straw and llanero grass) in cows. Rumen liquor was collected before the morning feeding from 2 cows (450 ± 6 kg BW) fitted with permanent rumen cannula. In vitro gas production (GP) was recorded at 2, 4, 6, 8, 10, 12, 24, 48 and 72 h of incubation. After 72 h, the incubation was stopped and the inoculants pH was determined and filtered to determine TDS. Ruminal fermentation parameters such as 24 h partitioning factor (PF24), gas yield (GY24), in vitro organic matter digestibility (IVOMD), metabolizable energy (ME), SCFA, and MP were also estimated. Data were analyzed as 4 (4 doses of ENZ) x 4 (4 FF) factorial experimental design. Interaction between FF × ENZ ($P < 0.05$) only occurred for gas production at 12 h (GP12) and 24 h (GP24) of incubation, but there were no interactions after 24 h of incubation. Relative to control, addition of ENZ increased ($P < 0.05$) accumulated gas volume of all FF during the 72 h of incubation compared with control (0 g ENZ/g DM). Among the FF species, gas production was higher ($P < 0.001$) in sorghum straw and lower ($P < 0.001$) in sugarcane leaves. There was no significant effect of ENZ on gas production parameters (i.e., b; asymptotic gas production, c; rate of gas production and L; discrete lag time before gas production) of all FF. Addition of ENZ doses increased ($P < 0.05$) gradually gas production and this increase was higher ($P < 0.05$) for 0.24 g ENZ/g DM. addition of ENZ was increased ($P < 0.05$) some fermentation parameters (i.e., IVOMD, ME, GY24 and SCFA) were higher ($P < 0.05$) of all FF, while the highest ($P < 0.05$) increased were in sorghum straw with a lower values in sugarcane leaves. Results indicated that exogenous enzymes preparation probably improve the ruminal fermentation activities of fibrous feeds in cows. The authors wish to acknowledge the financial support from IAEA/FAO project MEX 16307.

Key Words: exogenous enzymes, fibrous feeds, gas production

W377 Nutrient intake and ruminal parameters in response to *Bacillus subtilis* included on beef steer diet.

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The objective of this experiment was to evaluate the inclusion of *Bacillus subtilis* on the diet of 4 Nellore steers, with rumen cannulas and allocated on a Latin square design, with inclusion of Biotop (a probiotic product containing 10^9 colony-forming unit (cfu) *Bacillus subtilis*/g, as main plots and sampling time as subplots. The period last 20 d each and it was evaluate the dry matter (DM), organic matter (OM), crude protein (CP), ether extract (EE), neutral detergent fiber (NDF), non fiber carbohydrates (NFC) total carbohydrates (TC) and total digestible nutrients (TDN) intakes and, was measured the ruminal pH and N-ammonia. Treatments were defined as control (no addition of) and 3 doses (1, 2 and 4g.day^{-1}). The sampling times for pH and ammonia were at the time (0), at 3, 6, 9, 12 and 24 h after the morning the diet. The forage utilized was corn silage, in a 40:60 forage and concentrate ratio. The DM, OM, CP, EE, NDF and TC intakes were not different (Table 1). However, TDN intake increased with the addition of the probiotic. The pH and the N-ammonia were not affected by treatment, but a quadratic equation was adjusted as a function of sampling time, with a minimum point at 6.2 and 6.2 h after feeding for pH and N-ammonia with values of 5.88 and 24.17mg. dL^{-1}, respectively. It can be concluded that the addition of Biotop on beef cattle diet on the doses between 1 and 4g.day^{-1} do not affect ruminal pH and N-ammonia but can improve the TDN intake.

Table 1. Nutrient intake (%BW) of animals fed with Bacillus subtilis (Bs) in the diet

		Bs			
Item	C	1g	2g	4g	CV (%)
DM	1.91	1.99	1.99	1.86	8.76
OM	1.80	1.87	1.88	1.79	9.47
CP	0.24	0.25	0.25	0.23	8.88
EE	0.05	0.05	0.05	0.05	6.95
NDF	0.54	0.56	0.56	0.54	9.54
NFC	0.98	1.02	1.01	0.96	8.95
TC	1.52	1.57	1.58	1.50	9.25
TDN	1.36^{b}	1.41^{a}	1.42^{a}	1.40^{a}	7.32

[a,b]Means followed by different letter in row differ at 5% probability by Tukey test.

Key Words: ammonia, pH, probiotic

W378 Effect of exogenous fibrolytic enzymes on *in vitro* rumen fermentation of corn silage.

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The aim of this study was to investigate the effect of exogenous fibrolytic enzymes (EFE) as potential additives to improve the utilization of corn silage. A total of 11 commercial EFE, including 5 cellulase and 6 xylanase products, were used. Endoglucanase and xylanase were considered as key enzymatic activities for cellulase and xylanase products, respectively. One unit of enzyme activity was expressed as the amount of enzymes needed to release 1 μmol xylose or glucose per min per gram of enzyme products at 39°C and pH 6.6. Corn silage as substrate was added without (control) or with cellulase (30 units/g DM), xylanse (40 units/g DM). Rumen content was collected from 3 donor animals before feeding in the morning. Gas pressure measurements were recorded at 3, 6, 9, 12, 24 and 48 h of incubation and then converted to gas volume. At the end of the incubation, the fluid was sampled to determine the pH and volatile fatty acids (VFA). The contents in the bottle were completely rinsed out to determine the degradation of DM and neutral detergent fiber. Methane production was determined at 6, 12 and 24 h of incubation. Addition of cellulase resulted in a decreased potential gas production ($P < 0.05$) but increased rate of gas production ($P < 0.05$) with the highest rate being 83.7% compared with the control. Total VFA concentrations were increased ($P < 0.05$) for some EFEs, but degradation of DM and neutral detergent fiber was enhanced ($P < 0.05$) for all enzyme additives with highest value at 65.4%. The enzymes showed various effects on methane production. From the results of this study, it is indicated that addition of EFEs has potential to inhibit methane production while increasing fiber digestibility of corn silage.

Key Words: corn silage, exogenous fibrolytic enzymes, rumen fermentation

Small Ruminant: Reproduction, Parasites, and Environment

W379 Effects of meat goat breed, sex, and conditions before and between measures on behavior in pens with barb wire and electric fence strands. Y. Tsukahara,* T. A. Gipson, G. D. Detweiler, T. Sahlu, and A. L. Goetsch, *Langston University, Langston, OK.*

Growing meat goats of 4 types (Boer (B) wethers and doelings, 25 ± 1.0 and 22 ± 0.7 kg BW; Spanish (S) wethers and doelings, 17 ± 0.3 and 16 ± 0.2 kg BW, respectively) were used to evaluate conditions for a method to test efficacy of electric fence strand addition to barb wire fence for cattle to contain goats. Animals were allocated to 8 sets of 20, consisting of 5 groups/set and 1 animal type/group. There were 5 2.4 × 3.7 m test pens consisting of 3 sides of metal panels and 1, adjacent to a pasture with abundant vegetation, of barb wire strands at 30, 56, 81, 107, and 132 cm from the ground. Fence treatments were electric strands at 15 and 43 (LH), 15 and 23 (LM), 15 (L), 23 (M), and 43 cm (H) at 6 kV. Adaptation procedures entailed 4 sequential weekly exposures to test pens: no electric strands, 1 strand at 0 kV, LH, and LH. Two preliminary treatments were imposed the week before the first observation period in wk 1: barb wire with no electric strands vs. LH. All sets were observed for 1 h in wk 1, and 4 sets were exposed to the same fence treatment in wk 6. During the 5 wk between observations, sets were exposed to 2 washout treatments while on pasture: without or with electric strands at ≥6 kV situated next to concentrate feeders. There were no effects of gender, preliminary, or washout treatments ($P > 0.05$). The % of animals exiting test pens differed ($P < 0.05$) among fence treatments in wk 1 (25, 47, 38, 66, and 84%; SE = 7.7) and in wk 1 and 6 (6, 22, 22, 63, and 81% for LH, LM, L, H, and M, respectively; SE = 4.9) and between breeds in wk 1 (34 and 70%) and in wk 1 and 6 (28 and 50% for B and S, respectively). The % receiving a shock was similar among fence treatments in wk 1 and in wk 1 and 6, although for the latter analysis the value was greater ($P < 0.05$) in wk 1 vs. 6 (11 vs. 1%). In conclusion, dissimilar behavior of B and S is a consideration for the testing method being developed and adaptation procedures employed appeared generally conducive to use of an experiment with one observation period, whereas repeated observations would necessitate evaluation of other washout treatments.

Key Words: goat, fence, containment

W380 GIS grid analysis of utilization of adjacent pastures by two herds of goats. T. A. Gipson*[1], S. P. Hart[1], and R. Heinemann[2], [1]*Langston University, Langston, OK,* [2]*Kiamichi Forestry Research Station, Oklahoma State University, Idabel.*

Many goat producers divide their herd into 2 or more groups for grazing in adjacent pastures with or without other livestock species. The objective of this study was to observe the spatial patterns of 2 adjacent herds of goats pastured with and without cattle. A 15.8-ha pasture was stocked with 36 Spanish goats and 12 Angus cows (GC), and a 14.1-ha pasture was stocked with 36 Spanish goats without cattle (GO). Neither group of goats had been exposed to cattle before. The pastures consisted of fescue, bermudagrass, various *Panicum* such as switchgrass, bahiagrass, and broomsedge bluestem, but areas were reverting to woody plant species such as sapling-sized trees of pecan, elm, and honey locust. Eleven goats in GC and 10 goats in GO were fitted with GPS collars that recorded a fix every 5 min in the first 2 wk. A GIS point-in-polygon analysis using a 10 × 10 m grid was conducted for each pasture. The GO had greater ($\chi2 = 858$, $P < 0.01$) explored space (65% of 1473 grids) compared with GC (13% of 1584 grids). Of the grids explored, GO had a higher percentage with a density of 100 or more fixes than did GC (55 vs. 33%; $\chi2 = 11$, $P = 0.01$), indicating a wider area of methodical exploration or habituation. Only 21% of fixes were within 100 m of the water point. Goats in GO preferred pasture locations closer ($\chi2 = 15106$, $P < 0.01$) to the water point than did GC (200 vs. 300 m); however, GC came to the water point earlier ($P < 0.01$) than did GO (0730 vs. 1000 h). The favored location in the morning for each pasture was near the water point in the eastern intersection of the pastures. During the remainder of the day GC favored the southwestern-most corner of their pasture near a central fence line. In the afternoon, GO preferred the location near GC but also had a favorite location shaded by trees in the center of the pasture. The spatial behavior of the groups of goats appeared to be influenced by each other, and presence of cattle may have inhibited GC from fully exploring their pasture.

Key Words: goats, GPS, grid analysis

W381 Ruminal methane emission by Boer and Spanish does supplemented with garlic. R. Puchala,* Z. Wang, A. L. Goetsch, and T. Sahlu, *Langston University, Langston, OK.*

Twenty Boer (B; 2–7 yr of age and 48.5 ± 2.2 kg) and 20 Spanish (S; 4–6 yr of age and 39.3 ± 1.5 kg) does were used to examine effects of garlic on ruminal methane emission and heat production. Ten does of each breed were randomly allocated to control (C) and garlic (G) treatments. All does received 200 g/d (as-fed basis) of a concentrate mixture consisting of 54.4% ground corn, 26.0% soybean meal, 12.9% molasses, and 6.7% mineral and vitamin sources. The G does also received 20 g/d (as-fed basis) of garlic powder. For at least 2 mo does grazed grass/forb pastures in the summer. Thereafter, sets of 4 does consisting of 1 doe per treatment (CB, CS, GB, and GS) were sequentially placed in metabolism crates for 2 wk, continued to receive supplements, and were fed coarsely ground alfalfa hay free-choice. Gas exchange was measured on the last day for 24 h in an indirect, open circuit respiration calorimetry system with 4 metabolism cages fitted with head-boxes. There were no interactions between breed and supplement treatment ($P > 0.10$). Alfalfa hay DMI during the calorimetry measurement period was greater ($P < 0.05$) for G vs. C (781, 742, 934, and 853 g/d for CB, CS, GB, and GS, respectively; SEM = 29). Ruminal methane emission was less ($P < 0.05$) for G than for C in g/d (12.0, 10.8, 8.5, and 6.4, respectively; SEM = 0.56) and relative to intake of DM (15.2, 14.6, 9.1, and 7.6 g/kg; SEM = 0.44) and GE (4.31, 4.12, 2.58, and 2.14% for CB, CS, GB, and GS, respectively; SEM = 0.124). Treatment did not affect ($P > 0.10$) respiratory quotient (1.012, 1.004, 1.003, and 0.994), heart rate (73, 72, 72, and 70; SEM = 1.6), heat production (450, 444, 447, and 432 kJ/kg $BW^{0.75}$; SEM = 10.7), or the ratio of heat production:heart rate (6.18, 6.19, 6.18, and 6.21 kJ/kg $BW^{0.75}$ per heart beat for CB, CS, GB, and GS, respectively; SEM = 0.056). In conclusion, supplementation with garlic decreased ruminal methane emission and increased DMI by Boer and Spanish does consuming alfalfa hay.

Key Words: goats, garlic, methane

W382 Effects of Roscovitine on maturation and fertilization of ovine oocyte in vitro. S. Nasrollahi,* A. Z. Shahneh, S. Zeinoaldini, H. Kohram, and M. Poorhamdollah, *University of Tehran, Karaj, Tehran, Iran.*

The purpose of this study was to determine the effect of Roscovitine on maturation and fertilization of Ovine oocyte. Roscovitine was added in doses of 0, 6.25, 12.5, 25, 50 and 100µM with control group to maturation culture. Ovaries were collected from abattoir in normal saline at approximately 30°C and transported to the laboratory within 2 to 3 h from collection. After washing with fresh normal saline, cumulus-oocyte complexes (COCs) were recovered by aspiration. Cumulus-oocyte complexes were collected under a stereomicroscope and washed in the passed-through washed aspiration containing HEPES-TCM-199 culture supplemented with 2% fetal Bovine serum, 2/0 µM sodium pyruvate and 1% penicillin-streptomycin and then COCs were delivered into plates containing maturation medium and cultured for 24 h in 5% CO2 at 39°C and maximum humidity. In the first step, nuclear situation was assessed by removing of cumulus cell and oocyte staining. Then, oocytes were cultured without Roscovitine for 24h to determine the inhibitory effects of treatment and then again strained. Finally, oocytes were washed with fertilization medium and the fertilized with fresh semen. Data were analyzed by ANOVA and G mode procedure of SAS (version 9.1). Results showed those expansions level and mucosal rates were not influenced by different concentrations of Roscovitine ($P < 0.05$). Although, there was no difference in nuclear maturation between control treatment and 6.25 micro molar Roscovitine, other concentrations increased the nuclear maturation in oocyte ($P < 0.05$). All of treatment increased reaching to M-II phase than control treatment ($P < 0.05$). In conclusion, treatments 6.25, 12.5 and 25 were selected for in vitro fertilization. The results obtained of these treatments indicated that the oocyte affected by Roscovitine (25µM), could make the better fertilization ability than control group.

Key Words: Roscovitin, fertilization, sheep

W383 Anthelmintic efficacy of medicinal herbs in goats infected with nematode parasites. R. Z. Zhong[1,2], Z. Wang*[2], D. Zhou[1], A. L. Goetsch[2], S. P. Hart[2], and T. Sahlu[2], [1]*Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, Changchun, China,* [2]*Langston University, Langston, OK.*

Thirty high-percentage Boer does (2.9 ± 0.12 yr; 48 ± 1.9 kg BW) naturally infected with *Haemonchus contortus* from grazing pasture of Langston University were allocated to 5 groups and moved to a barn to investigate anthelmintic efficacy of 3 medicinal herbs, *Rheum palmatum* L. (rhubarb; R), *Meliae cortex* (melia bark; M), and *Quisqualis indica* L. (rangoon creeper; Q). Does were given ad libitum access to grass hay and water, along with 200 g/d per doe of a concentrate-based pelleted supplement. Treatments were control (C), R, M, Q, and a 1:1:1 mixture of the 3 herbs (RMQ). The herbs in powder form were mixed with water at 20 g/100 mL just before drenching. After being acclimated for 7 d, does were drenched with 100 mL of water alone or with the respective herbs at 20 g/d for 10 d. Fecal samples were collected on d 0, 3, 6, 9, 13, and 16 after the start of drenching for worm egg count (FEC). Blood samples were taken on d 0 and 13 for measuring packed cell volume (PCV). Initial FEC was 2,208, 3,933, 3,025, 2,350, and 3,033/g for C, R, M, Q, and RMQ, respectively (SEM = 425.2; $P > 0.05$). After 10 d of treatment, none of the herbs showed anthelmintic effects. The FEC on d 16 was 1,350, 3,058, 1,525, 825, and 2,067/g for C, R, M, Q, and RMQ, respectively (SEM = 332.9, $P > 0.05$). Change in PCV was 1.8, 20.1, 9.1, 10.7, and 13.3% for C, R, M, Q, and RMQ, respectively (SEM = 1.68). Compared with C, the PCV value increased in does treated with R and RMQ ($P < 0.05$); however, the increases may have been due to scouring in response to treatment with R. In conclusion, these herbs were not effective anthelmintics for the most problematic internal parasite of goats, *H. contortus*, in much of the US.

Key Words: goats, anthelmintic herb, *Haemonchus*

W384 The effects of confinement and protein levels on the growth and parasitic loads of kids raised under mixed-species grazing system. S. Gebrelul, L. Gray,* R. Marshall, and Y. Ghebreiyessus, *Southern University Ag Center.*

A long-term mixed-species grazing project was designed to determine the performance of goats and cattle grazing together or separately in continuous or rotational systems. To evaluate the potential of producing kids of desirable market weight of 20 kg or more, 50 kids that were born and weaned under the mixed-specie system were randomly assigned to 4 treatments in a 2 × 2 factorial arrangement. The treatments were housing (confinement vs. semi-confinement) and protein levels in the diet. Kids under confinement system were divided into 2 groups and fed ad lib rations which contained 13% or 16% CP. Kids under semi-confinement were allowed to graze on Bermuda grass pastures during the day (for 8h) and supplemented with the same experimental rations during the night. After an adjustment period of 2 weeks, initial measurements of BW, BCS, (1 = thin, 5 = fat) and FAMACHA scores (FS, 1 = red, healthy, 5 = white, anemic) were taken. These measurements were taken every 14 d for 8 wk. Data were analyzed using SAS MIXED procedure where kids were considered random effects. Kids under confinement were 1.7 kg heavier ($P < 0.05$) than kids under semi-confinement housing. Male kids were 3.0 kg heavier ($P < 0.05$) than female kids. No differences in BCS or FS were observed due to housing effect. Level of CP in the diet had no effect ($P > 0.05$) on BW, BCS or FS. Kids from pastures that were comingled with cattle had higher BW (19.1 ± 0.4 vs. 17.9 ± 0.4 kg) and BCS (2.6 ± 0.05 vs. 2.4 ± 0.05), and lower FS (1.8 ± 0.1 vs. 2.4 ± 0.1) than kids that originated from goats-alone pastures. Kids that were confined and fed 16% CP were heavier ($P < 0.05$) than any other group. BW was positively correlated (0.48) to BCS but negatively correlated (−0.34) to FS. BCS and FS were negatively (−0.28) correlated. Results showed that kids raised under mixed-species system can be confined and fed for 8 wk to achieve desirable market weights.

Key Words: mixed-grazing, FAMACHA, confinement

W385 The anthelmintic effect of Juniper and Tifton 85 on the infective larval stage of *Haemonchus contortus* in an in vitro system. S. A. Armstrong*[1], B. D. Lambert[1,2], T. R. Whitney[3], J. P. Muir[2], and A. McEwin[1], [1]*Tarleton State University, Stephenville, TX,* [2]*Texas Agrilife Research, Stephenville,* [3]*Texas Agrilife Research, San Angelo.*

This experiment tested the effect of inclusion of buffered rumen fluid with and without Tifton 85 bermudagrass (T85) or Juniper in an in vitro larval migration assay (LMI) for *Haemonchus contortus* (HC). Inclusion of a forage material in control samples is time consuming, risks introducing unknown compounds that could reduce larvae viability in the control treatment, and limits the number of test compounds that can be studied in a single assay. Rumen fluid from a mature ruminally-cannulated goat was mixed with McDougall's buffer in a 1:4 ratio. Aliquots of buffered rumen fluid were placed in an anaerobic incubator along with one of 3 forage treatments. Treatments included control (no forage material), control plus T85 or control plus dried juniper. Treatment solutions were incubated for 18 h to extract any potential bioactive anthelmintic compounds. Ivermectin (40 µg/ml) was included as a positive control treatment. Following the 18-h incubation, solutions were centrifuged. Five milliliters of supernatant was added to individual 100-mL plastic cups containing approximately 1000 ensheathed HC larvae. All treatment cups (buffered rumen fluid, buffered rumen fluid + Tifton 85, buffered rumen fluid + Juniper and buffered rumen fluid + ivermectin) were anaerobically incubated for 4 h. Following incubation, larvae were transferred onto a screen in a 96-well plate which contained the same treatment rumen fluid mixture (9 replicate wells per treatment). Larvae were incubated overnight; those which passed through a screen were considered to be viable. Percent larval migration inhibition was calculated as: % LMI = [(A − B)/A] × 100 where A is the number of viable larvae in the control wells, B is the number of viable larvae in the test wells. Juniper and ivermectin treatment resulted in similar LMI, which was greater ($P < 0.05$) than control or control plus T85. We conclude that inclusion of dried juniper was as effective at inhibiting larval migration as ivermectin at 40 µg/mL and future LMI assays need not include forage in the control treatment.

Key Words: *Haemonchus contortus*, anthelmintic, in vitro

W386 Panicled tickclover, a native herbaceous legume, suppresses internal parasites without negative effects on kid performance.

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This trial looked at the effects of 2 condensed tannin (CT) containing legumes, *Lespedeza cuneata* (sericea lespedeza; SL), *Desmodium paniculatum* (panicled tick-clover; PTC), and a non-CT containing legume, *Medicago sativa* (alfalfa) on growth and fecal egg counts (FEC) in goat kids. The 3 legumes were each 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 BW in a 4 wk feeding trial with 36 Boer × Spanish doe kids with an average BW of 19.1 kg. Goats were weighed every 14 d, refusals were collected throughout the study and weighed on d 14 and 28, blood samples were collected on d 25 and 28, and rumen fluid was collected at slaughter. Fecal eggs counts were done every 7 d. Compared with alfalfa, SL decreased feed efficiency and ADG, and had no effect on dressing percentage, BUN, and ruminal NH3-N. In contrast, PTC had the same feed efficiency, ADG, dressing percentage, BUN, and ruminal NH3-N as alfalfa. Sericea lespedez and PTC increased feed intake overall ($P < 0.05$) by 5.1 and 4.3 kg, respectively, compared with alfalfa, and kids consuming pellets with SL and PTC also showed 44% reduced FEC ($P < 0.05$) compared with alfalfa. If PTC, native in North America from Texas to Georgia and north to Canada, can be cultivated as easily as SL and alfalfa, it may be an alternative for small ruminant systems looking for natural means of reducing internal parasites or as a protein source in regions such as central Texas where alfalfa and SL are not easily cultivated.

Key Words: goat, internal parasites, legume

W387 Relative resistance to gastrointestinal nematode parasitic infection in sheep and goats.

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Co-grazing of parasite resistant and susceptible animals may aid in on-farm control of parasite load and offer a system for reducing production losses in goats. An experiment was conducted to evaluate the effect of nematode infection in goats co-grazed with St Croix sheep reported to be parasite resistant under fall and summer grazing conditions. St. Croix sheep (10), Boer goats (10), and Spanish Boer cross goats (10) were co-grazed on the same pasture. A second group of Boer (5) and Spanish Boer cross (5) goats were grazed on a separate pasture. The duration of both fall and summer trials was 56 d. Fecal and blood samples were collected on d 0, 28 and 56. Fecal egg counts, packed cell volumes, FAMACHA scores, BW and white blood cell differentials were used to assess relative resistance to parasite infection using SAS PROC GLM and PROC TTEST. Goats had higher levels of infection than sheep. The parasite resistant St Croix sheep had higher percentages of eosinophils in peripheral blood when compared with co-grazed goats or goats on a separate pasture ($P < 0.05$). During the fall co-grazed sheep and goats had lower percentages of neutrophils in peripheral blood than goats grazing on a separate pasture ($P < 0.05$). Parasite resistance in sheep was associated with low fecal egg counts and increased eosinophil levels. In goats parasite burden and the neutrophil mediated inflammatory response may be influenced by management practices such as co-grazing.

Key Words: parasitic infection, parasite resistance, goats

W388 Effects of supplementing fat sources in pre-mating ewe diets on reproductive performance.

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A major challenge in management of most sheep breeds especially low prolific sheep is low lambing rate. Ewe feeding in pre-mating with glucogenic ingredient such as cereal grain has used as a strategy in several past years. Fat supplements have caloric and noncaloric effects that can change energy status of ewes. An experiment was conducted to determine noncaloric effect of some fat supplements in pre-mating ewe diets on reproductive efficiency of Afshari ewes. Afshari sheep are major fat-tail sheep breed in northwest of Iran. Thirty 2 estrus-synchronized Afshari ewes (62 ± 7kg) were assigned randomly to 4 diets containing a basal diet (alfalfa, barley, soybean meal, and a blend of mineral and vitamin) and different fat supplements, 3% of dry matter. Fat supplement were consisting 1) sunflower oil (SFO), 2) fish oil (FO), 3) rumen protected calcium salt of palm oil (RPO), and 4) an equal blend of SFO+FO. For adapting ewes to concentrate (35% of total diet), they were individually fed with basal diet for 7 d and then they were fed with basal diet and fat supplements for 14 d until the day of mating (d 14). Estrus-synchronizing was conducted using intravaginal progesterone releasing device (CIDR) for 12 d and a single dose injection of 400IU PMSG immediately after CIDR withdrawal. Ewes were exposed to rams 24–36 h after PMSG injection. Body weight, BCS, back fat thickness, blood sampling, and ultrasonography were conducted in initial (0), CIDR withdrawal (12), estrus days (13) and 30 d after mating. Data were analyzed using the PROC MIXED of SAS software. Three covariance structures were tested and the best was fitted. The results showed that ewes fed with fat sources had no differences in daily DMI, BW, and BCS and also glucose, cholesterol, and albumin as well in aforementioned days. The ewes fed FO compared with SFO, RPO, and SFO+FO diets had lower ($P < 0.05$) insulin concentration, 19.5 vs 19.5, 22.6, and 21.2 IU/mL respectively, on d12 and 20.4 vs 20.4, 23.2, and 21.8 IU/mL respectively, on d13, and greater ($P < 0.01$) estradiol concentration, 69.2 vs 57.5, 54.2, and 53.5 pmol/mL respectively. There was no difference in progesterone concentration among diets. The ewes fed FO diet had greater ($P < 0.05$) large follicle (>5 mm diameter) number, 1.5 and 2.25, in d 12 and 13, respectively compared with SFO, RPO, and SFO+FO (d12: 1.15, 1.13, and 0.7; d13: 1.5, 1.63, and 1.00, respectively). Also, ewes fed with FO diet had larger follicle size ($P < 0.05$) than ewes fed to other diets (5.7 vs 5.5 5.23, and 3.9 mm) in d13. Number of lambs born per ewe exposed ranked FO > SFO > RPO > SFO+FO (175, 150, 138, and 114%). It was concluded that short-term supplementing fish oil in pre-mating diets can have a beneficial effect on reproductive performance of Afshari ewes.

Key Words: fish oil, sunflower oil, pre-mating ewes

W389 Effect of equine chorionic gonadotropin dosage and administration moment on reproductive performance in Pelibuey ewes. A. González-Reyna[1], J. Hernández-Meléndez[1], F. A. Lucero-Magaña[1], J. Cedillo-Monroy[2], and J. F. Vázquez-Armijo*[2], [1]*Universidad Autónoma de Tamaulipas, Facultad de Ingeniería y Ciencias, Cd. Victoria, Tamaulipas, Mexico,* [2]*Centro Universitario UAEM Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, México, Mexico.*

This study was conducted to evaluate the effects of 4 doses of eCG and 3 application times on the estrus percentage (EP), time to estrus (TE), ovulation rate (OR), and prolificacy (PR) in hair sheep ewes, under a synchronization of estrus program. Ninety 7 Pelibuey adult ewes were treated with vaginal sponges impregnated with 40 mg of fluorogestone acetate during 12 d, at −48, −24, and 0 h before the sponge withdrawal. The ewes were assigned to the following treatments: 1 = 0; 2 = 100; 3 = 200 and 4 = 400 IU of eCG; and ewes showing estrus were mated by natural service. The statistical analysis was carried out using GLM procedure of SAS, and chi-squared tests. There was no effect of eCG dose on EP; however, the application time affected ($P < 0.01$) the EP. The application time ($P < 0.0006$) and the eCG dose ($P < 0.0001$) had important effects on TE. The dose of eCG affected ($P < 0.003$) the OR, and the OR for the dose of 400 IU of eCG was greater ($P < 0.05$) than the OR for the 0, 100 or 200 IU of eCG doses. These values were of 3.5 ± 2.5, and 2.05 ± 0.9, 1.86 ± 0.7 and 2.26 ± 1.3, respectively. The application time did not have effect on the lambing rate, but the eCG dose did ($P < 0.05$), showing superior values of 83 and 75%, respectively for the 100 and 400 eCG doses, versus 48 and 63% for the 0 and 200 eCG doses. PR was affected ($P < 0.05$) by the eCG dose, being greater for the 400 eCG dose (2.28). Based on the results of this present study, the use of eCG did not affect EP; however, it reduced the interval TE and increased the OR and PR.

Key Words: gonadotropins, reproductive behavior, hair sheep

W390 Blood metabolites and insulin concentrations during pregnancy in ewes carrying one to five fetuses and supplemented with propylene glycol. H. Honig,* A. Rozov, E. Gootwine, L. Lifshits, and U. Moallem, *Volcani Center, Bet Dagan, Israel.*

Our previous studies demonstrated the susceptibility of prolific ewes to metabolic disorders during late pregnancy. In this study we examined blood metabolites and insulin concentrations in 60 Afec Assaf ewes carrying 1 to 5 fetuses from 60 d of pregnancy (DOP), and investigated the effect of supplementation from 110 DOP of propylene glycol (PGLY) to ewes carrying ≥ 3 fetuses. Ewes were examined for number of fetuses by ultrasonography at 35 DOP. At 110 DOP ewes carrying ≥ 3 fetuses were divided into 2 groups: (i) control — ewes were fed daily with an average of 0.70 kg of grain mix, 0.35 kg of corn silage and 1.34 kg of oat hay (DM basis); and (ii) PGLY — ewes were fed similar diet which included 55 g/d ProGlyc-55 thatcontained 55% 1.2 propaniol. Blood samples were collected every 2 wk from 60 to 100 DOP and then weekly until lambing, and concentrations of glucose, β-hydroxybutyrate (BHBA), nonesterified fatty acids (NEFA) and insulin were determined. Glucose concentrations decreased gradually from 95 DOP. Insulin concentrations elevated between 70 and 100 DOP, which followed by a dramatic decline in ewes bearing 3-5 fetuses. The increase in NEFA concentrations started moderately between 80 to 95 DOP and then rose rapidly until a peak at lambing. Average concentrations of BHBA (12.2 and 11.3 mg/dL, $P > 0.10$), NEFA (866.4 and 888.1 μEq/L, $P > 0.10$) and insulin (7.3 and 5.9 μIU/ml, $P > 0.10$) during the last 40 DOP were not different between control and PGLY groups, whereas glucose concentrations were lower in PGLY than in the control ewes (50.0 and 58.5 mg/dL, respectively; $P < 0.02$). In conclusion, our results indicate that the metabolic stress in prolific ewes starts early during pregnancy, at 70 DOP, most likely due to the high metabolic demands of the placenta being in its maximal growth rate during this period. In addition, PGLY supplemented from 110 DOP was not effective in improving the metabolic status of ewes conceiving multiple fetuses.

Key Words: Afec Assaf, multiple fetuses, propylene glycol

W391 Withdrawn by author

W392 Bone morphogenetic protein 15 (BMP-15) in crossbred goat fertility. R. Hill, L. Canon, H. Ismail, R. Noble, and M. Worku,* *NC A&T State University, Greensboro.*

A study was conducted to identify bone morphogenetic protein 15 (BMP-15) in goat genomic DNA, to evaluate its role in fertility. Bone morphogenetic protein 15 is a growth factor and a member of the TGFβ superfamily that is recognized by the bone morphogenetic protein receptor. It is specifically expressed in oocytes and is important for ovulation and for increasing litter size. Blood was collected from does and their kids of 2 goat breeds, Boer (n = 3 does each) and Spanish x Boer (n = 3 does each), on FTA elute cards (Whatman Inc.). Genomic DNA was extracted from the FTA card according to the manufacturer's protocol. Specific primers for BMP-15 and the loading control GAPDH were used for PCR amplification. Amplified products were run on a 1% agarose gel with DNA markers. Gels were stained with ethidium bromide and visualized using a gel documentation system. All Boer goats and their offspring had the BMP-15 gene. The BMP-15 gene was also detected in does and twin offspring of Boer x Spanish goats. However, Boer × Spanish cross goats that did not have the BMP-15 gene had single offspring. These offspring also did not have the BMP-15 gene. This preliminary evidence indicates that BMP-15 might be a gene that influences prolificacy of crossbred goats, but further research is needed to reach a final conclusion.

Key Words: goat, bone morphogenetic protein 15, fertility

W393 Induction of sexual activity of male goats during the reproductive resting season. O. Angel-Garcia[1], J. M. Guillen-Muñoz[1], M. A. De Santiago-Miramontes[1], P. A. Robles-Trillo[1], R. Rodriguez-Martinez[1], C. A. Meza-Herrera[2], F. G. Véliz[1], and G. Arellano-Rodriguez*[1], [1]*Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México,* [2]*URUZA, Universidad Autónoma Chapingo, Gómez Palacio, Durango, Móxico.*

The aim of this study was to evaluate different protocols to induce the sexual behavior in male goats during the season of reproductive arrest in northern Mexico. Adult male goats (n = 24; dairy crossbred genotype) were divided into 4 experimental groups (n = 6, each) which were homogeneous regarding to BW, BCS, scrotal circumference and smell at the onset of the experimental period. Animals received alfalfa hay ad libitum and 200 g per animal per day of a commercial concentrate (14% CP). On May 15, one group of males (G-T4) was treated with 25mg of testosterone per male, every third day during 3 weeks. A second group (G-GnRH) was treated with 25 ug of GnRH per male every third day, during 3 weeks. A third group (G-females) of males was set in contact with 3 estrogenized females, separated by a fence that permitted visual contact between them. Each of these females received 0.3 mg of estradiol cypionate every third day. A fourth group (G-Control) of males was treated with a saline solution each every third day during 3 weeks. At the end of the experimental period (April 11) each male was submitted to a behavioral test. Each male was exposed to an estrogenized female for 15 min. The behavioral test considered the number of sniffing, vocalization, approaches, complete mounts, mounts with ejaculation as well as latency to first ejaculate. The odor of the males was measured at the end of the experimental period, considering a 0–4 scale; 0 = female odor, 4 = very active male odor. The sexual behavior data were compared with x^2. The smell intensity and latency to ejaculate were compared with ANOVA as well as paired-mean comparisons with a "t" of student test (SYSTAT 10, Evanston, IL, USA, 2000). Data regarding sexual behavior, smell and latency to the first ejaculate for all groups is shown on Table 1. The results for the present study allow us to conclude that GnRH and testosterone administration besides the exposure to estrogenized females to dairy crossbred male goats in northern Mexico during the sexual resting season can promote a clearly active sexual behavior.

Table 1. Number of registered behavior during the behavior test for the four groups exposed to an estrogenized female during 15 min

	Vocalization	Approaches	Complete mount	Mount & ejaculation	Ejaculate latency (s)	Odor (0-4 scale)
G-Control	7^{a}	53^{a}	5^{a}	3^{a}	436 ± 121^{c}	0.7 ± 0.1^{a}
G-GnRH	84^{b}	210^{b}	16^{b}	10^{b}	187 ± 89^{b}	1.4 ± 0.3^{b}
G-Female	60^{b}	168^{b}	3^{a}	2^{a}	507 ± 93^{c}	1.4 ± 0.1^{b}
G-T4	1^{a}	114^{b}	27^{b}	17^{b}	24 ± 8^{a}	1.3 ± 0.2^{b}

$^{a–c}$Different letters in columns mean significant statistical differences ($P < 0.05$).

Key Words: sexual behavior, goat, season

W394 Induction to sexual activity of goats from the Mexican semidesert during the seasonal anestrous throughout the "female-to-female effect."

J. M. Guillen-Muñoz[1], O. Angel-Garcia[1], M. A. De Santiago-Miramontes[1], G. Arellano-Rodriguez[1], C. A. Meza-Herrera[2], M. Mellado[3], F. G. Véliz[1], and R. Rodriguez-Martinez*[1], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]URUZA, Universidad Autónoma Chapingo, Gómez Palacio, Durango, México, [3]Universidad Autónoma Agraria Antonio Narro, Saltillo, Coahuila, México.*

The aim of this study was to determine if administration of PMSG during the seasonal anestrous stimulates sexual activity of goats exposed to the "female-to-female effect" (FTF) in northern Mexico (26° N). The FTF effect considers that direct contact of estrus females with anovulatory females, stimulates reproductive function. Crossbred adult goats (n = 138) under grazing conditions were divided into 4 experimental groups and received alfalfa and water ad libitum. On May 13, all anestrous goats received a single i.m. injection of 25 mg progesterone in 1 mL vegetable oil, to reduce the occurrence of short luteal cycles. On May 14 (d 0), a group of females (PMSG-G; n = 30) was treated with 240 IU of PMSG and 50 ug of cloprostenol i.m. per animal, a second group of females (FTF-G; n = 39) was untreated but interacted with the first treated group. The third and fourth groups were set 300 m apart from the previous groups; while the third group (CS, n = 30) received 0.5 mL of saline i.m. per animal, the fourth group (control, CG; n = 39) remained untreated. At this time 3 males were introduced in every group of females. Female estrus activity was registered twice per day (0800 and 1800 h) during 15 d. On day-45 after male introduction, the proportion of pregnant goats was determined by ultrasonographic scanning. The percentage of estrus females, diagnosed as pregnant and giving birth were compared with a x^2. The latency of the first estrus was compared with a Student t-test (SYSTAT 10, Evanston, IL). Reproductive outcomes considering estrus females, pregnant females, first heat latency and prolificacy in the 4 experimental groups is shown in Table 1. Results of this study clearly demonstrated that anovulatory females can be induced to sexual activity by the female-to-female effect.

Table 1. Percentage of females (no./no. in parentheses) that demonstrated estral activity, diagnosed as pregnant

	Estrus females (%)	Pregnancy rate (%)	Time to onset of estrus (h)	Litter size	Kidding rate (%)
PMSG-G	97 (29/30)^{a}	83 (25/30)^{a}	54.2 ± 1.3^{b}	1.9 ± 0.1^{a}	77 (23/30)
FTF-G	95 (37/39)^{a}	85 (33/39)^{a}	72.6 ± 2.8^{a}	1.7 ± 0.1^{a}	70 (27/39)
CS	0 (0/30)^{b}	0 (0/30)^{b}			
CG	0 (0/39)^{b}	0 (0/39)^{b}			

^{a,b}Different letters between columns indicate statistical differences at $P < 0.01$.

Key Words: sexual activity, female effect, goat

W395 Influence of different GnRH treatments in an 11-d CIDR timed AI synchronization program in Santa Inês ewes.

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The aim of this study was to determine the effect of GnRH doses at different times on reproductive performance of Santa Inês ewes (n = 299) synchronized with 11-d CIDR timed AI (TAI) program. Ewes were blocked according to BW (45.8 ± 0.39) and BCS (2.22 ± 0.03, scale 1 - 5). The treatments were: 25μg/12h (n = 52) and 10μg/12h (n = 51) which means that ewes received 25 μg or 10 μg of GnRH 12h before TAI; 25μg/TAI (n = 47) and 10μg/TAI (n = 51) which means that ewes received 25 μg or 10 μg of GnRH at time of TAI; no-GnRH (n = 46); and NM (n = 52) bred by natural mating. The CIDR was inserted on day −11 and it was removed 11d later (d 0). All ewes received 5 mg PGF (Lutalyse) and 300 IU eCG (Novormon) on d 0. Estrus detection was performed for 55 h after CIDR withdrawal. Ewes were exposed to rams 10 d after CIDR removal for rebreeding for 7 d. Pregnancy diagnoses by ultrasonography were performed 30 and 50 d after TAI. Data were analyzed using GLIMMIX procedures of SAS. Estrus detection was greater ($P < 0.05$) for 10μg/12h (96.1%) treatment compared with 25μg/TAI (74.5%), 10μg/TAI (60.8%), no-GnRH (73.9) and NM (55.8%), where the 25μg/12h (86.5%) did not differ from any of the treatments. The time of onset of estrus did not differ among treatments (29.9 ± 0.56 h). TAI pregnancy rate was greater ($P < 0.05$) in 10μg/12h (60.8%) and 25μg/TAI (63.8%) compared with 10μg/TAI (41.2%), no-GnRH (30.4%) and NM (42.3%), where the 25μg/12h (51.9%) did not differ from any of the treatments. Natural mating rebreeding pregnancy rate was greater ($P < 0.05$) in no-GnRH (47.8%) when compared with 25μg/12h (28.8%), 10μg/12h (17.6%), 25μg/TAI (19.1%) and NM (28.8%). Final pregnancy rates did not differ among treatments. In conclusion, 10 μg of GnRH 12 h before TAI was effective in promoting estrus response and had a similar AI pregnancy rate as when 25 µg of GnRH was given at TAI. However, the convenience of a single injection of GnRH at TAI makes this approach more desirable in sheep operations.

Key Words: ewes, timed AI, laparoscopy

W396 Effect of AI method on pregnancy rate following an 11d-CIDR estrus synchronization program in Santa Ines ewes. M. V. Biehl*[3], A. V. Pires[2,3], I. Susin[2], R. S. Gentil[2], E. M. Ferreira[2], M. V. C. Ferraz Junior[3], D. D. Nepomuceno[2], F. M. Abreu[1], L. H. Cruppe[1], and M. L. Day[1], [1]*The Ohio State University, Columbus,* [2]*University of Sao Paulo, Piracicaba, SP, Brazil,* [3]*University of Sao Paulo, Pirassununga, SP, Brazil.*

The objective of this study was to compare reproductive performance of nonlactating Santa Ines ewes (n = 267) synchronized using an 11-d CIDR program and a laparoscopic AI followed by different insemination methods following estrus detection. Ewes were blocked by BW (53.4 ± 0.42) and BCS (3.08 ± 0.04; scale 1 – 5). The treatments were: 1) timed AI (n = 65), when half of the ewes were detected in estrus, and AI was performed on the whole group; 2) AM/PM rule (n = 66), AI 12 h after estrus detection; 3) timed AI-48h (n = 67) AI 48 h after CIDR withdrawal; or 4) control (n = 69), ram exposure for 60 h after CIDR withdrawal. After insertion, CIDRs remained in place for 11 d. Upon CIDR removal, all ewes received 5 mg PGF (Lutalyse®) and 300 IU eCG (Folligon®), and estrus detection was performed for 60 h thereafter. Fresh semen from 5 proven rams was used for AI. Ten days after the initial AI, ewes were exposed to rams for rebreeding for 7 d. Pregnancy diagnosis by ultrasonography was performed 30 and 50 d after AI. Data were analyzed using GLIMMIX and MIXED procedures of SAS. Estrus detection within 60 h was 82.8% across treatments and was greater ($P < 0.05$) for timed AI, AM/PM rule, and control (86.2, 87.9 and 85.5%, respectively) than timed AI-48h (71.6%). The moment of AI was greater ($P < 0.05$) for the timed AI (47.1 h), AM/PM rule (46.3 h), timed AI-48h (48.8 h) compared with the control (34.4 h). Pregnancy rate of the synchronized estrus did not differ among treatments (timed AI, 41.5%; AM/PM rule, 53.0%; timed AI-48h, 41.8% and control, 59.4%). Rebreeding pregnancy rate was greater ($P < 0.05$) for the timed AI (32.3%) compared with the AM/PM rule (15.2%) or control (13.0%), however, the timed AI-48h (25.4%) group did not differ from any of the treatments. Final pregnancy rate was 70.4% and did not differ among treatments. In conclusion, timed AI was comparable to AM/PM breeding and natural mating in Santa Ines ewes.

Key Words: ewes, timed AI, laparoscopy

Swine Species III

W397 Industry productivity analysis—Sow farm traits. C. E. Hostetler*[1] and M. T. Knauer[2], [1]*National Pork Board, Des Moines, IA,* [2]*North Carolina State University, Raleigh.*

The objective of this study was to quantify US swine production benchmarks and trends for sow farm traits from a representative database. Data were provided by a data management company representing 1.8 million sows in North America. Production records were available from 2005 to 2010. Traits included piglets per mated female per year (PMFY), litters per mated female per year (LMFY), total number born (TNB), number born alive (NBA), number weaned (NW), preweaning mortality (PM), weaning age, weaning weight (WWT), replacement rate (RR), culling rate (CR), sow mortality, lactation feed intake (LFI) and gestation feed intake (GFI). Data were analyzed in SAS using PROC MIXED. Models included year and month as fixed effects. Standard errors for PMFY, LMFY, TNB, NBA, NW, PM, weaning age, WWT, RR, CR, sow mortality, LFI and GFI were 0.12, 0.010, 0.029, 0.033, 0.035, 0.27, 0.08, 0.015, 1.42, 1.17, 0.15, 0.050 and 0.016, respectively. Means for sow reproductive efficiency and sow removal traits are shown by year in Table 1. Piglets per mated female per year, LMFY and NW increased ($P < 0.05$) from 2005 to 2010 (21.5 to 23.4, 2.31 to 2.34 and 9.30 to 10.08, respectively). Replacement rate did not differ ($P > 0.05$) between 2005 and 2010 (54.1 and 52.2%, respectively) and sow mortality decreased ($P < 0.05$) from 11.2 to 10.4%. Total number born and NBA increased ($P < 0.05$) from 11.82 to 13.03 and from 10.77 to 11.83, respectively. Weaning age and WWT increased ($P < 0.05$) from 18.9 to 20.6 d and 5.46 to 5.86 kg, respectively. Lactation feed intake increased ($P < 0.05$) from 6.11 to 6.62 kg per d and GFI decreased ($P < 0.05$) from 2.33 to 2.27 kg per d. Producers and scientists can use these sow farm benchmarks to better understand industry trends.

Table 1. Sow reproductive efficiency and removal means from 2005 to 2010

	Year					
Trait	2005	2006	2007	2008	2009	2010
Reproductive Efficiency						
PMFY	21.5^{a}	21.9^{b}	22.4^{c}	22.9^{d}	23.4^{e}	23.6^{e}
LMFY	2.31^{a}	2.34^{b}	2.34^{b}	2.35^{b}	2.34^{b}	2.34^{b}
NW	9.30^{a}	9.39^{b}	9.55^{c}	9.72^{d}	9.98^{e}	10.08^{f}
PM, %	13.7^{a}	14.1^{a}	14.0^{a}	14.2^{a}	14.0^{a}	14.8^{b}
Sow Removal						
Replacement rate, %	54.1^{ab}	57.8^{c}	56.0^{bc}	56.1^{bc}	51.4^{a}	52.2^{a}
Culling rate, %	41.9^{a}	44.2^{b}	43.4^{ab}	48.2^{c}	48.7^{c}	47.5^{c}
Sow mortality, %	11.2^{d}	10.7^{c}	10.4^{bc}	10.3^{b}	9.8^{a}	10.4^{bc}

$^{a–f}$Means within a row with different subscripts differ ($P < 0.05$).

Key Words: benchmark, reproduction, sow

W398 Welfare of Camborough sows in gestation crates or pens. W. Chaya*[1] and J. McGlone[2], [1]*Department of Animal and Food Sciences, Texas Tech University, Lubbock,* [2]*Pork Industry Institute, Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

A randomized complete block design experiment with 2 × 2 factorial rearrangement of treatments was conducted to study the effect of 2 housing systems, group pens and crates and 2 feeding systems, single drop and trickle feeding systems on lactating sow reproductive performance, litter performance, behavior, physiology and skin lesion scores. A total of 40, Camborough (Yorkshire x Landrace) gilts were allocated into groups of 5/pen or crates. Behaviors such as feeding, drinking, standing/walking, lying, sitting, agonistic behavior, and oral-nasal-facial (ONF) behavior were video recorded for 24 h at 50 to 60 d of gestation and transformed before analyses. Behavior data were collected hourly based on a 5 min interval between scan samples. Whole blood was collected via jugular puncture over heparin for determinations of plasma cortisol, white blood cell counts, % differential WBC count, neutrophils:mononuclear cell ratio, neutrophil phagocytosis, and neutrophil oxidative burst a week after behavioral observations. No significant differences were identified among housing and feeding systems for reproductive or physiological measures (except for plasma cortisol, neutrophil phagocytosis, and neutrophil oxidative burst that had not yet been assayed). Gilt ONF behavior was higher ($P < 0.05$) among crated gilts than penned gilts (LSmeans 12.7 ± 1.13 vs. 7.6 ± 1.19%). The interaction between penning and feeding system was significant for head lesion score (LSmeans for pen-drop, pen-trickle, crate-drop, crate-trickle were, respectively: 1.0 ± 0.07, 0.0 ± 0.06, 0.0 ± 0.06, and 0.13 ± 0.06; $P < 0.01$). Crated and group-penned sows had similar reproduction. With only minor differences in skin lesion score, each sow penning/feeding system supported similar sow welfare. However, the finding that Camborough gilts had more ONF behavior in crates (than pens) and more head skin lesion score in pens (than crates) differed from our previous work with Camborough-22 gilts in which these differences were not observed. Genotypes may respond differently to group housing than individual housing.

Key Words: pigs, welfare, housing

W399 Relationships of birth weight and weaning weight on performance traits in purebred pigs. R. L. Cutshaw*[1], A. Schinckel[1], J. Fix[2], M. Brubaker[3], and M. Einstein[1], [1]*Purdue University, West Lafayette, IN,* [2]*National Swine Registry, West Lafayette, IN,* [3]*Whiteshire Hamroc LLC, Albion, IN.*

The purpose of study was to evaluate the relationships of birth weight (BTW) and weaning weight (WW) with off test performance traits: Days to 113.4kg (DAYS), real-time ultrasound backfat depth (BF), and loin muscle area (LMA). Data analyses were conducted separately for sire line (SL, Hampshire and Duroc n = 2,388) and maternal line breeds (ML, Yorkshire and Landrace, n = 11,163). The data were fitted to a model that included significant ($P < 0.05$) fixed effects for breed, parity (1–6), sex, ultrasound time period, and random effects of contemporary group and sow. Significant ($P < 0.05$) covariates including WW, WW2, BTW, BTW2 were then added to the model. It was found that pigs from parity 1 dams had 1.44 (SL) and 2.21 (ML) greater ($P < 0.05$) DAYS than pigs from parity 2 and 3 dams. When covariates were added to the model, pigs from parity 1 dams averaged 1.41 (SL, $P < 0.05$) and 0.46 (ML, $P = 0.32$) less DAYS than pigs from parity 2 and 3 dams. Effects of BTW (linear and quadratic) and WW (linear and quadratic) were significant ($P < 0$ 0.01) for DAYS and accounted for 20 and 22% of the residual variance respectively. For the BF data, in the SL only BTW linear was included (−0.013 cm per kg, $P < 0.01$) while for the ML, BTW (linear and quadratic), and WW were significant ($P < 0.01$). For LMA in the SL pigs, WW (linear and quadratic) were significant ($P < 0.01$) and for the ML pigs the effects of BTW (linear and quadratic, $P < 0.01$) were significant. The inclusion of the covariates to the LMA and BF models produced small reductions in residual variances. Pigs that were the lightest at birth or weaning had smaller LMA, greater BF and required additional DAYS.

Key Words: swine, birth weight, weaning weight

W400 Length of productive life and lifetime production of Landrace, Yorkshire and crossbred sows raised under Thai tropical conditions.

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Length of productive life (LPL) and lifetime production of sows are important for commercial swine operations. These traits need to be considered for the improvement of sow productivity and efficiency. The aim of this study was to characterize factors affecting LPL and lifetime piglets born alive (LB), lifetime piglets loss (LL), lifetime weaned piglets (LW), and lifetime non-productive sow days (LN) in Landrace (L), Yorkshire (Y) and F1 crossbreds between L and Y (C) sows evaluated in a Thai commercial farm. Data included records of 1,239 L, 397 Y and 153 C sows born between 2001 and 2010. The LPL was defined as the number of days between sow age at first farrowing and sow age at weaning of her last farrowing. The LB, LL, LW, and LN were the sum of all individual measurements of each trait during this period. The model included year-season and breed group (L, Y, and C) as subclass fixed effects, age at first farrowing (9 to 17 mo) as a fixed covariate, and residual as a random effect. Least squares means (LSM) were estimated for all breed groups. Year-season effects were important for all traits ($P < 0.01$). Sows that began to farrow at older ages had significantly shorter LPL (−17.4 ± 7.1 d/mo; $P = 0.01$), lower LB (−1.2 ± 0.5 piglets/mo; $P = 0.03$), and lower LW (−1.2 ± 0.5; piglets/mo; $P = 0.009$) than sows that started farrowing at younger ages. Breed group effects were significant ($P < 0.05$) for LL, LW and LN, but not for LPL and LB. Yorkshire sows had the highest LL (8.5 ± 0.4 piglets) and LW (47.6 ± 1.3 piglets), L sows had the lowest LL (7.4 ± 1.0 piglets), LW (43.6 ± 0.7 piglets), and LN (30.3 ± 0.6 d), and C sows had the highest LN (33.5 ± 1.7 d) of all breed groups. Thus, Yorkshire sows were the most productive over their lifetime (highest LW) of all breed groups in this commercial herd. This study needs to be repeated with a large number of herds in Thailand to verify if results here apply to the whole swine population in this tropical country.

Key Words: pig, production, tropical

W401 In utero heat stress alters postnatal body composition parameters in growing pigs.

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Heat stress (HS) is a costly issue to the US swine industry as a result of losses in several production, reproductive, and health parameters. The study objective was to test the hypothesis that gestational HS would alter postnatal response to HS and body composition parameters. To investigate this, 48 offspring from 14 first parity crossbred gilts were exposed to 1 of 4 environmental treatments (TNTN, TNHS, HSTN, or HSHS) during gestation. TNTN and HSHS sows were exposed to thermal neutral (TN, cyclical 18–22°C) or HS conditions (cyclical 28–34°C) for all of gestation, respectively. Sows assigned to HSTN and TNHS treatments were heat-stressed for the first or second half of gestation, respectively. After a TN nursery period, at 14 weeks of age, offspring were exposed to one of 2 postnatal thermal environments for 5 weeks: constant TN (21°C) or HS (35°C). Following the subsequent thermic bouts, offspring from the HSTN group had increased back fat depth compared with all other gestational treatments (20.3, HSTN vs. 17.0, TNTN; 16.0,TNHS; and 17.5, HSHS mm, $P = 0.01$) irrespective of postnatal HS. Further, irrespective of postnatal HS, pigs from sows that experienced HS during the first half of gestation (HSHS and HSTN) had increased (13.5%) back fat depth than pigs from sows exposed to TN conditions during the first half of gestation (18.8 vs. 16.5 mm, $P = 0.03$). There was an interaction ($P = 0.04$) between gestational and postnatal environments for loin eye area, as offspring from HSHS and HSTN sows had decreased loin eye area after postnatal HS compared with the postnatal TN offspring, whereas offspring from sows in TNTN and TNHS conditions had increased loin eye area following postnatal HS compared with postnatal TN. No gestational treatment effect was observed on heat indices, feed intake, or weight gain during postnatal HS. Together, these results demonstrate prenatal heat stress alters body composition parameters during growth and development without concomitant changes in feed intake or body weight. This work was supported by USDA NIFA grant #2011-67003-30007.

Key Words: swine/porcine, heat stress, body composition

W402 Implementing a total traceability system for the pig chain based on electronic ear tags and molecular markers.

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A total of 1,540 crossbreed pigs of similar origin and production conditions (weaned 28 d, slaughtered 100 kg BW) were used in 3 experiments to assess on the implementation of a total traceability system based on electronic identification (e-ID) and molecular markers (DNA). Pigs were tagged by 3 types of electronic ear tags and carcasses audited by DNA. In Exp. 1, piglets (n = 1,033) were e-ID at birth with ear tags (EF1, plastic double button FDX-B transponder, 2.6 g), biopsied (n = 30) and slaughtered under commercial conditions. No EF1 losses were reported until weaning, but fattening losses were 6.3%. Losses of EF1 during transportation and slaughtering were 41.9%, resulting in 54.3% overall traceability. Auditing 18 carcasses by a panel of 12 DNA microsatellites showed 83.3% matching rate. In Exp. 2, 133 weaned piglets were e-ID (EH, plastic double button HDX transponder, 4.4 g) and biopsied (n = 56). Fattening and slaughtering were done under experimental conditions. On-farm losses were 1.5% and no losses were observed at slaughter, overall traceability being 98.5%. Auditing 56 carcasses by DNA microsatellites showed 98.0% matching rate. In Exp. 3, 374 weaned piglets were e-ID with 453 ear tags of 3 types: EF1 (n = 151), EF2 (plastic double button FDX-B transponder, 4.2 g; n = 140) and EH (n = 162). Biopsies for auditing were 97. Fattening was done in the farm of Exp. 1 and slaughtering in 3 commercial slaughterhouses. By ear tag type (EF1, EF2 and EH), on-farm losses were 1.7, 1.9 and 0.9%, and failures 5.0, 5.6 and 0.9%. On-farm traceability was 93.3, 92.5 and 98.3% (the last differing at $P < 0.05$), respectively. Additionally 5.3, 4.0 and 0.9% ear tags were lost or failed during transportation, respectively. Slaughtering losses were 22.1, 13.3 and 4.5% and failures were 6.3, 5.3 and 0%, resulting in 71.6, 81.3 and 95.5% slaughterhouse traceability, respectively. Overall traceability was 63.6, 70.1 and 92.4% for EF1, EF2 and EH, respectively ($P < 0.05$). Auditing 23 carcasses by DNA microsatellites resulted in 85.1% matching rate. Ten samples of each ear tag type were collected across the experiments for studying their features and performances under laboratory conditions. Separation

strength of EF1 from Exp. 1 was weaker ($P < 0.05$) than the rest of ear tags and reading distances varied dramatically according to the reader, technology and orientation toward the antenna used (0.3 to 33.4 cm). In conclusion, the EH ear tags were more efficient than EF1 and EF2 for tracing pigs under commercial conditions. On-farm traceability depended on piglet age, device used and fattening and slaughtering conditions. Traceability auditing by DNA varied by sample quality and matching rates ranged between 83.3 and 98.0%. Finally, the use of quality electronic ear tags and DNA analysis are recommended for implementing a total traceability system in the pig industry.

Key Words: traceability, electronic identification, ear tag

Wednesday, July 18, 2012

SYMPOSIA AND ORAL SESSIONS
Alpharma/Beef Species Joint Symposium: Redefining the Replacement Heifer Paradigm

602 Pubertal issues for beef replacement heifers. C. L. Gasser,* *Southern Utah University, Cedar City.*

Heifers that reach puberty and experience multiple estrous cycles before the onset of their initial breeding season have a greater probability for early conception and optimal lifetime productivity. Peripubertal changes include increases in LH secretion, estradiol production, follicular development, and reproductive tract size. Positive feedback stimulation from estradiol eventually causes a hypothalamic surge of GnRH, leading to a surge of LH from the pituitary and the initial ovulation. Attainment of puberty typically occurs around 12 to 14 mo of age in beef heifers but varies greatly. Genetic differences and environmental factors contribute to this variation. In typical US cow-calf operations, calves are generally weaned at approximately 200 d of age. The effect of postweaning management on age at puberty in heifers has been demonstrated, and there is considerable flexibility in the timing of gain from weaning to breeding. However, even when heifers are grown to the desired BW before the start of breeding, there remains a pronounced variation in the timing of puberty, which affects pregnancy rates. Less attention has been focused on the effect of preweaning management on age at puberty. Many changes occur during early reproductive development. Wave-like patterns of follicular development have been observed in heifer calves as early as 2 weeks of age. Some dramatic changes occur from about 2 to 5 mo of age, most notably the transient rise in LH secretion. Most components of the hypothalamic-pituitary-ovarian axis are fully competent by approximately 5 to 6 mo of age. Heifer calves with increased growth rates from birth to weaning have reached puberty at earlier ages. Precocious puberty has also been induced in most heifers with early weaning and feeding a high-concentrate diet. Nutritional control during early maturation in heifers exerts substantial influence on the timing of puberty. Understanding the mechanisms involved in reproductive development increases our ability to effectively manage replacement beef heifers for reproductive efficiency.

Key Words: heifer, puberty, development

603 Development systems for replacement beef 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

604 Interactions of feed efficiency with beef heifer reproductive development. R. D. Randel*[1] and T. H. Welsh Jr.[2], [1]*Texas AgriLife Research, Overton,* [2]*Texas AgriLife Research, College Station.*

The influence of nutrition on puberty in beef heifers is complex and under neuroendocrine control. The stores of body fat in mammals are a determinant of the onset and maintenance of puberty. Body fat stores are greater in heifers with higher residual feed intake than in their more efficient herdmates. A one-unit increase in residual feed intake resulted in a reduction of 7.54 d in age at puberty in *Bos taurus* beef heifers. However, *Bos indicus* influenced heifers which reach puberty at older ages were not found to have sexual maturity influenced by selection for residual feed intake. The strong influence of body fat stores on return to estrus after calving does indicate that selection for leaner beef heifers could affect reproductive performance relative to puberty and postpartum rebreeding of first calf heifers. The influence of intermediary metabolism through signals at the central nervous system regulates the GnRH pulse generator thereby influencing pituitary and ovarian function culminating with puberty and return to ovarian cydicity following calving. Tropically adapted cattle (Santa Gertrudis and Brahman) selected for low residual feed intake had a lesser response of insulin to a glucose challenge than their less efficient herdmates. These studies indicate the possibility that animals with differing residual feed intake (efficiencies) may have differing intermediary metabolism and therefore differing rates of reaching puberty.

Key Words: heifers, feed efficiency, reproduction

605 Enterprise level implications of heifer development. R. L. Endecott*[1], A. J. Roberts[2], and J. T. Mulliniks[3], [1]*Department of Animal and Range Sciences, Montana State University, Miles City,* [2]*USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT,* [3]*Department of Animal and Range Sciences, New Mexico State University, Las Cruces.*

Research emphasis has been placed on heifer development strategies in recent years, comparing traditional, more intensive systems to more extensive systems using less feed and relying on compensatory gain to reach a target BW. Recent research has suggested that developing heifers to a lighter target BW at breeding (50–57% of mature BW compared with 60–65% BW) reduced development costs while not impairing reproductive performance. One limitation of most research concerning influences of nutrition on heifer development and cow reproductive performance is little or limited consideration of long-term implications. Longevity has a relatively low heritability; thus heifer development and other management strategies have a greater potential to affect cow retention. While limited information exists about the effects of heifer development strategies on cow longevity, data from other species implies that limiting caloric intake during juvenile development can increase lifespan. Establishing the effect of heifer development protocols on longevity is complex, requiring consideration for nutritional factors following the start of breeding and through subsequent calvings. Factors to consider include the resulting maintenance requirements and behavior traits associated with development protocols. For example, developing to lighter target weights may be advantageous in maintaining positive energy balance or adapting to negative energy balance through the breeding season in many range settings. Likewise, heifers developed under a range setting may be better adapted to maintain desired metabolic status during breeding than heifers reared in a pen or developed at a high rate of gain. Adequate growth and development to ensure little calving difficulty can be of critical importance for longevity; however, providing additional supplemental feed during postweaning development to accomplish this may be less efficient than later in development. Ultimately, financial requirements of any development system must be evaluated in conjunction with duration of production to establish implications on production enterprises.

Key Words: replacement heifers, feed inputs, cow longevity

Breeding and Genetics: Beef Cattle Breeding II–Applied Genomics

606 Genomic technologies to increase production of Certified Angus Beef (CAB). J. D. Nkrumah*[1], P. Boddhireddy[1], M. Kelly[1], S. L. Northcutt[2], M. McCully[3], K. Anderson[1], J. Rumph[1], W. Herring[1], J. Osterstock[1], and S. DeNise[1], [1]*Pfizer Animal Genetics, Kalamazoo, MI,* [2]*Angus Genetics Inc., St Joseph, MO,* [3]*Certified Angus Beef, Wooster, OH.*

Genomic technologies can be used as part of genetic improvement strategies to allow Angus cattle producers to both improve growth performance and increase the potential for animals to achieve the Certified Angus Beef (CAB) brand quality specifications. We applied data mining and machine learning methods to genotype and phenotype data on a total of ~4,000 animals with AAA marbling and postweaning gain EPDs and ~9,600 animals with feedlot growth and carcass marbling phenotypes to select an optimum subset of markers from the Illumina BovineSNP50 chip. Selected SNPs predict the genetic potential of Angus cattle to qualify for the CAB brand due to superior genomic merit for marbling, and to affect profitability through growth. Marker effects estimated based on cross-validations using 2/3 of each data were used to compute molecular breeding value predictions, which were then tested in the remaining independent 1/3 of each data set. The independent internal validation results showed that the markers explained between 17 to 36% of the genetic variation in both the EPDs and phenotypes for marbling and growth, depending on the trait. Subsequently, the SNP effects were used to generate predictions on a second completely independent set of ~5,400 animals with genotypes. These new molecular breeding value predictions were sent to Angus Genetics Inc. (AGI), where they were combined with their respective phenotypes and evaluated for their genetic correlations with phenotypes using single-trait animal models. The estimated genetic correlations in the AGI analysis ranged from 0.40 to 0.50, depending on the trait. These predictions provide commercial cattlemen the opportunity to use simple and cost-effective genomic tools to inform early selection, management, and marketing decisions related to genetic potential for marbling and growth.

Key Words: Certified Angus Beef, genomic technologies, molecular value predictions

607 Genomic selection for dry matter intake using a combined European and Australian reference population. Y. de Haas*[1], J. E. Pryce[3], M. P. L. Calus[1], E. Wall[2], M. P. Coffey[2], H. D. Daetwyler[3], B. J. Hayes[3], and R. F. Veerkamp[1], [1]*Animal Breeding and Genomics Centre of Wageningen UR Livestock Research, Wageningen, the Netherlands,* [2]*Sustainable Livestock Systems Group at Scottish Agricultural College, Easter Bush, Midlothian, United Kingdom,* [3]*Biosciences Research Division of Department of Primary Industries Victoria, Bundoora, VIC 3083, Australia.*

Dairy cow dry matter intake (DMI) data from Australia (AU), the United Kingdom (UK) and the Netherlands (NL) were combined (1801 cows) for this study. The aim was to explore the impact on the accuracy of genomic estimated breeding values of pooling data across key reference populations. A total of 843 Australian growing heifers with records on DMI measured over 60 to 70 d at approximately 200 d of age, 359 Scottish and 599 Dutch lactating heifers with records on DMI during the first 100 d in milk were included in the data set. Genotypes were obtained using the Illumina BovineSNP50 BeadChip for European (UK+NL) cows, and Illumina High Density Bovine SNP chip for AU heifers. The AU and EU genomic data were matched on SNP-name and genotypes were compared for quality control using 40 bulls that were genotyped in both data sets. This resulted in a total of 30,949 SNPs being used in the analyses. Genomic predictions were with both single-trait and multi-trait genomic REML models, using ASReml. The accuracy of genomic prediction was evaluated in 11 single-country validation sets, and the reference set (where animals had both DMI phenotypes and genotypes) were either a reference set within AU or EU, or with a multi-country reference set consisting of all data except the validation set. When DMI was considered to be the same trait for each country, using a multi-country reference set, the accuracy of genomic prediction for DMI increased for EU and UK, but not for AU and NL. Extending to a bivariate (AU-EU) or trivariate (AU-UK-NL) model increased the accuracy of genomic prediction for DMI in all countries. The highest accuracies were estimated for all countries when data was analyzed with a trivariate model, with increases of up to 5.5% compared with a single-trait analysis with a multi-country reference set.

Key Words: genomic selection, dry matter intake, international collaboration

608 Whole transcriptome sequencing of seven bovine tissues reveals gene expression profiles, splicing variants, and novel coding regions to improve genome annotation. J. Thomson*[1], U. Basu[1], Y. Meng[1], X. Liao[1], S. Moore[2], and P. Stothard[1], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*University of Queensland, Brisbane, Qld, Australia.*

A comprehensive annotation of the transcriptome is essential for understanding the genome biology of cattle. The objectives of this work include characterizing the transcriptome of 7 bovine tissues with the aim of identifying additional splice variants, novel coding regions, and tissue-specific gene expression. Liver, adipose, hypothalamus, muscle, kidney, duodenum, and lung tissues were profiled using RNA-Seq Reads were mapped to the bovine reference sequence using TopHat and gene expression values normalized as FPKM (fragments per kilobase of exon per million fragments mapped) were generated using Cufflinks. A total of 24,617 genes were identified and quantified in at least 1 of the 7 tissues. Several thousand transcript variants were also identified. Functional annotation of the expressed genes will provide insight into tissue functions and may stimulate future lines of research. This work adds to the current knowledge base by identifying expressed transcripts and quantifying their expression in several important tissues. Novel transcribed regions that are not currently available in the database may be identified. Additional information about gene function can be used to improve our understanding of ruminant biology.

Key Words: gene expression, genomics, physiology

609 An ensemble-based approach to imputation of high-density genotypes for genomic selection with application to purebred Angus cattle.

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Imputation of high-density genotypes from low-density panels is of increasing interest in genomic selection because it can reduce genotyping costs markedly. Imputation software packages vary in imputation accuracy, and imputed genotypes may be inconsistent among procedures. Hence, an AdaBoost-like approach is proposed to combine imputations from several different software packages. Six such packages were used: Beagle (v3.3), IMPUTE (v2.0), fastPHASE (v1.4), AlphaImpute, findhap (v2), and Fimpute (v2), each serving as a basic classifier in an ensemble-based system. This method computed weights sequentially for all classifiers, and then combined results from the component methods via weighted majority voting, to produce a final vote for unknown genotypes. The data included 3,078 purebred Angus cattle, each genotyped with the Illumina BovineSNP50 BeadChip. SNP genotypes on 3 chromosomes (BTA1, BTA16, and BTA28) were used to compare imputation accuracy among various methods, and the application involved imputation of 50k genotypes covering 29 chromosomes based on a set of 7k SNPs contained on the Illumina BovineLD chip. Beagle and Fimpute had the greatest accuracy, which varied between 0.87 and 0.99, among the 6 imputation softwares. The ensemble method outperformed the independent packages; however, the sequence of independent packages in voting affected imputation accuracy. The ensemble systems yielding the best imputation accuracies were those that had Beagle as the first classifier, followed by one or 2 methods that utilized pedigree information. A salient feature of the ensemble method is that it provides a way of solving imputation inconsistencies among different imputation methods, hence leading to a more reliable system for imputing genotypes relative to any of the individual procedures.

Key Words: AdaBoost, imputation, ensemble-based system

610 Gene expression analysis of longissimus and semitendinosus muscle from Angus and Charolais finishing steers.

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Fatty acid profile is an important component in determining the healthfulness of beef products. However, the fatty acid profile of beef is variable among breeds and within different cuts in the same breed. Genetic regulation of fatty acid profile is known to vary among breeds and within different muscles. The objective of this study was to analyze gene expression in both longissimus and semitendinosus muscles in 6 Angus and 6 Charolais heifers finished on concentrate for 140 d. Expression of *ADIPOQ* (*adiponectin*), *FASN* (*fatty acid synthase*), *DGAT2* (*diglyceride acyl transferase 2*), *PPARG* (*peroxisome proliferator activated receptor gamma*), and *GPAM* (*glycerol-3 phosphate acyltransferase muscle type*) were analyzed for differences between both muscle and breed. Total RNA was extracted from intramuscular samples and gene expression was quantified using SYBR Green real-time PCR. Delta CT (threshold cycle) values for each gene were analyzed for differences between breed and muscle using the GLM procedure in SAS (Cary, NC) and means were separated with the PDIFF option. In Angus cattle, *ADIPOQ* and *FASN* were upregulated 6.7- and 4.1-fold respectively in semitendinosus compared with longissimus muscle ($P < 0.05$). In Charolais, *PPARG* was upregulated 43-fold in semitendinosus compared with longissimus ($P < 0.05$). In longissimus, *ADIPOQ*, *FASN*, *PPARG*, and *DGAT* were upregulated 7.6-, 6.0-, 5.0-, and 6.1-fold in Charolais compared with Angus ($P < 0.05$). In semitendinosus, *PPARG* was upregulated 35.8-fold in Charolais compared with Angus ($P < 0.05$). Significant differential expression differences across both muscle and breed indicates these genes are likely affecting fatty acid metabolism in the tissues analyzed.

Key Words: beef, fatty acid, gene expression

611 Single nucleotide polymorphisms in the NPY, leptin, and IGF-1 genes in Angus cattle: I Effects on feed efficiency.

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Single nucleotide polymorphisms (SNP) that showed associations with residual feed intake (RFI) may be useful for marker-assisted selection. There is limited research about specific gene mutations and RFI. Neuropeptide Y (NPY), leptin (LEP), and insulin-like growth factor-1 (IGF-1) are candidate genes due to their role in the regulation of feed intake, growth and energy balance. Thus, our aim was to study the associations of SNP previously identified in NPY (A/G, intron 2), LEP (C/T, exon 2) and IGF-1 (C/T, promoter region) genes to dry matter intake (DMI), metabolizable energy intake (MEI), average daily gain (ADG) and RFI. Female Angus calves carrying 3 putative favorable alleles simultaneously (V = validation group; n = 19; 187 ± 33 kg BW, 260.6 ± 34 d old at the beginning of test (BT)) and calves carrying 3 putative unfavorable alleles (C = control group, n = 19, 185 ± 33 kg BW, 263.9 ± 17 d old at BT) were fed a TMR diet (60:40 concentrate: alfalfa hay, as fed) twice a day during 56 d. DMI was estimated by the difference between feed offered and refused; BW was recorded every 2 wk. RFI_{K} was residual from a regression of DMI on ADG and mid-test $\text{BW}^{0.75}$. RFI_{SCA} was residual from regressing DMI on DMI predicted from Australian feeding standards. RFI_{NRC} was residual from regressing DMI on DMI expected from net energy system (NRC_{1984}) and RFI_{ME} was the same as RFI_{NRC} but expressed in ME values. Mean DMI, MEI, ADG and RFI_{K} were 7.16 ± 1.08 kg DM, 18.53 ± 2.78 Mcal ME, 1.24 ± 0.19 kg BW, and 0.00 ± 0.41, respectively. Mean values for RFI_{SCA}, RFI_{NRC}, and RFI_{ME} were 0.00 ± 0.49, 0.00 ± 0.50, 0.00 ± 1.27, respectively. Calves of V group had lower DMI and MEI ($P = 0.046$, $P = 0.032$, respectively) and similar ADG ($P = 0.195$) than calves of C group when initial BW (covariate) and age (random effect) were included in a linear mixed model. Calves of V group were more efficient ($\text{RFI}_{\text{NRC}} = -0.181$, $\text{RFI}_{\text{SCA}} = -0.171$, $P < 0.05$; $\text{RFI}_{\text{ME}} = -0.3279$, $\text{RFI}_{\text{K}} = -0.111$, $P < 0.1$) than calves of C group. Spearman rank correlation between RFI methods was highly significant ($P < 0.001$). These results indicate that there is an association between the SNP of NPY, LEP and IGF-1 and RFI.

Key Words: beef cattle, residual feed intake, single nucleotide polymorphism

612 Single nucleotide polymorphisms in the NPY, Leptin, and IGF-1 genes in Angus cattle: II Effects on serum IGF-1 and leptin concentrations.

A. I. Trujillo,* A. Casal, and P. Chilibroste, *Universidad de la Republica, Facultad de Agronomia.*

Single nucleotides polymorphisms (SNP) in the leptin (LEP) and insulin-like growth factor (IGF-1) genes or its promoters, have been associated with differences in serum LEP and IGF-1 concentrations and others relevant traits including residual feed intake (RFI). The aim of the study was to evaluate the relationship of the SNP, previously identified in NPY (A/G, intron 2), LEP (C/T, exon 2) and IGF-1 (C/T, promoter region) genes, with serum LEP and IGF-1 concentrations. Female Angus calves, genotyped at mentioned SNP, were classified as carrying 3 putative favorable alleles simultaneously (n = 19; 187 ± 33 kg BW; 260.6 ± 34 d old; V = validation group), or 3 putative unfavorable alleles (n = 19; 185 ± 33 kg BW; 263.9 ± 17 d old; C = control group). Calves were fed a TMR diet (60:40 concentrate: alfalfa hay, as fed) during 56 d. Dry matter intake (DMI) was estimated as the difference between feed offered and refused; BW was recorded every 2 weeks. RFI_{ME} was residual from regressing energy metabolizable intake (EMI) on EMI expected from net energy system (NRC1984). Blood samples were collected by jugular venipuncture at sampling date at the beginning (SD1) and at the end of test (SD2). Data was analyzed as a repeated measure using a mixed model and means were considered to differ when $P < 0.05$. Mean serum concentration of IGF-1 and LEP were 281.8 ± 110.8 and 2.92 ± 0.97 ng/mL, respectively. IGF-1 concentration did not differ between groups, was affected by initial BW (iBW; $P < 0.0001$) and was greater in SD2 than in SD1 (348.8 vs. 214.9 ± 12.2 ng/mL, respectively). LEP concentration did not differ between groups and tended to be affected by iBW ($P < 0.1$). In addition, IGF-1 concentration was moderate and positively correlated with DMI (r = 0.40, $P < 0.05$) while LEP concentration was moderate and negatively correlated with RFI_{ME} (r = −0.40, $P < 0.05$). Although the SNPs considered were not associated with any of the studied hormones our data show a correlation between LEP concentration and RFI_{ME}. Further studies are needed but these results suggest that LEP serum concentration could be use as an indicator of efficiency in beef cows.

Key Words: single nucleotide polymorphism, IGF-1, leptin

613 A distributed parallel computing approach for tuning Bayesian regression models for genomic selection with application to Angus cattle.

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Predicting genetic merit of candidates for breeding purposes using an optimal subset of whole-genome markers is a model selection problem. A BayesCπ model, for example, postulates that a portion, π, of all SNP markers have no effect on the quantitative trait. Inferring π, however, adds extra complexity to the Bayesian regression model, which is dependent on the extent of data and the underlying trait genetic architecture, and requires more computing time. It is also questionable whether the π parameter optimized in training data necessarily leads to best prediction when generalized to testing data particularly for traits governed by the infinitesimal model. Here, we propose a distributed parallel computing (DPC) approach to choose optimal π values in Bayesian regression models, based on their cross-validation performance in testing data sets. Several Bayesian regression models were computed in parallel in computer clusters, each assuming a distinct value of π. These 2 approaches to choosing π were applied to prediction of marbling score in 3,078 registered Angus bulls. It was found that the π values obtained directly from BayesCπ fitted to the training data were smaller than those obtained from the DPC approach as supported by testing data. This reflected that BayesCπ fit more SNP markers in the model than the DPC approach. In general, the π obtained from BayesCπ was > 95% with a 50K SNP panel, and it was moderate (40–70%) with a 3k SNP panel. In contrast, the DPC approach consistently yielded the best predictions using from 600 to 900 SNP markers. Hence, a model that describes variation in a training set well does not necessarily lead to the best predictions when generalized beyond the training set. With a low-density SNP panel, however, interpretation of SNP markers having putatively nonzero effects should be done with caution, because many could be distant from functional genes or quantitative trait loci.

Key Words: distributed parallel computing, genomic selection, single nucleotide polymorphism

614 Quantitative traits and genomics of heterosis in Wagyu × Angus F_1 progeny.

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The objective of the present study was to understand the genetic complexity of economically important traits in beef cattle. A total of 91 genes were investigated for their associations with 6 carcass and 24 fatty acid composition traits in a Wagyu × Angus population, including 43 Wagyu bulls and their potential 791 F1 progeny. Parentage assignment was performed using the Cervus package, while the association analysis was conducted using the PROC MIXED procedure of SAS. All significant markers along with their quantitative trait modes (QTMs) for each phenotype were then integrated into a linear regression analysis to identify genetic networks. Of the 182 SNPs evaluated, 102 SNPs that were in Hardy-Weinberg equilibrium with minor allele frequencies (MAF) > 0.15 were selected for parentage assignment. Linkage disequilibrium analysis further identified 75 of these 102 SNPs derived from 54 genes as tagged SNPs for association analysis. After Bonferroni correction, single-marker analysis revealed a total of 113 significant associations between 44 genes and 29 phenotypes (adjusted $P < 0.05$). Multiple-marker analysis confirmed single-gene associations for 10 traits, but revealed 2-gene networks for 9 traits and 3-gene networks for 8 traits, respectively. These associations/networks were orchestrated by only 19 genes, including ATP-binding cassette A1, apolipoprotein B, ankyrin repeat and SOCS box-containing 3, calpains 1 and 12, calpastatin, corticotropin releasing hormone, dermatan sulfate epimerase-like, EGF containing fibulin-like extracellular matrix protein 1, fatty acid desaturase 2, guanine nucleotide binding protein gamma 3, lipase, hormone-sensitive, phospholipid transfer protein, regulator of calcineurin 1, solute carrier family 27 A1 and A2, tumor necrosis factor, transcription factor B2, mitochondrial and urotensin 2 receptor. In addition, we observed an interesting phenomenon that crossbreeding of different breeds might change gene actions to dominant and overdominant modes, thus explaining the origin of heterosis in their F1 progeny. The present study further confirmed that these pathway-based genes are useful targets for improving meat quality traits and healthful beef products in cattle.

Key Words: quantitative traits, genetic networks, beef cattle

Companion Animals

615 Use of genomic biology to study companion animal microbiota. K. S. Swanson,* *University of Illinois, Department of Animal Science, Urbana.*

The gastrointestinal (GI) tract of dogs and cats contains a complex and dense population of microbiota, including bacteria, archaea, fungi, protozoa, and viruses. Depending on its composition, the microbiota may be beneficial or harmful to the host. Commensal microbes may be a burden in some respects, but is outweighed by the role they play in GI immunity, resistance to pathogenic colonization, short-chain fatty acid production, and epithelial gene expression. The knowledge pertaining to GI microbiology and health has largely been obtained using traditional (i.e., plating) techniques over the past several decades. A hindrance to this field has been the inability to effectively identify and quantify microbial species. Molecular tools, such as quantitative polymerase chain reaction (qPCR), fluorescent in situ hybridization (FISH), denaturing gradient gel electrophoresis (DGGE), quantitative dot blot hybridization, restriction fragment length polymorphism (RFLP), and high-throughput DNA sequencing, have dramatically changed the research landscape. Our lab has recently used such techniques to characterize the phylogeny and functional aspects of canine and feline GI microbiota and identify the effects of diet and age on these communities. Several hundred phylotypes, predominated by members of *Firmicutes*, *Fusobacteria*, *Proteobacteria*, *Bacteroidetes*, and *Actinobacteria*, inhabit the dog and cat gut. Although these populations are quite stable over time, our data have demonstrated that dietary macronutrient profile (e.g., dietary protein: carbohydrate ratio), fiber amount and type, and form of food (e.g., raw vs. extruded) may affect the number and/or metabolism of the colonic microbiota. Continued use of DNA-based techniques to characterize microbial phylogeny and metabolic capacity, along with other technologies to analyze microbial RNA, protein, and metabolite profiles, will increase our understanding of host-microbe relationships. Despite the challenges that surround this field, these powerful tools will enhance our ability to understand GI health and diseases in pets on a molecular level, leading to improved disease diagnosis and treatment in coming years.

616 Pheromones and interomones that change heart rate and behavior of anxious dogs. G. Thompson* and J. J. McGlone, *Texas Tech University, Lubbock.*

Pheromones are species-specific odors used in communication. Interomones are pheromones in one species, but have diverse effects on other species. The objective of this study was to assess efficacy of pheromones/interomones to modulate heart rate and behavior in adult anxious dogs (trembling, cowering, shy). The dogs (8.1 ± 0.18 kg; estimated 5–12 yr intact males) were obtained from a local research facility. Body weights and feed intake were recorded. Each dog was housed in a separately ventilated room with a minimum of 12 m^2 of floor space. Heart rate (HR) and surface temperature was measured using a telemetry system (Data Science International, St. Paul, MN). Behavior was recorded on a DVR and later reviewed by a trained individual. A scan sample was used with a recording interval of 5 min over 24 h. At the end of 24 h with a given pheromone collar, each dog was startled with a 110 db foghorn 12 cm from the dog's head while behavior and heart rate were recorded. Each dog received each treatment in a Latin square design with repeated measures over time. This model allowed evaluation of effects of treatment, dog, treatment by dog, time, treatment by time and dog by time. Treatments were given in the form of a collar containing each pheromone/interomone and included placebo (collar without pheremone), Sergeant's (SERG), 2-methylbut-2-enal–Rabbit Pheromone (RP), or a SERG+RP combined collar. Baseline HR did not differ among treatments (avg = 110.1 ± 13.3 bpm). After startle, the RP lowered ($P < 0.01$) HR compared with placebo (124.5 ± 7.2 vs. 157.8 ± 7.2 bpm); however, the treatment by dog interaction ($P < 0.01$) indicated certain dogs were more responsive than others. Dogs with RP collars spent more time lying down (87.4 ± 5.4 vs. 63.2 ± 4.8% of time, $P = 0.01$) and less time pacing (3.0 ± 0.2 vs. 3.8 ± 0.02%, $P < 0.05$) than placebo-treated dogs. Pace/walk changed differentially among treatments and dogs (dog by RP and SERG effects for pace/walk, $P = 0.05$). In summary, RP lowered HR while SERG and SERG+RP did not change dog HR. However, pheromone/interomone treatments had differential effects on individual dog behavior and HR. Pheromones/interomones can cause meaningful changes in dog behavior and HR among certain anxious dogs.

Key Words: pheromone, behavior, dogs

617 Genome-wide linkage scan for loci associated with canine hypoadrenocorticism. A. M. Oberbauer* and J. M. Belanger, *University of California-Davis, Davis.*

Canine hypoadrenocorticism (Addison's disease) results from reduced adrenal production of corticosteroids and mineralocorticoids. Within the dog population, the disease is relatively uncommon but some breeds, bearded collie, great danes, leonbergers, Portuguese water dogs, standard poodle, and west highland white terriers are at increased risk for developing hypoadrenocorticism. This disease can be lethal or require lifelong hormonal therapy. Prior studies have indicated a genetic component to the expression of the disease in these breeds. The aim of this study was to employ a genome-wide linkage scan to interrogate the canine genome and identify genomic regions associated with hypoadrenocorticism in the dog. Extracted DNA from bearded collies (43), great danes (11), leonbergers (4), Portuguese water dogs (11), standard poodles (91), and west highland white terriers (11) were genotyped using the newly developed high-density genotyping array consisting of over 170,000 evenly spaced single nucleotide polymorphisms (SNP). Association analyses were conducted using the software package PLINK. Dogs were classified as having a positive diagnosis of hypoadrenocorticism if they failed to respond to an adrenocorticotropic hormone stimulation test and unaffected controls if they were over 7 years of age and healthy. The analysis included 96 confirmed cases and 75 control dogs. When considered in this manner, based on 50,000 permutations, 4 chromosomal regions reached genome wide significance: chromosomes 3 ($P < 0.006$), 6 ($P < 0.008$), 16 ($P < 0.04$), and 30 ($P < 0.04$). Chromosome 3 appears to be associated with a protective allele while 6, 16, and 30 confer a 3- to 4-fold risk. Each chromosomal region encompasses several genes that will require additional fine mapping to resolve the region that contributes to expression of the disease. Identifying the underlying causal mutations and implementing genetic testing will reduce the incidence of hypoadrenocorticism in dogs.

Key Words: hypoadrenocorticism, genome scan, dog

618 Effects of dietary macronutrient composition on postprandial endocrine response in domestic cats.

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Obesity is now the most common metabolic disease in cats, having adverse effects on quality of life. Identifying dietary effects on appetite-regulating hormones in cats may enhance our understanding of appetite control and obesity development in this species. The objective of current study was to investigate the effects of dietary macronutrient composition on appetite-regulating hormone release. Twelve neutered male adult domestic shorthair healthy cats were fed 4 nutritionally complete diets [control, high-fat (HF), high-protein (HP), high-carbohydrate (HC)] at amounts to maintain ideal BW and body condition score. The control diet provided 33% kcal from each macronutrient, while the other provided 50% of kcal from the macronutrient highlighted. Cats were randomly allotted to diets in a 4 × 4 Latin square design experiment for a total of 64 d (four 16-d periods). After a 15-d adaptation phase, blood samples were collected before (0 min) and 10, 20, 30, 60, 90, 120, 150, 180, 240, 300, 360, 720 min after the morning meal was consumed. Glucose, insulin, total ghrelin, and leptin concentrations were measured. Data were analyzed by comparing change from baseline and postprandial incremental area under the curve (IAUC) among treatments. Baseline concentrations of glucose, insulin, leptin, and ghrelin were not different among treatments. However, glucose $\text{IAUC}_{0\text{–}6\ \text{h}}$ and $\text{IAUC}_{0\text{–}12\ \text{h}}$ were higher ($P = 0.028$) in cats fed control and HC compared with those fed HF and HP. $\text{IAUC}_{0\text{–}6\ \text{h}}$ and $\text{IAUC}_{0\text{–}12\ \text{h}}$ of insulin, leptin, and ghrelin were not different among treatments. In conclusion, while diets containing higher carbohydrate content increased blood glucose, they did not appear to affect appetite-regulating hormone concentrations. More studies on macronutrients are required to identify any effect they may have on appetite.

Key Words: appetite-regulating hormones, macronutrients, cat

619 Digestibility of day-old, whole ground, extruded, and canned chicken-based diets in African wildcats.

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Small captive exotic cats are commonly fed whole prey to supplement traditional diets, such as raw-meat based, canned, and extruded diets. Data regarding the digestibility of these diet types is lacking. The objective of this study was to compare apparent total tract macronutrient digestibility differences of whole chicks [WHO; 24% DM, 76% crude protein (CP)], ground chicken (GRO; 31% DM, 43%CP), chicken-based canned diet (CAN; 40%DM, 47% CP), and chicken-based extruded (EXT; 92%DM, 36% CP) diets fed to captive African wildcats. Four animals were utilized in a crossover design. Apparent DM digestibility (81 to 85%) was not affected by treatment; however, apparent organic matter (OM) digestibility was higher ($P < 0.05$) in cats fed GRO (94%) compared with those fed WHO, CAN, and EXT (85 to 87%). Apparent CP digestibility was higher ($P < 0.05$) in cats fed GRO (91%) compared with those fed EXT (80%). Because the GRO had high digestibility and low levels of fiber or bulking materials (i.e., feathers), cats fed this diet had high fecal DM (68%), which was reflected in the fecal scores (1 out of 5; 1 = hard, dry pellets). Cats fed the other diets had fecal scores close ideal (2.6 to 3.6; 3 = ideal). In conclusion, all diets had high digestibility (>85% OM digestibility), maintained BW and health short-term. Inclusion of whole-prey (WHO and GRO) as dietary items for AWC is appropriate; however, if fed as the sole dietary item additional nutrient supplementation, including fiber or fiber-like material, may be necessary. Further research is needed on the ability of whole prey to meet the nutritional needs of small exotic cats, including compositional analysis, bioavailability, and research including more species.

Key Words: digestibility, feline, whole prey

620 Dietary protein:carbohydrate ratio alters kitten fecal microbiota as analyzed by 454 pyrosequencing.

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The dietary protein: carbohydrate ratio may affect the gut microbiota of growing kittens, but this aspect of the diet has not been well studied. This study was conducted to test the effects of moderate and high protein intake on the composition of the gut microbiota of growing kittens using 454 pyrosequencing. Male domestic shorthair kittens were raised by mothers fed moderate-protein, moderate-carbohydrate (MPMC; n = 7) or high-protein, low-carbohydrate (HPLC; n = 7) diets, then weaned at 8 wk of age onto the same diet. Fresh fecal samples were collected at 8, 12 and 16 wk of age; DNA was extracted, followed by amplification of the V4-V6 region of the 16S rRNA gene using barcoded primers for pyrosequencing. Pyrosequencing of barcoded amplicons resulted in a total of 384,588 sequences, with an average of 9,374 sequences per sample. The difference in protein:carbohydrate ratio resulted in dramatic differences in fecal microbiota, primarily in the *Actinobacteria* and *Fusobacteria* phyla; the abundance of fecal *Actinobacteria* being greater ($P < 0.05$) in MPMC-fed kittens and increased with age ($P < 0.05$). In contrast, the proportion of fecal *Fusobacteria* was greater in HPLC-fed kittens ($P < 0.05$). Among the well-characterized genera *Clostridium*, *Fecalibacterium*, *Ruminococcus*, *Blautia*, and *Eubacterium* predominated ($P < 0.05$) fecal samples of HPLC-fed kittens. In contrast *Dialister*, *Acidaminococcus*, *Bifidobacterium*, *Megasphaera*, *Mitsuokella*, and *Subdoligranulum*, were greater ($P < 0.05$) in MPMC-fed kittens. Kittens fed MPMC also had higher ($P < 0.05$) fecal Lactobacillus at 8 wk of age and then decreased ($P < 0.05$) at 12 and 16 wk of age. Further research is required to identify the physiological relevance of these diet-induced changes in gut microbiota during the nursing and weaning period, and test how important the weaning diet is on long-term microbiota populations and gut health-related outcomes.

Key Words: protein carbohydrate ratio, gut microbiome, 454 pyrosequencing

621 Influence of indigestible starch content in dry expanded diets on stool characteristics of dogs differing in body size.

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Large breed dogs are known to be more sensitive to diet than smaller ones, and consequently to produce feces of poorer quality. This could be due to larger amounts of indigestible residues reaching the large bowel and leading to increased fermentative activity. The aim of this study was 1/ to determine whether variation in dietary indigestible starch level could affect fecal characteristics in small and large dogs and 2/ to assess if large dogs have a higher digestive sensitivity to indigestible starch than small ones. Five German shepherds (GS), 5 beagles (BE), and 5 miniature schnauzers (MS) were used in the study. Two dry expanded diets were tested in a crossover design. They only differed in their source of corn starch: purified (CS) or high-amylose (HA), and contained respectively 0.4 and 3.6% of indigestible starch (i.e., resistant starch). Fecal quality, nutrient digestibility and fermentation by-products (SCFA and lactate) were measured. Effects of diet or breed on fecal parameters were statistically tested (Wilcoxon and Kruskal-Wallis tests). Contrary to CS diet, HA diet tended to modify fecal characteristics in the 3 tested breeds ($P < 0.059$). When HA diet was fed, higher fecal SCFA (GS, BE) or lactate (GS, BE, MS) concentrations, lower pH (GS), and poorer fecal quality (GS) were observed, and animals presented a lower apparent digestibility of starch. Compared with small ones, large dogs fed with the HA diet presented stools with lower consistency ($P < 0.003$) and higher moisture ($P < 0.003$). Fecal SCFA and lactate concentrations were higher ($P < 0.003$ and $P < 0.014$ respectively), and stool pH tended to be lower pH ($P < 0.055$). Starch apparent digestibility was higher in GS ($P < 0.01$). Those results show that indigestible starch level tends to increase colonic fermentative activity in all dogs whatever their size. However, small and medium dogs showed less sensitivity to indigestible starch based on fecal scores, while large dogs were quite responsive. These results suggest that indigestible starch content (strongly affected by source and processing) is a critical step for petfood manufacturer, especially regarding diets for large breed.

Key Words: dog, starch, fermentation

622 Influence of fresh citrus pulp and apple pomace on the digestibility of nutrients in dogs.

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Six adult cocker spaniel dogs were used to evaluate whether the dietary inclusion of fresh citrus pulp and apple pomace affect the digestibility of nutrients. Dogs (3 female, 3 male; BW: 12.7 ± 0.7 kg) were assigned randomly to treatments in a double 3 × 3 Latin square design (3 treatments, 3 experimental periods). Treatments consisted in a commercial dog food (CON) with or without the addition of 70 g/kg of either fresh citrus pulp (CIT) or fresh apple pomace (APP). Each experimental period consisted in a 5-d diet adaptation phase and 3-d for fecal collection. Diets and feces were analyzed for DM, OM, CP, NDF and ADF, and digestibility of each fraction calculated. Data was analyzed by PROC MIXED considering the treatment and period effects and means were separated by orthogonal contrasts. Digestibilities of nutrients were higher when dogs received CON than when fed diets containing both citrus and apple. Dogs fed CIT presented higher digestibility values than dogs fed APP for most of the nutrients analyzed. Despite there was a reduction in digestibility values with the inclusion of fiber in the diets, overall digestion was widely acceptable.

Table 1. Effect of diets on coefficients of total tract apparent digestibility of nutrients

	Treatment				Contrast (*P*-value)[1]	
	CON	CIT	APP	SEM	Fiber	Source
DM	0.850	0.811	0.804	0.011	0.005	0.020
OM	0.888	0.845	0.841	0.012	<0.001	0.003
CP	0.863	0.835	0.817	0.011	0.012	0.081
NDF	0.777	0.680	0.649	0.022	<0.001	0.001
ADF	0.575	0.383	0.340	0.030	<0.001	<0.001

[1] Fiber = effect of fiber inclusion (CON vs CIT+APP); Source = effect of fiber source (CIT vs APP).

Key Words: fiber, canine, digestion

Dairy Foods: Microbiology and Chemistry

623 Impact of NaCl substitution with KCl on cell-wall extract and cell-free supernatant proteinase activities of *Lactobacillus delbrueckii* ssp. *bulgaricus* and *Streptococcus thermophilus* and *Lactobacillus acidophilus* and *Lactobacillus casei* at different pH and salt levels. M. M. Ayyash[1], F. Sherkat[2], and N. P. Shah*[1,3], [1]*Victoria University, Melbourne, Vic, Australia,* [2]*RMIT University, Melbourne, Vic, Australia,* [3]*The University of Hong Kong, Pokfulam, Hong Kong.*

To reduce salt concentration in cheeses by substitution with KCl, it was important to study the effect of salt substitution on starter culture proteinases which play a vital role in ripening and texture profile of cheeses. The objective of this study was to examine the effect of NaCl substitution with KCl at different pH levels (6.0, 5.5, and 5.0) and salt concentrations on proteinases activity of cell-wall and supernatant of *Lactobacillus delbrueckii* ssp. *bulgaricus* 11824, *Streptococcus thermophilus* MS as well as of *Lactobacillus acidophilus* and *Lactobacillus casei* was investigated. MRS broths were mixed with 4 salt substitutions at 2 different concentrations (5% and 10%) and incubated individually at 37°C for 22 h. The collected cell pellets were used to prepare cell-wall proteinases and the cell-free supernatants were used as source of supernatant proteinases. The proteolytic activities and protein contents of both portions were determined. The supernatants after incubation of both portions with 3 milk caseins (α, β, kappa-casein) were subjected to ACE-inhibitory activity and proteolytic activity by OPA method. Significant differences were observed in ACE-inhibitory activity and OPA between salt substitutions of cell-wall extract and cell-free supernatant of LB and ST at same salt concentration and same pH level. The conclusion is that there were significant effects of pH and salt substitution on all measured variables.

Key Words: salt substitution, proteinase activity, ACE-inhibitory activity

624 Survival of microencapsulated probiotic *Lactobacillus paracasei* LBC-1e during manufacture of Mozzarella cheese and simulated gastric digestion. F. Ortakci,* J. R. Broadbent, W. R. McManus, and D. J. McMahon, *Western Dairy Center Department of Nutrition, Dietetics, and Food Science, Utah State University, Logan.*

An erythromycin resistant strain of probiotic *Lactobacillus paracasei* ssp. *paracasei* LBC-1 (LBC-1e) was added to part skim Mozzarella cheese in alginate microencapsulated or free form at a level of 10^8 and 10^7 cfu/g respectively. The objective of this study was to investigate the survival of LBC-1e and total lactic acid bacteria through the pasta filata process of cheese making where the cheese curd was heated to 55°C and stretched in 70°C-hot brine, followed by storage at 4°C for 6 wk and subjected to simulated gastric and intestinal digestion. This included incubation in 0.1 *M* and 0.01 *M* hydrochloric acid, 0.9 *M* phosphoric acid and a simulated intestinal juice consisting of pancreatin and bile salts in a pH 7.4 phosphate buffer. There were some reductions in both free and encapsulated LBC-1e during heating and stretching with encapsulated LBC-1e surviving slightly better. Changes in total lactic acid bacteria losses during heating and stretching did not reach statistical significance. During storage there was a decrease in total lactic acid bacteria but no statistically significant decrease in LBC-1e. Survival during gastric digestion in HCl was dependent on extent of neutralization of HCl by the cheese with more survival in the weaker acid in which pH increased to 4.4 after cheese addition. The alginate microcapsules did not provide any protection against the HCl. Interestingly, there was greater survival of the encapsulated LBC-1e during incubation in H_3PO_4. Proper selection of simulated gastric digestion media is important for predicting delivery of probiotic bacteria into the human intestinal tract. Neither free nor encapsulated LBC-1e was affected by incubation in pancreatin/bile solution. It was concluded that based on survival during simulated gastric digestion, the level of probiotic bacteria that would need to be added to cheese to provide a beneficial health benefit is lower than is generally assumed for other fermented dairy foods or when consumed as supplements.

Key Words: microencapsulation, probiotic, Mozzarella

625 Characterization of *Lactobacillus* sp. GF103 as potential probiotics in vitro. X. L. Dong[1], Q. Y. Diao*[1], N. F. Zhang[1], Y. Tu[1], M. Zhou[1,2], L. H. Zhao[1], and X. H. Gao[1], [1]*Key Laboratory of Feed Biotechnology of Ministry of Agriculture/Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China,* [2]*College of Animal Science Xinjiang Agricultural University, Urumqi, China.*

Probiotics are living microbial feed supplements which beneficially affect the host animal by improving its intestinal microbial balance. A potentially probiotic strain is expected to have several desirable properties to exert its beneficial effects. The purpose of this study was to characterize the strain *Lactobacillus* sp. GF103 as potential probiotics. The strain was identified as *Lactobacillus plantum* by 16S rRNA sequence analysis (GenBank accession number: JQ411248). It was further characterized for acid and bile salt resistance, simulated gastrointestinal fluid tolerance and antibacterial activity. Results showed that *Lactobacillus* sp. GF103 can fully resist to pH 3 and 0.3% bile salts. The percentage of bacteria viable count was 85% during 3 h under the conditions of the simulated gastric fluid. Viability was not affected during 3-h culture in the simulated intestinal fluid. Antibacterial activity found the strain has ability to inhibit the growth of 2 pathogens, *Escherichia coli* K88 and *Staphylococcus aureus*. The results suggest that the strain *Lactobacillus* sp. GF103 has potential probiotics properties. It can survive and propagate in animal intestinal tract as probiotics additives.

Key Words: probiotics, 16S rRNA, characterization

626 Microbial safety assessment of Juustoleipa cheese manufacture. B. Ganesan,* D. Irish, and C. Brothersen, *Western Dairy Center, Utah State University, Logan.*

Juustoleipa cheese is manufactured by direct acidification of milk and stored either refrigerated or frozen. The cheese has a shelf life ranging from 2 weeks to over several months depending on mode of storage. The cheese is cooked (either toasted or mildly sautéed) before use in foods, which is a post-manufacture step that helps destroy unwanted bacteria. However, even such heat treatments do not exclusively limit bacterial load. To understand microbial quality, spoilage-, and safety-related issues arising from Juustoleipa cheese-making, we hypothesized that survival of unwanted bacteria in Juustoleipa cheese is reduced by frozen storage, thereby altering its shelf life, quality and safety. The objective of the study was to understand how storage conditions and pre-storage baking of Juustoleipa cheese affect its microbial quality. Juustoleipa cheese was made in 3 replicates. *Escherichia coli* and *Pseudomonas fluorescens* were added to separate cheese portions at an initial level of 10^4 cfu/g cheese along with a control (bacteria not added). Bacterial addition was performed 30 min after salting and cheeses were further pressed for 1.5 h and stored refrigerated or frozen with or without pre-storage cooking in a pizza oven (internal temperature of 82°C). We compared the survival of these bacteria by plate counts on selective media in refrigerated and frozen storage conditions that were sampled at a) 0, 14, and 28 d for refrigerated cheese and b) 0, 30, and 90 d for frozen cheese. Bacterial survival was reduced ($P < 0.05$) by 1,000 to 10,000-fold when samples were stored frozen, justifying our hypothesis. Pre-storage cooking of cheese reduced *E. coli* and *Pseudomonas* below detection by plate counts, but aerobic thermoduric bacteria that were incident during manufacture survived cooking at 82°C. As expected, microbial counts in cheeses that were not cooked were higher ($P <$ 0.05) by 10- to 1000-fold compared with those in cooked samples. Characterization of the thermoduric bacteria is underway to comprehend their survival mechanisms. We concluded that pre-storage cooking and frozen storage reduce survival of but do not fully eliminate thermoduric bacteria in Juustoleipa cheese, which might affect its shelf life and microbial quality.

Key Words: Juustoleipa cheese, *E. coli*, *Pseudomonas*

627 Viability of probiotic bacteria and yeasts in traditional and commercial kefir following frozen storage. K. V. O'Brien,* C. A. Boeneke, K. J. Aryana, and W. Prinyawiwatkul, *Louisiana State University, Baton Rouge.*

Kefir is a fermented milk traditionally made from a unique starter culture, which consists of numerous bacteria and yeast species bound together in an exopolysaccharide matrix produced by certain lactic acid bacteria. Many health benefits are associated with traditionally produced kefir; however, bulging and leaking packaging, caused by secondary yeast fermentation during storage, has limited large-scale manufacture of traditionally produced kefir. Commercial kefir products have been designed to reduce these effects by using a pure starter culture consisting of a mixture of bacteria and yeast species that give a flavor similar to traditional kefir; however, some health benefits may be lost in commercial production such as reduced microbial diversity and lack of beneficial exopolysaccharides. The objective of this study was to examine the effects of various periods of frozen storage on the survival of probiotic species in traditional and commercial kefir. The traditional kefir was prepared by inoculating 1 L of pasteurized whole goat milk with approximately 30 g of kefir grains. Commercial kefir was prepared by inoculating 1 gallon of full fat, pasteurized goat milk with a commercial kefir starter (Lifeway Foods, Morton Grove, IL). The milk was allowed to ferment at room temperature (24–28°C) until pH 4.6 was reached. Samples were frozen (−8 to −14°C.) immediately following the completion of fermentation and were thawed and plated for lactobacilli, lactococci and yeasts on d 0, d 7, d 14 and d 30 of frozen storage. Statistical analysis was performed using the variance analysis (ANOVA) F-test ($P < 0.05$). Means were compared by the least squares difference (LSD) test. Lactobacilli, lactococci and yeasts were significantly reduced in number during frozen storage ($P < 0.05$); however, the traditionally produced kefir was shown to have significantly higher counts of bacteria and yeast at each sampling ($P < 0.05$). It was concluded that the development of frozen kefir products would eliminate most packaging concerns associated with large-scale production of traditionally produced kefir, resulting in increased manufacture and marketability of this healthful product.

Key Words: kefir, probiotics, frozen dairy

628 Probing the foaming characteristics of milk proteins. J. A. Stankey*[1] and J. A. Lucey[1,2], [1]*University of Wisconsin-Madison, Department of Food Science, Madison,* [2]*Wisconsin Center for Dairy Research, Madison.*

The strength of protein-protein interactions in foams gas-liquid interface dictate stability and formation of the dispersed gas phase. Molecular properties of proteins determine its overall foamability. Intermolecular interactions within and between casein can be modulated through the addition of salts, which affect the hydrophobic interactions. The Hofmeister salt (HS) series modifies hydrophobic interactions by strengthening (Na_2SO_4) or weakening (NaSCN) protein-protein interactions due to their preferential interactions with water or protein. Comparisons were made with the Hofmeister-neutral NaCl. This study evaluates the importance of hydrophobic interactions in milk protein foams by modifying casein interactions with HS. Mechanisms responsible for foam structure are of practical interest within the food industry. Foams were made from milk protein concentrate solutions (5% protein, w/w; pH 6.6) and HS were added (0.05–1.0 *M*) at 22°C. Protein solutions were whipped in a KitchenAid mixer for 5, 10, 15, or 20 min at the highest speed. Yield stress of foams was measured immediately after 20 min whipping using a rheometer with a vane attachment. Foam overrun and stability were measured at each time point. Foams made with high levels (≥0.5 *M*) HS exhibited salt-specific effects. Foams made with HS that decreased hydrophobic interactions (≥0.05 *M* NaSCN) formed quicker and were more voluminous, less stable, and weaker (yield stress) foams than the other treatments ($P < 0.05$). Foams made with HS that increased hydrophobic interactions (0.05–0.75 *M* Na_2SO_4) required longer time to foam, and produced denser, stronger, and overall more stable foams ($P < 0.05$). At high levels (1.0 *M*) of Na_2SO_4, foams formed slowly due to the high ionic strength and its salting-out effect on proteins. Overrun of foams made with NaCl decreased with increasing concentrations but stability and yield stress increased. Fluorescence microscopy was performed after whipping 20 min. Foams with 0.5 *M* NaSCN had fewer, larger air cells compared with foams made with 0.5 *M* NaCl or Na_2SO_4, which had smaller, more numerous air cells. Hydrophobic interactions between milk proteins at the gas-liquid play an important role in the strength and stability of foams.

Key Words: milk protein concentrate, foaming, Hofmeister series

629 The influence of Bactoscan total bacteria counting (TBC) and preliminary incubation (PI) counting on subsequent infrared milk component results. K. L. Wojciechowski and D. M. Barbano,* *Cornell University, Department of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY.*

Our objective was to determine if sampling and sample handling for TBC and PI counting using a Bactoscan FC influences milk component test results by mid-infrared (IR) milk analysis. Raw milk was gravity separated for 22 h at 4°C. After 22 h, the lower 90% of milk was removed from the cone bottom gravity separation tank and then the cream layer was collected in 6 sequential fractions. The cream from the upper most fraction (highest bacteria count) was used to blend with a portion of the lower 90% (gravity skim about 2% fat) to produce milks with 3, 4, and 5% fat in addition to the gravity separated milk with no added cream. Milk at each fat concentration was mixed and split into 60 vials. If the removal of a test portion from a sample container by the auto-sampler of the Bactoscan when the milk was cold removed a non-representative portion of fat, then the effect of sampling on IR results would be expected to increase progressively with increasing fat concentration. The TBC count is done on fresh cold milk while the sample for the PI is incubated for 18 h at 14°C before testing. Within each fat level, 20 vials of milk were tested by IR only, 20 vials by Bactoscan TBC followed by IR, and 20 vials by Bactoscan TBC and PI, followed by IR. This was replicated 3 times with a new batch of milk and the samples were tested using a different Bactoscan FC in a different laboratory in each replicate. Running TBC with a Bactoscan first followed by IR milk analysis had minimal effect (<0.01%) on milk component tests when milk bacteria counts were within Pasteurized Milk Ordinance limits <100,000 cfu/mL. For milks with bacteria counts of > 500,000 cfu/mL, there was an effect on the fat test results. Running PI counts had an effect ($P < 0.05$) on IR component tests. The effect on component testing by IR was due to microbial growth in the samples, not the physical process of sampling by the Bactoscan. The effect of microbial growth was the largest on fat tests. The direction and magnitude of change in component tests will vary depending on the bacteria count, the type of bacteria that grow and the compounds they product in the milk.

Key Words: milk payment testing, bacteria testing, Bactoscan

630 Protective action of serum amyloid A3 against *Salmonella* Dublin infection.

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Milk is an important source of antimicrobial compounds. Serum amyloid A3 (SAA3) is an acute phase protein expressed at high levels in colostrum and may be an important candidate for the protection of calves against intestinal infections. Previous studies have explored its protective role in the gastrointestinal tract indicating that it inhibits the binding of enteropathogenic bacteria in cell cultures. However, the SAA3 potential at regulating the intestinal immune response has been poorly explored. The objective of this study was to evaluate the SAA3 effects in infected and non-infected tissues ex vivo, quantifying the associated immune response and bacterial internalization. A total of 28 punches of 8-mm diameter from jejunal bovine Peyer patches were cultured in 24-well plates with Krebs media and assigned to 2 different treatments: with or without recombinant SAA3 (n = 14 per treatment). Tissues were incubated for 3 h at 37°C and 5% CO2. After the first hour of incubation, jejune explants were challenged with 10^2 cfu/well of *Salmonella* Dublin (n = 20), according to previous optimization of the ex vivo enteropathogenic model, or incubated with media (n = 8). For cytokine quantification, total RNA was extracted from the tissue and IL-8 and INF-γ levels were quantified by qPCR. To determine internalized bacteria, tissue fragments were homogenized and viable cell counts were enumerated by colony counting after serial dilution plating. Data were analyzed using an ANOVA test. In non-infected tissues, pro-inflammatory IL-8 response increased ($P < 0.05$) with the presence of SAA3. Moreover, the SAA3 treatment tended ($P = 0.08$) to double the expression of IL-8, and increased ($P < 0.05$) the expression of INF-γ in infected tissues. Furthermore, SAA3 clearly decreased ($P < 0.05$) *Salmonella* Dublin infection ($5.1 \times 10^3 \pm 1.3 \times 10^3$ cfu/mL versus $1.6 \times 10^3 \pm 0.46 \times 10^3$ cfu/mL with SAA3). In conclusion, SAA3 enhances inflammatory immune response in the gastrointestinal tract and suggests a direct protective effect against intestinal infections such as that caused by *Salmonella* Dublin.

Key Words: SAA3, intestine, *Salmonella* Dublin

Dairy Foods: Physico-Chemical Properties

631 Development of whey protein concentrate incorporated dietetic kulfi. H. G. Ramachandra Rao*[1] and A. Giri[2], [1]*Dairy Science College, Bangalore, Karnataka, India,* [2]*National Dairy Research Institute, Karnal, Haryana, India.*

Kulfi, a traditional Indian frozen dairy product has a similar composition to that of ice cream. Kulfi is made by concentrating whole milk (5% fat and 8.5% SNF) by 2 fold and then added with sugar, sodium alginate, glycerol monosterate and cardamom. The mix is then pasteurized, placed in molds and hardened to the consistency of ice cream. The objective of our study was to produce kulfi with reduced sugar and enriched with whey protein concentrate without compromising the sensory quality. Stevia, non-caloric natural sweetener, which is about 300 times sweeter than sucrose and heat stable up to 200°C was used as a sugar replacer to an extent of 50, 60 and 70 by 0.05, 0.06 and 0.07% respectively. At higher levels of sugar replacement, there was significant decrease of specific gravity, melting rate, and significant increase of freezing point, hardness and fat, protein, ash and moisture percentage. 50% sugar replaced kulfi was adjudged by a panel of 5 experts (using ice cream score card) on par with the control in sensory characteristics. Above 50% sugar replacement there was lack of brownish appearance, increased bitterness and presence of icy texture. Further, the study was conducted with incorporation of different levels of whey protein concentrate (WPC) at 0, 2, 3 and 4% respectively on the basis of concentrated milk and mixing thoroughly and hardening at −20°C for 8 h. When the levels of WPC addition increased there was significant decrease of freezing point (due to higher levels of soluble constituents - whey protein, lactose and mineral from WPC), melting rate (for improved water binding ability and stability for whey proteins), hardness (for water binding property which imparts reduced iciness) and moisture percentage but significant increase of specific gravity (for increase water binding ability of WPC), protein percentage and total calorie content. Among control and treated samples up to 3% addition of WPC overall acceptability score increased due to increase body and texture for excellent functional properties of whey protein but above 3% addition of WPC there was detectable whey flavor and excess softness. Statistically significance was tested by employing ANOVA and comparison between means was made by critical difference (CD) value. It was concluded that kulfi made with 50% replacement of sugar using stevia and 3% WPC incorporation was acceptable.

Key Words: kulfi, stevia, whey protein concentrate

632 Application of ultrasound spectroscopy to monitor lactose crystallization. J. K. Amamcharla*[1], L. E. Metzger[1], and R. Tweedie[2], [1]*Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings,* [2]*Industrial Tomography Systems plc, Manchester, UK.*

Lactose accounts for about 75 and 85% of the solids in whey and deproteinized whey, respectively. Production of lactose is usually carried out by a process called crystallization. Several factors including rate of cooling and mixing speed influence the crystal characteristics. Therefore, it is important to monitor the crystallization process. The objective of the present work was to use ultrasound spectroscopy as a tool to monitor the lactose crystallization process. Unlike conventional optical spectroscopy techniques, ultrasound spectroscopy can be used to characterize highly concentrated or optically opaque samples. An in situ ultrasound probe operating in pulse-echo mode connected to an ultrasound spectrometer (U2s, Industrial Tomography Systems, Manchester, UK) was used to acquire attenuation and velocity of ultrasound over the frequency range 5 and 20 MHz. In the first preliminary experiment, it was found that the attenuation of ultrasound in under-saturated lactose solutions was not influenced by temperature and lactose concentration. In the second preliminary experiment, it was found that the ultrasound attenuation increased along with an increase in the amount of crude lactose crystals. Lactose crystallization studies were conducted in a batch crystallizer (1000 mL). Supersaturated lactose solutions (70 g/100 g water) were prepared and crystallized using an isothermal batch process at 25°C. At regular intervals, 1mL of the crystal suspension was removed from the crystallizer and centrifuged to separate the crystals from the aqueous phase. The dissolved lactose in the aqueous phase was measured using a refractometer to determine crystallization kinetics. The separated crystals were washed with cold water (<5°C) and an image was acquired under 10× magnification using a camera attached to a microscope. As soon as the crystals appeared (20 μm), the ultrasound attenuation increased at frequency 12 MHz. Subsequently, the attenuation at other frequencies also increased as the concentration of lactose in soluble phase decreased. Overall ultrasound spectroscopy shows potential for monitoring the lactose crystallization process.

Key Words: ultrasound, lactose crystallization, in situ

633 Heat induced aggregation of whey proteins as influenced by shear, pH, and protein concentration. M. Dissanayake, L. Ramchandran, and T. Vasiljevic,* *Advanced Food Systems Faculty Research Unit, School of Biomedical and Health Sciences and Institute for Sustainability and Innovation, Victoria University, Werribee Campus, VIC, Australia.*

Microparticulation of whey proteins (WP) is understood to improve their functional properties that could enhance their utilization. However, shear forces used in microparticulation of WP can modulate their functional properties by altering their structure. The main objective of this study was to monitor the effect of simultaneous heating (90°C/20 min) and shearing (100, 500 or 1000/s) on WP aggregation at different protein concentrations (5, 10, 17.5 or ~25% w/w) and pH (3, 5 or 7). WP retentates (Warrnambool Cheese and Butter Factory, VIC, Australia) were simultaneously subjected to shear and heat using rheometer geometry. The sheared and heat treated WP were then analyzed for the conformational and structural changes by measuring turbidity, gel color, PAGE and surface hydrophobicity. Results from these tests indicated that application of shear reduced the formation of molecular associations including covalent bonds particularly at pH 7 while the reverse was true at pH 5. Surface hydrophobicity of WP increased significantly ($P < 0.05$) when sheared at pH 5 suggesting greater denaturation than the control and at pH 3 and 7, which further increased significantly ($P < 0.05$) with increase in shear rate at protein concentrations up to 10%. Turbidity tests indicated that shear forces significantly increased ($P < 0.05$) aggregate growth at pH 5, while at pH 3, protein concentration significantly increased ($P < 0.05$) the size of aggregates. Thus, the rate of denaturation and size of resulting aggregates was dependent on pH, protein concentration, and intensity of the shear forces applied. However, shear rate alone did not affect ($P > 0.05$) the color (lightness, L*) of the shear heat-induced WP gels but the effect was significant ($P < 0.05$) along with changes in pH and protein concentration. It was concluded that simultaneous heating and shearing of WP could modify the surface properties of the WP that could change the direction and extent of heat-induced WP denaturation and aggregation.

Key Words: whey proteins, aggregation, heat/shear

634 Effect of pH and protein concentration on denaturation kinetics of whey proteins.

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Microparticulation of whey proteins (WP) has been implied to help overcome the loss of protein functionality accruing from traditional heat processing. This study examined the reaction kinetics of WP aggregation as a function of pH (4–6) and protein concentration (10, 17.5 and 25%, wt/wt) to help devise a more feasible pathway to produce microparticulated WP powder having small particle size. WP retentates (Warrnambool Cheese and Butter Factory, VIC, Australia) were heat treated at 140°C for 5–20 s in an oil bath. The thermal behavior of the WP was assessed using differential scanning calorimeter while the kinetics of denaturation was examined using capillary electrophoresis. The extent of protein aggregation was monitored by measuring solubility and turbidity. The denaturation and aggregation of β-Lg appeared to follow the first order reaction kinetics under steady state conditions. The reaction rate constant (k) obtained suggested distinctly higher rate of denaturation and aggregation when WP dispersions having 10% protein concentration were heated at pH 5. Also, the decline in k values was more noticeable at pH 4 than at pH 6 indicating a slower rate of denaturation at pH 4. At higher concentrations of protein, the rate of aggregation was not prominent at pH 5. Heat induced changes at low protein concentration reduced the solubility of WP regardless of pH, the reduction being significant ($P < 0.05$) during the first 5 s of heating at pH 5 and 6. The rate of decrease in solubility was significantly ($P < 0.05$) greater at pH 6 than at pH 4 and 5. The turbidity of WP dispersions at pH 4 were significantly higher ($P < 0.05$) than those at pH 5 and 6, suggesting that WP were most stable against heat induced denaturation at high protein concentration and low pH. Results from differential scanning calorimetric studies indicated that rate of WP denaturation varied with protein concentration and pH, being highest at 10% concentration and pH 5. It was concluded that microparticulation of WP at low pH and high protein concentration could produce heat stable WP ingredients.

Key Words: whey proteins, kinetics, denaturation

635 Comparison of heat stability of bovine milk subjected to UHT and in-container sterilisation.

B. Chen,* F. Ren, A. Grandison, and M. Lewis, *University of Reading, Reading, UK.*

The objective of this study was to compare how the heat stability of bovine milk was affected by the UHT and in-container sterilization. In addition, stabilizing salts are added to bovine milk to decrease ionic calcium concentration in milk and the roles of different stabilizing salts (di-sodium hydrogen phosphate and tri-sodium citrate) in both heat treatments were evaluated. Heat stability was assessed by measuring the amount of sediment in the bovine milk. Sediment formation provides a robust way of measuring heat stability during in-container sterilization, as standard deviations were small for replicated determinations of the same sample. Without stabilizing salts, bovine milk produced more sediment when subjected to UHT processing compared with in-container sterilization. Addition of up to 12.8 m*M* stabilizing salts resulted in a significant ($P < 0.05$) increase in sediment for in-container sterilization. This arises due to the considerable increase in measured casein micelle size during in-container sterilization. The existence of this lower heat stability region has not been specifically pointed out previously, since it is not intuitive that reducing ionic calcium will decrease heat stability. In contrast, adding 6.4 m*M* DSHP (di-sodium hydrogen phosphate) initially reduced sediment formation in UHT treated milk but this increased on addition of 12.8 m*M* DSHP. However, Adding up to 12.8 m*M* TSC (tri-sodium citrate) resulted in a continuous increase in sediment in UHT processing. Adding these stabilizing salts to bovine milk increased pH, decreased ionic calcium and increased casein micelle size. Adding up to 2 m*M* calcium chloride increased sediment formation significantly ($P < 0.05$) more after UHT treatment than after in-container sterilization. These results for bovine milk are in agreement with trends found for heat stability of caprine milk, which have been published previously. It was concluded that there is no single mechanism or set of reactions that cause milk to produce sediment during heating and that the kinetics are different for UHT and in-container sterilization processes. Poor heat stability could be induced by both increasing and decreasing ionic calcium.

Key Words: heat stability, UHT, in-container sterilization

636 Investigating the influence of phospholipids on the viability of *Streptococcus thermophilus* and *Bifidobacterium lactis.*

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The potential health benefits and improved extraction methods of dairy phospholipids from by-products such as buttermilk and whey have opened new avenues for dairy phospholipids (PL) application in foods; one such application is fortification of yogurt with PL. However, before fortification, it is critical to evaluate if PL inhibit common lactic acid bacteria (LAB) used in yogurt. The objective of this research is to determine the influence of PL on viability of *Streptococcus thermophilus* (ST), *Bifidobacterium lactis* (BL), *Lactobacillus delbrueckii* ssp. *bulgaricus* (LB) and *Lactobacillus acidophilus* (LA) in yogurt. In preparation for work in yogurt, ST and BL were grown in M17 and MRS broth respectively, fortified with one of 5 PL: phosphatidylcholine (PC), phosphatidylethanolamine (PE), phosphatidylinositol (PI), phosphatidylserine (PS), and sphingomyelin (SM). Growth was monitored at a) optimum growth temperatures and b) 5°C above the optimum growth temperatures (42°C ± 1and 47°C ± 1 for ST and 37°C ± 1 and 42°C ± 1 for BL, respectively). The temperature spike of 5°C from optimum growth temperatures was selected to "stress" bacteria in a way that may occur during yogurt processing. The PL were fortified at the rate of 0.01% wt/vol. The LAB were enumerated at 0, 3, 6 and 9 h time intervals using the pour plate technique. At optimum temperature, after 9 h, ST and BL counts tended to be higher when media were fortified with PL than when not. At elevated temperatures, most PL showed a similar trend, except ST, which was slightly inhibited by PS and PI, and BL by PE. No statistically significant differences ($P > 0.05$) were recorded in the viability of ST and BL in the presence or absence of PL or across temperatures. The results suggest that phospholipids do not have profound beneficial or inhibitory influences on ST and BL. However, viability studies in yogurt and on the remaining lactic acid bacteria must be conducted to determine fortification of PL in yogurt is a promising venture.

Key Words: phospholipids, *Streptococcus thermophilus*, *Bifidobacterium lactis*

637 Elucidating the role of α_{s2}-casein in the superior functionality of acid gels prepared from high-pressure-treated milks compared with heat-treated milks.

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The objective of this study was to compare the functional properties of heat- and high-pressure-treated milks and elucidate the mechanisms

for differences in their functionality. Samples of low heat skim milk powder reconstituted to 10% total solids (wt/wt) were heat treated at 90°C for 10 min or pressure treated at 600 MPa for 3 min. Acid gels were prepared from these heat- and pressure-treated milk samples and rheological measurements (G′, G″, tanδ) were carried out. Samples were also centrifuged into a soluble (serum) phase and an insoluble casein micelle (pellet) phase and analyzed using PAGE techniques to study the interactions of proteins as affected by heat and pressure treatments of the samples. Both the heat- and pressure-treated samples generated a range of disulfide-linked aggregates, which were much larger in the heat-treated samples than the pressure-treated samples. The acid gel strengths were significantly greater in pressure-treated samples (1000 Pa) compared with heat-treated samples (200 Pa). The PAGE techniques suggested that the casein-whey protein (WP) complexes in the soluble phase consisted mainly of disulfide-linked complexes of κ-casein with β-lactoglobulin and other WPs, with little evidence of the presence of α_{s2}-casein, in the heat-treated samples, but contained significantly higher proportions of both α_{s2}- and κ-casein in the pressure-treated samples. The higher acid gel strengths of the pressure-treated samples, compared with the heat-treated samples, can be explained by the presence of greater amounts of soluble casein-WP complexes and the involvement of α_{s2}-casein (in addition to κ-casein) in the disulfide-linked interactions with WPs. Generally, α_{s2}-Casein is buried inside the casein micelles and is not easily accessible for casein-WP interactions whereas κ-casein protrudes outside the micelles and is readily available. High-pressure treatment affects the colloidal calcium phosphate complex; it dissociates/solubilizes the casein micelles, therefore exposing α_{s2}-casein and making it readily available, whereas only the κ-casein is accessible in heat-treated samples. These results clarify that α_{s2}-casein has a special role to play in improving the functional properties of high-pressure-treated milks.

Key Words: high pressure, heat, casein

638 Coagulation properties of the casein micelle by combination of ultrafiltration and dilfiltration measured using rheology and diffusing wave spectroscopy. J. G. Luo*[1,2], E. Kristo[1], and M. Corredig[1], *[1]Department of Food Science, University of Guelph, Guelph, ON, Canada, [2]Gay Lea Foods Co-operative Ltd., Guelph, ON, Canada.*

The objective of this work is to understand how casein micelles (CM) are affected during milk protein concentrates (MPC) manufacturing and what effect this may have on its coagulation properties. The changes in structure function of the CM occurring in MPC are a topic of great interest in dairy technology. There is limited research of coagulation properties of the casein micelle during MPC manufacturing. This study investigates the changes in the renneting functionality of fresh retentates and reconstituted retentates by combination of ultrafiltration and dilfiltration. Reconstitution was carried out in milk or milk serum (permeate). The rennet gelation behavior of reconstituted retentate was also compared with a control reconstituted freeze-dried skim milk powder (6% protein level). The renneting behavior of the CM was followed using rheology and diffusing wave spectroscopy (DWS). The release of caseinomacropeptide was also quantified. Soluble calcium and total calcium were measured to understand the effect of this ion on the mechanism of the gelation. Concentrated fresh retentate and reconstituted MPC (17.5% protein) formed significantly stiffer gels than regular samples (6% protein) due to increased number of bonds in the network. There were no significant difference in casein micelle size between fresh retentate and reconstituted retentates. The reconstituted retentates at 6% protein were dialyzed against skim milk to ensure the ionic equilibrium of the samples were similar to skim milk. The release of the caseinomacropeptide during renneting was also not significantly different among the samples tested at the same protein concentration. No significant differences were noted in the rennet coagulation time as tested by both DWS and rheology. After dialysis against milk, the gelation time of the samples was shorter and the gel modulus higher than for the nondialyzed samples. Based on our result, we conclude that ionic equilibrium is important in the reconstitution of MPC for rennet-induced gelation of milk.

Key Words: ultrafiltration, dilfiltration, rennet

639 Composition and physical properties of dairy products in the UK. B. Chen,* A. Grandison, and M. Lewis, *Univerisity of Reading, Reading, UK.*

The objective of this study was to investigate the effect of raw milk composition on some selected properties of milk products. Raw bulk cow milk was collected and its composition and physical properties were measured every 2 weeks. This milk was then converted to a range of products using standardized methodology and selected properties of these products were measured. Products include evaporated milk, soft cheese, skim milk powder, whipping cream, UHT milk and in-container sterilized milk. Results presented are those from the first 6 batches of raw milk, collected over the period August to December 2011. This project is ongoing and will be replicated with a minimum of 25 batches of raw milk. The range of values for fat and protein were 4.04 to 4.77% and 2.89 to 3.29% respectively. Ranges for lactose (4.26 to 4.69%), total solids (12.45 to 13.32%), pH (6.74 to 6.78), buffering capacity (pH change from 0.83 to 0.88) and ethanol stability (87 to 94%) were narrower. Ca^{2+}concentration ranged from 1.75 to 2.55 m*M*. Sediment in raw milk was very low, ranging from 0.10 to 0.12% (dry weight basis). Viscosity ranged from 1.56 to 2.31 cp and density from 1.026 to 1.031 g/cm^3. Casein micelle size ranged from 160 to 200 nm and freezing point depression from −0.525 to −0.514. The longest foaming times were 75 and 61 s for raw and skim milk, respectively, and the shortest were 24 s and 19 s. Foam stability was more variable, ranging from 76 s and 72 s to 213 s and 435 s for raw and skim milk, respectively. The viscosity range for evaporated milk was wide and was also affected by the level of added stabilizer. The range of for sediment for UHT and in-container sterilized milk was from 0.16 to 0.29% and from 0.18 to 0.31% respectively. Sediment formation was always accompanied by an increase in casein micelle size. For the whipping cream, the overrun and hardness were constant, ranging from 151 to 153% and 0.13 to 0.15 N, but the range of stability was more variable (14.63 to 18.75 mL). The heat stability of skim milk powder showed considerable variability. The ranges of the moisture content and hardness in soft cheese were 55.5 to 59.1% and 1.27 to 2.26 N respectively. It was concluded that variations in raw milk composition influence the properties of manufactured milk products.

Key Words: raw milk quality, physico-chemical properties, best use for milk

Extension Education II

640 Assessing a team-based educational program designed to build communication skills for practicing dairy veterinarians. G. M. Schuenemann*[1], D. J. Klingborg[2], D. A. Moore[3], and J. D. Workman[1], [1]*Department of Veterinary Preventive Medicine, The Ohio State University, Columbus,* [2]*School of Veterinary Medicine, University of California, Davis,* [3]*Department of Veterinary Clinical Sciences, Washington State University, Pullman.*

The purpose of the study was to assess the effectiveness of a team-based educational module designed to build communication skills for practicing dairy veterinarians. A comprehensive program on leadership and communication skills 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 advanced module (~2 d and ~20 h of learning) in 2011. The program consisted of the following topics: insights of participants; communication styles; personality influences; group dynamics/effective teams; rationale and interpersonal skills in team problem solving; communication lab-survival; communication model; re-write messages; elements of effective listening; conflict management; critical thinking, decision making and priority setting; elements of effective management of meetings and facilitation; message mapping; and communication limitations. Educational materials were delivered through in-class lectures followed by case-based learning, group discussions, and participant presentations resulting from an out-of-class assignment. Attendees were assessed using pre- and post-tests of knowledge to determine the level of knowledge gained during the module. Participants evaluated the program and provided feedback at the conclusion of each module. Veterinarians (100%) reported that the overall program, presentations, and discussions were useful. Attendees found the presented information relevant for their work (neutral = 2.3%, agree = 38.3% and strongly agree = 59.4%), and of great immediate use to them (neutral = 1.7%, agree = 43.9% and strongly agree = 54.4%). The presented materials and the implemented educational delivery methods substantially increased the knowledge level of the attendees (13.6% points increase from pre- to post-test scores; $P < 0.05$). Importance of teamwork and communication styles, developing and improving messages, elements for effective management of meetings, and conflict management styles were listed as learned concepts that participants can apply in their practices. This program has important implications for dairy veterinarians because they are a vital source of information for dairy producers.

Key Words: communication, veterinary, continuing education

641 Assessing a team-based educational program on nutrition and reproductive management for small dairy producers. G. M. Schuenemann*[1], W. P. Weiss[2], and J. D. Workman[1], [1]*Department of Veterinary Preventive Medicine, The Ohio State University, Columbus,* [2]*Department of Animal Sciences, The Ohio State University, Wooster.*

The purpose of the study was to assess the effectiveness of a team-based educational program designed to enhance the transfer of applied research-based practices to dairy producers and their veterinarians to enhance sustainability of small dairy operations. A comprehensive program on nutrition and reproductive management was developed and participants from 2 veterinary practices and 69 dairy producers (<100-cow herds), attended the on-farm modules (~6 h of learning). The nutrition program consisted of the following topics: corn silage harvesting (moisture content, particle size, cut length, and inoculants); silage management (spoilage); choosing feeds; and maintaining ration consistency. The reproductive program consisted of the following topics: estrous cycle, synchronization strategies (estrus detection and compliance to protocols); factors affecting reproductive performance; record analysis; and AI technique. Educational materials were delivered through on-farm lectures followed by case-based learning, and group discussions. Attendees were assessed using pre- and post-tests of knowledge to determine the level of knowledge gained during the module. Participants evaluated the program and provided feedback at the conclusion of each module. Dairy producers (100%) reported that the overall program, presentations, and discussions were very useful. Attendees found the presented information relevant for their work (neutral = 3%, agree = 45% and strongly agree = 52%), and of great immediate use to them (neutral = 13%, agree = 43% and strongly agree = 44%). The presented materials and the implemented educational delivery methods substantially increased the knowledge level of the attendees (23 percentage point increase from pre- to post-test scores; $P < 0.05$). Additionally, >80% of participants indicated that they were highly confident (>75%) that they will apply the new learning into their operations. Handling corn silage, value of reproductive management, effect of nutrition and health management on herd performance, assessment of feed prices before buying, and teamwork and communication were listed as learned concepts that participants can apply in their operations. This program has important implications for small dairy operations and their sustainability.

Key Words: small dairy herd, reproduction, nutrition

642 I. Interactive index to identify and rank risk factors affecting reproductive performance of lactating dairy cows under field conditions. S. Bas*[1], P. Federico[2], and G. M. Schuenemann[1], [1]*Department of Veterinary Preventive Medicine, The Ohio State University, Columbus,* [2]*Department of Mathematics, Computer Science, and Physics, Capital University, Columbus, OH.*

Many factors influence the reproductive and productive performance of dairy herds, thus, profitability. It is common to observe large between-herd variation in pregnancy rate (PR) of lactating dairy cows. Successful identification of factors affecting reproductive performance at herd level can be challenging due to their multi-factorial nature. The objective was to develop an interactive dairy herd index (DI) to aid in decision making about reproductive management of dairy cows. The DI was developed to identify and rank risk factors (stillbirth, retained fetal membranes, metritis, mastitis, lameness, body condition score, estrus detection, conception risk, labor-cow ratio, and stocking density) affecting PR according to their weights. Novel components of the DI included: 1) Desirable values for the selected risk factors (DV; estimated from the literature as reference for desirable PR), 2) Contribution weights for individual risk factors (CW; computed using linear regression), 3) Relative difference [RD = (DV-value of individual risk factor from herd to be assessed)/DV], and 4) DI by component (DI = RD*CW), 5) Ranking of risk factors according to their DI, 6) Overall DI for the herd (Positive or negative values move around the DV). The incidence of selected risk factors, collected from on-farm records, is compared with the DV and their individual CW to obtain individual and overall DI. Additionally, the regression nature of the DI helps the decision makers to be aware of the CW of each risk factor on PR due to herd management. Often time dairymen, consultants, and veterinarians trouble-shoot poor reproductive performance within-herd and the incidence of risk factors and their CW on PR varies greatly from farm-to-farm. Therefore, ranking within-herd risk factors with greater CW on PR is critical to implement corrective strategies step-by-step. Through a mechanistic approach, we ranked real herd risk factors affecting PR according to their CW (e.g., stocking density).

Key Words: dairy herd index, risk factor, pregnancy

643 Using real-time futures market simulation to teach dairy risk management. M. E. Sowerby* and J. J. VanSickle, *University of Florida, Gainesville.*

Less than 5% of all dairy producers use hedging strategies to manage price risk on their operations. To help producers gain knowledge, experience and confidence in using futures and options, a program featuring FACTSim, a financial and agricultural commodity trading simulator which uses real-time market data, was developed. FACTSim gives producers the opportunity to apply risk management concepts without losing real money. By using FACTSim, producers have gone beyond concepts to put together marketing goals to service farm debt needs and profit strategies to realize their farm goals. In the process of learning the fundamentals behind primarily milk, corn and soybean market movement, dairy producers have also become better at advanced ordering feed and using livestock gross margin (LGM)-Dairy insurance. Producers who have been involved in the program are now using futures options to hedge, gaining savings on advanced ordered feed and finding peace of mind using LGM-Dairy insurance.

Key Words: risk management, futures market, FACTSim

644 A decision support tool for investment analysis of new dairy housing facility construction. R. A. Black* and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this research was to develop a decision support tool, in the form of a user-friendly dashboard, for investment analysis of new dairy housing facility construction. User inputs included milking herd size, daily milk yield per cow, long-term milk price (MP), daily lactating cow feed cost, hourly labor cost, time to move cows, SCC bonus structure, SCC, and clinical mastitis and lameness incidence rate. New facility inputs included per cow barn cost (CBC), bedding cost (BC) and usage rate, tax rate, discount rate, interest rate, predicted daily increase in production per cow (PPC), predicted time to move cows, predicted time to stir the pack or rake stalls, and predicted reduction in SCC (PSCC), lameness incidence (PL) and clinical mastitis incidence (PCL). Investment analysis outputs included net present value (NPV), internal rate of return (IRR), breakeven barn cost, and payback period (PP). Model assumptions were obtained from published literature and farm surveys. This dashboard did not account for manure handling or culling costs. To compare alternative facilities with all model assumptions held equal except CBC, CBC were set at $850 per cow space for a compost bedded pack barn (CBP), $1,306 for a freestall barn with mattresses (FSM), and $1,021 for a freestall barn with sand (FSS). The NPV, IRR, and PP for the alternative facilities were CBP: $5,042, 9%, and 6.1y, respectively; FSM: $5,673, 9% and 6.8y, respectively; and FSS: $27,844, 13%, and 5.1y, respectively. A breakeven analysis was conducted for each of the 3 systems that would return a NPV of zero by changing BC, CBC, MP, PPC, PSCC, PL, or PCL. Results are depicted in the table below.

Table 1. Breakeven analysis for each of the 3 systems

System	BC	CBC	MP	PPC	PSCC	PL	PCL
CBP	$566	$909	$18.24	1.9kg	22.8%	44.1%	29%
FSM	$167	$1,061	$21.80	2.4kg	NA	NA	NA
FSS	$578	$1,214	$16.67	1.8kg	55.2%	80.8%	29%

Key Words: economic dashboard, compost bedded pack barn, freestall barn

645 Quantifying the effect of an extension programme (InCalf) on the reproduction performance of New Zealand dairy herds using a randomized controlled study. T. S. Brownlie*[1,2], J. M. Morton[3], C. Heuer[2], and S. McDougall[1], *[1]Cognosco, Anexa Animal Health, Morrinsville, New Zealand, [2]Epicentre, Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand, [3]Jemora Pty Ltd., Geelong, Victoria, Australia.*

There has been a national decline in the herd average reproductive performance and an increase in between herd variation of the New Zealand dairy herd. A national reproductive extension program (InCalf) has recently been introduced. A study was established to quantify the effects of this program on the reproductive performance of enrolled herds as well as benchmarking the reproductive performance of the national herd. The study was a multi-herd, multi-year randomized controlled study in 4 key dairy regions of New Zealand. In total, 168 herds were ranked based on estimates of the proportion of cows pregnant in the first 6 weeks of the seasonal breeding programs ("6-wk in-calf rate") and randomly allocated to either 1 of 2 control groups (n = 95) or the treatment group (n = 73) that received a 12 mo series of structured meeting with trained advisors ('farmer action groups'). The herds were monitored in the year of the farmer action group and the subsequent year. Monitoring included collection of cow demographic data, BCS, heifer weights, all breeding and disease events and 180,000 pregnancy tests. Social science interviews were conducted to capture the attitudes, priorities and constraints perceived by farmers. Preliminary results indicate that the mean 6-wk in-calf rate for the control group remained similar across years at 67% (95% CI: 66–68). The median 3 week submission rate (i.e., proportion of the herd bred in the 1st 3 weeks of the breeding program) remained at 81% (95% CI: 80–82) across years but the median conception rate to first breeding declined to 48% (95% CI: 47–49). A multivariable model including biophysical and demographic explanatory variables (including region and season) found allocation to treatment was associated with a small but not statistically significant increase in 6-wk in-calf rate. More variation was explained by reproductive performance at allocation and variation between herds was greater than between years. Determinants of changes in herd reproductive performance will be explored to refine expectations and strategies for delivery of extension programs.

Key Words: dairy, extension, reproduction

646 Stochastic simulation of the impact of commodity price variation on mastitis costs. D. Liang*[1], M. M. Schutz[2], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]Purdue University, West Lafayette, IN.*

The objective of this research was to evaluate the impact of varying commodity prices on 2012 mastitis costs. The dynamic, stochastic, simulation farm-level model described by Bewley et al. (2010) and constructed using Microsoft Excel (Microsoft, Seattle, WA) and the @ Risk Monte Carlo simulation add-in (Palisade Corp., Ithaca, NY) was used to calculate mastitis costs and associated sensitivities. Baseline milk, replacement cow, slaughter, corn, soybean, and alfalfa prices were established using USDA NASS prices from 1971 to 2011 and stochastic predicted prices were modeled using FAPRI (Food and Agricultural Research Institution, Columbia, MO) estimates for 2012 to 2021. Feed cost was calculated using corn, soybean and alfalfa prices based on the USDA feed cost formula. A 163 cow US dairy, with default herd parameters established using DairyMetrics (Dairy Records Management Systems; Raleigh, NC) and published literature, was simulated through 5000 iterations. Mean (±SD) mastitis costs for parity 1 (P1) and later parity (P2) cows were \$240.98 ± 31.95 and \$192.08 ± 24.28 per case, respectively. For P1, costs (mean ± SD) were as follows: veterinary and drug costs (\$18.33 ± 1.83), labor costs (\$20.00 ± 2.00), discarded milk (\$55.21 ± 8.55), lost milk (\$93.78 ± 21.96), reduced days open (\$0.98 ± 1.78), culling (\$43.45 ± 10.80), and death (\$9.24 ± 1.27). In P1, mastitis costs were highly correlated with milk price ($r = 0.81$), moderately correlated with replacement price ($r = 0.464$) and feed cost ($r = -0.47$), and lowly correlated with slaughter price ($r = -0.18$). For P2, costs were as follows: veterinary and drug costs (\$18.33 ± 1.83), labor costs (\$20.00 ± 2.00), discarded milk (\$55.21 ± 8.55), lost milk (\$62.53 ± 16.56), reduced days open (\$0.98 ± 1.78), culling (\$25.11 ± 5.43), and death (\$9.93 ± 1.36). In P2, mastitis costs were highly correlated with milk price ($r = 0.88$), moderately correlated with feed cost ($r = -0.43$) and replacement price ($r = 0.28$), and lowly correlated with slaughter price ($r = -0.09$). These estimates may be used in on-farm mastitis decisions reflecting varying commodity prices.

Key Words: mastitis economics, commodity prices, stochastic simulation

647 A model: The Alabama Coalition for Farm Animal Care and Well-Being–A unified approach to animal care and well-being.

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The purpose of the Alabama Coalition for Farm Animal Care and Well-Being is to provide a unified approach to animal care and well-being across all farm animal species in Alabama. The Coalition serves as a body of knowledge for legislators and political groups on issues of farm animal care and well-being; provides a unified approach on animal care and well-being; is an advocate for a safe and abundant food supply; serves as a spokes-group for animal care in Alabama; is proactive in education for producers, consumers, and policy makers on animal care and well-being; provides a science perspective on issues affecting animal agriculture; provides training forums on issues of animal agriculture to producers, and regulators; is a forum of consensus building on animal agriculture. The governance of the Coalition is by a board of trustees (BOT) with an executive committee (EC) supported by a well-founded membership. The BOT consists of one voting member from each of the full-member partners of the Coalition. The EC consists of a president, vice-president, secretary-treasurer, and 4 directors at large. The Coalition membership consists of 1. full member: farm animal related organizations directly involved with animal agriculture and Alabama Land Grant Universities agriculture programs and Colleges of Veterinary Medicine, and 2: associate member: organizations indirectly involved with animal agriculture. Two major standing committees of the Coalition are (1) Education and (2) Legislative. The education committee works for the development of educational programs for stakeholders. The legislative committee provides a linkage to the state's legislative activities effecting farm animal care and well-being. Through the educational efforts of the Coalition, the Animal Agriculture 101 program, a training course in basic concepts of animal care and well-being, was delivered to educate law enforcement on adequate farm animal care. The course creates a resource for local officials in dealing with animal care complaints. The Coalition member organizations were an integral part in passing Alabama's HB561: Animal Industry Bill, a bill which strengthens the authority of the state veterinarian regarding setting the standards and procedures for animal protection within the state.

Key Words: well-being, coalition, welfare

Food Safety: Advances in Food Safety

648 Antimicrobial use in preweaned calves: Effects on fecal *E. coli* resistance.

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Antimicrobial use in food animals can potentially lead to resistant bacteria and future inability to use some antimicrobials for humans. The objective of this study was to determine the effect of fed antimicrobials and antimicrobial treatment on resistance in calf fecal *E. coli*. Newborn calves (n = 118) were allocated to 1 of 4 groups and monitored for 28 d. Calves in the conventional therapy group were treated as per dairy protocol with trimethoprim-sulfa, spectinomycin, penicillin, and bismuth-pectin for diarrhea. The targeted therapy group included a physical examination and treatment with bismuth-pectin for diarrhea and ceftiofur and trimethoprim-sulfa in cases of fever. Within treatment groups, calves were equally assigned to receive neomycin and tetracycline in their milk for the first 2 weeks of life or not. Daily health evaluations and treatments were recorded. Fecal swabs, taken on d 1 and at 2 and 4 weeks were cultured for *E. coli*, 3 isolates of which were tested for susceptibility to 12 antimicrobials. Resistance patterns were designated susceptible; resistant to at least streptomycin, sulfa and tetracycline (SSuT); or resistant to all β-lactams and SSuT. On the first sampling, 86% of isolates were mostly susceptible but by 14 d only 7 isolates were susceptible. Isolates were 3.1 times more likely to have β-lactam/SSuT resistance at 2 weeks compared with 4 weeks ($P < 0.001$). Using ordinal logistic regression, feeding antibiotics in milk did not result in higher levels of antibiotic resistance ($P = 0.52$). However, at the 14-d sampling, an isolate was 10 times more likely to have a higher level of resistance (either SST or β-lactam/SSuT) if the calf had been treated compared with no treatment (95% CI 3.7, 30.7). At 4 weeks, neither antibiotics in the milk for the first 14 d nor treatment were associated with resistance patterns seen ($P = 0.12$). In conclusion, antimicrobial treatment has a significant effect on recovery of multidrug resistant fecal *E. coli*, but the effect is not completely sustained over time.

Key Words: antimicrobial, resistance, calf

649 Effect of pre-slaughter stressors on intestinal microbial populations of pigs.

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The swine intestinal microbiota is a complex ecosystem, which may be disturbed by many factors. Studies have focused on the relation between antimicrobial use and resistance in intestinal microbial populations, whereas the effect of non-antimicrobial factors, such as stress, remains unknown. During the process of being transported from production farms to abattoirs, market pigs are exposed to several stressors. The occurrence of antimicrobial resistance in market pigs is critical, since the most likely transmission route from animals to humans is through contamination of carcasses. Therefore, 2 experiments were conducted to determine the effect of common pre-slaughter stressors (feed withdrawal, transportation, and lairage) on levels of antimicrobial resistance in commensal coliforms and lactobacilli in market pigs. In the first study, no effect of transportation and lairage on total fecal coliforms or its subpopulations resistant to antibiotics was observed ($P > 010$). Also, no effect was observed on total fecal lactobacilli populations, as well as on subpopulations resistant to tetracycline and erythromycin ($P > 0.10$). However, a significant increase of the fecal levels of ampicillin-resistant lactobacilli was caused by transportation and lairage ($P < 0.05$). In the second study, while total ileal coliforms were not affected by feed withdrawal and/or transportation ($P > 0.10$), populations of lactobacilli resistant to tetracycline and erythromycin decreased ($P < 0.05$) in response to the stress of feed withdrawal and transportation. Interestingly, no effects of the investigated stressors were observed in any of the cecal microbial populations analyzed. These studies show that stress does affect intestinal microbial populations in market pigs with lactobacilli being more susceptible to the effects of stressors compared with coliforms. Moreover, it was revealed that interactions between type of stress, region of the intestinal tract, and microbial population analyzed may influence the pattern of antimicrobial resistance observed. There is a critical need for further investigation of the quantitative effect of stressors on intestinal microbial populations of pigs, and its food safety implications.

Key Words: swine, stress, microbial ecology

650 Screening of antimicrobials and salt substitutes for use in reduced sodium dairy products.

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Pressure has been put on the food industry to reduced sodium levels. Since reduction or elimination of salt from dairy products could potentially change the microbial stability an alternative antimicrobial agent may be needed. In addition to the use of antimicrobials salt replacers could be used to maintain acceptable flavor. To determine which antimicrobials have potential for success in reduced sodium dairy products, this study evaluated 8 commercially available antimicrobials (lauric arginate, natural enzyme systems and various fermentates). Antimicrobials were also tested in combination with 6 commercial sodium reduction agents to determine if their use would interfere with antimicrobial activity. Sodium reduction agents contained one or more of the following components calcium salt, potassium salt, sodium chloride, cultured corn sugar and trehalose. Milk and low-sodium cheese agar systems were used as the growth medium for screening. Antimicrobials with and without sodium reduction agents were added to the agar systems, then a 5-strain cocktail of *Listeria monocytogenes*, *Salmonella* or *Escherichia coli* O157:H7 was spread plated at 3 concentrations: 10^1, 10^2 and 10^4 cfu/plate. Samples were then incubated at 30°C and observed for growth after 24 and 48 h. A nisin-containing antimicrobial blend, lauric arginate, a natural enzyme system and a fermentate inhibited growth of all pathogens on milk agar after 48 h. In the cheese agar, pathogen growth was observed after 48h with the nisin-containing antimicrobial blend, and the fermentate, whereas while lauric arginate showed pathogen growth in 48 h or less. No pathogen growth was observed in the cheese agar containing the enzyme system. When the nisin-containing antimicrobial blend, lauric arginate and fermentate were tested in combination with sodium reduction agents containing potassium chloride, growth of *Salmonella* and *E. coli* O157:H7 was observed within 48h. Regardless of the salt substitute, there was no pathogen growth when the natural enzyme system was tested. Results from this study can aid in the selection of antimicrobials and sodium reduction agents for use in dairy products. However, testing in the dairy product itself is needed to confirm screen results and ensure a safe product.

651 Control of native microbiota in skim milk by pulsed electric fields and tangential-flow microfiltration versus high-temperature short-time pasteurization. D. Khanal,* A. Chugh, M. Walkling-Ribeiro, L. Duizer, and M. W. Griffiths, *University of Guelph, Guelph, Ontario, Canada.*

Conventional high-temperature short-time pasteurization (HTST) is the established food preservation technology for commercial processing of milk. However, during HTST treatment degradation of valuable nutrients and loss in sensory quality in milk occurs due to substantial heat exposure. Pulsed electric fields (PEF) and tangential-flow microfiltration (TFMF) are emerging food processing technologies that could represent a non-thermal alternative to heat pasteurization for skim milk processing. This study investigated the effect of non-thermal technologies on the reduction of native microbiota in skim milk and compared PEF and TFMF efficacies to that of HTST. Fresh raw skim milk (0.05% fat) was incubated at 8°C for 96–120h to promote the native microbial growth up to 10^8 cfu/mL. Incubated milk was treated with PEF for electric field strength, product flow rate and maximum processing temperature combinations using 28 kV/cm, 20 mL/min and 40°C (PEFL), 40 kV/cm, 35 mL/min, and 55°C (PEFM), and 40 kV/cm, 25 mL/min, and 65°C (PEFH) that led to respective treatment times of 2805, 1122, and 1571 µs, while TFMF-treated milk was processed at a flow rate of 300 mL/min and 35°C with membranes of different pore sizes (0.2, 0.45, and 0.65 µm). Thermal control treatments were carried out with HTST at 75 and 95°C for respective holding times of 20 and 45 s. ANOVA was used for all treatments ($n = 3$). Microbial loads in stand-alone PEFL- and PEFM-treated milk were reduced by respective 1.3 and 2.3 log10 ($P < 0.05$), in contrast to higher inactivation ($P < 0.05$) of 4.5 and 3.7 log10 achieved by similarly effective PEFH and 0.65 µm pore-sized TFMF ($P \geq 0.05$), respectively. However, these treatments were all less effective for microbial decontamination than microfiltration at 0.2 and 0.45 µm ($P < 0.05$) inactivating respective 6.0 and 5.9 log10, which was comparable to the low and high HTST treatments ($P \geq 0.05$) that led to 5.7 and 5.8 log10 reductions of native microbiota in skim milk, respectively. Results obtained in this study highlight the potential of TFMF and heat-assisted PEF for skim milk processing and suggest their combination in a hurdle technology as non-thermal processing alternative to HTST.

Key Words: pulsed electric field, tangential-flow microfiltration, high-temperature short-time

Horse Species Symposium: Equine-Assisted Therapies: Incorporation into university programs

652 Partnering therapeutic riding and higher education. C. Burke,* *University of New Hampshire, Durham.*

The field of equine-assisted activities and therapies (EAAT) is a growing segment of the equine industry in the US. Research in this area continues to support anecdotal evidence that EAAT works as a treatment modality for individuals with a wide range of disabilities. As a result, the need for knowledgeable, qualified, and diversely educated individuals with practical experience in EAAT is rising. Additionally, as the breadth and depth of this field increases, so do career opportunities, and therefore more college students wishing to pursue this course of study. Since 1969, the Professional Association of Therapeutic Horsemanship International (PATH Intl; formally NARHA) served as the primary educational body in this field. Today, there are increasing educational opportunities at the collegiate level available for the pursuit of EAAT as a degree option. In 2010, PATH Intl developed Higher Education memberships for colleges and universities in an effort to aid in curriculum development for EAAT. Many institutions are in the process of evaluating whether to offer EAAT as a course of study and if so how best accomplish this goal. In this session career options in EAAT will be explored and many related questions answered. What job opportunities are available for graduates with a 2- or 4-year degree in EAAT? How can universities best prepare students to succeed in this industry? Should institutions of higher education partner with a local EAAT center or start their own program? What other university resources are required to incorporate EAAT and what are some benefits to the university? What opportunities for cross-disciplinary studies exist? How would a PATH Intl Higher Education Membership fit into the curriculum and is it a worthwhile endeavor? Questions of liability, legal structure, and faculty qualifications will also be explored.

Key Words: equine-assisted activities and therapies (EAAT), PATH International Higher Education

653 Equine-assisted therapy and recovery from combat trauma. J. M. Kouba*[1], B. L. McDaniel[1], E. A. Eason[2], and K. G. Odde[1], [1]*Kansas State University, Manhattan,* [2]*Fort Riley, KS.*

After more than a decade of conflict in the Middle East, the number of soldiers being diagnosed with posttraumatic stress disorder (PTSD) and mild traumatic brain injury (mTBI) is steadily increasing. Population surveys on post-deployment soldiers report a prevalence rate of 10 to 20% for some type of combat-related stress disorder. The diagnosis of PTSD and mTBI presents challenges for mental health providers, and relies heavily on screening instruments and clinician interviews. Treatment options for soldiers routinely involve various types of counseling or psychotherapy, along with psychotropic medications. Despite these established approaches, a need still exists for novel treatment interventions. Although equine-assisted therapy (EAT) has been used as an adjunct therapy for a variety of health conditions, it is gaining popularity as an alternative treatment modality for veterans at private EAT facilities and some military institutions. Despite the positive results reported by these facilities, research supporting the effectiveness of EAT on alleviating the symptoms of PTSD or mTBI in our military population is limited. Therefore, a 14-wk study will examine the efficacy of EAT with active-duty military personnel who have experienced psychological and/or physical injury in a tour of duty and been diagnosed with PTSD or mTBI. Twenty-four subjects from the Warrior Transition Battalion at Ft. Riley, Kansas, will be randomly assigned to either a treatment (T, n = 12) or control (C, n = 12) group, each consisting of 6 soldiers diagnosed with PTSD and 6 with mTBI. The T group will be taught basic horsemanship skills in weekly small group sessions. The participants mental status will be assessed several times during the trial using survey instruments. Salivary cortisol will also be measured. The T group will also complete an EAT questionnaire and be interviewed upon completion of the trial to evaluate their perceptions of the program. We anticipate that the results will demonstrate a benefit of EAT in reducing symptoms associated with PTSD and mTBI, and help improve the quality of life of soldiers transitioning to the next phase of their military or civilian career.

Key Words: equine-assisted therapy, posttraumatic stress disorder (PTSD), mild traumatic brain injury

654 Research in equine-assisted activities and therapies. E. L. Berg,* *North Dakota State University, Fargo.*

A growing body of evidence exists supporting the benefits of equine assisted activities and therapies (EAAT) for individuals with a wide range of diagnoses including cerebral palsy, autism, stroke, multiple sclerosis, spinal cord injury, and attachment disorder. Research in the field of EAAT is necessary to demonstrate effectiveness of EAAT for individuals with disabilities, to validate and standardize industry practices, to garner support from the medical community, and to work toward reimbursement for these services from insurance companies. The objective of this session will be to highlight research in the field of EAAT, examine collaborative opportunities for institutions of higher education with industry and private organizations, discuss who would be integral members of a research team, as well as available funding sources in the area of EAAT.

Key Words: equine-assisted therapy, higher education, research

Meat Science and Muscle Biology Symposium: Pre-Slaughter Stress, Postmortem Glycolysis, and Biophysical Mechanisms of Meat Quality

655 Preslaughter stress and pork meat quality. L. Faucitano,* *Agriculture & Agri-Food Canada, Sherbrooke, Canada.*

At all times before slaughter pigs may experience stress from a range of handling practices, such as feed withdrawal, loading and transport, mixing, human interventions and slaughter. Frequently used welfare indicators for preslaughter treatment are behavioral and physiological (heart rate, hormones, and body temperature) responses. However, preslaughter stress is not only an animal welfare issue but also a meat quality issue as it may have short- and long-term effects on ante-mortem muscle metabolism and thereby on meat quality. The 2 major preslaughter stress-induced meat quality defects are PSE (pale, soft, exudative) and DFD (dark, firm, dry) pork. Acute short-term stress, such as no or short rest time after transport, rough handling while moving pigs toward the stunning area and the stunning process itself, can stimulate sympathetic arousal and adrenaline release triggering a rapid glycogenolysis and excessive lactate and heat production. This muscle metabolic condition may result in the formation of PSE pork depending on the glycogen content at the time of slaughter. A major effect of long-term stress, such as too extended feed withdrawal, transport and lairage times, and mixing of unfamiliar groups of pigs, is the reduction of muscle glycogen levels at slaughter leading to an insufficient acidification of the meat (higher ultimate pH) and production of DFD pork. However, the relationship between behavioral and physiological variables and meat quality parameters is sometimes conflicting. This discrepancy might depend on the different reaction to physical and psychological stressors of muscles differing in muscle fiber contractile properties, being the glycolytic muscles more prone to develop PSE pork and the oxidative ones to develop DFD pork. The objective of this review is to overview research findings related to the effects of preslaughter practices on ante-mortem animal physiological response, including muscle metabolism, and to provide recommendations aiming at limiting the effect of preslaughter handling on pork quality variation.

Key Words: meat quality, pigs, stress

656 Muscle glycogen and postmortem glycolysis. E. Poulanne,* *Department of Food and Environmental Sciences, University of Helsinki, Helsinki, Finland.*

Glycogen is a branched polysaccharide with linear chains of 12 to 14 glucosyl groups linked by 1,4-bonds. Glycogen has a variable molecular weight from about 600 000 up to 10^7 with 55,000 glucosyl units and 4000 chains, of which 2100 chains are on the outermost tier. The structure is optimized to provide the maximum number of available branches in a minimum volume. The chains (B chains) have 2 branching points where further chains are linked by 1,6-bonds to form the next tier up to 12 tiers. On the outermost tier, the chains are unbranched (A chains). Glycogen phosphorylase is able to degrade glycogen at a very high speed thus providing the energy substrate, glucose-1-phosphate, in periods of intensive exercise and stress. Glycogen phosphorylase can cleave the glucosyl units down to the fourth unit from the 1,6-bond. Following this, the glycogen debranching enzyme is required first to remove 3 glucosyl units and move them to another A chain, and then to degrade the 1,6-bond resulting in one free glucose molecule, which allows the further action of glycogen prosphorylase. In glycolysis, glucose-1-phosphate is converted to glucose-6-phosphate and then broken down to pyruvate by 9 different enzymes, yielding 3 ATP per glucose-1-phosphate (2 ATP of glucose molecules coming from the action of the glycogen debranching enzyme). Pyruvate is used oxidatively in the citric acid cycle or non-oxidatively to regenerate NAD+, resulting in 2 lactate molecules and the binding of 2 protons per glucosyl unit. Simultaneously, there is a net production of 2 protons per glucosyl unit which originate from the glycolytic pathway from different intermediates, depending of the pH of the medium at a given time.

657 Biophysical approaches for improving our understanding of meat quality. A. Karlsson* and D. Brüggemann, *University of Copenhagen, Frederiksberg C, Denmark.*

The texture and water-holding of meat are of utmost importance for consumer acceptance. Meat consists of approx. 70% water and approx. 20% protein, the latter being crucial for holding the myo-water in place. Proteins are also the main constituents that make up the structure of meat and meat products. Even minor structural and chemical changes as well as degradation of the proteins post-mortem, are therefore very important for the major meat quality attributes, including water-holding, color and texture. The proteins also undergo structural changes on heating, resulting in protein denaturation, which includes among other processes protein unfolding, and protein-protein interactions leading to protein aggregations. Therefore the quality of meat products, which is mainly governed by the meat structure, also changes drastically after cooking. Due the complexity of muscle tissue and meat raw material, our knowledge in this field is far from complete, and therefore there is a need for research to understand basic and underlying mechanisms involved to explain the variation of the important meat quality attributes, thereby making it possible to control the meat quality. Biophysics, where physical methods are used to explain and study biological phenomenon, has the potential for being a new way for a meat science paradigm shift, thereby making it possible to increase our understanding of mechanisms involved in the development of meat quality attributes, and also to obtain a more detailed understanding of the complex matrix of raw and processed meat. In this presentation we will show some preliminary results of biophysical approaches for improving our understanding of meat quality attributes using techniques including fluorescence lifetime microscopy, second harmonic generation microscopy, differential scanning calorimetry and high field NMR.

Key Words: meat quality, biophysics

Nonruminant Nutrition: Amino Acids and Energy

658 Influence of net energy content of the diet on productive performance and carcass merit of gilts, boars, and immunocastrated males fed barley-based diets and slaughtered at 119 kg of BW. L. Cámara[1], M. Romero[1], M. P. Serrano[1], J. L. Sánchez[2], E. Alcázar[2], and G. G. Mateos*[1], [1]*Departamento de Producción Animal, Universidad Politécnica de Madrid, Madrid, Spain,* [2]*SAT Vallehermoso S.A, Ciudad Real, Spain.*

In total, 540 crossbred pigs with an initial BW of 28.5 ± 4.1 kg were used to investigate the effects of increasing the level of NE of barley based diets (2.450, 2.410, 2.370, 2.330, and 2.290 Mcal/kg) on growth performance and carcass and meat quality traits of gilts, boars, and immunocastrated males (IMC) slaughtered at 119 kg BW. The IMC pigs were immunized against GnRF with Improvac at 90 and 143 d of age (18 and 71 d on trial). Each treatment (5 × 3) was replicated 3 times (12 pigs per pen). Gilts, boars, and IMC pigs responded similarly to NE concentration of the diet. For the entire experimental period, an increase in NE concentration of the diet improved linearly NE intake ($P < 0.05$), ADG ($P < 0.05$), and feed efficiency ($P < 0.001$) but ADFI and NE efficiency (g of ADG/ Mcal NE intake) were not affected. Backfat depth (linear, $P < 0.05$, quadratic; $P = 0.078$), fat at m. *Gluteus medius* (linear, $P < 0.05$), and trimmed ham yield (linear, $P < 0.05$) increased as the NE concentration of the diet increased but carcass yield was not affected. The IMC pigs had higher ADFI ($P < 0.001$) and ADG ($P < 0.05$) than gilts and boars. Net energy efficiency was higher for boars than for gilts with IMC being intermediate ($P < 0.001$). Carcass and loin yields were higher for gilts than for boars and IMC ($P < 0.001$). Backfat depth ($P < 0.01$) and fat at m. *Gluteus medius* ($P < 0.001$) were higher for gilts and IMC than for boars. The results indicate that an increase in NE concentration of the diet improved growth performance and increased the amount of fat carcass independent of gender. The IMC pigs had higher ADG, backfat, fat at m. *Gluteus medius*, intramuscular fat, and similar carcass and primal cut yields than boars. The use of diets with NE content above 2.330–2.370 Mcal /kg is recommended for the production of pigs destined to the dry cured industry because of its beneficial effects on growth performance, backfat depth, and intramuscular fat that improved the quality of the final products.

Key Words: growth performance and carcass merit of pigs, inmunocastration, net energy

659 Influence of increasing levels of lysine in the diet on growth performance and carcass quality of entire and inmunocastrated females. L. Cámara[1], M. P. Serrano[1], A. López[2], J. M. González[2], F. Ortin[2], and G. G. Mateos*[1], [1]*Departamento de Producción Animal, UPM, Ciudad Universitaria, Madrid, Spain,* [2]*Piensos Jiménez S.L., Lorca, Murcia, Spain.*

In total, 320 crossbred pigs (70 d of age) were used to study the influence of increasing levels of standarized ileal digestible lysine (Lysd) in the diet on growth performance and carcass and meat quality of gilts and inmunocastrated gilts (IMG). The IMG were immunized against GnRF at 89 and 161 d of age. The feeding program consisted of 3 periods with 5 dietary Lysd levels used within each period. Diets within period were formulated to have the same net energy (NE) content (2,470 kcal/kg) but differed in Lysd concentration (control diet and ± 5% and ± 10% over the control diet). The Lysd concentration of the control diets was 1.01% from 70 to 89 d of age, 0.95% from 89 to 140 d of age, and 0.83% from 140 to 185 d of age. All the other indispensable amino acids were formulated on an ideal protein bases. Each treatment was replicated 4 times and the experimental unit was the pen for all traits (8 pigs each for growth performance variables and 4 carcasses chosen at random for carcass and meat quality traits). From 70 to 89 d of age, ADFI was similar for pigs fed diets with −5% to +5% Lysd and decreased with −10% (linear, $P = 0.088$; quadratic, $P = 0.003$). Pigs fed −10% Lysd diet had worse G:F than pigs fed −5% to +10% Lysd diets (linear, $P < 0.001$; quadratic, $P = 0{,}010$). From 161 to 185 d of age, IMG had higher ADFI ($P < 0.001$) and ADG ($P = 0.023$) than gilts. Cumulatively, neither Lysd content of the diet nor inmunocastration of gilts had any influence on growth performance of the pigs. Inmunocastrated gilts tended ($P = 0.073$) to have higher fresh ham yield than gilts but none of the other carcass quality variables measured, were affected by Lysd content of the diet or inmunocastration of the gilts. An increase in Lysd concentration in the diet increased protein content (linear, $P = 0.0185$) and reduced (linear, $P = 0.0373$) fat content of the meat measured at m. *Longissimus dorsi*. It is concluded that, under the conditions of the current experiment, the use of 1.01%, 0.86%, and 0.74% digestible Lys is recommended in each of the 3 feeding periods considered, in diets containing 2,470 kcal NE/kg.

Key Words: carcass quality of pigs, digestible lysine, inmunocastration

660 The standardized ileal digestible (SID) tryptophan to lysine ratio to optimize performance of 25 to 50 kg pigs fed low protein diets. G. Zhang[1], S. Qiao[1], and J. K. Htoo*[2], [1]*China Agricultural University, Beijing, China,* [2]*Evonik Industries AG, Hanau, Germany.*

Published data about the optimal SID Trp:Lys ratios for growing pigs fed low CP, AA-supplemented diets are rather inconsistent. Two 35-d experiments were conducted to estimate the optimal SID Trp:Lys in 25–50 kg pigs under commercial conditions. In Exp. 1, 144 pigs (Landrace × Large White; initial BW of 25.3 kg) were used to identify a diet deficient in Lys. Pigs were fed either a corn, soybean meal based high CP (18.6%) diet with 1.02% SID Lys or one of 2 low CP diets (14.6% CP but supplemented with Lys, Thr, Met, Thr, Trp, Val and Ile) to contain 0.90 or 1.02% SID Lys, respectively. All diets were formulated to contain 2400 kcal/kg NE and AA except Lys were adequate. Each diet was assigned to 6 pens with 4 barrows and 4 gilts per pen. The ADG (688 g/d) of pigs fed the low CP diet containing 0.90% SID Lys was lower ($P < 0.05$) than that of pigs fed the diet containing 1.02% SID Lys with a high (758 g/d) or low (747 g/d) CP content confirming that 0.90% SID Lys was deficient for these pigs. In Exp. 2, 300 pigs (same genetic and BW as used in Exp. 1) were allotted to 5 diets with 5 barrows and 5 gilts per pen and 6 replicates per treatment. Diets 1 to 5 contained SID Trp content of 0.12, 0.14, 0.17, 0.20 and 0.23%, respectively and the same suboptimal SID Lys level of 0.90% (dietary SID Trp:Lys of 13, 16, 19, 22 and 25%). The ADG increased linearly ($P < 0.05$) as the SID Trp:Lys increased while a linear effect of ADFI ($P < 0.05$) and a quadratic effect of FCR ($P < 0.05$) were observed. The d 36 plasma Trp concentration was highest ($P < 0.05$) at 25% SID Trp:Lys while plasma urea N concentration was lowest ($P < 0.05$) at 22% SID Trp:Lys. The SID Trp:Lys to optimize ADG, FCR and plasma urea N were 19.7, 20.0 and 20.8% using a linear broken-line model, and 22.6, 23.2 and 23.6% using a curvilinear-plateau model, respectively. On average, the optimal SID Trp:Lys was estimated at 22% for 25 to 50 kg pigs fed low CP, AA-supplemented diets under commercial conditions.

Key Words: growing pigs, lysine, tryptophan

661 Changes in amino acid accretion during immune activation of the chicken immune system by *E. coli*.

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The immune system requires appropriate levels of nutrients to support changes in leukocyte numbers and effector proteins during immune activation. However, a quantitative estimate of the amount of nutrients needed for maintenance and the additional amounts needed for a robust response has yet to be attempted. Thus, we quantified the total amino acid content of leukocytes in blood and tissues, protective plasma proteins, liver and pectoralis muscle in adult chickens before and after injected intravenously with dead *E. coli*. The amount of amino acids accreted during the early (first 2 d) and late (first 21d) response were calculated. When comparing amino acids used for leukocytes and protective proteins relative to that in skeletal muscle, lysine was limiting during the early response and leucine, threonine, and valine were limiting for the late response. For liver, phenylalanine, asparagine, lysine, and valine were limiting relative to muscle during the early response and phenylalanine during the late response. Summing accretion for expansion of leukocytes, protective proteins and liver showed that lysine and asparagine were limiting during the early response and leucine, threonine, and valine were limiting during the late response. Supported by USDA Regional Research project 1013.

Key Words: chicken, *E. coli*, amino acids

662 Restricting sulfur amino acid intake in immune system stimulated pigs decreases plasma protein and albumin synthesis.

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Chronic sub-clinical levels of disease occur frequently in intensive pork production and compromise nutrient utilization efficiency. Sulfur amino acids (Met+Cys; SAA) are involved in the pig's response to immune system stimulation (ISS) as substrates for generating compounds involved in the immune response, such as glutathione and acute phase proteins (APP; haptoglobin, fibrinogen, albumin). This study was conducted to determine the impact of ISS and SAA intake (high vs. low; 4.0 vs. 2.2 g/d) on the fractional synthesis rate (FSR) of albumin and protein in blood plasma, liver, and small intestine (SI) of pigs. Fifteen pigs (9.8 ± 1.4 kg BW) were allotted to one of 3 treatments: 1) Control (ISS-; high SAA), 2) ISS+ and high SAA, or 3) ISS+ and low SAA. For inducing ISS, pigs were injected intramuscularly twice, with a 48 h interval, with increasing doses of *E. coli* lipopolysaccharide (LPS); an ISS protocol that has been proven effective in previous studies. One day after the second LPS injection, FSR was determined using an intravenous infusion of a flooding dose of L-[ring-2H5]-Phe. Plasma levels of APP were not affected by ISS ($P > 0.10$; Control vs. ISS+ and high SAA). Only plasma albumin levels decreased with reduced SAA intake (29.0 vs. 24.2 g/L; ISS+ and high SAA vs. ISS+ and low SAA; SEM = 1.26; $P = 0.02$). Molar enrichment of free Phe in the liver and SI ranged from 86 to 91% of that in plasma, indicating adequate flooding. In plasma, total protein FSR was increased during ISS (50.3 vs. 56.9%/d, SEM = 1.64; $P = 0.01$) and plasma FSR tended to decrease with reduced SAA intake (56.9 vs. 52.5; SEM = 1.64; $P = 0.08$); albumin FSR was not affected by ISS ($P > 0.10$), but decreased with reduced SAA intake (49.5 vs. 41.9%/d, SEM = 1.57; $P = 0.01$). There were no treatment effects on FSR in liver and SI. The FSR of plasma proteins appears a more sensitive indicator of liver protein synthesis. Overall, these results suggest that restricting SAA intake during ISS decreases total plasma protein and albumin synthesis, implicating SAA as important nutrients involved in the immune response.

Key Words: immune system stimulation, protein synthesis, sulfur amino acids

663 Response to dietary L-glutamine supplementation in weaned piglets: A serum metabolomic comparison and hepatic metabolic regulation analysis.

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A novel metabolomic method based on gas chromatography/mass spectrometry was applied to investigate the serum metabolite in response to dietary L-glutamine (Gln) supplementation in piglets. Sixteen 21-d-old piglets were weaned and randomly assigned into 2 groups, one with the Gln group and the other with the control group, representing 1% Gln (wt:wt) and isonitrogenous L-alanine, respectively. Serum samples were collected to characterize metabolites after a 30-d treatment. Additionally, 4 liver samples per group were collected to examine the enzyme activity and genes expression involved in metabolic regulation. Results showed 12 metabolites were significantly altered by Gln treatment, including carbohydrates, amino acids, and fatty acid. A leave-one-out cross-validation of random forest analysis indicated that proline and glycerol were the most important metabolites among the 12 different metabolites. These data demonstrated that the control and Gln-supplemented pigs showed a wide range of metabolic difference across carbohydrate metabolism, arginine and proline metabolism, tyrosine metabolism, and glycerophospholipid metabolism. Principal component analysis yielded separate clustering of profiles between the 2 treatment groups. Metabolic enzyme activity of alanine aminotransferase and hexokinase increased by 26.77% ($P = 0.026$) and 26.18% ($P = 0.004$), respectively, in the liver of Gln-supplemented pigs over the control, whereas pyruvate kinase (PK) activity decreased by 29.08% ($P = 0.001$). The mRNA level of PK decreased by 66.10% ($P = 0.034$) in the liver. No significant difference was observed for the mRNA level of mammalian target of rapamycin and peroxisome proliferator-activated receptor gamma. Based on the data, correlation networks for the Gln-supplemented and control pigs revealed that Gln treatment changed carbohydrate, lipid and amino acid metabolism in the whole body of the early weaned piglets. These findings provide fresh insight into specific metabolic pathways and lays the groundwork for the complex metabolic alteration in response to dietary Gln supplementation in pigs.

Key Words: glutamine, metabolomics, piglets

664 Effects of dietary glutamine supplementation on nutrient absorption and activity of enzymes involved in glutamine metabolism and energy production in the jejunum of weaned piglets.

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The influence of L-glutamine (Gln) on the coefficient of total tract apparent digestibility (CTTAD) and apparent ileal digestibility (AID), the jejunal enzyme activity associated with nutrient absorption, and the energy production in weaned piglets has not been sufficiently studied. The aim of the present paper is to provide a profile of the effects of Gln on CTTAD, AID, the activities of jejunal enzymes in connection with nutrient digestion and absorption and energy production. The piglets were weaned at 21 d of age. There were 2 groups in Exp. 1 and Exp. 2, representing supplementation with 0 or 1% Gln to the basal diet. In Exp. 1, the CTTAD of the dietary components and energy was assessed at 3, 5, 10, 15, and 30 d after weaning. In Exp. 2, productive performance, AID, jejunal enzyme activities, and expression of peroxisome proliferator-activated receptor gamma (PPARγ) were measured at 10 and 30 d post-weaning. Results showed that dietary Gln supplementation significantly improved the CTTAD of DM, OM, GE, and AA, and the CTTAD increased significantly with the extension of days after weaning. For the entire experiment, the average daily gain increased by 12.40% ($P = 0.049$) in the Gln group. Dietary Gln supplementation increased the AID of GE, Leu, Lys, Cys, and Pro by 12.50 ($P = 0.047$), 7.03% ($P = 0.041$), 5.95% ($P = 0.036$), 9.30 ($P = 0.025$), 11.17% ($P = 0.009$), respectively, at 10 d post-weaning; Pro by 6.11% ($P = 0.044$) at 30 d post-weaning. Jejunal brush border membrane-bound alkaline phosphatase activity increased in the Gln-supplemented pigs by 30.36% ($P = 0.048$) and 6.21% ($P = 0.30$) at 10 and 30 d post-weaning, respectively. Compared with the control pigs, the mRNA level of PPARγ decreased by 10.85% ($P = 0.14$) and 41.88% ($P = 0.023$) after the administration of 1% Gln for 10 and 30 d, respectively. The activity of glutamine synthetase decreased by 48.89% ($P = 0.044$) at 10 d post-weaning, and pyruvate kinase by 13.13% ($P = 0.036$) at 30 d post-weaning in the Gln-supplemented pigs. In conclusion, 1% Gln supplementation to the post-weaned piglet diet enhanced the CTTAD and AID of diet, improved intestinal absorption, and modified jejunal enzyme activities related to Gln metabolism and energy production.

Key Words: L-glutamine, nutrient absorption, weaned piglets

665 Effects of oral supplementation with glutamate or combination of glutamate and N-carbamylglutamate on intestinal mucosa morphology in weanling piglets. W. Xin[1,2], P. Zhangzhi[1,2], L. Zhiqiang[1], L. Tiejun[1], and Y. Yulong*[1,2], [1]*Key Laboratory for Agro-ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy of Sciences, China,* [2]*State Key Laboratory of Food Science and Technology and College of Life Science and Food Engineering, Nanchang University, China.*

To evaluate the effects of glutamate (Glu) or combination of glutamate and N-carbamylglutamate (NCG) on intestinal mucosa in weanling piglets, 18 Duroc × Landrace × Yorkshire piglets weaned at 28 d (BW 5.56 ± 0.51 kg) were grouped into 3 treatments, and fed one of the following diets for 30 d: a standard diet (SD), SD+Glu (1%), SD+Glu (1%)+NCG (0.05%). All the piglets were killed for blood and tissue collection. The results showed that compared with the control group, Glu increased concentration of blood glucose and glucagon ($P < 0.05$) and reduced plasma insulin ($P < 0.05$) in weaned piglets. Both of Glu or combination of Glu and NCG decreased serum urea nitrogen and ammonia concentration ($P < 0.05$), and Glu+NCG increased average intestine weight significantly ($P < 0.05$). Compared with the control group, adding Glu to the diet resulted in a higher villus height ($P < 0.05$) in both of duodenum and jejunum. However, there was no difference in crypt depth at the 2 different locations, and the villus height/crypt depth ratio was unaltered ($P > 0.05$). The RT-PCR results showed that combination of Glu and NCG significantly increased PCNA mRNA abundance in both jejunum and ileum ($P < 0.05$), while they also significantly increased β-catenin and decreased VEGF in ileum ($P < 0.05$). There were no differences in expression of these genes between the Glu and Glu+NCG groups ($P > 0.05$). Only Glu increased ($P < 0.05$) PCNA mRNA abundance in jejunum. and Glu+NCG significantly decreased VEGF mRNA in jejunum ($P < 0.05$). These results indicated that oral supply of Glu improved intestinal mucosa morphology, and combined Glu and NCG had more favorable effects on self-renewing of intestinal mucosa than supply of glutamate alone.

Key Words: glutamate, N-carbamylglutamate, mucosal morphology

Physiology and Endocrinology I

666 Gram-negative or gram-positive toxin-induced subclinical mastitis affects preovulatory follicle responses in cows. O. Furman[1], G. Leitner[2], Z. Roth[1], Y. Lavon[3], S. Jacoby[4], and D. Wolfenson*[1], [1]*Faculty of Agriculture, Food and Environment, the Hebrew University, Rehovot, Israel,* [2]*The Veterinary Institute, Bet Dagan, Israel,* [3]*Israel Cattle Breeders Association, Caesarea, Israel,* [4]*Institute of Animal Science, Agricultural Research Organization, Bet-Dagan, Israel.*

Long-term, subclinical mastitis lowers conception rate. The objective of this study was to induce subclinical mastitis by gram-positive (G+) exosecretions (*S. aureus* ex.) or gram-negative (G-) endotoxin (*E. coli* LPS), and examine its effects on preovulatory follicle responses. Throughout the study, cows were synchronized with series of GnRH and $PGF_{2\alpha}$ administered every 8 d. Cows received intramammary injections every 48 h for 20 d with minimal doses of either G+ (10 µg, n = 10) or G- (0.5 µg, n = 6) toxin, or saline (n = 6). Follicular fluids were aspirated before, at the end of (immediate effect), and 16 and 32 d after toxin exposure (carryover effect). Data were analyzed by ANOVA. During G+ or G- exposure, somatic cells count was higher ($P < 0.05$) than in controls, but body temperature (38.8 ± 0.1°C), plasma cortisol and haptoglobin concentrations did not differ among groups. In the G- group, a 50 to 60% immediate and 16 d-carryover decrease ($P < 0.05$) in plasma estradiol concentration relative to controls (11.0 ± 1.0 pg/ml) was noted; in the G+ group, only a 16 d-carryover decrease of 25% in plasma estradiol was noted ($P < 0.05$). Neither toxin induced an immediate drop in follicular steroids; however, an immediate decrease in the number of medium-size follicles was noted in the G+ group compared with controls (1.3 ± 0.2 vs. 3.0 ± 0.7 follicles;, $P < 0.05$). Most G- group cows (5/6) exhibited a 32 d-carryover decrease ($P < 0.05$) of 70% and 62% in estradiol and androstenedione concentrations, respectively, in the follicular fluids. In the G+ group, only half of the cows exhibited a 33% and 60% carryover decrease in follicular estradiol and androstenedione concentrations, respectively ($P < 0.05$); in the other half, steroid levels were not altered. Results indicate that growth dynamics of medium-size follicles is attenuated mainly by *S. aureus* ex. Small, pre- to early antral follicles are susceptible to both *S. aureus* ex. and *E. coli* LPS toxins, and the induced damage is then carried over to the preovulatory follicles; this corresponds well with the long-term chronic nature of subclinical mastitis.

Key Words: mastitis, steroid, follicles

667 Blood constituents in milk due to changed blood-milk barrier integrity during mastitis. O. Wellnitz, M. Lehmann, and R. M. Bruckmaier,* *Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland.*

Mastitis is accompanied by changes in milk composition. Besides changes of mammary secretions the blood-milk barrier integrity is impaired and molecules can cross the border from blood into milk or vice versa. This study aimed to investigate the transfer of several blood constituents into milk during a mammary immune response due to intramammary endotoxin challenge. Five cows who received a β-hydroxybutyrate (BHB) clamp infusion to increase BHB in blood to a steady concentration (1.5 to 2.0 mmol/L) were challenged intramammarily into one quarter with 200µg *E. coli* lipopolysaccharide (LPS). They were immunized against bluetongue virus (BTV) 2 years before. Blood and milk were analyzed hourly. Changes were considered significant if $P < 0.05$. Blood concentrations of LDH, IgG, and specific antibodies against BTV did not change. In milk the somatic cell count increased in LPS challenged quarters within 4h but not in controls. Lactate dehydrogenase (LDH), BHB, lactate, and immunoglobulin (Ig) G was 33 ± 8 U/L, 0.08 ± 0.01 mmol/L, 8 ± 2mg/L, and 0.1 ± 0.0 mg/L, respectively, and increased within 3 h and continued to increase through 8h to concentrations of 326 ± 146 U/L, 0.56 ± 0.01 mmol/L, 182 ± 26 mg/L, 0.72 ± 0.24 mg/L, respectively, in milk of LPS challenged quarters but not of control quarters. IgG increase in milk was paralleled by an increase of antibodies against BTV. Lactate concentrations in blood and milk of control quarters increased 2h after challenge and were correlated (r = 0.74). The blood constituents LDH, BHB, IgG, and lactate increase in milk after LPS challenge. The increase of antibodies against BTV in milk suggests that the primary mechanism of IgG transfer is opening of the blood-milk barrier and not specifically targeted to mastitis pathogens. In conclusion, opening of the blood-milk barrier during mammary inflammation increases the presence of blood constituents including antibodies in milk, and this does not appear to be a specific immune function response.

Key Words: blood-milk barrier, mastitis, antibody

668 Characterizing the temporal and seasonal pattern of plasma lipopolysaccharide binding protein during the transition period. A. Nayeri*[1], N. C. Upah[1], M. V. Sanz-Fernandez[1], E. Sucu[1,2], A. L. Gabler[1], R. L. Boddicker[1], D. B. Snider[1], J. M. Defrain[3], and L. H. Baumgard[1], [1]*Iowa State University, Ames,* [2]*Uludag University, Turkey,* [3]*Zinpro Corporation, Eden Prairie, MN.*

During the periparturient period and heat stress (HS), dairy cows are more susceptible to rumen acidosis, which may compromise the gastrointestinal tract's (GIT) barrier function. Infiltrating lipopolysaccharide (LPS) is bound by LPS binding protein (LBP), but the role of LBP in dairy cow physiology is not well known. To investigate this, production data and blood samples were collected on lactating Holstein cows (n = 40) housed in a freestall barn and fed individually from −21 to 21 DIM. Two analyses were conducted: 1) good vs. poor transition cows and 2) winter vs. summer (July 2011) calving cows. It is important to note that data from 5 of the 40 cows were used as part of the winter and good transition analyses. Poor transition cows (n = 7) were defined as those treated for ketosis within 22 d after parturition. Conversely, good transition cows (n = 9) were void of a diagnosed health problem during the transition period. Cows included in the winter (n = 24) vs. summer (n = 5) analysis did not experience a diagnosed health event. Irrespective of classification, plasma LBP levels were lowest before calving and peaked at 3 DIM then slowly returned to pre-parturition concentrations by 21 DIM. Overall, poor transitioning cows had increased (21%, $P = 0.04$) circulating LBP compared with good transition cows and the difference was most pronounced (>2 fold) on 3 DIM. Nonesterified fatty acid and BHBA levels were not different between good and poor transitioning cows. However, we observed strong correlations between peak LBP and the transition success measures, milk yield slope ($r = -0.58$, $P < 0.05$) and BHBA area under the curve ($r = 0.72$, $P < 0.01$). Interestingly, winter calving cows had 52% ($P = 0.05$) greater LBP than summer calving cows and the difference was most pronounced (82%) at 3 DIM. In these cows, peak LBP was also negatively associated with average milk yield ($r = -0.49$, $P < 0.01$) and d 1–21 dry matter intake slope ($r = -0.57$, $P < 0.05$). Taken together, we hypothesize that circulating LBP concentration may play a role in determining seasonal and transition period success, or at least is closely associated with periparturient performance.

Key Words: dairy cow, LPS, transition

669 Effect of dry period length on rumen adaptation in dairy cows.

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The objective of this study was to evaluate the effect of length of dry period on rumen papillae dimensions of dairy cows around parturition. Twelve rumen-cannulated Holstein dairy cows were assigned to a dry period length of 60 (G60), 30 (G30) or 0 (G0) days. The experiment started 60 d before expected calving date and lasted until wk 8 postpartum for each individual cow. Cows received ad libitum forage mixtures of corn silage, grass silage and straw (containing 12% CP, 5.3 MJ NEL/kg DM for dry cows and 15% CP, 6.4 MJ NEL/kg DM for lactating cows). Concentrates were fed individually starting 10 d antepartum with 1.0 kg/d, gradually increasing up to 8.5 kg/d at d17 postpartum. Milk yield and DMI were recorded daily. The rumen contents of each cow were evacuated at wk-9, wk-6, wk-2, d3, d7, d14, d28 and d56 relative to parturition. At each time, biopsies were taken to determine papillae dimensions at 3 locations: the right dorsal sac cranially of the dorsal coronary groove (DS), the right wall of the caudodorsal blind sac (DB) and the ventral wall of the caudoventral blind sac (VB). Treatment effects were tested by mixed model analysis using REML procedure. Data are presented as means ± SE. Mean DMI postpartum was 21.2, 22.2 and 23.7 (±0.6 kg/d) for G60, G0 and G30 respectively ($P < 0.05$). Average daily milk yield postpartum was significantly lower for G0 ($P < 0.05$) compared with G30 or G60 (35.1 vs. 41.4 and 41.8 ± 3.1 kg/d, respectively). For cows with a dry period (G30 and G60), papillae surface area decreased prepartum ($P < 0.05$). More importantly, during the first 2 weeks postpartum the papillae growth was significantly delayed for G60 compared with G30; mean papilla surface was 42.5, 58.6 and 60.6 (±7.1, $P < 0.05$) mm^2 for G60, G30 and G0 respectively. Irrespective of treatment, rumen papillae were largest at VB and smallest at DS and papilla surface increased approximately 50% postpartum ($P < 0.05$). In conclusion, a shortened dry period of 30 vs. 60 d increases papillae surface in the first weeks of lactation and herewith may improve absorption capacity of volatile fatty acids, without a negative effect on milk yield as found with 0 d dry.

Key Words: dairy cow, rumen papillae, dry period length

670 Sodium salicylate administration during the first 7 days of lactation has effects that extend through the entire lactation in dairy cattle.

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Inflammation has been proposed as a contributor to fatty liver disease, and this disorder has negative effects on milk production in dairy cattle. Our objective was to determine if administration of sodium salicylate (SS), a non-steroidal anti-inflammatory drug (NSAID), in the first week of lactation changes whole-lactation productivity and retention in the herd. At calving, 78 cows (n = 39 primiparous [1P]; n = 24 2nd lactation [2P]; n = 15 ≥ 3 lactations [3P]) were alternately assigned to either control (CON) or SS treatment for 7 d postpartum. SS treatment was administered via individual water bowls at a concentration of 1.68 g/L, delivering a mean of 113.5 ± 6.8 g SS/d during the 7 d of treatment. Cows were followed through the lactation by monthly milk yield and component testing, and the effects of treatment on the risk of leaving the herd and on 305-d milk, fat, and protein yields were determined by Fisher's exact test and mixed model analysis, respectively. Predicted transmitting abilities (PTA) for milk, fat, and protein yields were not influenced by treatment or treatment by parity interaction (all $P > 0.17$); nevertheless, PTA values were included as covariates in the statistical models. Treatment by parity interactions were detected for 305-d milk and fat yields, and a tendency for an interaction was detected for protein yield. Milk yield was 2,469 ± 646 kg greater over the lactation in 3P SS cows compared with 3P controls (21% increase, $P < 0.01$), but milk yield tended to be 980 ± 375 kg less for 1P SS cows compared with 1P controls (8% decrease, $P = 0.07$); no effects were detected in 2P cows. Furthermore, 3P SS cows produced 130 ± 23 kg more milk fat over the lactation (30% increase, $P < 0.001$) and tended to produce 49 ± 18 kg more protein (14% increase, $P = 0.06$). No effects on fat or protein yield were detected for 1P or 2P. A treatment by parity interaction was observed for the risk of leaving the herd. First parity cows treated with SS cows tended to have greater risk of leaving the herd than controls (30% vs. 6% risk, $P < 0.10$). However, treatment did not alter herd retention in 2P or 3P groups, and SS had no effect on the risk of leaving the herd overall ($P = 0.59$). Results indicate that sodium salicylate has long-term effects on lactation of aged cows, particularly on fat metabolism, but has potential negative effects for primiparous cows.

Key Words: inflammation, milk production, non-steroidal anti-inflammatory drug

671 Responses to a nutritional challenge in early and late lactation.

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Characterizing robustness at the level of the individual animal would be valuable for refining management and selection strategies. Accordingly, to explore differences in adaptive capacity we studied responses of animals to a short-term nutritional challenge. Measurements of performance, milk composition and plasma metabolites were made in 16 dairy goats exposed to a 2-d nutritional challenge (underfeeding), at 2 different stages of lactation. Each challenge consisted of a 1-wk control period with standard TMR, 2 d of straw feeding, and a 1-wk recovery period on the TMR. All feeds were offered ad libitum. The 1st challenge was in late lactation (mean DIM, intake, milk yield: 280, 2.55 kg/d, 1.85 kg/d, respectively), the 2nd challenge was early in the following lactation (mean DIM, intake, milk yield: 26, 3.07 kg/d, 3.99 kg/d, respectively). Relative to the control periods, the challenges (means in late and early lactation, respectively) resulted in large drops in DMI (−1.78, −2.48 kg/d) and milk yield (−1.32, −2.46 kg/d) with increases in milk fat (+3.71, +4.65%) and milk protein (+0.91, +0.55%). For intake and milk yield, the size of the drop was strongly related to the pre-challenge values indicating that these 2 measures were tightly clamped by the challenge. For all other measures (milk fat, milk protein, NEFA, BHB, glucose, urea, insulin) the pre-challenge values had no significant effect, except for BHB in early lactation. Significant within animal repeatability between lactation stages in size of response for intake, milk yield, plasma urea, and BW were found (i.e., significant regression slopes; early vs late). Responses in milk fat, milk protein and the plasma metabolites (other than urea) were not significantly related, indicating that the metabolic adaptations to nutritional challenge vary not only between animals but also between stages of lactation. This was confirmed by principle components analysis which revealed different response patterns between individuals with regard to energy partitioning in milk. In conclusion, there is significant variation between individuals in response to a nutritional challenge and this can be used to develop a quantitative description of adaptive capacity.

Key Words: robustness, individual variation, ruminant

672 Supranutritional levels of antioxidants maintains feed intake and reduces heat stress in sheep. S. Chauhan[1,2], P. Celi[3], B. Leury[2], and F. Dunshea*[2], *[1]CSK, HP Agriculture University, Palampur, Kangra, India, [2]The University of Melbourne, Parkville, Victoria, Australia, [3]The University of Sydney, Sydney, Australia.*

The present study was undertaken to investigate the impact of heat stress and dietary antioxidant supplementation on the oxidative status and physiology of sheep. Twenty-four Merino × Poll Dorset crossbred sheep were housed in one of 2 climatic chambers and offered either a control (10 IU Vitamin E and 0.24 mg Selenium/kg DM) or high antioxidant [100 IU Vitamin E and 1.20 mg Se (as SelPlex)/kg DM] diet. The sheep were subjected to 2 thermal treatments [Thermoneutral (TN): 18 to 21°C and 26–30% relative humidity and Heat Stress (HS): 28–40°C and 40–50% relative humidity] for 2 weeks in a single reversal design. After one week of dietary treatment, animals in one chamber were subjected to HS for one week, with the temperature being increased to 40°C between 9.00 h to 17.00 h and then maintained at 28°C overnight. Those sheep in the TN group were maintained at 18–21°C. Physiological parameters (respiration rate, rectal temperature, skin temperature and heart rate) were recorded 4 times a day (9.00 h, 13.00 h, 17.00 h and 21.00 h and blood samples were collected on d 1 and 7 of heat treatment at 0hr, 8hr and 12hrs of start of heat. The temperature treatments were then reversed. The data was analyzed by undertaking REML (restricted minimum likelihood) variance component analysis using GenStat for windows (12th edition). All the physiological parameters recorded were elevated significantly ($P < 0.001$) by heat treatment. Respiration rate was reduced by antioxidant supplementation as indicated by a diet x temperature x time interaction ($P = 0.010$). There was 13% decline ($P = 0.014$) in feed intake of the control animals during heat stress whereas feed intake was maintained in sheep supplemented with antioxidants. Therefore, these data demonstrated that the negative effect of heat stress on feed intake and respiration rate can be reversed when sheep receive dietary antioxidant supplementation.

Key Words: heat stress, antioxidants, sheep

Ruminant Nutrition: Beef: Feed Additives

673 Feeding monensin or functional oils in high corn finishing diets for Nellore bulls. L. J. Chagas, R. S. Marques, C. Sitta, C. Guerra, V. N. Gouvea, J. Souza, F. Batistel, and F. A. P. Santos,* *University of São Paulo, Piracicaba, SP, Brazil.*

A feedlot experiment was conducted to evaluate the effects of functional oils in substitution of monensin on feedlot cattle performance and carcass characteristic. Two hundred forty Nellore bulls (339 ± 18 kg initial BW) were blocked by initial BW and allotted to 40 dry lot pens (6 head/pen). The animals received their respective dietary treatment for 124 d (including 21 d of adaptation). Treatments were: 1) control (CON), no additives; 2) monensin (MON), 30 mg/kg of DM (Rumenpac); 3) Functional oil (FO3), 0.3 g/kg of DM (commercial additive extracted from castor and cashew oils, Essential); and 4) Functional oil (FO5), 0.5 g/kg of DM. The diets contained 80.6% ground corn, 12% Tifton 85 hay, 4% soybean meal, 0.9% urea, and 2.5% minerals (DM basis). During the 21 d adapting period (step up), when comparing CON, MON, FO3 and FO5 treatments respectively, monensin (MON) decreased ($P < 0.01$) DMI (7.96, 6.49, 7.83, 7.71 kg/head/d) and ADG (0.95, 0.76, 1.11, 1.12 kg/head) ($P < 0.06$) compared with other treatments. Supplementing functional oils at 0.3 g/kg of DM (FO3) increased ($P < 0.06$) G/F (Gain/Feed) (0.120, 0.105, 0.141, 0.145) compared with MON treatment. Supplementing functional oils at 0.5 g/kg of DM (FO5) increased ($P < 0.06$) G/F compared with CON and to MON treatments. Considering the whole feedlot period (124 d), when comparing CON, MON, FO3 and FO5 treatments respectively, no treatment effects ($P > 0.05$) were observed for DMI (9.84, 9.52, 10.28, 10.26 kg/head/d), for ADG (1.27, 1.24, 1.31, 1.34 kg/head), for G/F (0.129, 0.131, 0.128, 0.131) and for carcass characteristics. In conclusion, functional oils from castor and cashew oils may have some beneficial effect on cattle performance during the first 21 d adapting period to high grain diets. In this trial the feed additives tested did not improve cattle performance during the whole feedlot period.

Key Words: antibiotics, feedlot, ionophores

674 Feeding monensin, functional oils and combination of feed additives in high by-products finishing diets for Nellore bulls. L. J. Chagas, R. S. Marques, C. Sitta, C. Guerra, V. N. Gouvea, J. Souza, F. Batistel, and F. A. P. Santos,* *University of São Paulo, Piracicaba, SP, Brazil.*

Monensin, functional oils and a combination of both were evaluated in diets for feedlot cattle for 102 d. One hundred seventy-six Nellore bulls (310 ± 29 kg initial BW) were blocked by initial BW and allotted to 16 dry lot pens. The animals were fed once a day and treatment diets were restricted to 1.5% of BW at the first experimental day. The amount fed was increased 0.4 kg of DM/head per day whenever the feedbunk was clean. Treatments were: 1) control (CON), no additives; 2) monensin (MON), 25 mg/kg of DM (Rumensin); 3) Functional oil (FO5), 0.5 g/kg of DM (commercial additive extracted from castor and cashew oils, Essential); and 4) (M+FO3) monensin, 25 mg/kg of DM plus functional oil, 0.3 g/kg of DM. The 4 treatment diets contained 5% sugar cane bagasse, 50% wet corn gluten feed, 43.5% soybean hulls and 1.5% mineral-vitamin mix and the respective fee aditive. Data were analyzed using the mixed procedure of SAS (1999) with pen as experimental unit. During the first 34 experimental days, comparing CON, MON, FO5 and M+FO3 respectively, cattle fed FO5 diet presented greater DMI (8.95, 8.62, 9.38, 8.69 kg/animal per day) than cattle fed MON and M+FO3 diets ($P < 0.05$). The ADG (1.66, 1.60, 1.75, 1.79 kg/animal per day) was greater for FO5 and M+FO3 than for MON ($P < 0.08$). No differences ($P > 0.05$) were observed for G/F (ADG/DMI) (0.186, 0.186, 0.187, 0.206). During the 102 d of the whole experimental period, comparing CON, MON, FO5 and M+FO3 respectively, DMI (10.30, 10.30, 10.54, 10.46) was not affected by treatments ($P > 0.05$), ADG (1.73, 1.86, 1.77, 1.82 kg/animal per day) was greater for MON and M+FO than for CON treatment ($P < 0.05$) and G/F (0.171, 0.183, 0.171, 0.177) was greater for MON than for CON and FO5 treatments ($P < 0.08$). In conclusion, during the adapting period to high concentrate diets, feeding functional oils or the combination of both feed additives was superior to feeding monensin alone. During the whole feedlot period, monensin was superior to control and to functional oils as a feed additive for feedlot cattle fed high by-product diets.

Key Words: antibiotics, feedlot, ionophores

675 Effect of Rumensin, Micotil, and Component TE-G with Tylan on health, growth performance, and carcass merit of stocker cattle grazing wheat pasture. E. D. Sharman*[1], P. A. Lancaster[1], B. D. Wallis[1], G. W. Horn[1], and G. D. Hufstedler[2], [1]*Oklahoma Agricultural Experiment Station, Stillwater,* [2]*Elanco Animal Health, Guthrie, OK.*

Crossbred steers (n = 207; 200 ± 22 kg) were used in a split plot design to determine the additive effects of metaphylactic treatment with Micotil on arrival, inclusion of Rumensin in an energy supplement, and use of a combination grazing implant on wheat pasture growth performance and carcass merit. On arrival, half of the steers were randomly treated with Micotil (1.5 mL/cwt BW) and held in receiving pens for 42 d. Following receiving, steers were stratified by BW and randomly assigned to 1 of 16 wheat pastures (7.3 to 9.7 ha) at a stocking rate of 1.5 steers/ha for a 112-d winter grazing phase. Pastures were blocked and randomly assigned to 1 of 2 supplement treatments that consisted of a corn and wheat middling-based energy supplement that contained 0 or 220 g/metric ton monensin fed at a rate of 0.91 kg/steer per day. Prior to turnout, half of the steers within each pasture and within Micotil treatment were implanted with Component TE-G with Tylan. Steers were then transported to a commercial feedlot, implanted with Component TE-S with Tylan and fed in a single pen for 137-d before harvest. Growth performance and carcass merit were analyzed using PROC MIXED procedure of SAS. The model included Rumensin treatment as the whole-plot and Micotil and implant treatments as the sub-plot. The 2- and 3-way interactions were not significant ($P > 0.10$). There were no differences ($P > 0.87$) in receiving health parameters or economic impact among Micotil treatments, but no steers were treated for respiratory issues. Inclusion of Rumensin in the supplement increased ($P < 0.01$) final BW and grazing ADG compared with the non-medicated supplement (349 vs. 340 kg; 1.07 vs. 1.01 kg/d, respectively). The grazing ADG of implanted steers was 0.13 kg/d greater ($P < 0.01$) than non-implanted steers (1.10 vs. 0.97 kg/d). Steers implanted during grazing had greater HCW and REA compared with non-implanted steers with no differences in backfat, marbling score, or quality grade distribution. Since the interactions between Micotil, Rumensin, and implant were not significant, we conclude that these technologies are independent and, therefore, additive.

Key Words: grazing implant, Micotil, Rumensin

676 Effects of dietary *Aspergillus oryzae* extract containing α-amylase activity on feedlot performance and carcass characteristics of finishing beef cattle fed steam-flaked corn-based diets.

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Two hundred seventy crossbred yearling steers were used in a randomized block study to evaluate the effects of supplementing steam-flaked corn-based finishing diets with *Aspergillus oryzae* extract containing α-amylase activity on feedlot performance and carcass characteristics. Steers were ranked by weight and allocated into 15 weight block replicates (9 steers/pen). Within each weight block replicate, steers were randomly assigned to one of 2 treatments. The treatment diet (AMZ) contained 5 g/head daily *Aspergillus oryzae* extract containing α-amylase (Amaize, Alltech Inc., Nicholasville, KY). The control diet (CON) provided 5 g/head daily of a corn meal placebo. Each gram of Amaize provided 750 fungal α-amylase units (FAU) which was defined as the amount of enzyme that will dextrinize soluble starch at the rate of 1 mg/min at 30°C and pH 4.8. Individual full weights were obtained on d −1, 0, 33, 70, 105, 159, and 160. All weight data were subjected to a 4% pencil shrink before analysis. Treatment differences for final BW, ADG, DMI, and gain-to-feed ratio were not significant ($P > 0.10$). Steers consuming AMZ achieved greater ($P < 0.07$) dressing percentage (63.7 versus 63.2%); greater ($P < 0.05$) hot carcass weight (358.4 versus 352.1 kg); and greater ($P < 0.08$) kidney, pelvic and heart fat (2.08 versus 1.99%) as compared with controls. Steers fed the AMZ diet also exhibited a reduced ($P < 0.10$) liver abscess rate (17.7 versus 27.7%) as compared with steers receiving the CON diet. Remaining carcass variables were not affected ($P > 0.10$). Data indicate that AMZ supplementation has minimal effects on live cattle performance but alters dressing percentage and carcass weight. Additional research studying the mode of action for this response is warranted.

Key Words: beef feedlot, carcass merit, α-amylase

677 Accelerated step-up regimens for feedlot heifers following oral dosing with Lactipro (*Megasphaera elsdenii*).

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A finishing study was conducted using crossbred heifers (n = 378; 385 ± 10.9 kg BW) to evaluate the potential for employing accelerated step-up regimens following oral dosing with *Megasphaera elsdenii* (Lactipro; MS-Biotec, Inc., Wamego, KS). Upon arrival at the feedlot cattle were given *ad libitum* access to alfalfa hay, and 36 h later were stratified by weight and randomly assigned to 54 pens (7 cattle/pen) within strata. Pens were randomly assigned to one of 6 step-up regimens that utilized between 1 and 5 diets. Diet 1 = 50% corn silage (CS) and 50% concentrate; 2 = 40% CS and 60% concentrate; 3 = 30% CS and 70% concentrate; 2 = 20% CS and 80% concentrate, and the final finishing diet (F) contained 10% CS and 90% concentrate. The control treatment (1234F; no Lactipro) consisted of feeding diets 1 through 4 for 5 d each before feeding F on d 21 and thereafter. Accelerated regimens consisted of a single oral dose (100 mL; 109 cfu/mL) of Lactipro drench administered at processing, followed by the following diet regimens: 234F, 34F, 3F, 4F, and F. Diets 2 through 4 were fed 5 d each before progressing to the next diet in sequence. All diets were based on dry-rolled corn and wet corn gluten feed. Treatment tended (quadratic effect, $P = 0.07$) to influence DMI, with cattle started on intermediate diets (3F and 34F) having lower DMI than other groups. Heifers fed 1234F or F tended to have greater ADG (quadratic, $P = 0.10$) and were more efficient than other groups (quadratic, $P < 0.01$). Treatments did not differ with respect to liver abscess incidence or severity, HCW, dressing percentage, yield grade ($P > 0.10$) or digestive upsets. Treatment affected LM area (quadratic, $P = 0.01$), and was smallest for carcasses from heifers fed the 4F regimen. Marbling score generally increased with the accelerated step-up regimens (linear, $P = 0.12$; quadratic $P = 0.02$) with the greatest improvement in carcasses of heifers placed directly onto the finishing diet. Heifers can be transitioned rapidly to high concentrate diets following oral administration of *Megasphaera esldenii* without compromising performance or carcass quality.

Key Words: diet adaptation, *Megasphaera elsdenii*

678 Oral dosing with Lactipro (*Megasphaera elsdenii*) decreases roughage required for feedlot finishing.

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A completely randomized study with crossbred steers (n = 443; initial BW = 400 ± 2.4 kg) was used to evaluate performance and carcass traits after oral dosing with *Megasphaera elsdenii* (Lactipro; MS-Biotec, Wamego, KS) and placed directly onto finishing diets. Steers grazing pastures in Wells, NV were transported to the Beef Cattle Research Center in Manhattan, Kansas, placed into feedlot pens, and provided ad libitum access to brome hay and water. Approximately 24 h after arrival, steers were weighed and randomly assigned to one of 2 treatments based on order of processing. Steers were placed in 36 pens, 24 containing 14 or 15 steers/pen and 12 containing 7 or 8 animals/pen (18 replicates/treatment). A traditional, 4-diet step-up regimen (control) utilizing 3 step-up diets (40, 30, and 20% corn silage and the balance as concentrate) fed for 6 d each, followed by a finishing diet (10% corn silage and 90% concentrate) fed for the remainder of the study was compared with a Lactipro treatment, which consisted of a single oral drench of Lactipro (100 mL, providing 109 cfu/mL *Megasphaera elsdenii* strain NCIMB 41125) and direct placement onto the finishing diet. Diets contained steam-flaked corn and wet corn gluten feed, and were fed once daily ad libitum. Lactipro steers consumed 17% less silage than control steers over the 115-d feeding period ($P < 0.01$). Dry matter intake tended to be lower for steers in the Lactipro group ($P = 0.07$), but gain and gain efficiency were not different ($P > 0.10$). Dressing percentage, HCW, LM area, 12th-rib fat thickness, and incidence of liver abscess were unaffected by diet regimen. Percentage of YG 1 carcasses tended to be higher for steers in Control group ($P = 0.10$) compared with cattle placed directly onto the finishing diet. Dosing with Lactipro and placing cattle directly onto the finishing diet yielded more Choice ($P = 0.07$) and fewer Select carcasses ($P = 0.06$) compared with the control treatment. Steers receiving Lactipro at processing can be placed directly onto a finishing diet, decreasing roughage use while maintaining acceptable cattle health, performance, and carcass quality.

Key Words: diet adaptation, Lactipro, roughage

679 Effect of Optaflexx level on growth performance and carcass characteristics of feedlot steers.

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Three thousand and twenty-four steers (588 kg) were allotted to 40 pens in a randomized complete block design of 4 treatments at 2 trial sites with 5 replications per site to evaluate the effects of differing levels of Optaflexx on growth performance and carcass characteristics of finishing steers. Experimental treatments included: 1) Non-medicated control; 2, 3 and 4) Optaflexx fed continuously at 10.0, 20.1 and 30.1

mg/kg of the diet DM, respectively. Optaflexx was fed during the final 28 d before harvest. The basal diet contained Rumensin at 36.7 mg/kg and Tylan at 9.8 mg/kg of the diet DM. Data were analyzed using a mixed model with treatment as a fixed effect and site, block and site by block as random effects. Pen served as the experimental unit and initial weight was used as a covariate. Feeding Optaflexx resulted in improved ($P < 0.01$) average daily gain, harvest weight, feed conversion, carcass weight, dressing percentage and LM area compared with control. Feeding 20.1 or 30.1 mg/kg diet DM Optaflexx increased ($P < 0.05$) daily gain, harvest weight, feed conversion and carcass weight compared with 10.0 mg/kg diet DM. Optaflexx fed at 30.1 mg/kg diet DM resulted in increased dressing percentage and LM area compared with 10.0 and 20.1 mg/kg diet DM. Marbling score, quality grade and yield grade were not affected by feeding Optaflexx. Feeding Optaflexx increases daily gain, harvest, and carcass weight and improves feed efficiency while having minimal effects on carcass quality.

Table 1. Effect of Optaflexx level

	Treatments					
Item	Control	10.0 mg/kg	20.1 mg/kg	30.1 mg/kg	SEM	P-value
Final BW, kg	618.2^{a}	622.3^{b}	626.9^{c}	627.3^{c}	2.5	<0.01
DM Intake, kg/d	9.36	9.28	9.36	9.24	0.16	0.38
Daily gain, kg	1.08^{a}	1.23^{b}	1.38^{c}	1.41^{c}	0.09	<0.01
Feed/gain	8.71^{a}	7.63^{b}	6.84^{c}	5.70^{c}	0.33	<0.01
Carcass Wt, kg	397.8^{a}	401.2^{b}	404.0^{c}	406.3^{c}	0.9	<0.01
Dressing percent	64.3^{a}	64.5^{a}	64.5^{a}	64.8^{b}	0.1	0.02
LM area, cm^2	91.0^{a}	92.5^{b}	93.2^{b}	94.8^{c}	1.7	<0.01
Marbling	small^{29}	small^{22}	small^{24}	small^{19}	3.7	0.07

$^{a–c}$Row means without a common superscript differ ($P < 0.05$).

Key Words: Optaflexx, ractopamine, steers

680 Effect of an injectable amino acid solution in calves fed barley-based rations with supplemental lysine and methionine during a 65-d preconditioning program.

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High-risk steer calves (n = 160; BW = 297 ± 10.6 kg) were allocated to evaluate the effect of an injectable amino acid solution in combination with supplemental lysine and methionine in barley-based rations during a 65-d preconditioning program. The trial was conducted in Alberta, Canada. Animals were randomly assigned to a 2 × 2 factorial arrangement of treatments: saline × injectable amino acid (INJ-AA) versus control (CON) × dietary amino acid (DIET-AA) in a completely randomized block design. Animals were blocked by placement weight. Administration of saline or Vitamaster-NF (NF; Vétoquinol N.A. Inc., Lavaltrie, QC, Canada) was done intramuscularly at a dosage of 1 mL/45 kg of BW. Cattle receiving DIET-AA were fed supplements providing 15 mg/steer per day of both methionine (MetaSmart, Adisseo, Alpharetta, GA) and lysine (AminoShure-L, Balchem Corporation, Animal Nutrition and Health, New Hampton, NY). Cattle from the same treatment group were randomly allocated to one of 4 pens (40 steers/pen) equipped with individual feed intake data collection systems (GrowSafe Systems Ltd., Airdrie, Canada) and fed for 65 d. Performance was calculated with deads (2) and removals (6) excluded; only 6.0% morbidity and 1.3% overall mortality was experienced with no health differences across treatments ($P > 0.10$). 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 block nested within pen. There were no differences in placement BW ($P > 0.30$) or 65-d BW ($P > 0.30$). There were no effects of treatment on ADG ($P > 0.26$) or G:F ($P > 0.60$), throughout the 65-d period. A decrease in DMI was observed in animals receiving DIET-AA compared with CON (5.97 vs. 6.40 kg; $P < 0.01$) in the 65-d preconditioning program. These data indicate that dietary supplementation of amino acids resulted in a decrease in DMI in high-risk steer calves without hindering ADG. However, it should be noted that morbidity was only 6.0%.

Key Words: amino acids, cattle, feedlot performance

Small Ruminant: Production and Reproduction

681 Fabricated carcass measurements in terminally sired F_1 lambs. M. R. Mousel*[1], D. R. Notter[2], T. D. Leeds[3], H. N. Zerby[4], S. J. Moeller[4], and G. S. Lewis[1], [1]*USDA, ARS, U.S. Sheep Experiment Station, Dubois, ID,* [2]*Virginia Tech, Blacksburg,* [3]*USDA, ARS, National Center for Cool and Cold Water Aquaculture, Kearneysville, WV,* [4]*The Ohio State University, Columbus.*

Scientific data for carcass traits of terminal-sire sheep breeds can be used to improve the value of market lambs, but information is lacking for modern terminal-sire breeds in the United States. Thus, the effects of terminal-sire breed on 14 fabricated carcass measurements were determined in F_1 wether lambs. Columbia, USMARC-Composite (Composite), Suffolk, and Texel rams were mated with mature Rambouillet ewes over 3 yr. From weaning until harvest each year, F_1 lambs ($n = 518$) were fed a step-up finishing diet and harvested in 3 groups at targeted mean BW of 54.5, 61.4, or 68.2 kg. Carcasses were fabricated according to Style A of Institutional Meat Purchase Specifications. Weights were collected for the following carcass subprimal cuts: neck, foreshank, breast, square-cut shoulder (SCShoulder), rack, roast ready rack (RRR), loin, trimmed loin (TLoin), sirloin, boneless sirloin (BSirloin), flank, leg, boneless leg (BLeg), and hindshank. All traits were analyzed individually with a mixed model 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 ($P < 0.01$) in all models. Sire breed was significant ($P < 0.01$) for all traits except flank ($P = 0.05$). Suffolk-sired lambs had the heaviest neck (0.86 kg), breast (4.1 kg), SCShoulder (6.5 kg), rack (3.4 kg), RRR (1.5 kg), loin (3.2 kg), sirloin (3.1 kg), leg (10.6 kg), and BLeg (4.6 kg) compared with the other F_1 lambs. Suffolk-sired lambs had the heaviest foreshanks (1.7 kg) and TLoin (2.7 kg); then Columbia-sired, 1.5 and 2.6 kg, respectively; and Texel-sired lambs had the lightest, 1.4 and 2.4 kg, respectively. Suffolk-sired lambs had heavier BSirloin (1.7 kg) than Composite-sired lambs (1.5 kg), but Suffolk- and Composite- did not differ from Texel- (1.6 kg) or Columbia-sired (1.6 kg) lambs. Columbia- and Suffolk-sired lambs had heavier hindshanks than Texel-sired lambs, 0.94, 0.97, and 0.88 kg, respectively. Producers can use data such as these to select a terminal-sire breed of sheep that will improve the carcass value of market lambs.

Key Words: lamb, terminal sire, carcass

682 Awassi sheep productivity in central Anatolia region of Turkey. H. Üstüner* and M. Ogan, *Uludag University, Faculty of Veterinary Medicine, Department of Animal Science, Bursa, Turkey.*

The objective of this study was to investigate the reproductive and production performance of Awassi sheep in central Anatolia region of Turkey. A total 147 ewe production and reproductive performance records between January 2003 and December 2005 were used for this experiment. The data consisted of parity, birth type and year for reproductive and production performance, and birth type, birth date, sex and weight of lamb for growth performance. Growth and milk yield were recorded fortnightly. Average live weight of Awassi lambs at birth, 30th, 60th (weaning), 90th, and 120thday were found 4.5 ± 0.2, 9.9 ± 0.2, 17.3 ± 0.4, 23.3 ± 0.5, and 29.1 ± 0.7 kg, respectively. Average live weights of female Awassi lambs at d 150 and 180 were 32.8 ± 0.5 and 38.1 ± 0.7 kg, respectively. The effects of parity, birth year, sex, birth type (single or twin) and all interactions on growth performance were investigated using PROC MIXED of SAS. The birth weight was affected by sex ($P < 0.01$) and birth type ($P < 0.01$) but the effects of parity and year were not significant ($P > 0.05$). The average survival to weaning was 88.3%, representing a loss of 18 lambs. Lactation milk yield was found to be 196.5 ± 5.6 kg in 184.3 ± 2.1 d. The effects of year and parity and all interactions on milk yield were investigated using PROC MIXED of SAS. The effects of year and parity were found statistically significant ($P < 0.01$). Greasy wool production and mating weight of Awassi ewes were found 2543.0 ± 59.6 g and 58.8 ± 0.7 kg, respectively. General mortality rate was found 8.2% throughout research period. Greasy wool production was affected by year (first or second research year; $P < 0.001$) but not by parity ($P > 0.05$). The effects of parity and mating year on ewes' mating weight were highly significant ($P < 0.001$). As a result of this study, Awassi sheep can be successfully raised under central Anatolia conditions.

Key Words: Awassi, lactation yield, environment

683 Effect of lithium chloride for mid-term conditioned aversion to olive tree leaves in penned and grazing goats. C. L. Manuelian, E. Albanell, M. Rovai,* A. A. K. Salama, and G. Caja, *Grup de Recerca en Remugants (G2R), Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

With the aim of allowing the selective grazing of goats in olive tree fields, conditioned aversion was created by using 2 doses of lithium chloride (LiCl). Treatments were C (water blank), AV1 (175 mg LiCl/kg BW) and AV2 (200 mg LiCl/kg BW). Fifteen dry Murciano-Granadina does were randomly assigned to the 3 treatments, in which voluntary intake of olive leaves (used as novel feed) was individually measured after 1 h of allowance during the aversion induction period (d 1 to 3). A single dose of LiCl was orally administered by a drenching gun. Repeated exposure to the olive leaves for memory evaluation was performed in double-choice feeding (Italian rye-grass and olive leaves) tests of 60 min (d 4 to 8) and 30 min (d 16, 24, 31, 38 and 53). On d 9 a new dose of LiCl was administered to does consuming > 10 g/d olive leaves. No more LiCl was administered during the memory evaluation period. Thereafter, all groups were exposed (d 59, 90, 121 and 182) to simulated olive trees, placed in a rye-grass prairie for 30 min. Moreover, C and AV2 groups grazed (d 146, 211 and 363) on a commercial olive tree field with natural weeds for 30 min. Olive leave intake slightly increased during the memory evaluation period being greater on d 53 in the C does (99 ± 1 g; $P < 0.05$) than in the averted does (AV1, 42 ± 14 g; AV2, 34 ± 16 g) which did not differ. Four AV1 does needed a new LiCl dose to re-establishing the aversion. In addition AV1 does spent more time eating olive leaves under simulated field conditions than AV2 (333 ± 53 s and 149 ± 60 s; $P > 0.05$). A year after the induced aversion, AV2 does still presented greater preference (approaching, eating and climbing) for olive leaves than C does, when grazing in the commercial field. In conclusion, 200 mg LiCl/kg BW was the preferred dose for inducing an effective mid-term (12 mo) conditioned aversion in goats. The use of LiCl was considered as a useful tool for selective grazing and use in ecological bio-agriculture system.

Key Words: aversion, lithium chloride, goats

684 Milk production losses in early lactating dairy goats under heat stress. S. Hamzaoui, A. A. K. Salama,* G. Caja, E. Albanell, C. Flores, and X. Such, *Group de Recerca en Remugants (G2R), Universitat Autònoma de Barcelona, Bellaterra, barcelona, Spain.*

In a previous work we observed that heat-stressed goats at late lactation suffered no reductions in milk yield and milk fat, despite the lower milk protein. However, this response during early lactation remains unclear. Eight multiparous Murciano-Granadina dairy goats (43.3 ± 1.6 kg BW; 81 ± 3 DIM) were used. Goats were kept in metabolic cages and randomly assigned to 2 climatic treatments according to a crossover design (35 d periods). Treatments were (temperature, °C; humidity, %; THI, Thorn heat index):1) thermal neutral (TN, 15 to 20°C; 35 to 45%; THI = 59 to 64), and 2) heat stress (HS, 12 h/d at 37°C and 45%, and 12 h/d at 30°C and 45%, THI = 86 and 77, respectively). Goats received TMR and water ad libitum. Feed intake and milk yield were recorded daily. Milk, blood, and urine samples were collected weekly for the osmolality measurements. Additionally, blood samples were taken at d 7 and 28 of each period for the creatinine analysis. Urine uric acid concentration was used as an index (uric acid:creatinine × $BW^{0.75}$) of microbial protein synthesis. Feces and urine for digestibility and N balance (d 31 to 35) were also collected in each period. Compared with TN, HS goats had lower ($P < 0.01$) feed intake (1.75 vs. 2.47 kg/d), milk yield (1.53 vs. 1.68 L/d), milk fat (3.76 vs. 4.26%), and milk protein (3.26 vs. 3.74%). Osmolality (mosm/kg) of blood plasma (334) and urine (1449) was similar in both groups, but milk of HS had lower ($P < 0.05$) osmolality than TN (309 vs. 321). Creatinine concentration in blood was greater ($P < 0.05$) in HS than TN (0.81 vs. 0.62 mg/dL), which might indicate muscle degradation under HS conditions. The HS goats had lower ($P < 0.05$) microbial protein synthesis index (6.5 vs. 10.0). Digestibility of DM, OM, ADF, and NDF did not differ between TN and HS. Moreover, both TN and HS retained similar ($P = 0.557$) amount of N (19.3 g/d). In conclusion, early lactating dairy goats under HS suffer losses in milk yield, milk fat and protein contents. The reduced milk protein content under HS might be related to the lower microbial protein synthesis.

Key Words: heat stress, digestibility, dairy goat

685 Long-term effects of intrauterine rivalry on the reproductive performances of co-twin ewe-lambs.

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Intrauterine environment may permanently alter the genome expression through fetal programming. We hypothesized that the birth weight difference (BWD) between co-twins may be a representative measure of their experienced rivalry. With this regard, we tested the effect of variations in the BWD of co-twin ewes on their further average litter size. Data analyses were performed on 1,449 lambing records from 331 Ripollesa breed ewes averaging 1.502 ± 0.01 lambs per litter (singletons, 51.8%; twins, 46.2%; triplets, 2.0%). Ewes born as twins were classified in groups using BWD = 200 g as a discriminating threshold; i.e., equal twins (T0, BWD ≤ 200 g), and heavier (TH) and lighter (TL) co-twins of litters with BWD > 200 g. Ewes born as singletons were grouped in an additional control category (S). A mixed linear model accounting for BWD, ewe age (<3, 3, 4, 5 and > 5 yr), year of lambing (21 yr) and the random permanent effect of each ewe, was implemented with the Mixed procedure of SAS (SAS Institute, Inc., Cary, NC). Both the effects of birth weight and co-twin sex (male or female) were discarded ($P > 0.1$), whereas remaining effects reached statistical significance ($P < 0.05$). Singleton (n = 94; 1.49 ± 0.03 lambs), T0 (n = 73; 1.509 ± 0.03 lambs) and TH (n = 64; 1.52 ± 0.032 lambs) ewes showed similar reproductive performances ($P > 0.05$) whereas litter size decreased ($P < 0.05$) for TL ewes (n = 100; 1.40 ± 0.03 lambs). Indeed, TL ewes experienced a 6 to 8% reduction in the realized litter size along their whole productive life. Although physiological pathways underlying these reproductive departures were not elucidated, current knowledge on fetal programming postulates permanent alterations in the hypothalamic-pituitary-adrenal axis as the causal mechanism. In conclusion, fetal programming due to intrauterine competition is a fact that must be dealt with in sheep, with relevant economic consequences in the ovine sector worldwide.

Key Words: fetal programming, litter size, sheep

686 Fixed-time laparoscopic AI with frozen-thawed goat semen in progesterone and PMSG supplemented Cosynch protocol.

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The effects of progesterone and PMSG supplemented Cosynch (GnRH on d 0, PGF2α on d 7, with GnRH and timed AI (TAI) on d 9) on the estrus synchronization, follicular development and pregnancy rates (PR) after TAI were evaluated during the breeding season. The multiparous Saanen does (>40 kg BW) were used and assigned to 4 synchronization treatments. In group I, II and IV; all does received Cosynch plus intravaginal sponges on d 0 (choronogest) for 7 d. For the Groups I (n = 18) and III (n = 15) all does were received PMSG at PGF2α injection. The Groups I and II (n = 20) were laparoscopically and the Groups III and IV (n = 19) were intracervically inseminated with 50 × 10^6 motile spermatozoa after 2nd GnRH injection. The onset of estrus was determined with teaser bucks at 12-h interval for 30 min during 72h. Follicular development was monitored at d 7 and 9 by transvaginal ultrasonography (US) with 4–8 MHz endocavity array transducer. The data were subjected to Fisher′s exact test and the 95% significance level was noted. The mean time of the estrus onset, the mean of observed estrus, the biggest follicle diameters and follicle numbers (>0.3 cm) at the sponge removal and at the 2nd GnRH injection were 28.5h, 89%, 0.6cm, 2.6, 0.8cm, 2.2; 28.2h, 85% 0.8cm, 3.1, 0.8cm, 1.3; 24.0h, 27%, 0.7cm, 2.8, 0.7cm, 3.3 and 29.3h, 84%, 0.8cm, 2.2, 0.7cm, 2.9 for the Groups I, II, III and IV, respectively. Cosynch plus PMSG (Group III) was not successful to induce estrus ($P < 0.001$). There were no significant difference between evaluations for the follicle diameters ($P > 0.05$). The follicle numbers of the Group II were lower at the 2nd GnRH injection than at sponge removal ($P < 0.001$). PR were ultrasonographically determined as 56, 41, 0, and 33% for Groups I, II, III, and IV on d 35, respectively. The PR of Group III was the lowest ($P < 0.05$). Although, there was no difference between insemination protocols for PR of Groups II and IV; the laparocopically inseminated groups was higher than the intracervically inseminated groups. Choronogest supplementation of Cosynch improved the reproductive parameters.

Key Words: Cosynch, goat, laparoscopic AI

687 Pregnancy diagnosis in sheep using fecal near infrared reflectance spectroscopy.

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The development of quick and accurate methods for early pregnancy diagnosis is a key factor for livestock exploitation. Fecal near infrared reflectance spectroscopy has shown potential to be used to identify pregnancy in cattle. One hundred ten Brazilian

Somalis and 100 Morada Nova ewes' fecal spectra were used to evaluate the fecal NIRS for pregnancy identification in sheep. Fecal spectra were collect from the same animals in two different physiological stages: 67 ± 7 days of pregnancy and 30 days after weaning. Discriminant analysis with PCA/MDR algorithm coupled to Mahalanobis distance (MD), were used to identify pregnancy through spectra similarity, assuming three or more as dissimilar spectra. Spectra of pregnant or non-pregnant ewes from one breed were not consistently similar to other breed in the same reproductive stage, with a range of 33 to 89% of prediction accuracy in the spectral match. Greater breed effect was observed for pregnant ones, probably reflecting prolificacy differences. Spectra from pregnant animals were different from non-pregnant ones and vice versa (98 to 100% of prediction accuracy), regardless of the breed, suggesting they may be used to classify animals based on pregnancy. To minimize breed effect, all spectra were pooled to create two databases (pregnant and non-pregnant). From these data sets, a randomized subset of 42 fecal spectra, not used to equation calibration, were selected and used for validation of procedure. Both pregnant and non-pregnant discriminant equations were able to identify and classify the animals according to pregnancy with 100% of accuracy, confirming the potential of fecal NIRS to identify pregnancy in livestock. However, a statistical significant difference was observed for diet CP and organic matter digestibility (OMD) between pregnant and non-pregnant ewes (T-test, P <0,001), reflecting changes in pasture quality during data collection. Thus, the potential effect of season on pregnancy-related spectral differences remains to be investigated and also a larger database need be evaluated before this technique is recommended for early pregnancy diagnosis in sheep.

Key Words: discriminant analysis, gestation, NIRS

688 Ability to culture of cells from postmortem goat skin tissues stored at room temperature for different time intervals.

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Animal cloning technology has renewed the interest in postmortem tissue storage, since these tissues can be used to reintroduce the lost genes back into the breeding pool in animal agriculture, preserve the genetic diversity, and revive endangered species. Several studies have demonstrated that cell survival decreases with increasing postmortem tissue storage. However, the limits of time interval within which live cells can be recovered from dead animals is not adequately studied. Cell viability and their potential to in vitro culture ensure nuclear integrity, a requirement for successful cloning of animals. To test the postmortem storage limits of animal tissues, 2–3 mm^2 skin pieces (n = 70) from ears of 3 breeds of goats (n = 7) were cultured after 0, 2, 4 and 6 d of postmortem storage at 24°C. After 10 d of culture, outgrowth of fibroblast-like cells (>10 cells) around the explants was scored. All the explants irrespective of breed displayed outgrowth of cells on the dish containing fresh tissues (d 0). However, the number of explants exhibiting outgrowth reduced with increasing time interval. Only 53.8% explants displayed outgrowth after 2 d of tissue storage. The number of explants displaying outgrowth was much smaller after 4 d (16.7%) and 6 d (13.3%) of storage. In general, the number of outgrowing cells per explant, on a given day, also decreased with increasing postmortem storage time interval. To test the differences between cell cultures, obtained from postmortem fresh and stored tissues, secondary cultures were established from one of the goats exhibiting outgrowth of cells after 6 d of tissue storage. Comparison of both the cell lines revealed similar cell morphology and growth curves, and had doubling times of 23.0 h and 22.6 h, respectively. These results suggest that live cells can be recovered from skin tissues of goats and perhaps other animals even after 6 d of their death with comparable growth profiles.

Key Words: fibroblasts, postmortem tissue storage, goat skin

Symposium: Recent Advances in Swine Genomics

689 Pigs, feed intake, and genes. J. P. Cassady*[1], S. Jiao[1], C. Maltecca[1], K. A. Gray[2], and J. W. Holl[1], [1]*North Carolina State University, Raleigh,* [2]*Smithfield Premium Genetics.*

The objective of this research was to develop genomic strategies for improving nutrient utilization by identifying genomic regions affecting feed intake, growth rate, and ultrasound traits in a Duroc terminal sire population. Individual feed intake, growth rate, and ultrasound data were available on 1022 Duroc boars. Boars were genotyped at GENESEEK using the Illumina Porcine SNP60 BeadChip. The criteria for screening the genomic data was a call rate per animal of 0.9, call rate per SNP marker of 0.9, Hardy Weinberg equation test with $P < 0.001$, and minor allele frequency >0.01. After editing, 40,008 SNPs were retained for genome wide association analysis. The Bayes B and C options in GenSel 4.0.1 were used with pen and contemporary group included as fixed effects for all traits. A preliminary analysis of average daily feed intake, intramuscular fat, and muscle depth was completed. Regions on chromosomes 1, 6, 9, 10, 12, 15, and X were identified affecting average daily feed intake, intramuscular fat, and muscle depth. Additional regions affecting average daily feed intake were found on chromosomes 3, 4, 5, 7, 8, 11, 13, and 17. The markers explained 16% of the total variance for average daily feed intake, 44% for intramuscular fat, and 49% for muscle depth. Analyses of ADG and feeding behavior are currently in progress. Markers identified on chromosome 1 effecting average daily feed intake were in the general region of MC4R. Several other markers were also located in regions where QTL have previously been reported. It was concluded that opportunities exist to use genomic markers to increase accuracy of selection in a Duroc terminal sire population.

Key Words: denomics, SNP, Duroc

690 A review of swine genome-wide association studies at USMARC. J. F. Schneider,* *USDA, ARS, USMARC, Clay Center, NE.*

Reproductive efficiency has a great effect on the economic success of pork production. Traits including age at puberty (AP), ovulation rate, number born alive (NBA), and average piglet birth weight (ABW) contribute greatly to reproductive efficiency. To better understand the underlying genetics of reproductive efficiency, a series of GWAS were undertaken. Samples of DNA were collected and tested using the Illumina PorcineSNP60 BeadChip (Illumina Inc., San Diego, CA). The first analysis included total number born (TNB), NBA, number born dead (NBD), number still born, mummies, litter birth weight (LBW), and ABW taken from 1,152 first parity females. Chromosome and position assignments were based on Build 10. A total of 41,151 SNP were tested using a Bayesian approach. Beginning with the first 5 SNP on SSC1 and ending with the last 5 SNP on the SSCX, SNP were assigned to groups of 5 consecutive SNP by chromosome-position order and analyzed again using a Bayesian approach. These selected 5-SNP non-overlapping groups were defined as QTL. Of the available 8,814 QTL, 124 were found to be statistically significant ($P < 0.01$). Multiple testing was considered using the probability of false positives. QTL were found for litter traits on SSC1, SSC4, SSC6, SSC10, SSC11, SSC13, SSC14, SSC15, and SSC17. QTL were found for LBW and ABW on all chromosomes except SSC16 and SSCX. Several candidate genes have been identified that overlap QTL locations among TNB, NBA, NBD, and ABW. A second analysis measured AP on 752 gilts that showed estrous before 230 d of age. Chromosome and position assignments were made based on Build 10.2. Seventy-two QTL were found to be statistically significant ($P < 0.01$) and were found on all chromosomes except SSC17. One hundred fifty-seven gilts that failed to reach puberty were added to the data set and the 909 gilts were analyzed as a binomial trait. A similar number of QTL were found on all chromosomes except SSC11, SSC16, and SSC18. The results of these analyses demonstrate that opportunities exist to introduce QTL into genetic improvement programs designed to improve reproductive efficiency. USDA is an equal opportunity provider and employer.

Key Words: Bayes, GWAS, reproduction

691 The genetic basis of host response to experimental infection with the PRRS virus in pigs. J. Dekkers*[1], N. Boddicker[1], E. Waide[1], J. K. Lunney[2], R. R. R. Rowland[3], D. J. Garrick[1], and J. Reecy[1], [1]*Iowa State University, Ames,* [2]*USDA, ARS, BARC, Beltsville, MD,* [3]*Kansas State University, Manhattan.*

Porcine reproductive and respiratory syndrome (PRRS) represents the most costly disease in the US pig industry. Caused by an RNA virus, vaccination strategies have generally been ineffective. Thus, to investigate opportunities for genetic improvement of pigs for increased resistance or tolerance to the PRRS virus, the PRRS Host Genetics Consortium (PHGC) was established. Among others, the PHGC involves experimental challenge of piglets provided by commercial breeding companies with a specific strain of the PRRS virus shortly after weaning, evaluating piglet response in terms of viremia and weight gain, genotyping each piglet with the Porcine 60K SNP panel, and conducting genome-wide association studies to identify genomic regions associated with host response. The purpose of this presentation will be to review results of the first 6 challenge trials of 200 piglets each, with specific reference to a major QTL identified on chromosome 4, and to discuss future plans and implications. This work is supported by the PRRS CAP, USDA NIFA Award 2008-55620-19132, the National Pork Board, USDA ARS and the NRSP-8 Swine Genome and Bioinformatics Coordination projects.

Key Words: porcine reproductive and respiratory syndrome (PRRS), genetic markers, swine

Teaching/Undergraduate and Graduate Education Symposium: Giving Employers What They Want–How Ready is Today's Animal Science Graduate?

692 The animal sciences curriculum of 2025. M. A. Wattiaux,* *University of Wisconsin-Madison, Madison.*

A curriculum reflects subjects and experiences in a plan of study intended to prepare students for professional success in a chosen career. The core animal sciences curriculum has hardly changed in the last 50 years, but it has adapted to changes in scientific discoveries, departmental priorities, student and instructor demographics, and employers' demands. As the 21st century unfolds, our graduates will be asked to solve increasingly complex problems and address societal concerns, many of which will not have unique disciplinary answers. How can we capitalize on our strengths to prepare students for jobs that, in many cases, do not exist yet? How do we structure programs that foster skills and aptitudes that offer students with a degree that has long-term value? Animal sciences curricula will continue to expand (e.g., genomics, animal welfare) and interface with other disciplines (e.g., environmental, international, human health and social studies), but more importantly, our classrooms will become microcosms of society, and students will be challenged to face problems as they will encounter them in the workforce. Students will have to become critical thinkers and evaluators of information as the latest scientific facts and figures will be readily available through the World Wide Web. Because embracing diversity is an essential component of broad understanding, creativity and innovation, our students must be challenged with the conflicting perspectives of multiple stakeholders. Requiring multiple capstone-like experiences whereby a student addresses relevant real-world problems through properly structured internships, service learning, labs or undergraduate research projects, study abroad, and computer-based simulations will become ever more essential to our future pedagogy. Communication skills and leadership experiences will no longer suffice, as metacognitive and self-directed learning skills will be vital to one's successful career path. In short, learning how to learn is a lasting, transferable and life-long learning skills that will be as important as equipping our students with the latest knowledge at the time of graduation. These inevitable changes are already occurring in spite of numerous challenges.

Key Words: undergraduate, instruction, curriculum

693 Creating animal scientists from scratch–Meeting industry needs with today's students. J. A. Sterle,* *Iowa State University, Ames.*

Changing demographics of students majoring in animal science (AN S) are no surprise. However, coupled with decreased interest of AN S undergraduates in food production species, continued demand for "industry-ready" graduates, and the increased enrollment that many AN S departments are experiencing (along with decreasing resources), it becomes apparent that AN S faculty, departments and curriculum must adjust. Questions arise about changing goals and objectives of traditional departments, and the best use of available resources to meet these diverse interests and needs (and increasing student numbers). Incoming students today need more introduction to the livestock industry, including terminology, industry structure, heritage, and contributions to society. Safety around livestock and animal handling also need to be covered. These topics are not only necessary to provide frame of reference and perspective, they also draw the interest of students. There is pressure to create broader curricula to meet students' interest in species other than livestock. A department must consider whether the job market supports graduates in a new specialized area. If the answer is yes, then the question of available resources must be addressed. For example, many students come to AN S with a strong interest in zoo animals or exotics, but the job market makes it difficult to justify specific courses in this area. Many employers of animal scientists have expectations that graduates have some basic knowledge, experiences and skills (such as being comfortable around large animals), regardless of the position. Basic handling courses, experiential labs throughout the curriculum, and intense internship/student worker positions can prepare students who do not enter college with such experience. Over 95% of Iowa State AN S graduates, 55% of which would not be considered "traditional" or from a farm background, are placed within 6 mo of graduation, in a wide variety of positions. This suggests that AN S programs can still meet the needs of a variety of employers, regardless of the background of students entering the curriculum.

Key Words: teaching, undergraduates, non-traditional students

694 Critical skills and characteristics expected by employers of animal science graduates and strategies for equipping them. S. Robinson*[1] and D. Mulvaney[2], [1]*Oklahoma State University, Stillwater,* [2]*Auburn University, Auburn, AL.*

Employers and professional schools desire graduates in animal science programs who possess human capital (i.e., technical competencies, employability skills, and experiences) in the animal agriculture industry. Specifically, in addition to technical competencies, employers seek prospective employees who have evidence of practiced leadership and previous work experience that has enabled them to experience real-life issues, such as dealing with difficult people, resolving conflicts, making decisions and thinking at higher levels of cognition. According to employers, colleges of agriculture are effective in preparing prospective employees with technical skills and knowledge within a specific discipline; however, the development of interpersonal and emotional intelligence (EI) skills is not perceived as highly. Yet, in terms of importance, employers rank these latter skills ahead of disciplinary knowledge and technical skills. It is believed that disciplinary knowledge, skills and ability (KSA) are expected of all prospective employees, while "soft" cluster skills are those that differentiate the best from the rest. A recent study released by the Association of Public and Land Grant Universities (APLU) analyzed the importance of 7 "soft skill" clusters. Employers ranked them in importance from highest to lowest: (1) communications, (2) decision making/problem solving, (3) self-management, (4) teamwork, (5) professionalism, (6) experiences, and (7) leadership. These data provoked a call for more intentional integration of leadership and EI development into curricula and the establishment and promotion of leadership minors and/or certificates. Authors will address the readiness of the animal science graduate and offer strategies for developing the KSA expected by employers. Results of a study using the Delphi method to reach consensus of agreement among animal science industry experts on their thoughts regarding the skills college graduates need for employability in various sectors of the animal agriculture industry will be compared with other survey results and the APLU report. Additional inputs derived from interview processes conducted by prospective employers with applicants provide details about which aspects of human capital result in job offers. Of concern is how do programs reconstruct the frameworks of the higher education experience so that learning outcomes of soft skills, critical thinking skills, problem solving, experience and abilities needed for acquisition and access of information, knowledge and the contextual application are not mere aspirations in a strategic plan but tangible and measured. Classroom pedagogy may need to be changed - shifting from the emphasis on delivering content knowledge to a more robust intentional, experiential engagement of students around the acquisition of the desired skills. Based on these collective inputs, authors will offer suggestions for teaching and learning practices and curricular revision, which will lead to effective preparation of students for a dynamic, complex, global world of work.

Key Words: employer expectation, student development, animal sciences curricula

695 Custom tailoring class information to each student for their eventual use in the workplace.

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Teaching required classes within the animal sciences often involves students from a wide range of backgrounds and diverse future career interests. Thus, some class material may seem of more relevance to some than to others, and engagement and comprehension suffers among students who do not see an immediate need for learning the information. As a result, opportunities for critical thinking are lost and the student is subsequently ill-prepared for critical thinking after entering the workplace. To address this, 2 different strategies have been employed in 2 different courses. The first involves the use of comprehensive oral final exams in Anatomy and Physiology. This required class includes about 80 students each semester, with career interests ranging from family farming to veterinary medicine. Students take the oral final in groups of 4 to 6, and are first asked their career interests. As each student takes a turn answering questions about major class concepts, they are asked to describe the information in the context of their future career choice. The future farmer may be asked about heat stress and managing animal comfort in a feedlot, while the future veterinarian might be asked about the same concepts in the context of an animal recovering from surgery. Students are made aware frequently during the semester that they will be asked to apply the basic concepts during the oral final, and the idea of doing so in front of peers provides increased motivation for learning basic mechanisms. The second strategy involves an industry-style R&D team project in Physiology of Lactation. Students work in small groups of 3 or 4 and are asked to develop a business proposal focused on some aspect of lactation, and which uses class material on anatomy and function of the mammary gland in their chosen species. Critical thinking skills are practiced at numerous times as students are required to present a legitimate business model for their lactation-based business to the rest of the class at the end of the semester. Each strategy allows individual students to develop the context in which to apply basic course information and practice critical thinking in their chosen occupation area.

Key Words: critical thinking, oral final exam, industry-style project

Contemporary and Emerging Issues

696 Web forums as a method for engagement on contentious issues in dairying: Should pain relief be provided during disbudding and dehorning of dairy calves? D. M. Weary,* C. S. Schuppli, and M. A. G. von Keyserlingk, *University of British Columbia, Vancouver, BC, Canada.*

Many people have positive views about dairy farming but this goodwill may be eroded if industry practices fall out of step with changing public expectations. Previous work has indicated that a particularly contentious topic is the use (or lack thereof) of pain control during painful management procedures. To better understand the expectations of different stakeholders to the use of pain control during routine painful procedures, we used web-based virtual "town hall" meetings to provide some background information describing the procedures and issues and allow people to respond to the question: "Should pain relief be provided when disbudding and dehorning dairy calves"? Anybody with access to the Internet could participate, and individuals working in dairy industry were targeted via a short article and link to the forums published in Progressive Dairyman. Over 200 people participated in 5 different web forums; 36% were students or teachers, 10% animal advocates, 25% farmers, veterinarians, and industry professionals, and 29% had no involvement in the dairy industry. The majority (86%) responded "Yes"; 7% "Neutral" and 7% "No." Participants in any one forum could not see the responses in other forums, allowing the discussions to proceed independently. Despite this independence, the majority of respondents in every forum (varying from 82% to 90%) indicated that pain control should be provided (i.e., chose "Yes"). Responses varied with participant demographics; for example, only 64% of producers chose "Yes" versus 90% of veterinarians. However, within every demographic category measured (e.g., sex, age, etc.) the majority argued that pain control should be provided. These results suggest that practice on farms that do not routinely provide pain mitigation for these procedures is out of step with widely held values (including those of dairy producers), suggesting the need for new policy and better incentives to encourage use of appropriate methods of pain control.

Key Words: animal welfare, analgesic, survey

697 Preliminary assessment of graded *Garcinia kola* seed meal on the performance, hematology and serum enzymes of broilers. O. A. Ogunwole, E. A. Iyayi, M. D. Olumide,* O. Arinola, and O. A. Adebiyi, *University of Ibadan, Ibadan, Oyo State, Nigeria.*

A preliminary assessment of the incorporation of graded levels of *Garcinia kola* seed meal (GKSM) and a commercial symbiotic Biovet YC on the performance, serum enzymes, hematology and organ weights of broilers was undertaken in a trial lasting 6 weeks. One hundred and 50 chicks of Arbor acre strain were randomly assigned to 6 treatments comprising of 25 birds per treatment and 5 birds per replicate. Diets 1, 2, 3, 4, and 5 contained *Garcinia kola* meal at 0, 2.5, 5.0, 7.5 and 10.0g/100g and the sixth diet had Biovet-YC at 0.1g/100g of feed. Routine antiviral vaccinations were administered on the birds but without any medication throughout the course of the trial. Feed intake and weight gain were significantly ($P < 0.05$) lowered by increasing GKSM inclusion above in the feed. Values obtained for serum alkaline phosphatase (19.82, 21.40, 21.20, 21.05, 20.82 and 22.90 μg/L for birds on treatments 1, 2, 3, 4, 5 and 6 respectively) were significantly ($P < 0.05$) higher with increasing inclusion of test ingredient. The red blood cell counts and the weight of kidney were significantly ($P < 0.05$) higher for birds on treatment 5. *Garcinia kola* meal should be incorporated at lower levels below 2.5g/100g in broilers diet. The bioactive component of *Garcinia kola* could be extracted, characterized and exploited for poultry production.

Key Words: *Garcinia kola* meal, serum indices, organ weight

698 Water usage and discharge volumes on New Mexico dairy operations. T. M. Vander Dussen*[1], G. R. Hagevoort[1], J. Lazarus[2], E. Naumburg[2], R. Ganta[2], and K. D. Casey[3], *[1]Agricultural Science Center at Clovis, New Mexico State University, Clovis, [2]Glorieta Geoscience Inc., Santa Fe, NM, [3]Texas AgriLife Research, Texas A&M System, Amarillo.*

Water usage on western dairies has become a topic of much debate in recent years. Much of the debate is fueled by incomplete information about the volume of water pumped (total water diversion) and its subsequent distribution for dairy purposes or for irrigation. Water diverted to the dairy is consumed by the cows, used for cooling of milk or cows, or utilized for cleaning. The large majority of the cooling and cleaning water is discharged into the lagoon system and recycled as irrigation water. In New Mexico a discharge permit (DP) is required to discharge "green water" into the lagoon system, and the maximum allowed discharge volume is defined in the permit. Metered discharge volumes into the lagoon system are reported monthly. A review of New Mexico's State Engineer and Environment Department records attempted to determine how much water is actually discharged. Average discharge volumes varied largely depending on the waste water management practices, in particular the use of a flush system. Based on the average herd size in NM (2,293), the average discharge volume per milking cow in 2011 was 28 GPD. Dairies with direct land application or total evaporation systems (19% of DP's) discharged lowest water volumes, typically well below 10,000 GPD. Since individual herd sizes are not reported, it is unknown if large discharge volumes (>100,000 GPD) were simply due to a large herd size, a large flush-system, or poor water management. Over the 2006–2011 reporting period, average discharge volumes peaked in 2008 at 87,000 GPD but have since decreased 27%. Some of the noted measures producers have taken to reduce water usage are: switching from water- to air-cooling systems, abandoning the practice of flushing alleys, reducing hose sizes in barns and wash pens, installation of timers on hoses for wash pen cleaning, etc. Dairies surrounding the Rio Grande watershed reported lower discharge volumes than dairies along New Mexico's East side with little or no nearby surface water. A lower discharge volume ultimately reduces: 1) the risk of accidental non-permitted discharges to waters of the US, 2) the costs of production, and 3) the total water footprint of the dairy operation.

Key Words: water usage, discharge volume, water footprint

Beef Species

699 Evaluation of selecting half-sibling beef cows to increase calf crop uniformity.

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Increasing calf crop uniformity has long been regarded as a means to increase sale price in beef cattle operations. A lack of uniformity has also been reported as one of the top quality defects in the US beef industry according to the National Beef Quality Audit. In 2004, 200 half-sibling (HS) yearling heifers and 200 yearling heifers of similar phenotype (PS) but unknown genetic relationship were used to determine if selection of half-siblings would increase uniformity of the calf crop under commercial management. Females were bred by AI to either Angus or Limousin bulls and exposed to full brothers of the AI bull. Cows were managed in one herd under commercial conditions. Calf weaning weights were measured for 5 calf crops (calves born in 2005 – 2009). Adjusted weaning weights (BIF adjustments) were available for 853 calves (393 calves from 158 HS cows; and 460 calves from 156 PS cows). These adjusted weaning weights were evaluated in a repeated-measures ANOVA (PROC MIXED) with year, cow type, calf sire breed, calf sex and their interactions as fixed effects and cow as the repeated subject with an autoregressive covariance structure. Least squares means for adjusted weaning weight were 506 and 526 lb for HS and PS cows, respectively. Adjusted weaning weight residuals from the model were evaluated for homogeneity of variance with Levene's test in PROC GLM of SAS. Adjusted weaning weight SD was 49.4 and 47.7 for HS and PS cows, respectively ($P = 0.56$). Lifetime weaning weight production was calculated for each cow by summing all observed actual weaning weights across all 5 years. Lifetime production was 1358 ± 706 lb for HS cows and 1635 ± 705 lb for PS cows, and variances were not different ($P = 0.97$). A subset of calves from each year was finished in a commercial feedlot. Variance of HCW and REA of calves from HS cows tended to be less ($P < 0.14$) than variance of calves from PS cows. The opposite was true for finishing-period ADG variance ($P = 0.14$). Considering half-sibling relationships when selecting commercial cows, over and above phenotypic selection, appears to have limited ability to reduce variability of calf crops.

Key Words: calf crop uniformity, beef cows

700 Performance, residual feed intake, and carcass quality of progeny from Red Angus sires divergent for maintenance energy EPD.

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The maintenance energy (ME_M) EPD was developed by the Red Angus Association of America and is used as an indicator of energy expenditure, which may be closely associated with residual feed intake (RFI). The objectives of this study were to evaluate and quantify the following using progeny of Red Angus (RA) sires divergent for ME_M EPD: 1) post-weaning RFI and finishing phase feed efficiency (FE), 2) post-weaning RFI and carcass quality, and 3) post-weaning RFI and sire ME_M EPD. Studies were conducted over a period of 3 years (cohorts), and sires divergent for ME_M EPD were identified before breeding. Post-weaning RFI and finishing phase FE of steer progeny tended to be positively correlated ($r = 0.38$; $P = 0.06$) in cohort 1 and were positively correlated ($r = 0.50$; $P = 0.001$) in cohort 3. In addition, post-weaning RFI was not correlated ($P > 0.05$) with any carcass traits. Sire ME_M EPD was correlated ($P < 0.05$) with carcass traits in cohort 1 (HCW, LM area, KPH, fat thickness, and yield grade) and cohort 2 (KPH and fat thickness). Most correlations between sire ME_M EPD and carcass quality were explained by the genetic potential of the sires; however, variation in measured LM area was not explained by the genetic potential of ribeye area EPD, and therefore, the observed correlation between sire ME_M EPD and measured LM area may suggest an association between ME_M EPD and LM area. In addition, no relationship was observed ($P > 0.05$) between progeny post-weaning RFI and sire ME_M EPD. Therefore, results suggest the following: 1) RFI measured during the post-weaning growth phase is indicative of FE status in the finishing phase, 2) neither RFI nor sire ME_M EPD negatively affected carcass quality, and 3) RFI and sire ME_M EPD are not associated.

Key Words: maintenance energy, residual feed intake, carcass quality

701 The effect of limiting feed intake on concentration of proteins associated with energy balance in the pregnant beef cow.

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Twenty-two multiparous pregnant beef cows were used to investigate the effect of dietary restriction on the abundance of selected proteins regulating energy metabolism. Cows were fed at either 85% (n = 11; LOW) or 140% (n = 11; HIGH) of NEm. The diet consisted of a haylage-based total mixed ration containing 20% wheat straw. Cows were slaughtered by block (date of parturition), beginning on 83 d after the initiation of dietary treatments and every wk thereafter for 6 wks, such that each block was slaughtered at approximately 250 d of gestation. Tissue samples from liver, kidney, sternomandibularis muscle, ruminal papilli (ventral sac), pancreas, and small intestinal muscosa were collected at slaughter and snap frozen in liquid N_2. Western blots of total protein isolated from these tissues were conducted to quantify abundance of: PCNA, ATP synthase, ubiquitin, and Na/K+ ATPase for all tissues; PGC1α, PPARγ, AMPKα and phosphorylated AMPKα for liver, muscle, and rumen; and PEPCK for liver and kidney. Statistical analysis was conducted using proc Mixed in SAS and included the fixed effects of dietary treatment, cow age, block, and the random effect of pen. Pearson correlations were conducted within treatment to investigate relationships between protein abundance and performance characteristics. Dietary treatments resulted in cows fed HIGH having greater ($P \leq 0.04$) ADG and final BW then cows fed LOW. Abundance of ubiquitin in muscle was greater ($P = 0.009$) in cows fed LOW, and PCG1α in liver was greater ($P = 0.03$) in cows fed HIGH. In cows fed HIGH, DMI was negatively correlated ($P < 0.03$) with small intestinal PCNA, ATP synthase and Na/K+ ATPase abundance. This data indicates that feed intake can influence the quantity of important metabolic proteins. These results will further the understanding of maintenance requirements and feed efficiency in pregnant beef cows.

Key Words: beef cows, cellular energy metabolism, feed intake

702 Heifers with low antral follicle counts have low birth weights and produce progeny with low birth weights.

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Research has demonstrated that heifers with increased numbers of ovarian antral follicle counts (AFC) have improved hormonal profiles and improved fertility. Interestingly, heifers with low AFC had lower birth weights, suggesting that genes influencing growth and development also influence the development of the reproductive tract and establishment of the ovarian reserve. To determine the relationship of AFC to heifer BW, reproductive tract characteristics, and first calf performance, composite (MARC III x Red Angus) heifers (n = 362) were used over a 4 yr period. In yr 1 heifers grazed winter range or corn stalk residue and were offered no supplement or 0.45- 0.90 kg/d (31%CP, DM Basis) during development. In yr 2 and 3 heifers grazed winter range and were fed a dried distillers grain-based (DDG) or corn gluten feed-based supplement offered at 0.59% and 0.78% BW, respectively, throughout development. Supplements were formulated to be isocaloric but differed in undegradable protein. In yr 4 heifers were fed either 0.59% or 0.46% BW of the DDG based supplement offered in yr 2 and 3. All heifers in yr 2 to 4 were fed ad libitum meadow hay while grazing dormant pasture. Prior to breeding, heifers were transrectally ultrasounded to determine AFC and classified as high (≥26 follicles; HIGH) moderate (16–25; MOD) or low (≤15; LOW). There was no diet x AFC classification interaction. HIGH heifers have greater ($P \leq 0.05$) birth, weaning, and adjusted 205-d weaning BW compared with LOW. Pre-breeding BW, total AFC, and proportion of mature BW at breeding were greater ($P < 0.01$) for HIGH compared with LOW heifers. Overall pregnancy rate was similar ($P = 0.36$) among AFC classifications. Progeny birth BW was greater ($P = 0.03$) for calves born to HIGH compared with LOW heifers. Taken together these data indicate a relationship between AFC and BW through the first breeding season and progeny calf BW. The low birth BW in heifers with low AFC and in their progeny continues to support a possible link between genes that influence growth and development and establishment of the ovarian reserve. USDA is an equal opportunity provider and employer.

Key Words: beef, progeny, antral follicle count

703 Prediction of HCW of individual steers from partial live weight collected with an in-pen weighing device.

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Accurately and precisely predicting HCW of individual cattle several days before slaughter would enable more efficient management and marketing of slaughter cattle. Technology (GrowSafe Beef system, GrowSafe, Inc.) has been developed that estimates a partial body weight (pBW) by weighing the fore feet of an animal as it drinks water. Weights are measured at 1-s intervals. Our objective was to determine the degree to which pBW could predict HCW in steers. Four hundred and five steers (BW: 309 ± 28.5 kg) were fed in a commercial feedlot near Calgary, AB in the winter of 2010 – 2011. Steers were housed in dirt-surfaced pens equipped with the pBW measuring device. Cattle were slaughtered (HCW: 360 ± 33 kg) in 2 groups (n = 203 and 202). Cattle were on feed for 209 d, and recorded ADG of 1.21 kg, indicative of commercial management. Number of pBW observed ranged from 0 to 4,620 and averaged 602/steer per day. These pBW were filtered to remove extreme 1-s data points. The filtering algorithm removes 1-s observations were the residual pBW is more than 200 kg from the predicted pBW predicted from the linear regression of pBW over time. The filtering algorithm continues iteratively refitting the linear regression, decreasing the residual threshold in 5-kg increments in each iteration, and discarding the extreme observations until all the observed pBWs are within 25 kg of the predicted pBW. For each steer, this filter was applied to pBW from d −40 to −10 (relative to slaughter = d 0), and used to predict pBW at d 0 (slaughter). On average, this filtering algorithm removed 12% of the pBW data. Predicted pBW was then regressed on measured HCW ($r^2 = 0.86$). The Limit of Agreement was 25.2 kg, indicating that a 30-d history of pBW measurements could predict HCW of an individual steer 10 d before slaughter within 25.2 kg, 95% of the time. Theoretically, using this device and prediction method, mean HCW of a group of 100 steers could be predicted within 2 kg of the actual HCW 10 d before slaughter, 95% of the time. Further, if a large population of steers were available such that 100 steers could be identified that all had the same predicted pBW, mean HCW of that group would still be within 2 kg of the prediction and 95 of the steers would have a HCW within 25.2 kg of the predicted HCW.

Key Words: partial body weight, carcass weight prediction, technology

704 Effect of various feeding regimens pre-shipment on shrink and subsequent weight recovery in feeder calves.

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Shrink is a major factor in the marketing of feeder cattle. It is especially important for long hauls (20+ h) from southeastern backgrounders to Midwestern feedlots. Shrink occurs in 2 forms: 1) loss of body fill and 2) loss of tissue fluids, which is observed during longer periods of transport. Objectives of this research were to compare the effects of various pre-shipment feeding regimens on shrink and subsequent BW gain in shipped and unshipped feeder calves. Forty-eight British cross steers (initial BW 351 kg) were fed high moisture (HM) or dry feed (DF) for 45 d and then offered hay or no hay 48 h before shipment. Factors were imposed factorially (2 × 2), 3 pens/group and 4 steers/pen. Daily gain during the backgrounding period was not different for HM versus DF ($P > 0.10$) and averaged 0.93 kg/d. On d 45, 2 steers from each pen were shipped, while their 2 pen-mates remained in the pen of origin (24 shipped; 24 un-shipped). Steers were loaded on 2 trailers ($11.3m^2$; 12 steers/trailer; one from each pen) with an average stocking density of $413kg/m^2$. Average shipping BW was 393 kg. Transported calves remained on the trailers for 21 h during which the minimum temperature was 7.2°C and the maximum temperature was 11.6°C. Upon arrival, BW were decreased ($P = 0.02$) for transported steers (365 kg) versus their pen mates (392 kg). Neither HM nor DF or hay affected shrink ($P > 0.10$). Within 12 h, BW were similar for the shipped and un-shipped calves ($P = 0.08$; 371 and 392 kg, respectively). Pre-shipment diets or 48-h hay offering did not affect BW post-shipment ($P > 0.10$). Within 5 d of shipment BW of the transported calves (384 kg) and un-transported calves (393 kg) remained similar ($P = 0.36$). Following 21 h of trailer transportation feeder calves shrank 7.1% during mild temperatures (7.2°C to 11.6°C). Feeding HM or DF or offering hay 48 h before shipment had no effect on shrink or subsequent BW gain after transportation.

Key Words: shrink, transportation, feeder calves

705 Comparison of different feed additives for backgrounding of weaned beef calves.

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The use of feed additives in supplements is one means to positively affect the health status of newly weaned calves during backgrounding.

Our objective was to evaluate the response of weaned calves to different feed additives in a supplement (CP = 14.6%, TDN = 67%) to improve calf performance and mitigate the stress response observed during the backgrounding period. Following stratification by BW, calf gender, previous castration status, and breed, 160 calves (203 ± 2.3 kg) were randomly allotted to 1 of 4 treatments (n = 40 calves/treatment): 1) control (CON) were supplemented without additives; 2) supplement with added chlortetracycline, 350 g/d (CTC); 3) supplement with added Rumensin, 175 mg/d (RUM); 4) supplement with added Actigen, 10 g/d (ACT). Calves were held in 1 of 4 drylot treatment pens (n = 40 calves/pen) for 1 wk and offered ad libitum access to hay and 1.8 kg of supplement before placement in 1 of 32 0.8-ha pens (5 calves/pen) for a total of 8 pens/treatment. Calves had BW and blood samples collected on d 0, 1, 4, 7, 11, 14, 51 and 52. Data were analyzed by the MIXED procedure of SAS. The model included the main effects of treatment. All variables quantified by day were analyzed using repeated measures. Over the 52-d period, ACT resulted in the greatest ($P = 0.002$, 0.325 kg/d) gain response. CTC calves exhibited similar ($P = 0.35$) gains to ACT, which were both greater ($P \leq 0.005$) than RUM (0.228 kg/d). CON calves were similar ($P \geq 0.13$) to both medicated treatments, but did not gain more ($P = 0.02$) than ACT. Plasma concentrations of haptoglobin and ceruloplasmin were similar ($P \geq 0.70$) among treatments; however, a day effect ($P \leq 0.001$) was observed in both acute phase proteins measured. Feed cost of gain was not significantly different ($P = 0.19$, mean = \$2.93/kg) among treatments. Profitability for ACT and CTC were similar ($P = 0.16$, mean = \$23.84/calf) and more ($P = 0.002$) profitable than RUM (\$-3.66/calf), CON was intermediate. ACT may improve calf performance as effectively as CTC during a backgrounding period of this duration, but neither additive was effective at mediating stress post-weaning.

Key Words: backgrounding, stress, supplement

706 Comparison of different feeding levels of a recycled-product supplemented to weaned beef calves. M. Hersom,* T. Thrift, and J. Yelich, *University of Florida, Department of Animal Sciences, Gainesville.*

The objective of this study was to evaluate different feeding levels of dehydrated food products and recycled poultry bedding supplemented to weaned beef calves. In Exp. 1, 160 Angus and Brangus steers and heifers (218 ± 2.2 kg) were utilized. In Exp. 2, 160 steers and heifers (245 ± 3.6 kg) of Angus, Brahman, and 4 combinations of Brahman × Angus were utilized. For both experiments all calves grazed 0.81 ha bahiagrass-bermudagrass pastures and supplement was offered as a percent of initial pen mean BW. Treatments were 1) no supplementation (CON); 2) 1.0% of BW; 3) 1.5 of BW; 4) 2.0% of BW and calves were fed daily in the morning. In both experiments calves were stratified by BW, breed, gender, and implant status in Exp. 1, and randomly allotted to 1 of 4 treatments. Each treatment was replicated in 4 pastures for each experiment. All pastures were fertilized 7 d before the initiation of the experiment with 56 kg/ha of N. Calf BW were collected on d −7 for allotment, and d −1, 0, 22, 46 and 47. Data were analyzed as a randomized complete block design with a split-plot; supplement treatment was the whole plot and implant or breed type was the split-plot for Exp. 1 and 2, respectively. Forage mass decreased linearly ($P < 0.05$) from 3,839 to 1,998 kg/ha across the 46 d experiment. In both Exp. 1 and 2, final BW was greater ($P < 0.05$) for supplemented compared with CON. In Exp. 1, 46-d ADG was greater ($P < 0.05$) for supplemented compared with CON and calves supplemented at 2.0 had greater ($P < 0.05$) ADG than the 1.0 and 1.5 level. In Exp. 2, 46-d ADG was different ($P < 0.05$) among all treatment levels. Breed type affected 46-d ADG; 0.5:0.5 and 0.25:0.75 Angus:Brahman crossbred calves had greater ($P < 0.05$) compared with Angus, Brangus and 0.75:0.25. In both Exp. 1 and 2, final calf value (\$/calf) and profit/loss (\$/calf) were greater ($P \leq 0.005$) for supplemented compared with Con calves (Exp. 1: \$644.25 vs 601.64 and \$35.16 vs 6.33, respectively; Exp. 2: \$725.74 vs 648.31 and \$54.56 vs 6.36, respectively). Available forage and supplement level had a direct effect on calf BW gain, value, and weaned calf profitability.

Key Words: backgrounding, pasture, supplement

Breeding and Genetics: Dairy Cattle Breeding III–Genetic Evaluation

707 Extension of Bayesian procedures to integrate and to blend multiple external information into genetic evaluations. J. Vandenplas*[1,2] and N. Gengler[1], [1]*University of Liege - Gembloux Agro-Bio Tech, Gembloux, Belgium,* [2]*National Fund for Scientific Research, Brussels, Belgium.*

Current genetic evaluations are mostly based on local data, potentially followed by an international second step, as it is performed by Interbull (Uppsala, Sweden) for dairy breeds. However, reliability of estimated breeding values (EBV) for animals with few local data may be limited. Furthermore, the current development of genomic selection makes this issue more important and the blending of those multiple sources more necessary. Current methods are based on selection index and Bayesian procedures were proposed for a single external source. The aim of this research was to extend these methods to integrate information from multiple sources outside a given evaluation system, i.e., external information, into this genetic evaluation, i.e., internal evaluation, and to assess its potential to blend multiple sources of information when only external information is available. To allow simplifications of the computational burden and the propagation of all external information through the whole pedigree, all animals were considered as animals associated to external information thanks to the prediction of external information from available one for internal animals, i.e., animals with no external information. Multiple considerations of contributions due to relationships among animals were also taken into account. Two dairy cattle populations were simulated across 5 generations. Internal females were randomly mated with internal and 50 external males. Milk production for the first lactation for each female was simulated in both populations. Results for 100 replicates showed that average rank correlations among Bayesian EBV and EBV based on the joint use of external and internal data were close to 1 for both external and internal animals. The respective correlations for the internal evaluation were equal to 0.54 and 0.95. Mean squared error, expressed as a percentage of the internal mean squared error, was close to 0% for both external and internal animals. Thereby, the Bayesian procedure has the potential to integrate and to blend multiple sources of external information to evaluate animals more reliably.

Key Words: Bayesian, integration, multiple

708 Are in-line measurements of somatic cell counts equally or more useful for genetic evaluations as those from DHI? L. P. Sørensen* and P. Løvendahl, *Department of Molecular Biology and Genetics, Center for Quantitative Genetics and Genomics, Aarhus University, Tjele, Denmark.*

The aim was to estimate and compare genetic parameters for log-transformed somatic cell counts (SCC) based on in-line measurements (OCC, DeLaval) in automatic milking systems with monthly test-day SCC from traditional herd testing schemes. Data was collected during a 29-mo interval from 6 herds and 1294 first parity cows (5 to 305 d in milk). Cell counts were analyzed using a 2-trait linear animal model. There were a total of 298,988 records for OCC and 7779 for test-day SCC. The fixed part of the model included lactation curves fitted as a Wilmink function, and the random parts included animal and herd-test-day effects. Age at calving and days in milk was included as covariates. Estimates of heritability were similar for the 2 traits, $h^2 = 0.26$ and 0.25 for OCC and SCC, respectively, and the genetic correlation between the 2 traits was close to unity ($r_g = 0.98$). The results suggest that somatic cell counts based on in-line measurements are similar but not preferable to traditionally obtained SCC despite several OCC measurements per cow per day.

Key Words: dairy cattle, somatic cell count, genetic parameters

709 Prediction of residual feed intake for first and second lactation dairy cows. G. H. Manafiazar,* T. McFadden, E. Okine, L. Goonewardene, and Z. Wang, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.*

Individual daily feed intake of 77 heifers from calving to the end of their second lactation was recorded at the Dairy Research and Technology Centre of the University of Alberta. Individual milk yields, and milk composition data of these cows were obtained from Dairy Herd Improvement (DHI) program and their body weights were recorded on the same days as the DHI milk sampled. Daily animal solutions for metabolic body weight (MBW), milk production energy requirements (MPER), and empty body weight changes (EBWC) were predicted from 5 to 305 d in milk using random regression Legendre polynomial. Total MBW, MPER, and EBWC over 301 d were predicted as the summation of their respective daily solutions. The total actual energy intake (AEI) over 301 d was linearly regressed on total 301-d predicted MBW, MPER, and EBWC to develop expected energy intake (EEI) prediction equation. The EEI prediction equation for the first and second lactation had R^2 of 0.82 and 0.81, respectively. Individual RFI over 301 d was calculated as the difference between total AEI and EEI over 301-d. The averaged daily RFI value ranged from −3.95 to 5.11 MJ NE_L d^{-1} and −4.86 to 4.34 MJ NE_L d^{-1} for the first and second lactation period, respectively. The animals were grouped into 3 classes of Low (<0.5 SD), medium (±0.5 SD), or high (>0.5 SD) from the mean (0) based on SD of RFI within lactation. The results showed that 30% of animals remained their respective RFI group between lactations, 54% of animals changed their RFI by less than 0.5 SD, and 15% of animals changed their RFI group by 1 SD. The results indicate that the developed RFI prediction equations could be used to calculate RFI in the first and second lactation; however, reranking exists between animals in the first and second lactation.

Key Words: dairy, residual feed intake, random regression

710 Random forest approach for SNP effects of residual feed intake in dairy cattle. C. Yao*[1], D. M. Spurlock[2], K. A. Weigel[1], L. E. Armentano[1], C. D. Page[1], and M. J. VandeHaar[3], [1]*University of Wisconsin, Madison,* [2]*Iowa State University, Ames,* [3]*Michigan State University, East Lansing.*

The objective of this study was to identify significant associations between single nucleotide polymorphisms (SNP) markers and residual feed intake (RFI) in dairy cattle using a random forest (RF) algorithm. Genomic data included 54,609 SNP genotypes for 395 Holstein cows, whereas phenotypic data included RFI measurements from 50 to 150 d postpartum. Residual feed intake was defined as the difference between observed dry matter intake (DMI) and predicted DMI after accounting for year and season of calving, year and season of measurement, age at calving nested within parity, days in milk (DIM), milk yield, body weight (BW), and body weight change (ΔBW). Measurements of BW were smoothed by using the fitted value of a quadratic function of weekly weights regressed on DIM, whereas ΔBW was calculated as the difference between fitted values for BW on adjacent days. Random Forest is an ensemble-based machine learning algorithm that uses a collection of tree predictors and can be adapted to classification and regression problems. Variable importance scores of RF, which were based on increases in mean squared error after permutation, were used to rank individual SNPs with large effects. Important combinations of SNPs, which may indicate the presence of epistasis even in the absence of significant main effects, were identified by examining the structure of trees. A 2-step RF algorithm was implemented, and parameters were tuned through 5-fold cross validation. A total of 4411 SNPs were selected at the first step based on importance scores; in the second step, individual SNPs with the largest importance scores and pairs of SNPs that appeared most repeatedly in combination within decision trees were evaluated relative to previously published studies of RFI in livestock. Among the 15 SNPs that were identified in our study, 7 are located within reported quantitative trait locus intervals for RFI in beef cattle, 6 are associated with annotated genes, and 5 are located in the introns of known genes. Based on these results, RF algorithms may be an effective method for identifying individual SNPs with large additive effects and combinations of SNPs with epistatic effects for quantitative traits.

Key Words: feed intake, random forest, SNP

711 Use of milk fatty acids to substitute for body condition score in breeding purposes.

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The general objective of this research was to investigate whether fatty acids (FA) profile in milk could substitute for body condition score (BCS) as an indicator of energy balance status in genetic evaluations. First, genetic correlations between BCS and the content in milk of 10 major FA predicted by mid-infrared spectrometry (C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C17:0, C18:0, and C18:1 *cis-9*; in g/dL of milk) were estimated using 10 2-trait random regression models. Data included from 36,964 to 37,239 FA records depending on the trait and 30,500 BCS records collected in 85 herds from 7,623 first-parity Holstein cows. Genetic correlations among BCS and FA were at the highest in early lactation. At 5 d in milk, genetic correlations with BCS ranged from 0.26 to 0.32 for C4:0 to C14:0 and were 0.15 for C16:0, −0.01 for C17:0, 0.05 for C18:0, and −0.15 for C18:1 *cis-9*. These results could be explained by the release of long chain FA in milk in early lactation due to the body fat mobilization and the consequent inhibition of de novo FA synthesis in the mammary gland. Also, results indicated that FA contents in milk in early lactation would impact BCS during the whole subsequent lactation: genetic correlation between C18:1 *cis-9* at 20 d in milk was −0.14 with BCS at 20 d in milk and −0.25 with BCS at 305 d in milk. Second, the part of the genetic variance in BCS explained by FA contents in milk along the lactation was calculated using selection index theory. Results indicated that the part of genetic variance in BCS explained by FA was 38% at 5 d in milk, was at the highest (56%) at 150 d in milk, and then decreased to 44% at 305 d in milk. Future studies will aim at estimating the part of the genetic variance in fertility explained either by BCS or FA contents in milk or both and will further investigate if FA contents in milk could substitute for body condition score.

Key Words: fatty acid, body condition score, genetic correlation

712 Genetics of the mid-infrared prediction of lactoferrin content in milk for Holstein first-parity cows.

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Lactoferrin is an iron-binding protein present in bovine milk. Interests taken to this protein are related to its therapeutic properties. Lactoferrin can be isolated from whey and used as a specialty food ingredient or as an antimicrobial agent. Furthermore, lactoferrin content in milk has been demonstrated to be higher in (sub)clinical mastitic cows. The objective of this study was to assess the genetic variability of the mid-infrared prediction of lactoferrin content in milk (MIRLf) and to estimate its genetic correlations with milk, fat, and protein yields, somatic cell count (SCS), and contents in milk (g/dL) of 7 groups of fatty acids (FA) predicted by mid-infrared spectrometry (saturated, monounsaturated, polyunsaturated, unsaturated, short chain, medium chain, and long chain). Data included more than 88,000 milk, fat, and protein records, 85,000 SCS records, and 61,000 FA and MIRLf records from 9878 first-parity Holstein cows. Co(variances) were estimated using 11 2-trait random regression models. Heritability for MIRLf increased from 0.20 at 5 d in milk to 0.40 at 250 d in milk. Genetic correlations of MIRLf with milk, fat, and protein yields decreased along the lactation; from 0.50 to −0.50 for milk, from 0.40 to −0.10 for fat yield, and from 0.55 to −0.25 for protein yield. Genetic correlation between MIRLf and SCS increased along the lactation from 0.10 at 5 d in milk to 0.30 at 305 d in milk. This positive correlation substantiated the potential interest of MIRLf as an indicator of udder health. Finally, for all FA groups, genetic correlation with MIRLf increased along the lactation. Average daily genetic correlations between MIRLf and FA ranged from 0.25 to 0.40 and were higher for unsaturated FA, indicating that selection for higher MIRLf would increase the content of unsaturated FA in milk to a larger extent than saturated FA. Concomitant selection of MIRLf and unsaturated FA is therefore feasible and this could be considered as beneficial for the genetic improvement of nutraceutical properties of milk.

Key Words: lactoferrin, mid-infrared prediction, genetic correlation

713 Genetic parameters for methane indicator traits based on milk fatty acids in cows.

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Dairy production is pointed out for its large methane emission. Therefore, currently studies of factors affecting emission and methods to abate methane emission are numerous. However, an important issue is the development of easily obtainable indicators, because they would also allow estimating animal genetic variability of methane emission. Recently methane indicators were proposed using gas chromatography based milk fatty acid composition. We derived these published methane indicators using 1100 calibration samples directly from mid-infrared (MIR). For the published indicator showing the highest relationship ($R^2 = 0.88$) with sulfur hexafluoride (SF_6) methane emission data, genetic parameters for this MIR based indicator were estimated by single trait random regression test-day models from 619,272 records collected from 2007 to 2011 on 71,188 Holstein cows in their first 3 lactations at Walloon region of Belgium. The average daily heritability was 0.35 ± 0.01, 0.35 ± 0.02 and 0.32 ± 0.02 for the first 3 lactations, respectively. Similarly, the lactation heritability was 0.67 ± 0.02, 0.72 ± 0.03 and 0.62 ± 0.03. As expected, methane production was higher during the peak milk production depicting the normal lactation curve. The largest differences between estimated breeding values (EBV) of sires having cows in production eructing the highest and the lowest methane content was 21.80, 22.75 and 24.89 kg per lactation for the first 3 parities, the variances of the EBV of the sires with daughters were 10.67, 12.46, 12.18 kg^2. Results were similar for other indicators. This study suggested that methane indicator traits can be predicted by MIR. Genetic parameters also indicated a rather high heritability and genetic variability exist for these published indicators and consequently a potential high genetic variability of methane eructation by dairy cows. Therefore, these first finding might open new opportunities for animal selection programs that include the reduction of methane emission.

Key Words: methane, mid-infrared (MIR), heritability

714 Comparison of daughter performance of New Zealand and North American sires in US herds. H. D. Norman*[1], J. R. Wright[1], R. L. Powell[1], T. J. Lawlor[2], and C. W. Wolfe[3], *[1]Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, [2]Holstein Association USA Inc., Brattleboro, VT, [3]American Jersey Cattle Association, Reynoldsville, OH.*

To improve fertility or other desired traits, some US graziers have chosen bulls from New Zealand (NZ), which relies extensively on seasonal calving and grazing. To compare performance of daughters of NZ and North American (NA; Canadian and US) AI Holstein (HO) and Jersey (JE) bulls, the model included fixed effects for US herd-year-season, parity (≤5) and semen source. Cows that calved between January 2000 and July 2010 in all US herds were included as well as in a subset of seasonally calving herds (≥60% of calvings in February through April). First-lactation HO data included records from 438 herds with 1,443 daughters of 54 NZ bulls and 26,444 daughters of 3,055 NA bulls; JE first-lactation data included records from 538 herds with 2,714 daughters of 65 NZ bulls and 76,281 daughters of 1,631 NA bulls. The seasonal calving subset included 22 HO and 26 JE herds. All differences mentioned were significant ($P < 0.05$) unless designated otherwise. Mean milk and protein yields across all parities were higher for NA daughters than for NZ daughters (497 kg milk and 6 kg protein for HO; 264 kg milk and 3 kg protein for JE); mean fat yield was nearly equal for HO but lower (2 kg) for NA JE daughters. Mean somatic cell scores were higher for NZ than NA daughters (0.15 for HO; 0.08 for JE). Mean days open were fewer for HO (9.9 d) and JE (1.3 d, nonsignificant) NZ daughters. Difference between NZ and NA HO daughters for calving ease and stillbirth rate was small and nonsignificant. Results for seasonally calving herds were similar. For 17 HO type appraisal traits, NA daughters scored higher for stature, fore udder attachment, rear udder height, and udder depth. For 13 JE type appraisal traits, NA daughters scored higher for stature, dairy form, fore udder attachment, rear udder height and width, and udder depth but lower for strength and thurl width. Overall, NA HO bull daughters produced more milk and protein but were less fertile than NZ bull daughters. For JE, fertility was not different between NA and NZ daughters. Overall merit of various selection alternatives should be judged on performance of all traits with economic value considered.

Key Words: daughter performance, New Zealand, seasonal calving

715 Genotype environment interaction of Holstein-Friesian dairy cattle in eastern Libya. S. A. M. Bozrayda,* R. S. Gargoum, and I. A. S. Al-Drussi, *Department of Animal Production, University of Benghazi, Benghazi, Libya.*

Breeding values (BV) for some productive and reproductive traits of Holstein Friesian sires (6 North American, 57 European and 7 Libyan) under eastern Libyan conditions were estimated and compared with those estimated under, European, and North American conditions in an attempt to assess the genotype environment interaction. To investigate the effect of managerial conditions on the same traits, the heritability coefficients were also estimated under Libyan and Dutch managements. The trait's variance and covariance components and the breeding values of animal were computed using mixed model containing the fixed effects of month of calving, year of calving, management and generation and animal as random effect. The lactation period and age at calving were used as covariates. Genetic correlation values of sires BV for the milk yield under Libyan and European and North American conditions was less than 1. Differences in heritability estimates due to the management system and or to environmental factors reflect genotype × environment interaction. Milk yield traits except dry period had a higher BV during the Libyan than Dutch management. Reproductive traits except age at first calving also had a higher BV during Dutch than Libyan management. Correlations between BV for milk yield ranged between 0.16 and 0.56 under Libyan, European and North American conditions. Breeding values of both North American and European sires were medium, low and negatively ranked under Libyan environment. Breeding values of milk yield traits showed higher variability under the Libyan environment. Sires with low BV (≥ 500) revealed negative ranking under the Libyan conditions.

Key Words: breeding values, genetic correlations, genotype × environment interaction

716 Casein and fatty acid content in milk of crossbred dairy cows under grazing conditions. V. Artegoitia*[1,2], M. Carriquiry[1], A. Meikle[2], J. Dutur[1], L. Olazabal[3], J. Bermudez[1], A. Torre[3], and P. Chilibroste[1], *[1]Facultad de Agronomía, Universidad de la República Oriental del Uruguay, Montevideo, Uruguay, [2]Facultad de Veterinaria, Universidad de la República Oriental del Uruguay, Montevideo, Uruguay, [3]Laboratorio Tecnológico del Uruguay, Montevideo, Uruguay.*

Nutritional, physical, and flavor properties of milk are influenced by its casein and fatty acid (FA) content and they might have an effect on the consumer acceptance of dairy products. Therefore, the manipulation of their content in milk would have an effect on consumer demands, and on health recommendations [e.g., choosing between milks with greater proportion of conjugated linoleic acid (CLA)]. The objective of this study was to evaluate the casein and FA content of milk on Uruguay Holstein cows (UH; North American genetics), New Zealand Holstein and UH (NZH×UH), Jersey and UH (J×UH), and Swedish Red and UH (SRB×UH) under the same feeding strategies and herbage allowance. Forty primiparous cows were selected from a commercial Uruguayan dairy farm (UH, n = 8; HNZ×UH, n = 10; JXH×UH, n = 10; SRB×UH, n = 12). Milk samples were collected at wk 12 of lactation. Means were considered to differ when $P \leq 0.05$. Milk yield was greater in UH than RBS×UH and J×UH cows, while NZH×UH was greater than J×UH. Milk fat yield was greater in J×UH than the rest of the groups. Although milk protein yields were not affected by genotype, total casein production was greater in J×UH than UH cows and no other differences were found. Casein content was not affected by genotype. Saturated FA was greater and monounsaturated were less in milk fat of J×UH and HNZ×UH than RBS×UH. Polyunsaturated FA tended to have a lower concentration in J×UH than in the other groups ($P = 0.09$). Trans FA in milk fat were greater in RBS×UH, than J×UH. No differences among cows were found in CLA concentrations in milk. The results indicate that differences in genotype have an impact on the total casein production, as well as, saturated, monounsaturated, polyunsaturated and *trans* FA concentrations in milk from dairy cows under grazing conditions.

Key Words: crossbreeding, milk composition, grazing

717 Effect of the milk recording time on the genetic parameters of milk production and mid-infrared milk components in Luxembourg dairy cattle. V. M.-R. Arnould*[1,2], H. Soyeurt[2,3], and N. Gengler[2,3], [1]*CONVIS s.c., Ettelbruck, Luxembourg,* [2]*University of Liège, Gembloux Agro Bio-Tech, Animal Science Unit, Gembloux Belgium,* [3]*National Fund for Scientific Research (F.N.R.S.), Brussels, Belgium.*

Reducing the frequency of official milk recording and the number of recorded samples per test-day (vs. the conventional twice-a-day sampling) would have some advantages for dairy herd management. However, phenotypic variations in milk composition between morning (AM) and evening (PM) milkings are known and documented for major milk components but poor literature exist about genetic differences between AM and PM milkings. Therefore, the objective was to study the effect of milking time (AM or PM) on the estimation of the genetic parameters of milk yield, and mid-infrared milk components such as protein and fat yields and saturated and unsaturated fatty acids groups. A total of 44,833 milk samples were collected between October 2007 and November 2011 (from 9,602 Holstein cows in first lactation belonging to 491 Luxembourg dairy herds): 23,046 records from AM milking and 21,787 from PM milking. All milk samples were analyzed by mid-infrared spectrometry. The model included as fixed effects: herd × date of test, 3 classes of age, 24 classes of days in milk and month of test × year of test. Random effects were permanent environmental, additive genetics, and residual effects. Expect for milk yield ($P = 0.88$), it was observed that the evolution of the daily heritability among the first lactation was different according to the milking time for all studied traits ($P < 0.0001$). Preliminary results based on breeding values of bulls with daughters having records showed a rank correlation of 0.77 (milk yield). Given these results, genetic parameters of milk yield and studied milk components were affected by AM/PM milking.

Key Words: genetic evaluation, alternate milking recording scheme, milk component: heritability

718 Integration of experimental designs and analytical approaches to co-ordinate efficiency of global efforts to optimize environmental and genetic effects on reproductive performance of dairy cattle. E. Block[1], B. Bradford[2], W. M. Chalupa[3], I. J. Lean*[4], S. LeBlanc[5], M. C. Lucy[6], J. McNamara[7], J. Morton[8], A. R. Rabiee[4], J. E. P. Santos[9], W. W. Thatcher[9], M. Van Amburgh[10], and M. J. VandeHaar[11], [1]*Church & Dwight Co, Princeton, NJ,* [2]*Kansas State University, Manhattan,* [3]*University of Pennsylvania, Kennett Square,* [4]*SBScibus, Camden, New South Wales, Australia,* [5]*Population Medicine Ontario Veterinary College University of Guelph, Guelph, ON Canada,* [6]*Division of Animal Sciences, University of Missouri, Columbia,* [7]*Department of Animal Sciences, Washington State University, Pullman,* [8]*Jemora Pty Ltd., Geelong Victoria, Australia,* [9]*Department of Animal Sciences, University of Florida, Gainesville,* [10]*Department of Animal Sciences, Cornell University, Ithaca, NY,* [11]*Department of Animal Sciences, Michigan State University, E. Lansing.*

Our present knowledge of genetic and environmental processes that influence reproductive functions demands a systematic approach to design, conduct and analyze basic and applied studies of dairy cattle reproduction. The effects of genetic selection and population variation, nutritional intake and composition, climate and housing all interact to affect reproductive functions at cellular and molecular levels. Therefore, experiments must be designed to address specific mechanisms within a defined systems framework such that data will be integrated efficiently into knowledge bases, utilizing compilation methods such as meta-analysis and regression. Researchers with interests in reproduction have undertaken a project to produce guidelines to assist in efficient design, conduct, and analysis of experiments. The intent of the guidelines is to provide for design of studies that best fill the most critical knowledge gaps, enhance opportunities for research interaction, and provide new knowledge that can be integrated into our present understanding through appropriate data analyses and pooling methods. Similar guidelines have been developed for randomized controlled clinical studies in medicine, veterinary and animal science using a process of review and consensus. The guidelines will provide 1) clear definitions of experimental conditions, which include dietary, environmental, and reproductive conditions and responses, and 2) appropriate statistical designs and analyses to reduce bias, pseudoreplication, and the risks of Type I and Type II statistical errors. Critical knowledge gaps include the influence on reproductive outcomes of genetic selection and random genetic variation, diet content and intake, reproductive management and environmental conditions. Standardization is being developed for definitions of expression and detection of estrus and ovulation, cyclicity, fertilization, embryonic development, establishment and maintenance of pregnancy, and time to events such as pregnancy and for appropriate minimal sample sizes to detect economically or biologically important outcomes.

Key Words: reproduction, study design, nutrition

Breeding and Genetics: Small Ruminants, Poultry, and Nontraditional Species

719 Associations between candidate gene polymorphisms and milk production traits in Alpine goats farmed in Italy. P. Crepaldi[1], E. Mlanesi[1], B. Coizet[1], L. Nicoloso[1], P. Fresi[2], S. Murru[2], R. Steri[3], and N. P. P. Macciotta*[3], *[1]Università di Milano, Milan, Italy, [2]ASSONAPA, Rome, Italy, [3]Università di Sassari, Sassari, Italy.*

Milk fat yield and composition have a great economic importance in the goat industry being most of milk destined to cheese processing. The identification of genes associated with these traits could provide useful indications for breeding programs. In this work, an association study between 11 SNP polymorphisms at 3 candidate genes (acetyl-coenzyme A carboxylase, ACACA; stearoyl-CoA desaturase, SCD; lipoprotein lipase, LPL) was carried out on 59 Alpine bucks. Data from 13,331 daily records, for milk, fat, and protein yields (kg/d) and fat and protein contents (%) of 2,220 lactations were recorded on 946 goats, daughters of the 59 bucks. Associations were tested with a mixed linear model that included the fixed effects of flock, date of the test, lactation stage, kidding season, age of the goat at kidding, SNP genotype of the sire and the random effect of the goat. Four SNPs were found to be significantly associated to milk production traits (Bonferroni gene-wide adjusted significance $P < 0.01$). The GC substitution at exon 1 of the LPL locus had the highest effect on milk yield (difference of about 0.6 kg/day between the 2 homozygotes CC and GG, respectively, $P < 0.01$). The CT substitution at exon 45 of the ACACA locus affected milk yield and fat percentage. The deletion at the 3′ untranslated region of the SCD locus affected milk, and protein (undeleted homozygotes produced about 16 g/d more than deleted ones) yield and fat percentage. Finally, the CT mutation at exon 5 of the SCD gene was associated to milk yield. These interesting associations should be obviously validated on a larger sample. Moreover, effect on other traits as milk fatty acid composition could be considered in future analyses

Key Words: goat, candidate genes, dairy traits

720 Single nucleotide polymorphisms identified in polygenic traits through the use of the Ovine SNP50 BeadChip. R. R. Cockrum*[1], N. K. Pickering[2], R. M. Anderson[2], D. L. Hyndman[2], M. J. Bixley[2], K. G. Dodds[2], R. H. Stobart[1], J. C. McEwan[2], and K. M. Cammack[1], *[1]University of Wyoming, Laramie, [2]AgResearch Limited, Mosgiel, New Zealand.*

High-density single nucleotide polymorphism (SNP) chips have shown promise in genome wide association studies (GWAS) to target genomic regions that play key roles in traits of economic interest. The objective of this study was to use GWAS to identify SNPs affecting polygenic traits including backfat (BF), loin eye area (LEA), ADG, birth type (BT), and scrotal circumference (SC) in sheep. Phenotypic measurements were collected on rams from 2 separate ram tests (Dual Purpose Ram Test and Blackface Ram Test) at the University of Wyoming Ram Test ($n = 328$) from 2009 to 2011. Blood was collected via the jugular and DNA was isolated and diluted. Single nucleotide polymorphisms in ram DNA were genotyped using the Ovine SNP50 BeadChip on the Illumina Infinium HD BeadChip Assay. Percentage loci scored per animal and locus, Hardy Weinberg deviations, animal information comparison, replicate sample reproducibility, and unusual allelic ratio analyses were conducted through Genome Studio and R for quality control analysis. A GWAS analysis was conducted in R using the GenABEL package where a polygenic model, $Y = \mu + G + e$, where μ is the intercept, G is the polygene, and e is the random residual, was used to identify SNPs. The SNP associated with *RXFP2* was used to confirm the accuracy of the polygenic model resulting in a high association ($P = 9.283^{-04}$) with the horn phenotype. There were 11 and 5 SNPs for BF and ADG, respectively, that reached the genome-wide threshold ($P \leq 9.359^{-04}$). Genes associated with SNPs identified in BF include *EPHBA* and *B* family, *ANK* family, *REL, XDH, RPAIN*, and *FRMPD4*, while only *KLF12* was linked to ADG. Genome-wide threshold was reached ($P \leq 0.092^{-04}$) for BT (i.e., single, twin, or triplet) resulting in 10 SNPs. Genes linked to BT SNPs were *ODZ1, ODZ3, LTBP3*, and *DSCAM*. The top SNPs for SC and LEA did not reach optimum threshold as in BF, ADG, or BT; however, 3 SNPs for SC and 1 SNP for LEA achieved moderate threshold levels ($P \leq 0.0003$). No genes were associated to SNPs for SC, but one gene, *AAK1*, corresponded to the SNP for LEA. Results indicate that SNPs can be identified for polygenic traits using GWAS. However, further research and validation studies will be required before implementation of marker-assisted selection strategies.

Key Words: polygenic, sheep, single nucleotide polymorphism

721 Genetic parameter estimates for birth weight in three Yemeni indigenous sheep breeds. S. Al-Shorepy*[1], M. Al-Karmah[1], and Ab. Albial[1], *[1]United Arab Emirates University, Al Ain, United Arab Emirates, [2]Sana'a University, Sana'a, Yemen, [3]Agricultural Research & Extension Authority, Sana'a, Yemen.*

Genetic parameters for birth weight were estimated for 3 indigenous Yemeni sheep breeds (White Boni, Barri, and Black Boni breeds), using animal model. Data were analyzed by restricted maximum likelihood (REML) using MTDFREML program. Five different animal models were fitted. Model 1 considered the animal as the only random effect. Models 2 and 3 included in addition to the additive direct effect of the animal, the additive maternal and the permanent maternal environmental effects, respectively. Model 4 fitted both the additive maternal and permanent environmental effects. Model 5 was the same as model 4, except that a covariance between the direct and the maternal additive effects. Estimates of additive direct heritability were 0.19, 0.36, and 0.38 for White Boni, Barri, Black Boni lambs, respectively. Judged by log L, introducing either additive maternal effects (model 2) or permanent environmental effects (model 3) resulted in a similar fitting as compared with model 1 in the 3 breeds. Fitting additive maternal and permanent environmental effects (model 4) resulted in a significantly better fit ($P < 0.05$) compared with models 1, 2, and 3 for White Boni lambs only. Estimates of total heritability (h^2t) from model 5 were 0.14, 0.17, and 0.53 for Barri, White Boni and Black Boni lambs, respectively. These results indicate that moderate to high estimates of direct heritability suggest further scope for improvement due to selection for higher birth weight.

Key Words: birth weight, direct and maternal effects, Yemeni indigenous sheep breeds

722 Increased lean growth rate does not extend days to harvest in crossbred lambs. G. C. Márquez*[1], W. Haresign[2], M. H. Davies[3], D. R. Notter[1], R. Roehe[4], L. Bünger[4], G. Simm[4], and R. M. Lewis[1,4], *[1]Virginia Tech, Blacksburg, [2]Aberystwyth University, Aberystwyth, UK, [3]ADAS Rosemaund, Preston Wynne, UK, [4]Scottish Agricultural College, Edinburgh, UK.*

A lean growth selection index (LI) was designed for terminal sire sheep in the UK to increase lamb carcass lean weight while decreasing fat at a constant age end point. The purpose of this study was to investigate if lambs sired by high (leaner) versus low LI rams take longer to reach target harvest condition (fat cover). Data on 6,350 crossbred lambs sired by Charollais, Suffolk and Texel rams were available. From 1999 to 2002, 15 high and 15 low LI sires from each breed were mated to 1,984 crossbred ewes at 3 farms in the UK. Most rams were used for 2 mating seasons, and some were rotated among farms to create genetic links. Lambs were reared on pasture and, from 10 weeks of age, were visually assessed bi-weekly for fat cover until they reached a target condition of 11% subcutaneous fat (estimated) for harvest. The mean days to harvest (DTH) were 180 (SE 1.1) for high LI sires, 176 (SE 1.0) for low LI, 182 (SE 1.2) for Charollais, 182 (SE 1.3) for Suffolk, and 170 (SE 1.3) d for Texel. A semiparametric Cox proportional hazard model was fitted to DTH. The analysis was stratified by lamb rearing type because the hazard for DTH differed for single and twin reared lambs. Fixed effects were sire index, sire breed, dam breed, sex, age of dam, fat class (visual classification of harvest condition), birth year, farm, and birth year-farm interaction. Random effects were sire (considering the relationship matrix among sires) and rearing dam. Likelihood ratio tests indicated that all fixed effects were significant ($P < 0.001$) except sire index ($P = 0.5$) and dam breed ($P = 0.1$). There was no difference in hazard ratio (HR) between lambs sired by high and low index sires, or between lambs sired by Charollais and Suffolk rams ($P = 0.8$). However, Texel-sired lambs had fewer DTH than Suffolk-sired lambs (HR = 1.44, $P < 0.001$). No significant interaction between sire index and breed was found. The HR increased with increasing age of the dam. Heritability of DTH was estimated as 14%. The similar DTH in lambs sired by high as compared with low LI rams is favorable, because it implies that leaner lambs reach acceptable harvest condition without extending their finishing period.

Key Words: crossbred lambs, lean index selection, survival analysis

723 Evaluation of environmental factors affecting the speed of racing camels in the United Arab Emirates.

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Camel racing is a deep-rooted traditional sport that finds its origins in the desert culture of the Arabian Peninsula, North Africa, and the Middle East. In United Arab Emirates (UAE), camel racing is very popular and has become a part of tradition and culture. Therefore, the aim of the present study was to evaluate environmental factors affecting speed of racing camels in UAE. The data used in this study were obtained from UAE Camel Race Association, from year 2007 to 2011 and the trait evaluated was racing speed (m/s) for total distance and for the last 1000 m. Five hundred ten races with around 40 camels per race of varying distances were evaluated for which the first 10 winners were determined. The full linear model included the effect of year, age, sex, breed, racetrack, and type. In each race, 3 categories were considered for analysis; fastest 10, fastest 3, and the fastest camels. Overall average speed of the races was 10.40 m/s (SD = 0.37; range: 8.3–13.5 m/s), with a coefficient of variation of 3.6% and the effects included in the analytical model formed R^2 of 85.5%. The average speed for the last 1000 m was 10.87 m/s with maximum speed of 16.1 m/s. Speed significantly ($P < 0.05$) decreased with the age in the 3 categories (fastest 10, fastest 3 and the fastest). Females were significantly ($P < 0.05$) superior to males in the 3 categories evaluated. Similarly, purebred (thoroughbred) camels were faster ($P < 0.05$) than the crossbred camels in the tested categories. The sex by breed interaction had no significant effects on race speed in the 3 categories. Understanding the role of environmental factors in racing camels might assist owners, trainers, and others to optimize the performance of camels under their care. Moreover, determining these factors is a fundamental step in developing a selection program to improve the racing speed of racing camels.

Key Words: racing camels, environmental factors, racing speed

724 Influence of genomic predictors on yearling sales price and total career earnings in Thoroughbred racehorses.

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Many factors contribute to the yearling sales price (YSP) and total career earnings (TCE) of Thoroughbred horses. The aim of this study was to identify the most influential factors and determine if the addition of genomic information [e.g., genomic predictors (GP) provided by the Equinome Elite Performance Test; www.equinome.com] improves predictions of TCE. Individual, sire, dam, sale and racing information was collected for 256 Thoroughbreds from 4 countries (Ireland, Great Britain, United States, and France). Correlation and regression analyses were performed on the data. TCE had a correlation of 0.23 with GP and 0.15 with YSP. Linear mixed regression analysis identified the main contributing factors to YSP and TCE; the regression model for YSP obtained an $R^2 = 0.49$ without GP information and an $R^2 = 0.53$ with GP included. The main factors influencing sales price ($P < 0.05$) were identified as GP, year of sale, parity of the dam, number of winning offspring of the dam, number of races won per crop of foals of the sire and stud fee paid for the covering. The regression model for TCE (in the form of Earnings per start) obtained an $R^2 = 0.39$ without GP and an $R^2 = 0.57$ when GP information was included. These data indicate that genomic predictors have a considerable influence on the TCE of a horse. The most influential factors influencing TCE ($P < 0.05$) were GP, month of birth within the year of sale, sex, whether or not the dam was a winner, the number of black type offspring of the dam, parity of the dam and races won per crop of foals of the sire. The results showed GP to have a significant ($P < 0.05$) influence in both models and therefore highlights the contribution that genomic information can have in decision making. This study illustrates that genomic information can enable owners, breeders and trainers to better judge the value of a horse by determining its genetic potential for racing and breeding.

Key Words: genomic, performance, regression

725 Genetic variation study in Pakistani buffalo breeds using microsatellite markers.

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To assess the status of genetic diversity in Pakistani buffalo, 19 microsatellite loci were genotyped to obtain data on 184 DNA samples from all 5 native buffalo breeds (Nili, Ravi, Nili Ravi, Kundhi and Azakheli). All loci showed polymorphism in each breed. The observed number of alleles ranged from 8 (ETH10, ILSTS049, ETH225, CSSM66) to 24 (TGLA227) with a mean value of 13.368 alleles per locus. The effective number of alleles across all loci was as usual lower than the observed values with a mean value of 3.207 alleles per locus. The average observed and expected heterozygosity values across all polymorphic loci in all studied buffalo breeds were estimated to be 0.283 and 0.648

respectively. The overall value for Polymorphic Information Content (PIC) for all markers was 0.56 suggesting their appropriateness for genetic diversity analysis in buffalo. The mean Fis, Fit, and Fst values were 0.511, 0.570 and 0.120 respectively. The 5 buffalo populations were genetically less diverse as indicated by a small mean Fst value. The average gene flow (Nm) indicative of population migration was calculated as 1.817. The Nei's (1972) original measures of genetic distance (Ds) revealed ancient divergence of Nili-Ravi and Azakheli (Ds = 0.3018) and recent divergence of Nili and Ravi (Ds = 0.0468). These estimates of genetic diversity were seen in coincidence with phenotypic differentiation among the studied buffalo breeds. The present study results can facilitate the future researchers interested in further studies in buffalo as well as other livestock breeds of Pakistan.

Key Words: genetic diversity, microsatellite markers, buffalo breeds

726 Analysis of egg production using a random regression model with genomic relationships in layer chickens. A. Wolc*[1,2], J. Arango[3], P. Settar[3], J. E. Fulton[3], N. P. O'Sullivan[3], R. Preisinger[4], D. Habier[2], R. Fernando[2], D. J. Garrick[2], and J. C. M. Dekkers[2], *[1]Poznan University of Life Sciences, Poznan, Poland, [2]Iowa State University, Ames, [3]Hy-Line International, Dallas Center, IA, [4]Lohmann Tierzucht GmbH, Cuxhaven, Germany.*

Random regression models (RRM) can account for the longitudinal nature of egg production which, together with the use of genomic information, are expected to increase accuracy of selection compared with using only mean production and pedigree information. The objective of this study was to estimate variance components for egg production at various ages in a commercial brown egg layer population using genomic relationship information. A random regression reduced animal model with a marker-based relationship matrix (VanRaden, 2008) was used to estimate genomic breeding values of 3,908 genotyped animals from 6 generations. The first 5 generations were used for training, with predictions validated in generation 6. Daily egg production up to 46 weeks in lay was cumulated into 85,462 bi-weekly records for training, of which 17,570 were recorded on genotyped hens and the remaining on their non-genotyped progeny. The model for bi-weekly records included fifth-order Legendre polynomials nested within hatch-week as fixed effects. Random terms were quadratic polynomials for genetic and permanent environmental components, and residual variances that were uncorrelated and heterogeneous. Models with pedigree based or genomic relationships were used. Estimates of residual variation were very similar for both measures of relationship but the model with genomic relationships estimated a higher proportion of genetic variance. Heritability estimates increased with age up to mid production and decreased thereafter, resulting in average heritability of 0.20 or 0.33 for pedigree or genomic relationships. Predictions of total 46-week egg number and of most biweekly periods were more accurate with genomic than pedigree relationships (correlations with progeny performance of 0.26 vs. 0.16). In conclusion, random regression reduced animal models can be utilized in breeding programs using genomic information, resulting in substantial improvement of accuracy of selection for longitudinal traits. Practical implementation depends on computing and genotyping strategies to minimize costs to make such an approach cost effective.

Key Words: egg production, random regression model, GBLUP

Dairy Foods Symposium: Advances in Yogurt Manufacture and Product Functionalities

727 The impact of biopolymers on yogurt gelation and properties. J. A. Lucey,* *University of Wisconsin-Madison, Madison.*

Most yogurts in the US contain multiple stabilizers (polymers) that are added to try to control texture during storage. The nature of the interactions between these biopolymers and the milk proteins is poorly understood in yogurt systems. Often manufacturers add several different types of stabilizers in the hope of achieving the desired textural properties. Polymers can be added as stabilizers (e.g., pectin) or can be naturally produced in situ by certain bacteria in the form of exopolysaccharides (EPS). Most cultures supplied for commercial yogurt manufacture in the US contain an EPS-producer. Much confusion exists concerning the precise physico-chemical mechanism(s) by which EPS influences yogurt texture. Complicating factors include: variation in fermentation conditions (e.g., rate of acidification) also affect gel formation, it is not easy to accurately estimate the concentration of EPS in a yogurt matrix; it is usually unknown when in the fermentation process that the EPS was produced (before/during/after gelation), and the nature of the EPS (molar mass, degree of branching, etc) may also influence its interaction with the protein matrix. Better control of the interactions that occur between proteins and polymers during the fermentation process would help manufacturers to tailor-make a product with the desired physical and sensory characteristics. Examples of how different types of biopolymers (e.g., pectins, dextran and EPS) influence yogurt texture will be discussed.

Key Words: yogurt, texture, biopolymers

728 Advancements in yoghurt process design and unit operations. L.-E. Nilsson,* *Tetra Pak, Lund, Sweden.*

Yogurt is one of the fastest growing dairy products in many countries and has been so for many years. Yogurt is produced in different forms such as stirred, set, drink, concentrated, and frozen. Within each type there are many variants, including fat-free, low fat, high-fat, probiotic, prebiotic, lactose-free, mineral enriched, fruit added, fiber-added, etc. The quality of yogurt is influenced by several factors in the process line, most important of which are milk standardisation, deaeration, homogenization, heat treatment as well as culture type and overall plant design. Yogurt milk for stirred and set yogurt is most often increased in dry matter to obtain high viscosity and stability. This can be achieved by powder addition, evaporation or membrane filtration, of which each system has advantages and limitations. The most common fortification method today is powder addition. The basis for manufacture of high quality yogurt is predicated already in the milk treatment. Culture type has a large influence on the final yogurt taste and consistency, but also on the design of the yogurt line. Depending on culture activity in the range of pH 4.3, the design of incubation tanks, pipes, pumps, and cooler etc. are optimized. Some cultures are used which are specially adapted to provide improved functionality to the yogurt. Yogurt coagulum is sensitive to mechanical treatment and due to this fact, plant design is of utmost importance. Calculations of pumps, pipe dimensions, cooler configurations, and process layout must be carefully considered to maintain the natural viscosity built up during fermentation. Concentrated yogurts have recently been increasing in popularity. Traditionally the industry has used specialized separators to remove whey from the yogurt coagulum. Membrane filtration is another technique used for this process. This technique can retain more protein into the finished yogurt and achieve higher yields. Shelf life of yogurt, which is judged by microbiology, appearance, texture and flavor, depends on several factors, from milk quality to filling machine and packaging. There are different ways to extend the shelf life dependent on what limits the shelf life today.

Key Words: yogurt, process design

729 Impact of total solids, protein content, and protein source on the functionality of nonfat yogurt. L. E. Metzger* and K. N. Shah, *Midwest Dairy Foods Research center, South Dakota State University, Brookings.*

In the US, NDM is a commonly used ingredient in yogurt formulations. However, in International markets, skim milk powder (SMP) milk protein concentrate (MPC), and de-proteinized whey are also used in yogurt formulations. The total solids, protein content and source of the protein in a yogurt formulation can affect the functionality of the yogurt. Additionally, physicochemical changes during storage of powders can result in variation of the functional properties of powders as well as of the product in which they are used. The objective of this study was to evaluate the effects of storage of various milk powders (SMP, NFDM, MPC 40, MPC 70) on their functional properties and on the functionality of nonfat yogurt formulations at 3 different protein and total solids levels. Three different lots of SMP, NDM, MPC 40 and MPC 70 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. 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, MPC 40, and MPC 70. The data was analyzed by split plot design using PROC Mixed in SAS. Storage time had a significant effect ($P < 0.05$) on solubility and foaming properties where solubility of MPC70 and foam overrun of SMP, MPC40, and MPC70 decreased significantly ($P < 0.05$) with an increase in storage time of the powders. Emulsification properties of MPC70 were significantly higher ($P < 0.05$) than SMP, NDM, and MPC40. Storage time did not have significant effect on the yogurts from NDM, MPC40, and MPC70 at all protein/TS ratio. Viscosity of both MPC40 and MPC70 yogurts was significantly lower ($P < 0.05$) than SMP and NDM yogurts at each protein/TS ratio. The storage of milk powders has an effect on their functional properties but has a minimal influence on the textural properties of nonfat yogurt, whereas the use of MPC had a substantial effect on the functionality of nonfat yogurt.

Key Words: nonfat yogurt, viscosity

730 Advancements in starter technology and functional benefits in yogurt. DA Romero*[1], C. Fremaux[2], P. Fourcassie[2], S. Huppert[3], and P. Steele[1], [1]*DuPont/Danisco, Madison, WI,* [2]*DuPont/Danisco, Dangé-St.Romain, France,* [3]*DuPont/Danisco, Paris, France.*

Yogurt represents one of the oldest forms of biotechnology, employing lactic acid bacteria to ferment milk thus preserving it as a flavorful and healthy food. From the chance contamination of desirable bacteria the industry has progressed to the selection and development of highly specialized strains. Research that began with identifying and characterizing the responsible microbes has progressed to correlating starter metabolism in milk with technological attributes in yogurt. Today we have the complete genomes for traditional starters *Streptococcus thermophilus* and *Lactobacillus bulgaricus* and a host of probiotics cultures with which to map function to specific genes and pathways. Notwithstanding this revolution of genomics and bioinformatics, research has been grounded in a thorough understanding of microbial bioconversions to deliver rapid and reliable acid, flavor and texture development. In parallel to our increased understanding of starter functionality, there are ongoing and ever sophisticated studies focusing on the role of probiotics; in particular strains belonging to *Lactobacillus* and *Bifidobacterium*. As an excellent vehicle to deliver nutrition and health in food, the incorporation of live microbes to yogurt to provide additional nutrition and health attributes has helped drive the market forward in this age of health conscious consumers. Coupled with current studies of the human gut microflora, the role of probiotics in general wellbeing is transforming to more increasing rigorous scientific investigation in expectation of escalating regulatory expectations. We will present selected examples of strain (e.g., bacteriophage resistance, natural texture and flavor, strain safety) and probiotic (e.g., digestive health, gut transit time, immune health) development to highlight recent advancements and the current state of the yogurt culture development. Further, we will discuss how these technological developments positively affect the demands of the yogurt manufacturer and consuming public.

Key Words: yogurt, starter, probiotic

731 Fine tuning the structure of yogurt by changing the milk properties.

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During fermentation using lactic acid bacteria, as the pH decreases, colloidal calcium phosphate is released from the casein micelles, and the overall charge of the protein is reduced, ultimately causing colloidal destabilization of the protein particles and the formation of a protein network. Although the physico-chemical changes occurring to casein micelles during acidification of skim milk are well understood, the interactions occurring at the molecular level in a yogurt mix are less understood. Such mixes may vary in protein and fat concentrations, contain various stabilizers and different texturizing cultures. This presentation will review the interactions between the important building blocks of structure in acid gels. To better understand these interactions will allow for fine-tuning of the structure. The aggregation of whey protein complexes with caseins and the interactions between caseins and added stabilizers are known to play a major role in texture. The presence polysaccharide produced by lactic acid bacteria also needs to be considered. The interactions between these polysaccharides and milk proteins will vary in the type and extent with time, because of the changes in concentration and environmental conditions, namely pH and ionic strength. Fat globules are also an important building block of the structure and texture of yogurt, and their mode of incorporation in the gel will be modulated by changes to their size and interface. Another important aspect to consider is the pre-concentration of the milk. The processing history of the milk during membrane filtration will affect the gelation behavior of the casein micelles and the interactions between milk proteins. This presentation will provide an overall view of the factors involved in the formation of structure, and identify opportunities to improve or design new processes and product formulations.

Key Words: yogurt, structure, acid gelation

Extension Education Symposium: Does Extension Have a Future in Today's Agriculture?

732 National Science Foundation outreach: A non-traditional model. S. Ellis,* *Clemson University, Clemson, SC.*

Agricultural issues emphasized by extension personnel are obviously well-aligned with the mission of the US Department of Agriculture (USDA). But there are also substantial areas of overlap between missions of the National Science Foundation (NSF) and extension groups. Both groups seek to expand the pool of scientifically literate residents that can apply scientific advances to improve the health, prosperity, welfare, and security of the US. Both groups also support adult learners with interest in science, technology, engineering and mathematics (STEM) topics. So, while the NSF does not have a singular focus on agricultural issues, there are opportunities for Extension personnel to extend, improve, and adapt their practices with NSF support. As an example, a typical extension presentation might be directed toward a crowd of adult learners with common STEM interests (e.g., entomology or economics) but with varied educational backgrounds. Questions related to the effectiveness of curricular design, pedagogy or andragogy approaches, and outcomes assessment that are the mainstay of education researchers are just as valid and important for Extension personnel. The opportunity to involve Extension program participants as study subjects could improve our understanding of adult learning and lead to improvements in Extension service offerings. Another example of the potential to align Extension activities with NSF priority areas is in the Broader Impacts domain. All NSF proposals are rated for 2 merit criteria: intellectual merit and broader impacts. The broader impacts of a NSF research project frequently include public outreach and preparation of educational materials. Extension offerings that include similar activities are already exceptionally well-aligned with the NSF goals for broader impacts. Having access to producers, commodity groups, youth groups, and other interested consumers may thus provide a distinct advantage to Extension personnel who lead or collaborate on NSF research projects in either the physical or social science domains. The challenge is to recognize complementary or synergistic funding opportunities for which Extension personnel and their resources are at a competitive advantage.

Key Words: adult education, broader impacts, STEM learning

Graduate Student Symposium: From Hypothesis to Manuscript: How to Conduct Valuable and Efficient Research

733 Developing the research question, hypothesis, design, and protocol. D. E. Bauman*[1] and R. J. Collier[2], [1]*Cornell University, Ithaca, NY,* [2]*University of Arizona, Tucson.*

The first step in developing a research question is to undertake a thorough examination of the background literature. Review articles are often a good start to gain context, but this review should include specific investigations representing current and historical research. The end result is the investigator is able to identify current issues in this area. Nobel laureate physiologist Albert Szent-Györgyi described this as "seeing what everybody has seen and thinking what nobody has thought." The next step is to identify a researchable question and develop a hypothesis that will provide clarity and structure to the research question as well as a tentative explanation of the research problem and a potential outcome. Identifying a researchable question is one of the most challenging aspects of science. Nobel Prize-winning biologist Peter Medawar referred to science as "the art of the solvable," identifying which questions are solvable through scientific investigations, and then developing hypotheses and designs to address them. The research design needs to be structured to be quantifiable, verifiable, replicable, and defensible. The protocol is a logical outcome of the research design and should include methods for all of the procedures to be utilized. Methodology is a critical component of science; results will be judged on quality of the data, but also on the validity and accuracy of the methods used to derive the data. Likewise, variables being measured need to be thoroughly evaluated to ensure they are appropriate and essential to allow a critical evaluation of the hypothesis. The protocol should also include development of the data collection forms to be used for data entry. Presentations by others will discuss additional critical dimensions including statistical considerations, data collection and publication, but we emphasize that the principle investigator is responsible for the conduct of the study. This includes laboratory determinations and data analyses, summarization and interpretation of the results, and finally publication of the investigation in a peer-reviewed journal. Throughout the presentation, authors will draw on their experience to provide insight and examples.

Key Words: research, scientific method, review

734 Data collection and integrity. G. Hartnell,* *Monsanto Company, St. Louis.*

Accurate data collection is the foundation on which the integrity of research results is based. Procedures should be in place that results in the detection and minimization of errors (systematic and random) and ensures accuracy so results can be repeated with a high level of certainty by others. The protocol should contain sufficient detail so others can accurately repeat the study. Standard operating procedures should be in place to address the question "How do I know?" in regards to data and data collection. For example, how do I know the scale or balance is accurate? How do I know the corn used in feeding the animals was not contaminated with mycotoxins that could influence the outcome of the study? How do I know the animals were deemed healthy before the start of the study? How do I know the diets were mixed properly? How do I know the personnel were properly trained to collect and measure the information on the variables of interest? Good laboratory practice, quality assurance, and quality control are approaches to be considered. Researchers must be vigilant in preventing data integrity issues when selecting, collecting, recording, analyzing, handling, storing, reporting and publishing data. Data integrity must be preserved to ensure the scientific validity of study results and conclusions that in the end reflect on the integrity of the researcher.

Key Words: data collection, data integrity, GLP

735 I'm an animal scientist, why do I need statistics? D. K. Aaron,* *University of Kentucky, Lexington.*

The answer to the question posed in the title of this presentation should be obvious: Scientists conduct research and research is dependent upon statistics. Statistics plays an integral role in experimentation, starting with planning, continuing through execution, data collection and analysis, and ending with interpretation and presentation of results. This is the reason all graduate programs in animal (dairy) sciences require students to take one or more formal courses in statistics. The expectation is that understanding statistical theory and its application to experimental design and analysis makes better researchers. In other words, future researchers will know proper design, good execution strategies and correct data analysis procedures. Is this expectation being met? Are we training better scientists? Yes and no. On the positive side, completion of formal statistics courses results in graduate students who are generally adept in the computational aspects of experimentation; that is, they can "run" SAS (SAS Inst. Inc., Cary, NC). Give them a data set and the light comes on. On the negative side, graduate students often exit formal statistics courses deficient in the non-computational components (e.g., design, implementation, measurement, interpretation) of experimentation. Ask them to design experiments or interpret research results and the light flickers or doesn't come on at all. Whose fault is this? Whose responsibility is it to ensure that future researchers are proficient in both computational and non-computational aspects of experimentation? Is more formal statistical training the answer? Questions such as these will be addressed in this presentation. The importance of statistics will be discussed in a serious, but sometimes light-hearted, way. The result will be a greater appreciation and understanding of the role statistics plays throughout the entire process of research.

Key Words: science, statistics, research

736 It is not a scientific contribution until it is published: Tips from a journal editor. S. A. Zinn,* *University of Connecticut, Storrs.*

Graduate students meticulously plan and implement experiments. Data are generated, carefully analyzed, thoroughly discussed and presented at lab meetings and regional, national and international scientific meetings in a variety of formats. Students spend endless hours writing theses and dissertations to earn, and deservedly so, their advanced degrees in their chosen discipline. But without peer-reviewed publication of their work, a graduate student has little to show for their efforts, especially if they are trying to compete with their peers to be successful in a diminishing market of tenure-track faculty positions and laboratory-based industry positions. The focus of this talk will be on preparation of manuscripts from submission to acceptance in the *Journal of Animal Science*. Differences between thesis and manuscript writing will be covered and details regarding the submission and peer-revision process will be discussed.

Key Words: publication, peer-review, graduate students

Growth and Development Symposium: Participation of Adult Tissue-Restricted Stem Cells in Livestock Growth and Development

737 Regulation of skeletal muscle satellite cell chemotaxis. R. E. Allen* and X. Liu, *University of Arizona, Tucson.*

The objective of this study was to determine the role of the stromal derived factor 1 and its receptor CXCR4 in chemotaxis of skeletal muscle satellite cells. Skeletal muscle satellite cells in postnatal muscle serve as a pool of muscle precursor cells for muscle growth and muscle repair. Over the past 3 decades, a great deal has been learned about the regulation of satellite cell activation, proliferation and differentiation into muscle fibers; these events are associated with muscle fiber growth and hypertrophy. Repair of damaged muscle, however, requires an additional biological response, migration of satellite cells to the site of fiber damage. The response has not been well characterized. Recent experiments have identified the chemokine receptor CXCR4 and its ligand, stromal-derived factor 1 (SDF-1), as potential regulators of satellite cell chemotaxis. In experiments with rat muscle, CXCR4 was upregulated when satellite cells were activated from quiescence and entered the cell cycle. Furthermore, SDF-1 was not expressed in uninjured muscle, but it was found at the site of muscle injury. In vitro experiments demonstrated satellite cell chemotaxis in response to SDF-1. The ability of satellite cells to migrate toward SDF-1 in living muscle was demonstrated in experiments where isolated satellite cells were injected into the proximal end of rat tibialis anterior muscle, and SDF-1 was deposited in the distal end of the muscle in a collagen gel. In these experiments satellite cells were labeled with Quantum Dots in culture, before injection into muscle. Within 3 d labeled cells were found at the injury site. Treatment of rats with the CXCR4 inhibitor, AMD3100, inhibited cell migration to the SDF-1 injection site, and AMD3100 inhibited migration of injected cells to sites of muscle injury. Skeletal muscle sustains minor and even major injury throughout life, and normal muscle function and subsequent meat quality depend on the ability of satellite cells seek out sites of injury and repair the damage. Results from these and additional experiments suggest that CXCR4 and SDF-1 play a role in this process.

Key Words: muscle, satellite cell, chemotaxis

738 Potentials of male germline stem cells to influence the efficiency of beef cattle production. J. M. Oatley,* *College of Veterinary Medicine, Washington State University, Pullman.*

Genetic gain is the increase in performance characteristics from generation to generation and in cattle populations is primarily made through the male germline. Sperm are the vehicle by which male genetic contributions are passed to the next generation and expanded use of these cells from specific sires has a major impact on production characteristics of cattle populations. Artificial insemination technology has been widely used as a reproductive tool in dairy cattle production to exploit this concept; however, utilization in beef cattle production is limited due to intensive management required for effective implementation which is not conducive with current strategies for managing most the world's beef cattle populations. Thus, there is need for alternative reproductive tools that expand availability of sperm from specific sires. The foundation for spermatogenesis is provided by the actions of testicular germline stem cells which possess the capacity for unlimited self-renewal and generation of committed progenitor cells that terminally differentiate into sperm. Research with rodents has shown that these cells can be isolated from testes of a donor male and transplanted into testes of recipient males in which donor-derived spermatogenesis occurs and offspring with donor haplotype produced after natural breeding. Adapting this methodology for cattle could provide an efficient means to expand the use of germlines from specific sires without the requirement for intensive management. Because stem cells are rare, a period of in vitro expansion following isolation from donor testes is required to provide an abundance of cells for efficacious engraftment following transplant. In recent studies, we have developed a multiparameter selection approach for isolating a culture-viable cell fraction from bovine testes that is enriched for germline stem cells. Moreover, we have devised a method for long-term maintenance of these cells in vitro that is xeno-free, thereby meeting a key requirement for practical application. These advances provide crucial building blocks for developing germline stem cell transplantation methodology into a utilizable reproductive tool for modern beef cattle production that will influence genetic gain.

Key Words: germline stem cells, cattle, reproduction

739 Tenocytic potential of equine umbilical cord derived stem cells. S. A. Reed*[1] and S. E. Johnson[2], [1]*University of Connecticut, Storrs,* [2]*University of Florida, Gainesville.*

Mesenchymal stem cells offer promise as therapeutic aids in the repair of tendon, ligament, cartilage, and bone damage in the sport horse. Umbilical cord blood (UCB) contains a population of putative stem cells that may be harnessed to aid in the repair of these injuries. Equine UCB derived stem cells express Oct4, Nanog, and Sox2 in a manner similar to embryonic stem cells and can differentiate into a variety of less naïve cell types including those with osteogenic, chondrogenic, hepatogenic and myogenic properties. The objective of this work was to determine if equine UCB derived stem cells (eUCB-MSC) are capable of differentiation into tenocyte-like cells. Equine UCB stem cells ($n = 3$) were cultured on gelatin or matrigel coated dishes or gelatin coated beads and treated with 10 ng/mL fibroblast growth factor (FGF)-2, - 4, or −5. Expression of *scleraxis* (*scx*), a transcription factor required for tendon development, and *Tenascin-C* (*TnC*), a protein abundant in developing tendons, was measured by real-time PCR (reported as mean ± SEM). Growth kinetics were measured following FGF supplementation. Equine adipose derived stem cells (AdMSC) were used to compare eUCB-MSC to a more adult stem cell population. Both eUCB-MSC and AdMSC express *scx* and *TnC*. When cultured on varying matrices, eUCB-MSC and AdMSC adapted different morphologies. Further, culture in matrigel increased *scx* expression in both cell populations (eUCB-MSC: 6.73 ± 2.1 fold; AdMSC: 39.5 ± 26.6 fold, $P < 0.05$) and increased *TnC* 12.3 ± 1.85 fold in AdMSC ($P < 0.05$). In AdMSC culture in matrigel, supplementation with FGF2 or FGF5 increased *TnC* expression 1.84 ± 0.22 fold and 2.66 ± 0.48 fold, respectively. Fibroblast growth factors affected growth kinetics in AdMSC and eUCB-MSC. In conclusion, both eUCB-MSC and AdMSC express markers of early tenocytes. *Scx* expression is increased when cultured in matrigel, a 3 dimensional matrix. FGF supplementation further increased *TnC* expression in AdMSC. These results demonstrate a potential use for AdMSC and/or eUCB-MSC in future therapies to improve tendon healing.

Key Words: umbilical cord blood, horse, tendon

740 Development, characterization and use of a porcine epiblast-derived liver stem cell line: ARS-PICM-19. T. J. Caperna,* W. M. Garrett, and N. C. Talbot, *USDA/ARS, Beltsville, MD.*

Totipotent embryonic stem cell lines have not been established from ungulates, however, we have developed several somatic cell lines from the in vitro culture of pig epiblast cells. One such cell line, PICM-19, was isolated via colony-cloning and was found to spontaneously differentiate into hepatic parenchymal epithelial cell types, viz., hepatocytes (H) and bile duct cells (BD). Hepatocytes form as monolayers and BD as 3D bile ductules. PICM-19 cells are sensitive to variations in extracellular pH in that low pH induces H differentiation and high pH elicits BD differentiation. Transmission electron microscopy revealed that BD were composed of radially arranged, monociliated cells with their cilia projecting into the ductuleâ€s lumen, whereas H were arranged in monolayers with lateral canalicular structures containing numerous microvilli and connected by tight junctions and desmosomes. Extensive Golgi and rough endoplasmic reticulum networks were also present in H and BD, indicative of active protein synthesis. Analysis of conditioned media by 2D-electrophoresis and mass spectrometry indicated a broad spectrum of serum protein secretion by H. The PICM-19 cell line maintains a range of inducible cytochrome P450 activities, and, most notably, is the only non-transformed cell line that synthesizes urea in response to ammonia challenge. In collaboration with NASA, PICM-19 cells were placed on orbit (Shuttle Mission STS 126) where it was determined that short-term (14 d) microgravity exposure did not affect hepatic cellular differentiation. A PICM-19 subclone which only differentiates into H was isolated. It was evaluated as a platform for toxicity testing and has been utilized in a commercial artificial liver rescue device bioreactor (Hepalife Biosystems). Methods are currently under development to improve the growth of PICM-19 cells without feeder cells. Feeder-cell independent growth will facilitate the study of mesenchymal-parenchymal interactions that influence the divergent differentiation into H or BD, will enhance our ability to genetically modify the cells, and will provide a better model system to investigate porcine hepatic metabolism.

Key Words: liver stem cells, hepatocyte, bile duct

741 Mammary stem cells: Novel markers and novel approaches to increase lactation efficiency. A. V. Capuco*[1], R. K. Choudhary[1,2], C. M. Evock-Clover[1], and K. M. Daniels[3], [1]*Bovine Functional Genomics Lab, USDA-ARS, Beltsville, MD,* [2]*Department of Animal and Food Sciences, University of Kentucky, Lexington,* [3]*Department of Animal Sciences, The Ohio State University, Wooster.*

Mammary stem cells (MaSC) provide for net growth, renewal and turnover of mammary epithelial cells, and are therefore potential targets for strategies to increase production efficiency. Appropriate regulation of MaSC can potentially benefit milk yield, persistency, dry period management and tissue repair. Accordingly, we and others have attempted to characterize and alter the function of bovine MaSC. Approaches used have included flow cytometry and in vitro cultivation to enrich for and characterize these cells. Recent data indicate that MaSC retain labeled DNA for extended periods. Relying on this long-term retention of bromodeoxyuridine-labeled DNA, we identified putative bovine MaSC and hypothesized that the label retaining epithelial cells (LREC) present in the basal layer of the mammary epithelium represent MaSC. As in other species, these cells were present in low abundance within mammary epithelium (<1%) and were estrogen receptor-negative. We recently excised LREC and control cells from the mammary epithelium, using laser microdissection, and characterized their transcriptome by microarray analysis. Molecular profiles were consistent with the concept that LREC represent populations of MaSC and progenitor cells, that basal LREC are enriched for MaSC, and that LREC in suprabasal locations are enriched for committed progenitors. Analysis also provided novel candidate biomarkers for MaSC/progenitors. Potential biomarkers currently under investigation include NR5A2, NUP153, FNDC3B and HNF4A. Cells bearing these biomarkers are present in abundance and localization consistent with their utility as MaSC markers. We have attempted to modulate MaSC number in vivo and in vitro. Infusing a solution of xanthosine through the teat canal and into the mammary ductal network of prepubertal heifers and treatment of bovine mammary epithelial cells in vitro, increased the number of putative MaSC/progenitors. This was evidenced in vivo by an increase in the percentage of LREC and increased telomerase activity and in vitro by increased FNDC3B labeling and telomerase activity. The exciting possibility that stem cell expansion can influence milk production is under investigation.

Key Words: stem cells, progenitor cells, mammary

Lactation Biology Symposium: The Long-Term Impact of Epigenetics and Maternal Influence on the Neonate Through Milk-Borne Factors and Nutrient Status

742 Role of colostrum and colostrum components on glucose metabolism in neonatal calves. H. M. Hammon,* *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Mammalians undergo dramatic organ-specific as well as metabolic and endocrine changes after birth. Nutrient intake shifts from continuous glucose supply via the placenta to discontinuous colostrum and milk intake with lactose and fat as main energy sources. The development of the neonatal calf is influenced by colostrum intake when compared with colostrum replacement diets. Besides establishing a passive immunity, colostrum promotes maturation and function of the neonatal gastrointestinal tract (GIT) in calves. Nutrients and non-nutritive factors, such as hormones and growth factors, which are present in high amounts in colostrum of first milking, affect intestinal growth and function and enhance the absorptive capacity of the GIT. In addition, colostrum feeding improves the glucose status in neonatal calves. Glucose absorption increases and glycogen concentrations in liver rise much higher when colostrum instead of a milk-based colostrum replacer is fed. In contrast, first-pass glucose uptake in the splanchnic tissue is greater in calves fed colostrum replacer without growth promoting substances. The improved energy status in neonatal calves after enhanced colostrum intake leads to accelerated stimulation of anabolic processes indicated by an enhanced maturation of the postnatal somatotropic axis and increased production of endogenous IGF-I in neonatal calves. Besides the somatotropic axis, other endocrine changes such as higher postprandial insulin release, a reduced glucagon to insulin ratio and cortisol level in blood plasma, and an increased plasma leptin concentration after colostrum instead of replacer feeding support the concept of stimulation of anabolic processes. These endocrine changes may favor postnatal organ development and may improve growth and lactation performance in cattle in later life. Therefore, intensive colostrum and subsequent milk feeding by increasing amounts and frequency of colostrum and milk intake may have long-lasting effects on postnatal performances and might be a key factor of successful cattle breeding.

Key Words: neonatal calf, colostrum feeding, glucose metabolism

743 Nutrition of the dam affects mammary gland development and milk production in the offspring. P. Kenyon,* A. Paten, E. Garnett, H. Blair, S. Pain, C. Jenkinson, S. Peterson, and N. Martin, *Massey University, Palmerston North, New Zealand.*

In animal systems, the dam's milk production affects the growth and survival of its offspring. Further in agricultural systems any mechanism that can enhance milk production has the potential to increase financial returns. Our group has previously shown that maternal nutrition during pregnancy in sheep alters fetal mammary gland development and the volume and composition of milk produced by the offspring at their first lactation (fetal programming). Second generation offspring showed no difference in milk yield or composition. In 2009, 382 twin-bearing ewes (G0) were offered 1 of 3 nutritional treatments between d 21 and 50 of pregnancy: sub-maintenance (Sb), maintenance (M) or adlib (A) access to pasture. They were subsequently offered either M or A until d 139 of pregnancy. A sub-set of ewes were euthanized in late pregnancy. During 2010, puberty in ewe offspring (G1) was monitored and in 2011 G1 ewes were mated and a sub-set milked. At d 51 of pregnancy H G0 ewes were heavier than M which in turn were heavier than Sb ewes ($P < 0.05$, 69.5 ± 0.53 vs 65.1 ± 0.53 vs 62.2 ± 0.56kg). At P137, ewes offered H during d 51 to 139 of pregnancy were heavier than those offered M (88.2 ± 0.53 vs 82.6 ± 0.53). Fetal mammary gland weight was affected ($P < 0.05$) by ewe nutrition during d 21 to 50 of pregnancy, but not by nutrition in late pregnancy. Ewe nutrition during d 21 to 50 of pregnancy had no effect ($P > 0.05$) on G1 lamb birth weight, but during late pregnancy it did ($P < 0.05$). Ewe nutrition in either early or late pregnancy had no effect ($P > 0.05$) on puberty attainment in G1 ewes. Initial data analysis indicates G1 ewes born to G0 ewes fed M during d 21 to 50 of pregnancy produced a greater ($P < 0.05$) amount of milk over a 7-week, once-a-week milking period, compared with G1 ewes born to either G0 Sb or G0 H ewes. G0 nutrition in late pregnancy had no effect on G1 milk production. These preliminary results suggest that it is in the early pregnancy period that the fetal mammary gland is susceptible to the affects of dam nutrition. Molecular and physiological mechanisms for these effects are being examined.

Key Words: fetal programming, maternal nutrition, milk supply

744 Lactational programming of infant behavioral and somatic development. K. Hinde*[1,2], A. Foster[2], and J. P. Capitanio[2,3], [1]*Human Evolutionary Biology, Harvard University, Cambridge, MA,* [2]*Brain, Mind, and Behavior Unit, California National Primate Research Center, University of California-Davis,* [3]*Department of Psychology, University of California-Davis, Davis.*

Glucocorticoids in mother's milk have been associated with infant behavioral phenotype in rodents, macaques, and humans presumably by shaping the HPA axis. However, infant behavioral activity budgets are necessarily constrained by available energy. Cortisol, usually thought of only in the context of stress physiology, is actually a metabolic hormone that ties together both of these perspectives. Energy utilization, and the metabolic function of cortisol, becomes particularly critical during challenging conditions e.g., nutritional stress, predator encounters, and social conflicts- the same environmental conditions that have been implicated in the development of behavioral phenotype. We hypothesize that behavioral phenotype is organized in concert with the metabolism by energetic conditions during early development. Here we present data from rhesus macaque mother-infant dyads at the California National Primate Research Center, expanding upon previous findings that milk energy is correlated with milk cortisol and predicts infant behavioral phenotype. Changes in milk cortisol across lactation precipitate changes in infant growth velocity after controlling for maternal and infant covariates and predict infant temperament. In adulthood the HPA axis, metabolism, and behavior do not exist apart from one another. We present a synthesis of emerging evidence that suggests that the organization of these interconnected systems is likely shaped, in part, by mother's milk during ontogeny. Research supported by NSF BCS-0921978 and BCS-0525025 to KH and NIH RR019970 to JPC and NIH RR000169 to the CNPRC.

745 Lactocrine signaling and postnatal developmental programming. F. F. Bartol*[1], D. J. Miller[1], A. A. Wiley[1], J. C. Chen[2], A-L. Frankshun[2], M. E. Camp[2], K. M. Ferio[2], and C. A. Bagnell[2], *[1]Auburn University, Auburn, AL, [2]Rutgers, The State University of New Jersey, New Brunswick, NJ.*

Lactocrine signaling is defined as transmission of bioactive factors from mother to offspring as a consequence of nursing. Transmission of lactocrine-active signaling molecules is likely to be an evolutionarily conserved process through which bioactive factors of maternal origin necessary for support of neonatal development are delivered postnatally. Dependence on maternal resources for development in eutherian mammals extends into neonatal life for at least that period of time when nutrition is obtained solely from first milk (colostrum). Data for the pig (*Sus scrofa domesticus*) provide compelling evidence of lactocrine-mediated effects on development of female reproductive tract and other somatic tissues. Porcine uterine gland development is an estrogen receptor (ESR1)-dependent process that begins within 2 d of birth (postnatal d 0 = PND 0). A lactocrine-driven, ESR1-mediated process was proposed as a component of the regulatory mechanism governing onset of nascent uterine gland development and endometrial maturation in the neonatal pig. Compared with nursed controls, gilts maintained in a lactocrine-null state for 2 d from birth by being fed milk-replacer displayed altered patterns of endometrial gene expression and severely retarded uterine gland development by PND 14. For example, in the absence of lactocrine signaling, inhibition of endometrial ESR1 and vascular endothelial growth factor (VEGF) expression observed on PND 2 persisted to PND 14, even after gilts were returned to nursing on PND 2. Similar effects were observed in cervical and cardiac tissues and in male reproductive tissues at PND 2. Lactocrine induction of neonatal uterine and cervical ESR1 and VEGF expression is related directly to duration of nursing from birth and inversely to age at first colostrum consumption. Single feedings of porcine, equine or bovine colostrum (30mL/kg BW) to newborn gilts induced uterine and cervical ESR1 and VEGF expression. These effects were most pronounced with porcine colostrum. Collectively, data support a role for lactocrine signaling in regulation of critical neonatal developmental events. Maternal lactocrine programming of postnatal development may be essential to ensure healthy developmental outcomes.

Key Words: development, neonate, lactocrine programming

746 The effect of nutrient intake from milk or milk replacer of pre-weaned dairy calves on lactation milk yield as adults. F. Soberon* and M. E. Van Amburgh, *Cornell University, Ithaca, NY.*

Pre-weaning nutrition and management of dairy calves has generally focused on rumen development, starter intake and disease management. Recent data have shown that pre-weaning nutrition can have profound effects on development that enhance lifetime productivity. Using a combination of milk yield data from a test day model and a mixed model analyses incorporating pre-weaning nutrient intakes and growth rates of more than 1,800 calves on 2 dairy farms in NY, the relationship among growth and milk yield were evaluated. The relationship between pre-weaning average daily gain (ADG) and milk yield was positive and resulted in 850 and 1,113 kg more milk ($P < 0.01$) during first lactation for every kg of ADG before weaning for each farm, respectively. Further, pre-weaning ADG explained 22% of the variation in first lactation milk yield. In addition, for every megacalorie of intake above maintenance, calves yielded 235 kg more milk during first lactation. In addition, at least 11 studies have been reported describing milk yield of calves that had been fed various levels of pre-weaning nutrients, from both milk and milk replacer, which evaluated the effect of pre-weaning ADG and long-term productivity. A mixed model analysis of these studies was conducted, where study was considered a random effect and the analysis considered the number of animals per treatment in each study. Two models were utilized; the first model considered only treatment, high or low intake levels, and that analysis resulted in a prediction of 506.5 ± 99.1 kg ($P < 0.01$) first lactation milk yield in calves consuming higher levels of milk or milk replacer during the pre-weaning period. In a model that included pre-weaning ADG as a continuous variable with study as a random effect and weighted each study-treatment combination by the number of animals, the resulting equation was: $Y = 8{,}974$ kg + 1,404 ADG kg ($P < 0.001$) indicating that for every kg of ADG, heifers produced 1,404 kg more milk in the first lactation. This data reinforces the observation that early life nutrition of dairy calves positively impacts long-term productivity.

Key Words: pre-weaning nutrition, milk yield, dairy calves

Meat Science and Muscle Biology

747 Impact of stunning and carcass chilling on pork quality and post-mortem proteolysis. G. Petca and G. Bee,* *Agroscope Liebefeld Posieux, Research Station ALP, Posieux, Switzerland.*

The aim of the study was to evaluate the effects of stunning procedures (electrical (ES) vs. CO_2 (CS) stunning) and carcass chilling regimens (conventional [CC; 4°C for 23.5 h] vs. rapid chilling [RC; −30°C for 2.5 h; 4°C for 21 h]) on pork quality traits and post-mortem (pm) proteolysis in the LM. Twenty Swiss Large White × Piétrain crosses were randomly assigned to either ES or CS. Carcasses were then scalded (7 min; 65°C), eviscerated and split. At 45 min pm, the left and right carcasses were subjected to CC and RC, respectively. Compared with ES, the pH of the LM (10th rip) was greater ($P < 0.01$) at 45 min (6.5 vs. 6.0), 3 h (6.3 vs. 5.6) and 24 h (5.5 vs. 5.4) in CS. Stunning procedure affected muscle temperature being lower in CS at 45 min (38.3 vs. 38.8°C) but greater at 3 (18.8 vs. 16.2°C) and 24 h (1.8 vs. 1.5°C) pm. Regardless of the stunning procedure, pH of the LM was slightly greater ($P \leq 0.03$) in RC than CC at both 3 (6.1 vs. 5.9) and 24 h (5.5 vs. 5.4) pm. As expected, RC resulted in lower ($P < 0.01$) LM temperature at 3 h pm (13.7 vs. 21.4°C). Percentage drip loss (48 h) was lower ($P < 0.01$) in loin chops from CS pigs (3.5 vs. 4.5%). Considering the cooling regimen, RC resulted in greater ($P = 0.04$) drip loss than CC (4.3 vs. 3.7%). Maximal shear force was influenced both by stunning procedure ($P < 0.01$) and chilling regimen ($P < 0.01$), with greater values for CS (6.3 vs. 5.3 kg) and RC (6.4 vs. 5.3 kg). Intact desmin abundance determined at both 24 and 72 h pm was not affected by the stunning procedure ($P \geq 0.46$) or by the chilling regimen ($P \geq 0.07$). When CS is followed by CC and when ES is followed by RC, abundance of intact talin in the LM is lower at 24 but not ($P \geq 0.39$) at 72 h (stunning procedure × chilling regimen interaction; $P < 0.01$). Relative abundance of the unautolyzed 80 kDa μ-calpain unit at 24 h pm was influenced by stunning procedure ($P < 0.01$) and cooling regimen ($P < 0.05$), with greater abundance in the LM of CS and RC. By contrast, the relative abundance of the 78 kDa μ-calpain subunit was lower ($P \leq 0.06$) for the CS and RC. The results reveal an overall positive effect of CS, except for shear force values, and CC on LM quality traits.

Key Words: stunning procedure, chilling rate, proteolysis

748 Effects of cannabinoid receptor 1 on muscle fiber types and muscle oxidative metabolism. E. Xu*[1,2], L. N. Zhu[1], T. Wu[1], Y. N. Huang[1], and Y. Z. Wang[1], [1]*Institute of Feed Science, Zhejiang University, The Key Laboratory of Molecular Animal Nutrition, Ministry of Education, Zhejiang Provincial Laboratory of Feed and Animal Nutrition, Hangzhou, Zhejiang, China,* [2]*College of Animal Science, Guiyang, Guizhou, China.*

The cannabinoid receptor type 1 (*CNR1*) is a key component of the endocannabinoid system, which has been reported to play a pivotal role in modulating feeding behavior and energy balance. *CNR1*is expressed in skeletal muscle and has effects on skeletal muscle metabolism. However, how this gene regulates muscle fiber types and muscle oxidative metabolism remains un-elucidated. In this study, 2 different strategies have been carried out: siRNA suppression and overexpression of *CNR1*.Results showed that the *CNR1*-overexpressed L6 cells exhibit higher expression levels of oxidative type muscle gene myosin heavy chain typeIIα (MyHCIIα, $P < 0.01$) and oxidative enzyme succinic dehydrogenase(SDH, $P < 0.05$) compared with the control group. While knockdown the *CNR1* in L6 cells, MyHCIIα expression ($P < 0.01$) was decreased and the expression of glycolytic enzyme lactate dehydrogenase (LDH) was significantly increased ($P < 0.01$). Overexpression of *CNR1* in rat soleus muscle significantly increased MyHCIIα ($P < 0.01$), SDH ($P < 0.01$) and malate dehydrogenase (MDH, $P < 0.05$) mRNA expression. In addition, *CNR1* overexpression in vivo induced SDH ($P < 0.01$) and MDH ($P < 0.05$) enzyme activities and downregulated LDH ($P < 0.05$) enzyme activity. Furthermore, gene expression of extracellular-regulated kinase 1 (ERK1) and proliferator-activated receptor-γ coactivator-1α (PGC-1α) were remarkably increased in both overexpression L6 cells and rat soleus muscle. In contrast, we observed that PGC-1α gene expression was significantly decreased, but extracellular-regulated kinase2 (ERK2) gene expression significantly increased in siRNA cell lines. Based on these results, we conclude that *CNR1*enhance the MyHCIIα and oxidative enzyme MDH and SDH gene expression and activities, inferring that the gene may play an important role in muscle oxidative metabolism. Moreover, *CNR1* may affect muscle fiber types and muscle oxidative metabolism via ERK1/2 and PGC-1α. These results contribute to further understanding the role of *CNR1* in skeletal muscle energy metabolism, and also help to explore the key genes to improve meat quality.

Key Words: cannabinoid receptor type 1, muscle fiber types, oxidative metabolism

749 Fatty acid profile of meat from young bulls fed different levels of crude glycerin. M. M. Ladeira,* J. R. R. Carvalho, M. L. Chizzotti, E. M. Ramos, P. D. Teixeira, M. C. L. Alves, P. E. P. Barros, and O. R. Machado Neto, *Federal University of Lavras, Lavras, MG, Brazil.*

The fatty acid profile in beef has an extreme importance, because many of these fatty acids have beneficial and malefic actions to human health. The objective was to determine the fatty acid (FA) profile of muscle and subcutaneous fat of feedlot young bulls fed different levels of crude glycerin in the diet. The experiment was conducted in a completely randomized design, with 4 treatments and 11 repetitions. Forty-four Red Norte animals were slaughtered at average live weight of 519 ± 15 kg, and the levels of crude glycerin (83% glycerol) in the diet were: 0, 6, 12 and 18% DM. The basal diet consisted of 30% corn silage, 12% soybean meal, 56% corn grain and 2% mineral mixture. Corn was partially replaced by glycerin, and to achieve an isonitrogenous diet, corn gluten meal (21% CP) was used. After slaughter, samples were taken from the *Longissimus dorsi* muscle of the left half carcass, and fatty acids were quantified using gas chromatography (GC-MS Finnigan Focus Gas Chromatograph; Column CP-Sil 88). When there was significant effects ($P < 0.05$), regressions analysis using PROC REG of SAS 9.1.3 were done. There was a linear increase of oleic acid (C18:1 cis-9) content in subcutaneous fat ($P < 0.05$) and muscle ($P < 0.05$), which could be due to an inhibition effect of glycerol on rumen lipolysis and, consequently, on the biohydrogenation, resulting on greater flow of unsaturated fatty acids to small intestine. The octadecenoic acid (C18:1 trans-10, trans-11 and trans-12) content in muscle decreased ($P < 0.05$), and there was a tendency ($P < 0.10$) of reduction on palmitic acid (C16:0) content in the muscle and subcutaneous fat with the increase of crude glycerin in the diet. However, the linoleic acid (C18:2 ω-6), α-linolenic acid (C18:3 ω-3) and CLA (C18:2 cis-9, trans-11) contents were not affected ($P > 0.05$) by the levels of crude glycerin. In the muscle tissue, there was an increase ($P < 0.05$) in concentration of monounsaturated fatty acids, and unsaturated:saturated fatty acids ratio ($P < 0.01$). As a conclusion, the use of crude glycerin in the beef cattle diet improved the fatty acids profile of meat. Funded by Fapemig, CNPq, Capes and INCT-CA.

Key Words: biohydrogenation, CLA, glycerol

750 Effect of vitamin E inclusion on *trans*-18:1 isomers in subcutaneous fat of steers fed a high-barley grain diet.

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Beef from animals fed high-concentrate diets can contain more *trans* (t)10–18:1 than vaccenic acid (t11–18:1) and consumption of t10–18:1 is associated with unhealthy blood lipoprotein profiles in animal models. Vitamin E has been reported to alter the levels of biohydrogenation intermediates in the rumen and consequently the fatty acid composition of tissues. The objective of the current study was to determine the effect of different dietary vitamin E levels on t18:1 isomers in subcutaneous fat from steers fed a high-barley grain diet. Steers were fed 1 of 4 levels of supplementary DL-α-tocopheryl acetate (340, 690, 1040 or 1740 IU/steer/day) in a barley-based finishing diet for 120 d. Two pens of 7 animals were fed per diet. At slaughter, subcutaneous fat was collected from the grade site (12th rib), methylated with sodium methoxide, and analyzed by a combination of GC and Ag+-HPLC. Polynomial contrasts were used to test for linear and quadratic effects of increasing dietary levels of vitamin E on subcutaneous fatty acid composition. Addition of vitamin E led to linear reductions ($P < 0.05$) in t6-/t7-/t8–18:1 and t10–18:1, and linear increases ($P < 0.05$) in t11–18:1 and t11-/t10–18:1 ratio in subcutaneous fat. Although vitamin E led to improvements in the t18:1 profile of beef subcutaneous fat, t10–18:1 remained the predominant t18:1 isomer. Additional testing is, therefore, warranted where a greater range of vitamin E is fed combined with testing for interactions with other biohydrogenation modifiers.

Key Words: subcutaneous fat, *trans* fatty acids, vaccenic acid

751 Influence of gender on meat quality and skatole in the fat of lambs.

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Boar taint is a negative attribute of pork that occurs due to hindgut skatole production. The sheep rumen also produces skatole but there is no scientific evidence of ram taint. The objective was to investigate the influence of gender on lamb meat quality and fat skatole concentration. Five-month-old entire (n = 19) and castrated ram-lambs (n = 19) were grazed on autumn ryegrass pasture for 70 d. Live weight was measured at the start and before slaughter. Hot carcass weight was measured and the carcass chilled at 4°C for 24 h. After chilling the left loin was removed, vacuum-packed, chilled for a further 24 h at 4°C then stored at −20°C. Intermuscular fat was collected from the hind legs of the carcass and stored at −20°C. After thawing, muscle lightness and redness was assessed on a fresh slice of the loin after 30 min exposure to air (Minolta CR-200 chromameter calibrated to a white standard). Tenderness was assessed by the peak force required to shear 13 mm-square cores from loin steaks cooked in a water bath at 70°C for 90 min (Warner-Bratzler device, square blade and 30 kg load cell). Skatole concentration in the intermuscular fat was measured by GC-MS. Skatole concentration and peak shear force data required a log-transformation to achieve a normal distribution. Data were analyzed by *t*-test. The ram lambs had a greater pre-slaughter live weight (51.5 vs. 46.6 kg; $P < 0.001$) and carcass weight (22.0 vs. 20.5 kg; $P < 0.01$) due to a greater live weight at the start (40.3 vs. 37.7 kg; $P < 0.05$) and a greater growth rate (160 vs. 127 g/day; $P < 0.01$). Gender did not influence the lightness, redness or peak shear force. The skatole concentration was greater in the fat of the entire ram lambs (0.079 vs. 0.052 μg/g; $P < 0.05$). In production systems, rams are preferred over castrated male lambs due to their greater growth rates and ability to produce a heavier carcass, as observed in this study. The ram lamb was not associated with poorer meat quality in terms of tenderness and color compared with the castrated male. The greater skatole concentration indicates potential flavor issues for meat from ram lambs but the concentration was well below the 0.25 μg/g threshold at which boar taint is detected.

Key Words: lamb, skatole, gender

752 Comparison of skinning versus scalding and singeing: Effect on temperature, pH and meat quality in goats.

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The aim of this work was to investigate the effect of temperature and pH changes taking place at the slaughter line due to different post slaughter processing methods (PSPM) on meat of red Sokoto buck goats. A total of 27 good grade red Sokoto buck goats were slaughtered in batches of 3 and assigned randomly to the 3 PSPM of skinning, scalding, and singeing in a completely randomized design. Samples for pH analysis were taken from the Longissimus dorsi while the semi-membranosus muscles were used for evaluating shear force values (Kg/cm3) of the meat. Eating quality was estimated on aged semi-membranosus muscles using a trained taste panel on a 9-point hedonic scale. The internal temperature and pH values were taken at a depth of 2 cm at the Longissimus dorsi immediately after dressing and subsequently at 30 min intervals over a period of 3 h post-mortem. The rib-eye area was measured at the interface of the 12th and 13th rib while meat color was evaluated after freezing and thawing. Water Holding Capacity (WHC), drip loss and cooking loss were also evaluated. The ultimate pH was measured 24 h post-mortem. All data obtained were subjected to ANOVA. At the slaughter line, the skinned carcasses had a lower temperature ($P < 0.05$) compared with scalded and singed carcasses. The rate of pH fall was lowest ($P < 0.05$) in skinned carcasses from exsanguination until 3 h post-mortem while the ultimate pH was lowest ($P < 0.05$) in skinned (5.54) carcasses and highest ($P < 0.05$) in singed carcasses (5.70). Skinned carcasses showed a darker ($P < 0.05$) meat color compared with meat from scalded and singed carcasses. Scalding and singeing led to increased toughness by 26.21 and 50% respectively over meat from skinned carcasses. Drip and cooking losses were higher ($P < 0.05$) in meat from scalded and singed carcasses. WHC increased by 9.67% in meat from scalded carcasses while a decrease of 14.20% was obtained in meat from singed carcasses compared with those from skinned carcasses. The rib-eye area was not affected ($P > 0.05$) by the 3 PSPM. The trained panelist preferred ($P < 0.05$) meat from singed carcasses in terms of color, flavor, and overall acceptability.

Key Words: temperature, pH, postmortem processing

753 Organoleptic and shelf life of displayed Red Sokoto buck meat as influenced by post-slaughter processing methods. A. B. Omojola*[1], E. S. Apata[2], O. O. Olusola[1], and A. B. Omotosho[1], [1]*University of Ibadan, Ibadan, Oyo State, Nigeria,* [2]*Olabisi Onabanjo University, Ago-Iwoye, Ogun, Nigeria.*

While post-slaughter processing methods have the potential to add value, enhance shelf life and eating qualities of animal products, their effects on meat displayed for marketing as practiced in most developing nations needs to be evaluated. An experiment was carried out to investigate the effects of 3 post-slaughter processing methods (PSPM) of scalding, skinning, and singeing on eating and shelf life of displayed Red Sokoto buck meat. Twenty-seven (27) matured Red Sokoto buck goats weighing between 18 and 20 kg were slaughtered in batches of 3 and assigned to the 3 PSPMs. A completely randomized design in a 3 × 4 factorial arrangement was employed. After evisceration, the carcasses were split into symmetric halves and were fabricated into wholesale cuts. Meat from the leg cut (semi-membranosus) of each carcass from each treatment were displayed on a clean and sanitized table to simulate open market retail situations at an ambient temperature of 27°C. Meat samples were removed from the open displayed meat at intervals of 0, 3, 6 and 9 h for measurement of peroxide value, microbial load and organoleptic characteristics. The organoleptic score as measured on a 9-point hedonic scale was highest ($P < 0.05$) at 0 h of display for all parameters while the value reduced as time of open display increased. Irrespective of the time of display, meat from singed carcasses were scored highest ($P < 0.05$) for color (6.24), aroma (6.60), flavor (6.76) and overall acceptability (6.63). Tenderness and juiciness score were rated highest ($P < 0.05$) in meat from scalded carcasses. The peroxide value was least ($P < 0.05$) at 0 h of open display (0.43mEq) and increased as the display time increased. Displayed meat from skinned carcasses elicited the highest ($P < 0.05$) peroxide value (0.52 mEq) followed by meat from scalded carcasses (0.45 mEq). The microbial load of displayed meat from singed carcasses were least ($P < 0.05$) at various time of display while displayed meat from skinned carcasses had the highest microbial load at 0,3 6 and 9 h. Microbial load of all the displayed meat increased as time of display increased. Singeing enhanced shelf life and eating qualities of chevon displayed in open market situation.

Key Words: scalding, skinning, singeing

Nonruminant Nutrition: Feed Additives

754 Effect of different probiotics on diarrhea frequency and body weight of weaned piglets challenged with *Salmonella typhimurium*. L. J. Parazzi,* E. R. Afonso, S. M. M. K. Martins, T. A. Santo, A. F. C. Andrade, J. Diniz-Magalhães, and A. S. Moretti, *USP/FMVZ, Pirassununga, SP, Brazil.*

The aim of study was to test the effect of different probiotics fed to piglets on diarrhea frequency and body weight. The probiotic A (PA) mixture was composed of *B. subtilis, B. bifidum*, *E. faecium*, *L. acidophilus*, *L. casei*, and *L. lactis* and probiotic B (PB) contained *B. subtilis* and *B. toyoi* . A total of 160 crossbred piglets were weaned at 23 d of age, blocked by initial weight, equalized for sex, and distributed to 8 treatments: PA44 (4kg/ton) and PB44 (2kg/ton) fed through 44 d of age; PA65 (4kg/ton to 44 d and 2kg/ton to 65 d) and PB65 (2kg/ton to 44 d and 1kg/ton to 65 d) fed through 65 d of age; PA138 (4kg/ton to 44 d and 2kg/ton to 138 d) and PB138 (2kg/ton to 44 d and 1kg/ton to 138 d) fed through 138 d of age; control (C) without additives, and Antimicrobial (Atb), with antibiotic growth promoter. At 51 d of age, piglets received an oral dose of 1×10^5 UFC/pig of *S. typhimurium* (LSS-SR41). Feces from each experimental unit (4 pigs/pen) were visually examined every day (23 to 79d) to determine the diarrhea frequency using a subjective score on scale ranging from 1 to 3, where 1 = normal; 2 = soft feces; 3 = liquid feces. Piglets receiving Atb showed higher occurrence of normal feces compared with PA ($P = 0.0485$) and similar compared with PB during 23 to 79 d, independent of the administration period both PA and PB. Piglets fed PB138 demonstrated higher frequency of normal feces (32.75% vs 19.56%, respectively) and lower liquid feces (26.54% vs 35.62%, respectively) in relation to PA138. During 23 to 65 d of age, piglets fed Atb showed a higher body weight ($P < 0.05$) compared both PA and PB (25.99, 21.74 and 21.91 kg, respectively), but at slaughter (138 d) body weights were similar between all treatments ($P > 0.05$). In conclusion, the probiotic PA was not effective in reducing the incidence of diarrhea compared with PB and Atb, but the final body weights were similar, suggesting medium- and long-term actions of these probiotics on intestinal health.

Key Words: diarrhea, probiotics, *S. typhimurium*

755 Effect of mannan oligosaccharides on performance of weanling piglets. F. C. Horta, L. J. Parazzi,* S. M. M. K. Martins, O. H. O. Eckhardt, T. A. D. Santo, A. F. C. Andrade, J. Diniz-Magalhães, and A. S. Moretti, *USP/FMVZ, Pirassununga, SP, Brazil.*

The mannan oligosaccharides (MOS) have been used as prebiotics in the diets of pregnant and lactating gilts and weaned piglets. The aim of the study was to evaluate the effect of MOS in the diet on gestation and lactation of gilts and piglets during the weaning period on growth performance in the nursery. In a 2 × 2 factorial arrangement, 17 gilts and 140 weaned piglets (23 d of age) were used. There were 8 replicate pens (4 pigs/pen) per treatment, except CC and MM with 9 and 10, respectively. The compositions of diets for gilts and piglets were based on corn and soybean meal met NRC recommendations (1998). The groups consisted of gilts and piglets either fed with MOS (BioMOS, Alltech, 28% of the glucomannoprotein from *Saccharomyces cerevisiae*) or without it. The treatments were: MM (feeding MOS to gilts and piglets), MC (feeding MOS only to gilts), CM (feeding MOS only to piglets) and CC (control diets to gilts and piglets). The gilts received MOS at late gestation (81 ± 1.36 d) and lactation (0.1% MOS) and the piglets received MOS on the following schedule: 0.4% of the diet beginning on the last week of lactation to 37 d of age, 0.2% from 38 to 51 d of age, and 0.1% from 52 to 65 d of age. At 35 d of age, piglets were challenged orally (1×10^8 cfu/piglets) of *Salmonella* typhimurium. The weaning weight by the 5th week was higher ($P < 0.05$) in MM and MC treatments. Feed intake during first week post-weaning was higher ($P = 0.0449$) in MM and MC than CM and CC. The same result was observed for weight gain of piglets during the 2nd week ($P = 0.002$), but the CM and CC treatments showed a lower ($P = 0.0103$) G:F compared with MM and MC. In the 6th week, MM and MC treatments exhibited a higher feed intake ($P = 0.0007$), however, with no difference in the body weight of piglets. MM and MC piglets maintained highest body weight despite the challenge employed. In conclusion, supplementation with MOS in the diets of gilts increased the body weights of piglets by 5th week, independent the piglet MOS supplementation.

Key Words: mannan oligosaccharides, piglets, *S. typhimurium*

756 Multi-NSP enzymes improved growth performance and gut health in nursery pigs fed corn or rye and barley diets. J. Zhao,* F. Yan, D. L. Lichtenstein, A. Lawhorn, and M. Vazquez-Anon, *Novus International Inc., St Charles, MO.*

This study was conducted to investigate the benefits of an NSP enzyme blend in pigs fed either corn or rye and barley diets. A total of 128 nursery pigs (34 d of age, 9.95 ± 0.28 kg) were randomly assigned to 4 treatments with 8 replicates per treatment and 4 pigs per pen. The trial was a 2*2 factorial arrangement with 2 diet types (corn vs. rye and barley) with and without NSP enzyme for 3 phases (d 0–20, d 21–32, and d 33–55). Rye and barley were added at 30% and 15%, respectively. The enzyme (combination of Cibenza CSM and DE200, Novus International Inc., St. Charles, MO) is a blend of endo-xylanase, β-glucanase, α-galactosidase, and β-mannanase. Feed was withdrawn from all pigs from d 21–23 and d 28–30 to create a minor gut health challenge. Gain:feed was improved with enzyme supplementation in phase I and phase III in both corn (7 and 9%, respectively) and rye and barley diets (9 and 13%, respectively, $P < 0.05$). The presence of enzyme tended to improve daily weight gain (443 vs. 480 g, $P = 0.08$) and body weight in phase I (18.8 vs. 19.6 kg, $P = 0.08$) regardless of diet type. Daily feed intake was significantly decreased with enzyme supplementation in phase III (2.353kg vs. 2.209 kg, $P = 0.03$), perhaps due to improved energy utilization. No differences were observed on cecum viscosity, *E. coli*, *Clostridium*, and coliform counts among treatments ($P > 0.10$). Total aerobic counts were significantly reduced with enzyme supplementation at all 3 time points ($P < 0.02$). On d 55, cecum lactic acid bacteria counts were increased ($P < 0.01$) while pH was decreased (6.21 vs. 5.59, $P < 0.01$) with enzyme supplementation. Decreased intestinal pH is beneficial for controlling pathogenic bacteria in general. No significant effects of diet type or interaction of diet type and enzyme supplementation were observed on either growth performance or gut health measurements. In conclusion, enzyme improved feed utilization and weight gain in both corn and rye and barley diet in pigs. The benefits are partially associated with improved gut health.

Key Words: NSP, enzyme, swine

757 Effect of increasing concentrations of a novel β-glucanase to a constant β-mannanase in corn-soybean meal-corn distillers dried grains with solubles (DDGS) diets on grower pig performance. Z. Rambo[1], J. Ferrel*[2], D. Anderson[2], D. Kelly[1], and B. Richert[1], *[1]Purdue University, West Lafayette, IN, [2]ChemGen, Gaithersburg, MD.*

Two-hundred 52 pigs (initial BW = 26.0 kg ± 0.45) were used to evaluate the effect of adding a β-glucanase (ENz1) to a β-mannanase (ENz2) enzyme, titrated at 5 concentrations, in a corn-soybean meal-DDGS diet on pig growth and feed efficiency during the grower period. Pigs were allocated in a randomized complete block design of mixed sex pens, stratified by sex, litter and initial BW to 6 treatments with 7 pens/treatment. Dietary treatments were: T1-Negative Control (no enzymes), treatments 2–6 had a constant level of Enz2 at 0.16 MU/kg plus increasing levels of ENz1; T2 = 0 MU/kg, T3 = 0.044 MU/kg, T4 = 0.088 MU/kg, T5 = 0.132 MU/kg, and T6 = 0.176 MU/kg of ENz1. Pigs were fed 2 dietary phases (25 and 30% DDGS, respectively), each 3 weeks in duration. Individual BW and pen feed disappearance were recorded weekly. Phase 1 ADG was greater for T5 compared with T1 ($P < 0.05$) with all other treatments being intermediate (743, 768, 780, 768, 782, 772 g/d; T1-T6, respectively). Phase 1 G:F tended to linearly ($P < 0.07$) increase with increasing levels of ENz1 (0.449, 0.449, 0.456, 0.465, 0.473, 0.465, respectively). During phase 2 there were no differences in ADG among treatments; however, G:F linearly ($P < 0.02$) improved with increasing levels of Enz1 (0.372, 0.367, 0.378, 0.371, 0.382, 0.385, respectively). Overall ADG was greater for T3, T5, T6, compared with T1 ($P < 0.05$) with T2 and T4 being intermediate (788, 801, 825, 810, 817, 818 g/d; respectively). Overall G:F linearly ($P < 0.01$) improved with increasing levels of Enz1 (0.400, 0.397, 0.407, 0.405, 0.416, 0.414, respectively). Final BW was greater for T3 compared with T1 with all other treatments being intermediate (59.5, 60.2, 61.2, 60.6, 60.8, 60.8 kg, respectively). Increasing levels of β-glucanase (Enz1) linearly improved feed efficiency (4.8%) during the grower period and numerically improved ADG and final BW with corn-soybean meal diets containing up to 30% DDGS.

Key Words: swine, β-glucanase, β-mannanase

758 Evaluating nutritive value of pepper *Capsicum annuum* and garlic *Allium sativum* on performance, egg trait and serum parameters of old layers.

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This study was conducted to investigate the effects of garlic powder and dried pepper on the performance, egg traits, egg cholesterol and serum parameters of laying chickens. A 10-wk study was carried out using 90 ISA brown layers that have laid eggs for 2 years. The diets were formulated such that diet I with 0% pepper and garlic served as the control, while diets II and III had 4g/kg of dried pepper and powdered garlic, respectively. The layers were divided into 3 groups fed on these diets and replicated thrice. Data were analyzed by ANOVA using a completely randomized design. The results showed that there were no differences ($P > 0.05$) among the dietary treatments in feed consumption and feed efficiency; layers receiving garlic powder had better numerical values as compared with pepper and control. There were improvements ($P < 0.05$) in egg albumen index and Haugh unit of garlic-fed layers. There was also a reduction ($P < 0.05$) in egg yolk cholesterol concentration of layers fed the garlic-supplemented diet compared with the pepper and control diets. Serum total protein of garlic-fed layers increased ($P < 0.05$), while blood glucose and cholesterol levels decreased ($P < 0.05$). We concluded that garlic improved performance characteristics and may increase egg shelf life as indicated by egg quality measurements.

Key Words: garlic powder, dried pepper, layers

759 Defatted algae biomass may replace one-third of soybean meal in diets for laying hens.

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Although soybean meal is a commonly-used source of feed protein for laying hens and other food-producing animals, it is very expensive and limited in supply. Microalgae have recently been explored as a new exciting source of biofuel, and the residual biomass contains a good amount of protein and other nutrients. The present study was conducted to determine whether defatted algal biomass from biofuel production (Cellana, Kailua-Kona, HI) could replace a portion of soybean meal or a combination of corn and soybean meal in diets for laying hens. A total of 100 ISA Babcock White Leghorn laying hens (47 weeks old, *Gallus gallus domesticus*) were randomly assigned to 4 dietary treatments. There were 5 replicates for each treatment and each replicate consisted of 5 individually caged hens. The 4 experimental diets included a corn-soybean meal basal diet (BD), the BD with 7.5% defatted algae and the 5 most limiting amino acids substituting for 7.5% soybean meal, and the BD with 7.5% or 15% defatted algae substituting for soybean meal and corn. During the 8-week experiment, hens fed 15%, but not 7.5% defatted algae had lower ($P < 0.05$) egg production rate (−12%) and daily feed intake (- 9 g) than those fed the BD. There was no significant difference in egg weight (58–61g), shell strength (33–35 N), and shell specific gravity (1.08) or activities of plasma alanine aminotransferase (24–33 U/L) and alkaline phosphatase (112–155 U/mL) among the 4 dietary treatment groups at wk 4 and(or) wk 8. The inclusion of defatted algae tended to decrease the lightness (L value) and yellowness (b value) of the egg yolk color ($P < 0.05$), but increased the redness (a value; $P < 0.05$). In conclusion, it was feasible to substitute 7.5% defatted algae for soybean meal or for a combination of corn and soybean meal in the diets of laying hens without adverse effects on their health or egg production. Supported in part by a USDA/DOE Biomass R&D Initiative grant.

Key Words: algae, biofuel, laying hens

760 Effects of various replacements of corn and soy by defatted microalgal meal on growth performance and biochemical status of weanling pigs.

K. K. Lum,* K. R. Roneker, and X. G. Lei, *Cornell University, Ithaca, NY.*

Marine microalgae biomass derived from biofuel production has great potential as a nutrient-rich alternative feed protein or energy source. Our objective was to evaluate effects of partial replacements of corn and soybean meal by defatted algal meal in diets for young pigs on their overall growth performance and biochemical status. Weanling pigs (BW = 13.4 ± 1.6 kg; n = 8/treatment) were individually housed and fed for 6 wk with 1 of 4 diets: corn-soybean meal basal diet (BD), BD with 7.5% defatted algal meal (provided by Cellana, Kailua-Kona, HI) in replacing 7.5% soybean meal, and BD with 7.5 and 15% defatted algal meal in replacing 7.5 and 15% corn and soybean meal in combination, respectively. Data were analyzed using one-way ANOVA as complete random design with or without time-repeated measurements. Compared with those fed the BD, pigs fed 15% defatted algal meal had 9% lower final BW ($P < 0.05$) and 12% lower overall ADG ($P < 0.05$). The substitution of 7.5% defatted microalgal meal for the same amount of soybean meal also resulted in 12% lower overall ADG ($P < 0.05$) than the control. However, ADFI, gain/feed efficiency, and the percent body lean yield predicted by ultrasound scans at wk 6 were not significantly affected by the dietary treatments. Likewise, there were no treatment differences in the biweekly analyses of plasma biochemical indicators including urea nitrogen concentration, alanine aminotransferase, and alkaline phosphatase activities, and total triglycerides, cholesterol, and nonesterified fatty acid concentrations. In conclusion, weanling pigs manifested comparable growth performance and plasma biochemical status in responses to the replacement of 7.5% soybean meal and corn by defatted microalgal biomass, but failed to tolerate a higher level (15%) of such replacement, or the sole replacement of 7.5% soybean meal. Supported in part by a USDA/DOE Biomass R&D Initiative grant.

Key Words: microalgae, pigs, nutrition

761 Effects of a blend of essential oils on post-weaning growth performance of piglets.

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As a consequence of the ban on antibiotic growth promoters (AGPs) in several countries, piglets have been exposed to different challenges that have resulted in a notable deterioration in productive performance. The aim of this study was to investigate the effects of a phytogenic feed additive (PFA) on piglet performance and to evaluate it as an alternative to AGPs. A total of 360 weanling crossbred (Duroc × Yorkshire × Landrace) pigs with an initial body weight of 6.7 kg, weaned at 23 d of age, were used in 28-d growth feeding experiment. Pigs were randomly allocated to 1 of 3 experimental treatments. Each treatment had 30 pigs per pen and 4 replications (pens). Treatments were negative control (commercial diet based on corn and soybean meal), positive control (commercial basal diet + 100 mg/kg apramycin/ton), and PFA (commercial diet + 125 mg/kg Biomin P.E.P. 125). Two-phase feeding programs were implemented with phase 1 diet fed from 0 to 14 d and phase 2 diet fed from 14 to 28 d post-weaning. All experimental diets were fed in crumbled feed. The data set was analyzed using the GLM procedure of SAS (1998) with pen as experimental unit by adjusting initial body weight. Through the experimental period from d 1 to d 28 post-weaning, performance parameters including body weight, body weight gain, feed intake, feed conversion ratio and mortality were recorded. The results obtained revealed that piglets treated with PFA had 1 to 7% higher body weight than the negative control group and the AGP group respectively. Piglets treated with the PFA showed significantly higher ($P < 0.05$) average daily gain than the AGP group while the difference to the negative control group was numerically higher. At d 28, there were no significant differences in feed intake between the groups. Dietary supplementation with the PFA attained significantly lower ($P < 0.05$) feed conversion ratio values than the AGP supplemented group and insignificant values compared with the negative control group. No mortality was observed in the PFA group while dietary supplementation with AGP insignificantly ($P > 0.05$) reduced mortality by about 32%. The efficacy of any feed additive is judged by its potential to improve mainly feed utilization (feed conversion ratio) and other physiological parameters. The present study showed performance promoting effects in piglets fed the PFA, indicating its potential use as growth enhancer and as successful alternative to AGP piglet rations.

Key Words: phytogenics, growth performance, piglets

762 Effects of a dietary antioxidant blend on growth and plasma markers of oxidative status in pigs fed an oxidative stress diet.

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Crossbred barrows (n = 100, 10.9 kg BW, 36 ± 2 d of age) were used to assess inclusion of a commercial antioxidant (AOX; Agrado Plus, Novus International, St. Charles, MO) to diets formulated to increase oxidative stress. There were 5 pens of 4 pigs each in 5 treatments that included: 1) a negative control (NC) oxidative stress diet containing oxidized soy oil (5%) and a source of polyunsaturated fatty acids (PUFA, 10%) with no added vitamin E (VE) and no AOX; 2) the NC diet with 11 IU/kg of added VE; 3) the NC diet with AOX providing a proprietary antioxidant blend of ethoxyquin and propyl gallate; 4) the NC diet with AOX and VE; and 5) a standard control diet (SC) with no oxidized soy oil or PUFA source. Growth was assessed and plasma collected at defined time points throughout the 118 d study. No treatment effects were observed in performance by d 25 ($P > 0.33$), but at d 82 BW for pigs fed the NC, VE, AOX, AOX+VE and SC diets were 48.4, 69.5, 82.3, 81.7 and 85.3 kg respectively (NC pigs lower than all others, VE pigs lower than AOX, AOX+VE and SC, $P < 0.05$). At d 82, pigs fed the NC diet were switched to the SC diet due to very poor animal condition resulting in some recovery such that by d 118, BW for the respective treatments were 83.3, 92.9, 127.3, 130.6 and 135.1 kg, for NC/SC, VE, AOX, AOX + VE, and SC, diets respectively (AOX, AOX+VE and SC pigs greater than NC/SC and VE pigs, $P < 0.05$). Plasma concentrations of thiobarbituric acid reactive substances (TBARS) and carbonyl were consistent with growth data, being elevated ($P < 0.05$) in the NC compared with the SC pigs at d 55 but corrected to a level not different from the SC pigs at d 118. At d 118, TBARS (μM/mL) was 2.76, 10.56, 4.21, 4.10 and 2.33 and carbonyl (nmol/mL) was 25.94, 71.53, 24.21, 21.31 and 19.24 for the NC/SC, VE, AOX, AOX+VE and SC fed pigs, respectively, with both markers elevated in the VE pigs compared with all other treatments ($P < 0.05$). In the oxidative stress model used in this study, dietary addition of AOX or AOX plus VE was effective in improving growth and plasma markers of oxidative stress, but VE was not.

Key Words: pigs, oxidative stress, antioxidant

763 Effects of eubiotics (VevoVitall, Crina Piglets, Cylactin ME10) supplementation on growth performance, nutrient digestibility, fecal noxious gas emission, and fecal microbial shedding in weanling pigs.

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A total of 150 weanling pigs [(Landrace × Yorkshire) × Duroc, BW = 8.86 ± 0.43 kg] were used in a 42-d trial to evaluate the effects of eubiotics on growth performance, apparent total tract digestibility (ATTD), fecal microbial shedding, and fecal noxious gas emission. Pigs were randomly distributed into 1 of 5 dietary treatments on the basis of BW and litter. Each treatment had 6 replicate pens with 5 pigs per pen. Dietary treatments were as follows: T1, basal diet; T2, T1 + 0.5% VevoVitall + 0.01% Crina Piglets; T3, T1 + 0.5% VevoVitall + 0.007% Cylactin ME10; T4, T1 + 0.3% VevoVitall + 0.01% Crina Piglets; T5, T1 + 0.3% VevoVitall + 0.007% Cylactin ME10. VevoVitall is an ultrapure grade of benzoic acid, Crina Piglets contains around 10% essential oils (thymol, eugenol, and piperine), and Cylactin ME10 contains 1.0 × 10^{10} cfu/g of *Enterococcus faecium* NCIMB 10415. During 8–21 d, ADG and G/f in T2 and T3 treatments were improved ($P < 0.05$) compared with T1 and T5 treatments. Overall, pigs fed the T2 diet had greater ($P < 0.05$) ADG and G/f than those fed the T1 diet. Pigs fed the T2 diet significantly increased ($P < 0.05$) the ATTD of DM compared with those fed the T1 diet at d 21, while the ATTD of N in T2, T3, T4 treatments was increased ($P < 0.05$) compared with T1 treatment. The fecal *Lactobacillus* counts were increased ($P < 0.05$) by T2 treatment compared with other treatments, whereas the fecal *E. coli* population was decreased ($P < 0.05$) in T2 and T3 treatments compared with T1, T4, and T5 treatments. All the diets supplemented with eubiotics decreased ($P < 0.05$) the fecal NH_3, total mercaptans, H_2S emission compared with T1 treatment. Results indicated that 0.5% VevoVitall + 0.01% Crina Piglets could improve the growth performance, increase the fecal *Lactobacillus* population, decrease *E. coli* counts, as well as reduce fecal noxious gas emission in weanling pigs.

Key Words: eubiotics, noxious gas emission, weanling pigs

Physiology and Endocrinology: Nutritional Physiology

764 mRNA expression of a novel adipokine (pigment epithelium-derived factor, PEDF) in various tissues from dairy cows receiving supplements with or without conjugated linoleic acids (CLA). B. Saremi*[1], S. Winand[1], S. Dänicke[2], J. Pappritz[2], D. von Soosten[2], H. Sauerwein[1], and M. Mielenz[1], *[1]Institute of Animal Science, Physiology & 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.*

Pigment epithelium-derived factor (PEDF) is a recently discovered adipokine, a secreted glycoprotein belonging to the non-inhibitory serpin group; it is one of the most abundant proteins secreted by human adipocytes and is related to obesity, insulin resistance and inflammatory signaling. To our knowledge, no information is available on bovine PEDF expression and functions. Herein, CLA effects on PEDF mRNA abundance (Ab) were tested in tissues of dairy cows ante and postpartum (a.p., p.p.). In 2 trials, Holstein cows were allocated to a CLA (Lutrell, BASF, Germany) or control (Silafat, BASF) fat supplement at 100 g/day from d 1 to 182 p.p. in trial 1 and d 1 to 105 p.p. in trial 2. Trial 1: 21 multiparous cows at d 21 a.p. and d 1, 21, 70, 105, 182, 196, 224, 252 p.p. were biopsied from tail head adipose tissue (AT) and liver. In trial 2, 25 heifers were slaughtered on d 1 (n = 5; control), 42 and 105 p.p. (n = 5 per each group) and 3 visceral (Vc; mesenterial, omental and retroperitoneal) and 3 subcutaneous (Sc; sternum, withers and tail head) AT, liver, mammary gland, and muscle tissues were sampled. PEDF mRNA was quantified by qPCR. Data were analyzed using mixed model for trial 1 and GLM or nonparametric test for trial 2 (SPSS 17, $P < 0.05$). In trial 2, liver had 34.3, 15.1, 6.8 and 2.9 fold higher PEDF Ab than muscle, mammary gland, VcAT, and ScAT respectively. VcAT had 2.4 fold lower PEDF Ab than ScAT (trial 2). Liver PEDF Ab did not change with time in both trials. In AT, time-dependent changes were solely observed in the control group in which PEDF Ab increased after parturition, decreased until d 200, and increased thereafter (d 231 and 252). CLA effects were limited to trial 1 in which PEDF Ab in ScAT did not show the p.p. and late lactation increases of control cows. In trial 2, time-dependent changes were limited to mesenterial fat and to ScAT from sternum and withers with lowest values each on d 1. Our data confirm expression of PEDF for bovine AT with consistently higher Ab in Sc than in VcAT. Moreover, we identified the liver as a major site of PEDF expression.

Key Words: pigment epithelium-derived factor (PEDF), CLA, liver and fat

765 Effects of long-term hyperketonemia on metabolism and performance in lactating dairy cows. M. Zarrin*[1,2], L. De Matteis[1,3], M. C. M. B. Vernay[1], O. Wellnitz[1], H. A. van Dorland[1], and R. M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland, [2]Department of Animal Science, Yasouj University, Yasouj, Iran, [3]Istituto di Zootecnica, Università Cattolica S, Cuore, Piacenza, Italy.*

Hyperketonemia in dairy cows occurs frequently in early lactation. Previous studies observed that increasing plasma BHBA concentration decreases glucose levels in pigs and ewes through hormonal mechanisms or possible inhibition of gluconeogenesis. In cows, this has not yet been investigated. The objective was to study effects of a BHB infusion for 48 h in mid lactating dairy cows on metabolism and performance. Thirteen mid lactation dairy cows were randomly assigned to one of 2 treatments, including an intravenous infusion with Na-DL-β-OH-butyrate (1.7 mol/L) at a rate of 8.5 ± 0.6μmol/kg BW/min (HyperB, n = 5), or an infusion with a 0.9% saline solution (20 mL/h; NaCl, n = 8). The infusions started from 0900 h and continued to 0900 h 2 d later by use of a permanent catheter in the jugular vein. Blood was sampled before and on an hourly basis during the infusions for metabolite and hormone levels. In liver, mRNA transcripts of pyruvate carboxylase, mitochondrial phosphoenolpyruvate carboxykinase, and glucose-6- phosphatase were measured by real-time RT-PCR. GAPDH and ubiquitin were housekeeping genes. Cows were fed hay and concentrate and were milked twice daily throughout the study. Changes (difference between before and after 48h infusion) in the measured parameters were evaluated by ANOVA with treatment as fixed effect. The plasma BHB concentration reached and maintained during the study period in HyperB cows was 1.7 ± 0.2 mmol/L (mean ± SE) compared with 0.59 ± 0.02 mmol/L for NaCl cows. The change in feed intake, milk and ECM yield was not different between 2 groups. BHB infusion reduced the plasma glucose concentration (3.47 ± 0.11mmol/L) in HyperB compared with NaCl cows (4.11 ± 0.08mmol/L; $P < 0.05$). The other plasma factors were unaffected. In the liver, changes in mRNA abundance for the selected genes were similar between HyperB and NaCl cows. Results demonstrate that intravenous infusion of BHB decreased plasma glucose concentration in dairy cows but this decrease was not explained by alterations in insulin or key enzymes related to hepatic gluconeogenesis at a molecular level.

Key Words: hyperketonemia, metabolism, gluconeogenesis

766 Tissue-dependent expression of G-protein couple receptor (GPR) 40, 41, 43, 109A mRNA in early lactation dairy cows treated with conjugated linoleic acids (CLA) and long-chain fatty acids (LCFA). B. Saremi*[1], H. Sauerwein[1], D. von Soosten[2], S. Dänicke[2], and M. Mielenz[1], *[1]Institute of Animal Science, Physiology & 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 receptors GPR40, 41, 43, and 109A are a group of transmembrane receptors related to energy homeostasis through regulation of insulin and glucagon secretion, leptin release, adipogenesis and lipolysis, respectively. LCFA and CLA as ligands of GPR40 are insulinotropic in humans. We investigated GPRs mRNA abundance (Ab) in dairy cows tissues considering effects of CLA. From 25 heifers, 5 were slaughtered on d 1 postpartum (p.p.). Remaining heifers were randomly allocated to a CLA (Lutrell pure, BASF, Germany, n = 10) or a control fat supplement containing LCFA but without CLA (Silafat, BASF, n = 10) each at 100 g/d. Five animals per group were slaughtered at d 42 or 105. Subcutaneous (ScAT; sternum, withers and tail head) and visceral (VcAT; mesenterial, omental and retroperitoneal) adipose tissues, liver, mammary gland, and muscle were sampled. The mRNA was quantified by qPCR. GLM or nonparametric tests were used for statistical analysis (SPSS 17; $P < 0.05$). GPR40 was the only receptor which had a higher Ab in CLA group in liver ($P < 0.065$), omental and retroperitoneal AT. GPR41 and 43 Ab were higher (3.3 and 3.5 fold respectively) in VcAT in comparison to ScAT. GPR109A Ab was 1.4 and 33 fold higher in ScAT vs. VcAT and in AT vs. the mean of liver, muscle and mammary gland. Liver and mammary gland exhibited similar and muscle showed a lower GPR43 Ab in comparison to ScAT. Liver and muscle had the highest and lowest GPR40 Ab respectively, with the exception of equality of liver to ScAT from withers. GPR40 Ab increased from d 1 to d 42 and 105 p.p. in AT and was stably expressed in muscle and liver. GPR41 Ab decreased from d 1 and 42 to d 105 p.p. GPR43 Ab increased from d 1 to d 42 and 105 in ScAT and was consistently expressed in VcAT and non fat tissues. Different behavior of GPR40 Ab between CLA and LCFA in bovine AT and liver raises the differential regulation of the receptor in bovine vs. human. Differential expression of the GPRs in different fat or nonfat tissues might be a hint to their tissue specific roles.

Key Words: GPR40-43 and GPR109A, CLA, dairy cow

767 Is calcitonin involved in hypocalcemia of periparturient cows? E. M. Rodríguez*[1], A. Bach[1,2], M. Devant[1], and A. Arís[1], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain.*

Evidence for an association of calcitonin (CALC) in hypocalcemia in the cow is inconsistent: whereas some studies point out that this hormone secretion is increased, others state that it is diminished. The objective of this study was to elucidate the involvement of CALC on periparturient hypocalcemia establishing a comparative profile of the changes in calcium-regulating factors under high and normal dietary Ca supplies. Sixteen Holstein multiparous cows (674 ± 22.8 kg of BW and 3.9 ± 0.29 y of age) were distributed into 2 groups: a diet containing 1.64% Ca (HIGH) or a diet containing 0.87% Ca (CTR) during 3 wk before calving. Feed intake was individually recorded and blood samples were obtained daily from −7 to 7 d from parturition. Milk yield was recorded daily during 3 weeks after calving. Calcium was analyzed in plasma using a colorimetric method (SPINLAB 100) and in milk using atomic absorption spectrophotometry. Plasma parathyroid hormone (PTH) and 1,25-dihydroxyvitamin-D (1,25-vitD) were analyzed using ELISA, and plasma CALC was determined by RIA. Data were analyzed with a mixed-effect model with repeated measures. No differences in DMI were observed between groups. During the first 7 d after calving, milk yield tended ($P = 0.06$) to be greater in CTR than in HIGH cows (23.9 vs. 19.4 ± 1.56 L, respectively) and milk Ca concentration tended ($P = 0.08$) to be lower in CTR than in HIGH cows (1482 vs. 1627 ± 57.4 mg/kg, respectively), although total milk Ca production (31.7 ± 2.91g/d) did not differ between treatments. Seventy 5 percent of the cows incurred subclinical hypocalcemia (blood Ca concentrations <8 mg/dL). During hypocalcemia the CALC secretion was not increased and the hormone was maintained under basal concentrations. Blood PTH concentrations increased at d 1 postpartum as a reaction to Ca loss and 1,25-D concentrations increased at d 2. In conclusion, this study shows that CALC secretion is not increased on the hypocalcemic period of cows and as expected, the main Ca reduction was followed by an increase in PTH and 1,25-D secretion.

Key Words: hypocalcemia, calcitonin, parathyroid hormone

768 Reproductive performance of Ossimi rams fed biologically treated rations. E. B. Abdalla*[1], F. R. Abed El-Aziz[2], H. M. Gado[1], A. E. Hassan[2], and M. S. Ziada[3], *[1]Ain Shams University, Cairo, Egypt, [2]Anim. Prod. Res. Inst., Agric. Res. Center, Ministry of Agric., Giza, Egypt, [3]Anim. Reprod. Res. Inst., Agric. Res. Center, Ministry of Agric, Giza, Egypt.*

This experiment was conducted on 20 adult Ossimi rams (1–2 years old and averaged 44–48 kg live body weight) to evaluate the dietary supplementation of ZAD compound (patent product contains cellulases, xylanases, protease and α amylase) to improve overall nutritional status and consequently will improve semen quality characteristics in sheep. Rams were randomly divided into 2 equal groups (10 for each). The first group (G1) served as control and was fed rice straw without supplementation, while the second group (G2) was fed rice straw treated with ZAD compound. All rams received concentrate feed mixture (CFM) to cover 100% of their maintenance energy. Forage and CFM were adjusted biweekly according to live body weight changes and roughage to CFM ratio was 60:40 during the experimental period. The experimental feeding period lasted for 8 mo, the first 2 mo were a preliminary period and the other 6 mo were the main period of semen collection (once a week). General Linear Model (GLM) procedure of SAS, ANOVA and LSD test were used for statistical analysis. Results revealed that overall mean of semen characteristics were 0.54 vs. 1.21 mL, 77.81 vs. 85.18%, 2.15 vs. 2.85 × 10^9/mL, 75.90 vs. 78.05%, 12.10 vs. 9.68% and 5.20 vs. 5.91 for ejaculate volume, advanced motility, sperm cell concentration, live sperm, abnormal sperm and pH value of semen for control and treated group, respectively. Body weight changes were promoted ($P < 0.05$) by treatment as compared with the control group. Blood plasma concentrations of total protein, albumin and globulin were higher ($P < 0.05$) in G2 (8.22, 2.82 and 5.40 g/dL) as compared with those corresponding values in G1 (5.59, 2.18 and 3.41 g/dL, respectively). Blood plasma levels of thyroxine (T4) hormone showed a tendency of increases in G2 than in G1 (5.21 vs. 4.65 ng/dL). Similarly, triiodothyronine (T3) and testosterone concentrations were significantly higher in G2 than in G1 (164.8 vs. 138.3 ng/mL). Results of the present study indicated that feeding rams on ration containing ZAD compound had a beneficial effect on their semen quality characteristics, including sperm motility %, sperm cell concentration (× 10^9/mL), live sperm% and normal sperm % comparing with the control group .

Key Words: ZAD, hormone, semen

769 The effect of yeast cell wall supplementation on the metabolic responses of crossbred heifers to endotoxin challenge. N. C. Burdick*[1], T. R. Young[2], J. A. Carroll[1], J. R. Corley[3], R. J. Rathmann[2], and B. J. Johnson[2], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]Texas Tech University, Department of Animal and Food Sciences, Lubbock, [3]Lesaffre Feed Additives, Milwaukee, WI.*

This study examined the effect of feeding yeast cell wall (YCW) products on the metabolic responses of newly-received heifers to endotoxin (lipopolysaccharide; LPS) challenge. Heifers (n = 24; 218.9 ± 2.4 kg) were obtained from commercial sale barns and transported to the Texas Tech Univ. Beef Center. Heifers were separated into treatment groups receiving a Control Diet (C; n = 8), YCW A (2.5 g/hd per day; n = 8) or YCW C (2.5 g/hd per day; n = 8) and were fed for 52 d. Heifers were weighed on d 0, 14, 36, 38, and 52. On d36 heifers were fitted with indwelling jugular catheters and moved into a barn with individual stalls. On d37 heifers were challenged i.v. with LPS (0.5 μg/kg BW) and blood samples were collected every 0.5 h from −2 to 8 and again at 24 h relative to LPS challenge (0 h). Serum was isolated and stored at −80°C until analyzed for glucose, insulin, nonesterified fatty acid (NEFA), and blood urea nitrogen (BUN) concentrations. Heifer weight increased from d0–36 and from d38–52 ($P < 0.01$), but was not affected by treatment ($P > 0.32$). Post-LPS YCW A (−6.0 ± 0.9 kg) lost more weight (from d36–38) than C (−2.4 ± 0.9 kg) and YCW C (−4.2 ± 0.9kg; $P = 0.04$). Post-LPS glucose increased ($P < 0.001$) and was less in YCW A (98.5 ± 2.5 mg/dL) than C (105.6 ± 2.4 mg/dL) and YCW C (109.5 ± 2.4 mg/dL; $P < 0.01$). Pre-LPS insulin was greater in YCW A (0.80 ± 0.06 ng/mL) and YCW C (0.087 ± 0.06 ng/mL) than C (0.44 ± 0.06 ng/mL; $P < 0.01$). Post-LPS insulin increased ($P < 0.01$) with YCW C (0.95 ± 0.04 ng/mL) and YCW A (0.71 ± 0.05 ng/mL) having greater insulin than C (0.59 ± 0.04 ng/mL; $P < 0.001$). Pre-LPS NEFA tended ($P = 0.07$) to be less in YCW C (0.14 ± 0.01 mmol/L) than C (0.18 ± 0.01 mmol/L) and YCW A (0.17 ± 0.01 mmol/L). The difference in NEFA was significant post-LPS (0.18 ± 0.01, 0.21 ± 0.01, and 0.21 ± 0.01 mmol/L respectively for YCW C, C, and YCW A). Pre-LPS BUN was greater in YCW A (8.2 ± 0.3 mg/dL) than C (6.9 ± 0.3 mg/dL; $P = 0.03$). Post-LPS BUN was greater in YCW A (8.9 ± 0.2 mg/dL) than C (8.2 ± 0.2 g/dL) and YCW C (8.1 ± 0.2 mg/dL; $P < 0.01$). These data indicate that certain YCW products can enhance the energy metabolism during an immune challenge without causing lipolysis or muscle catabolism.

Key Words: cattle, metabolism, yeast

770 Effect of sward condition on metabolic endocrinology during the early postpartum period in primiparous grazing dairy cows and its association with productive and reproductive performance.

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The effect of differential sward herbage allowances and a total mixed ration (TMR) management on milk production, body condition, first postpartum ovulation and endocrine/metabolic parameters were investigated. Primiparous dairy cows (n = 44) were randomly assigned to one of the following grazing treatments (n = 11 each): high (HA, 30 kg DM/cow/d), medium (MA, 15 kg DM/cow/d) and low herbage allowance (LA, 5 kg DM/cow/d), and a TMR group fed ad-lib. Non esterified fatty acids (NEFA), β-hydroxybutyrate (BHB), cholesterol, protein, albumin, urea, insulin, insulin-like growth factor-I (IGF-I) and leptin were determined in plasma every 15 d. Progesterone was determined 2 times per week after parturition to determine first ovulation. TMR group had higher milk production than the HA and MA groups which did not differ, which were in turn greater than LA cows. Overall, the TMR and HA groups had a greater BCS, protein, albumin and urea concentrations than MA and LA groups, suggesting a better energy balance. While metabolic differences were observed among HA cows and MA cows early in the pospartum period (15–30 dpp), differences among HA and LA cows were observed later on (45–60 dpp). While IGF-I concentrations increased after calving in all groups, no increases were found in LA group, probably due to the energy restriction due to the nutrients offered. Greater insulin and IGF-I concentrations were found in the TMR group, which is consistent with the higher nutrient density offered to this group. The probability of cyclicity one month after calving was lower in MA cows than TMR and HA cows, which is consistent with the higher NEFA and lower urea concentrations found in this period. The lowest probability of first ovulation throughout the study was observed in LA cows. This study shows that different nutritional treatments affected several metabolites and hormones that reflect the nutritional partitioning toward milk and reproductive processes.

Key Words: dairy, metabolism, endocrinology

771 Association of biomarkers of stress, inflammation, and negative energy balance with milk yield and reproductive performance in Holstein dairy cows.

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The objectives were to evaluate the association between peripartum concentrations of fecal cortisol metabolites (11,17-dioxoandrostane; 11,17-DOA), plasma haptoglobin (Hp), and nonesterified fatty acids (NEFA), and milk yield and reproductive performance. Blood and fecal samples were collected weekly from 412 Holstein dairy cows from wk −3 through wk +1 relative to calving. Pregnancies by 150 DIM and projected 305ME milk yield based on the 3rd DHI test day (102 DIM) were measured. A range of concentration cutpoints were evaluated for each biomarker; associations of these cutpoints with 305ME or risk of conception were assessed using mixed effects or semiparametric proportional hazards models, respectively. Associations between the biomarkers and reproductive performance were strongest for primiparous (PP) cows during wk −1 or +1 relative to calving. Among multiparous (MP) cows, no biomarker measured during wk −1 or +1 was associated with reproductive performance ($P \geq 0.2$). Primiparous cows with Hp >0.4 g/L, 11–17-DOA >2300 ng/g fecal DM, or NEFA >0.40 mEq/L during wk −1 had a 41%, 42%, or 42% decreased risk of conception, respectively ($P \leq 0.05$), compared with PP cows below these cutpoints. Primiparous cows with Hp >1.3 g/L or NEFA >0.45 mEq/L during wk +1 had a 41% or 39% decreased risk of conception, respectively ($P = 0.02$). Associations between Hp and 11,17-DOA with 305ME milk yield were strongest when these analytes were measured during wk +1; however, wk −1 NEFA concentrations were a better predictor of milk yield than wk +1 NEFA. Postpartum Hp >1.1 g/L was associated with 947 kg lower 305ME milk yield for both PP and MP cows ($P = 0.001$). For MP cows only, 11,17-DOA >400 ng/g fecal DM during wk +1 was associated with a 663 kg lower 305ME milk yield ($P = 0.03$). Primiparous and MP cows with NEFA >0.55 mEq/L during wk −1 had a 1360 kg lower projected 305ME milk yield ($P = 0.002$). Biomarkers of stress, inflammation, and negative energy balance around calving can be used to identifying opportunities to improve milk yield and reproductive performance.

Key Words: biomarkers, milk yield, reproduction

772 Serum amyloid A3 (SAA3) mRNA in liver and adipose tissue of dairy cows supplemented with or without conjugated linoleic acids (CLA): A whole lactation cycle study.

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Serum amyloid A3 (SAA3) is an acute phase protein (APP) mainly expressed extrahepatically. Bovine adipose tissues (AT) are immune responsive and express SAA3. In monogastrics, CLA have anti-inflammatory and anti-lipolytic effects. We hypothesized that CLA might exert analogous effects in bovine tissues and be related to AT metabolism. Holstein Frisian cows received a CLA (Lutrell pure, BASF, Germany, n = 11) containing 12% each of the *cis*-9, *trans*-11 and the *trans*-10, *cis*-12 CLA isomers or a non-CLA fat supplement (Silafat, BASF, n = 10) from d 1 to 182 in milk. Biopsies were collected from subcutaneous (Sc) AT from tail head and liver tissue at d 21 ante partum (a.p.) and d 1, 21, 70, 105, 182, 196, 224, 252 postpartum (p.p.). SAA3 mRNA abundance (Ab) was measured by real-time PCR in all biopsies, but in the CLA group only on d 21 a.p. and d 21, 105, 196, 252 p.p. Detection of the SAA protein in AT was done by Western blot. Statistical analyses were done using the mixed model or Pearson correlation (SPSS 17; $P < 0.05$). Typical SAA protein bands were obtained from AT. CLA had no effect on SAA3 Ab in liver and ScAT. Liver SAA3 Ab exhibited a peak at the day of parturition (8 fold higher in comparison to the mean of the other d a.p. and p.p.) but remained stable throughout all other times. In ScAT, the day of parturition was significantly different in comparison to 196 and 252 d p.p. (7.7 fold higher SAA3 Ab). Liver and ScAT SAA3 Ab were positively correlated to haptoglobin plasma concentrations and ScAT and liver haptoglobin mRNA (r ranging from 0.30 to 0.62); ScAT SAA3 Ab was positively correlated to plasma NEFA (r = 0.31) (haptoglobin and NEFA from published data). The correlation of ScAT SAA3 Ab with plasma NEFA might be related to the homeorhetic adaptation regarding to the energy requirement during lactation. The peripartal peak of SAA3 in liver and ScAT is comparable to haptoglobin as another APP. The expression of SAA protein in bovine AT is a novel finding though the relevance of individual SAA isomers remains to be clarified.

Key Words: serum amyloid A3 (SAA3), CLA, cow liver and adipose tissue

773 Responses of mammary gland metabolism to long-term manipulated plasma concentrations of insulin and glucose in lactating dairy cows. J. J. Gross,* M. C. M. B. Vernay, L. Kreipe, O. Wellnitz, H. A. van Dorland, and R. M. Bruckmaier, *Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland.*

The regulation of genes involved in mammary gland metabolism was investigated during manipulated concentrations of insulin and glucose for 48 h. Six mid-lactating dairy cows each were assigned to a hyperinsulinemic hypoglycemic clamp (HypoG), a hyperinsulinemic euglycemic clamp (EuG) and a control treatment (NaCl). Blood samples were collected before and hourly during the infusions for measurements of glucose and insulin. Mammary gland biopsies were taken immediately before and at 48 h of infusion and mRNA abundance of genes involved in the mammary gland metabolism were measured by RT-qPCR with glycerinaldehyde-3-phosphate-dehydrogenase, ubiquitin and cyclophilin as static expressed housekeeping genes. Changes in the measured parameters, and the area under the curve of plasma parameters from 24 to 48 h of infusion were evaluated by ANOVA with the treatment as fixed effect. For HypoG, insulin infusion rate (IIR) was 0.46 ± 0.02 mU/kg/min from 24 to 48 h whereas IIR for EuG was maintained constant at 0.62 mU/kg/min, and the simultaneous glucose infusion rate in EuG was 2.47 ± 0.05 mmol/kg/min. From 24 to 48 h of infusion, HypoG had a lower glucose concentration (2.25 ± 0.05 mmol/L) in comparison to EuG (3.80 ± 0.16 mmol/L) and NaCl (4.17 ± 0.10 mmol/L; $P < 0.05$); HypoG and EuG had higher insulin concentrations than NaCl (41.9 ± 8.1, 57.8 ± 7.8, and 12.2 ± 2.8 mU/L, resp.; $P < 0.05$). In mammary tissue, the mRNA abundance of glucose transporter (GLUT) 4 was decreased in EuG compared with HypoG, and that of αS1-Casein and insulin receptor was decreased compared with HypoG and NaCl, while mRNA abundance of insulin induced gene 1 and UDP-glucose pyrophosphorylase was upregulated compared with NaCl and HypoG ($P < 0.05$), while mRNA abundance of κ-Casein and acetyl-CoA-carboxylase were increased in EuG by trend ($P = 0.06$). No differences between groups were found for mRNA abundance of GLUT1, E74-like factor 5, α-lactalbumin, sterol response element binding factor 1 and fatty acid synthase. In conclusion, most differences in gene expressions of mammary gland metabolism were found between HypoG and EuG indicating the regulatory role of glucose at simultaneously elevated insulin concentrations during an increased glucose turnover.

Key Words: mammary gland, metabolism, dairy cow

774 Tumor necrosis factor-α (TNF-α) mRNA expression in early lactation in different tissues of dairy cows with a focus on different fat depots. B. Saremi*[1], H. Sauerwein[1], D. von Soosten[2], S. Dänicke[2], and M. Mielenz[1], *[1]Institute of Animal Science, Physiology & 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 pro-inflammatory cytokine TNF-α is expressed in different cell types, mainly in stimulated monocytes and macrophages. In humans, TNF-α is involved in inflammation, apoptosis, insulin sensitivity, and induction of lipolysis. The *trans*-10, *cis*-12 isomer of conjugated linoleic acids (CLA) attenuates the release of TNF-α from bovine immune cells. Therefore, we investigated possible changes of TNF-α mRNA abundance (Ab) in tissues of dairy cows in postpartum (p.p.), considering effects of CLA. From 25 heifers, 5 were slaughtered on d 1 p.p. and remaining heifers were randomly allocated to conjugated linoleic acids (CLA) (Lutrell pure, BASF, Germany, n = 10) or control fat supplementation without CLA (Silafat, BASF, n = 10) each at 100 g/d. Five animals per group were slaughtered at d 42 or 105. Subcutaneous (Sc) (sternum, withers and tail head) and visceral adipose tissue (VcAT: mesenterial, omental and retroperitoneal), liver, mammary gland and muscle tissues were sampled. Quantification of TNF-α was done by qPCR. Fat mass and NEFA were adopted from published data on the same cows. Pearson correlation, GLM or non parametric tests were used for statistical analysis (SPSS 17; $P < 0.05$). From 1 to 105 d p.p. TNF-α Ab increased in ScAT and liver and decreased in mammary gland and retroperitoneal AT (from d 1 and 42 to 105 p.p.). In omental and mesenterial AT as well as in muscle, TNF-α Ab was stably expressed. Abundance of TNF-α mRNA was not affected by CLA except at d 42 in mesenterial AT (lower Ab in the CLA group). Liver, mammary gland and muscle TNF-α Ab was 5.3, 2.5 higher and 4.4 fold lower than that in AT. Within AT, Sc sternum and omental had the highest and mesenterial and retroperitoneal had the lowest TNF-α Ab. In contrast to AT, liver TNF-α Ab was correlated negatively to fat mass and positively to blood NEFA. As in humans, TNF-α in cattle might be linked to fat mobilization. Differential expression of TNF-α throughout lactation could be associated to paracrine mechanisms related to insulin sensitivity in the analyzed tissues.

Key Words: TNF-α, liver and fat tissues, dairy cattle

Production, Management and the Environment: Environmental Quality

775 Evaluation of a feeding strategy to reduce greenhouse gas emissions from milk production: The level of analysis matters. C. E. Van Middelaar*[1], P. B. M. Berentsen[2], J. Dijkstra[3], and I. J. M. De Boer[1], [1]*Animal Production Systems Group, Wageningen University, Wageningen, the Netherlands,* [2]*Business Economics Group, Wageningen University, Wageningen, the Netherlands,* [3]*Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands.*

The dairy sector contributes to climate change through emission of greenhouse gases (GHGs): carbon dioxide (CO2), methane (CH4), and nitrous oxide (N2O). From an animal perspective, a feeding strategy with high potential to reduce enteric CH4 emission is replacing grass silage by corn silage. Increasing corn silage in the ration, however, affects the farm plan (e.g., plowing grassland for corn cropping; type of concentrate), and consequently GHG emissions along the milk production chain. The level of analysis, therefore, can affect results and conclusions. This study evaluated effects of replacing grass silage by corn silage on GHG emissions, at 3 interdependent hierarchical levels; that is, the animal, farm, and chain level. Linear programming (economic optimization), mechanistic modeling of enteric fermentation, and life cycle assessment were combined to define an economically optimal basis farm (based on an average Dutch dairy farm) and to evaluate GHG emissions at animal, farm, and chain level. Subsequently, starting from the optimal ration, corn silage was fixed at a 1 kg dry matter (DM) higher level per dairy cow per day at the expense of grass silage, and the model was used again to determine the new optimal farm plan for the farm with this strategy, and to compare GHGs emitted with the basis farm. The basis farm has 35 ha of land and a fat- and protein corrected milk (FPCM) production of 8425 kg per cow per year. Per ton FPCM, replacing grass silage by corn silage resulted in an annual emission reduction of 11.2 kg CO2-e at animal level, 13.4 kg CO2-e at farm level, and 17.6 kg CO2-e at chain level. At farm and chain level, however, land use change (i.e., plowing grassland for corn cropping) resulted in non-recurrent CO2 and N2O emissions of 845 kg CO2-e per ton FPCM. From an animal perspective, therefore, this feeding strategy offers potential to reduce GHG emissions, whereas from a chain perspective it takes up to 47 years before annual emission reductions compensate for emissions related to land use change.

Key Words: dairy farming, greenhouse gas emission, feeding strategy

776 Are high production, low GHG emission dairy farms in New Zealand possible? R. E. Vibart*[1], T. White[2], D. Smeaton[3], S. Dennis[4], R. Dynes[4], and M. Brown[1], [1]*AgResearch Limited, Grasslands Research Centre, Palmerston North, New Zealand,* [2]*AgResearch Limited, Ruakura Research Centre, Hamilton, New Zealand,* [3]*DairyNZ, Hamilton, New Zealand,* [4]*AgResearch Limited, Lincoln Research Centre, Christchurch, New Zealand.*

Dairy farming in New Zealand (NZ) is under increasing scrutiny due to growing environmental concerns. Considerable investments have been made in the search for sustainable land management options and opportunities for mitigation of greenhouse gas (GHG) emissions and nutrient losses. High production, low emission systems are hard to run, but a small number of farmers are currently doing this. The objective of this study was to identify and examine dairy farms that were highly productive and profitable while maintaining reduced GHG emissions; these systems needed to carry reduced stock numbers (i.e., less than 3.3 cows/ha). Two suitable farms in the Waikato region and 2 in the Southland region were identified. The whole-farm system models FARMAX and OVERSEER were used to examine feed flow and nutrient balances, as well as profitability, of these systems. Although differing in size, all farms tended to be reliant on homegrown feeds for most of their needs; imported feed ranged from 2.2 to 9.7% of feed consumed. Stocking rates ranged from 2.5 to 3.3 cows/ha, annual production ranged from 377 to 464 kg milksolids (MS)/cow, and operating profits ranged from 1600 to 2350 NZD/ha. Wintering policies (i.e., the use of an off-farm block of land for dry cow wintering and young stock) differed between regions; the Waikato farms used these blocks only for young stock whereas the Southland farms used them for young stock and dry cows. Despite these differences, emissions intensity ranged from 8.4 to 9.6 kg CO_2-e/kg MS, thus below the average NZ farm range (11 - 13 kg CO_2-e/kg MS). Lower emissions intensity farms tended to be more profitable and achieve greater feed conversion efficiencies (kg MS/kg DM consumed). Although low stocked dairying often requires a high level of managerial skill to be successful, these systems were associated with low emission levels and highly competitive farm profitability. These farms are commercial working examples of the opportunities for highly profitable, emission efficient farms.

Key Words: dairy, livestock emissions, profitability

777 Impact of animal density on predicted greenhouse gas emission from selected conventional, organic and grazing dairy farms in Wisconsin. M. Dutreuil*[1], V. E. Cabrera[1], R. Gildersleeve[2], C. A. Hardie[1], and M. Wattiaux[1], [1]*University of Wisconsin-Madison, Madison,* [2]*University of Wisconsin Extension, Dodgeville.*

Our objective was to test the effect of animal density (AD) on predicted greenhouse gas emission (PGE) from 3 Wisconsin farms with contrasting management systems. A combination of farm data and model-based predictions, using the Integrated Farm System Model, was used to derive PGE on 1 conventional (C), 1 organic (O) and 1 grazing (G) farm at 2 AD. The farms had a herd size of about 80 cows, 133 ha of forage land, and 0.6 cows/ha. At this low AD (LAD), the PGE were 0.53, 0.70 and 0.77 kg of PGE (CO2eq)/kg of milk for the C, O and G respectively and the main source of PGE was from housing facilities (47, 39, and 31% of total PGE on C, O and G, respectively). The indirect emission sources (manufacture or production of fuel, electricity, machinery, fertilizer, pesticides, and plastic) accounted for 21, 12, and 30% of PGE on C, O and G, respectively. Other important PGE sources at LAD were feed production on C (19%), and grazing on O and G (35 and 14%, respectively). Doubling the AD (HAD, 1.2 cows/ha of forage land) increased PGE by 22.9% on C, mainly due to 48% increase from indirect sources. The emissions from feed production and indirect sources increased by 38 and 29%, respectively on O, but the emission from grazing and housing facilities decreased by 5 and 1.3%, respectively, which led to a 6.4% net increase. Finally, PGE decreased by 3.1% on G as the net result of a decrease in emissions from manure storage and fuel consumption (41 and 20%, respectively) but 8% increase in indirect sources. These results demonstrated that the effect of AD on PGE was different on the 3 selected farms because of different farm management practices such as feeding, manure storage, and housing facilities. Although increasing AD might have a beneficial effect in reducing PGE per unit of milk on the selected G farm, results predicted a slight negative effect in the O farm and a more substantial negative effect on the C farm. Although the scope of the study is limited to the 3 selected farms, combining farm data with model-based predictions may be useful to study the changes in farm-level management practices on PGE.

Key Words: greenhouse gas, Integrated Farm System Model (IFSM), animal density

778 Life-cycle assessment of greenhouse gas emissions from dairy production in eastern Canada: A case study.

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The objective of this study was to conduct a life-cycle assessment (LCA) of greenhouse gas (GHG) emissions from a typical non-grazing dairy production system in eastern Canada. Additionally, as dairying generates both milk and meat, this study assessed methods of allocating emissions between these co-products. The LCA was conducted over 6 yr for a simulated farm in the province of Quebec. The assessment considered 65 female Holstein calves, of which 60 heifers survived to first calving at 27 mo of age. These animals were subsequently retained for an average of 2.75 lactations. Progeny were also included in the analysis, with bulls and heifers in excess of replacement requirements finished as grain-fed veal (270 kg) at 6.5 mo of age. Cattle were housed indoors, and fed forages and grains produced on the same farm. Pre-farm gate GHG emissions and removals were quantified using Holos, a whole-farm model developed by Agriculture and Agri-Food Canada and based on the IPCC Tier 2 methodologies, with modifications for Canadian conditions. The LCA yielded a GHG intensity of 0.91 kg CO_2e/kg fat and protein corrected milk yield. Methane accounted for 56% of the total emissions, of which 86% originated from enteric fermentation. Nitrous oxide accounted for 40% of total GHG emissions. Lactating cows contributed 64% of the total GHG emissions while cattle under 1 yr contributed 10%, with the veal calves accounting for 3% of this figure. Allocation of GHG emissions between meat and milk were assessed as: a) no allocation, b) economics, c) dairy vs veal animal, and d) International Dairy Federation (IDF) equation using feed energy demand for meat and milk production. Comparing emissions from dairy vs veal calves resulted in 97% of the emissions allocated to milk. The lowest allocation of emissions to milk (78%) was associated with the IDF equation. This LCA showed that the greatest reductions in GHG emissions would be achieved by applying mitigation strategies to the lactating cow, with minimal reductions being achievable in young stock. Choice of co-product allocation method can also significantly impact the relative allocation of GHG emissions to milk and meat.

Key Words: life cycle assessment, dairying, eastern Canada

779 Effects of saponin extracts, in the diet of Holstein steers or added directly to their manure, on gaseous emissions from that manure.

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A series of experiments (Exp) were conducted to investigate the effects of saponin extracts, in the diet of Holstein steers or added directly to their manure, on gaseous emissions from that manure. Saponin extracts added to the feed or manure were from *Quillaja saponaria* (quillaja saponin), *Yucca schidigera* (yucca saponin) and *Camellia sinensis* (tea saponin). During Exp 1, manure from Holstein steers fed corn and corn silage based control diet (C1) was compared with manure from steers fed control diets plus 1.5% quillaja (QS) or 0.64% yucca (YS) saponins. In Exp 2, the effect of direct application of 2% yucca (CYS, wet basis) or quillaja saponin (CQS, wet basis) to manure collected from steers fed corn and corn silage based diet (C2) on manure air emissions was investigated. In Exp 3 the effects of dietary tea saponin supplementation (TS, 0.25% DM) and direct addition (CTS, 2% wet basis) to manure collected from steers fed corn and corn-silage based diet (C3) on manure air emissions were compared in the same experiment. Gaseous emissions methane (CH_4), ammonia (NH_3), hydrogen sulfide (H_2S), nitrous oxide (N_2O) and non-methane total hydrocarbons (NMTHC) were reported. When saponin extracts were fed, daily manure CH_4 emission mass was different among treatments ($P < 0.01$; 40.97, 58.12, and 71.49 mg/d, for YS, C1, and QS, respectively). Feeding YS resulted in less ($P < 0.01$) daily manure NH_3 emission mass than C1 and QS (318.18 vs. 391.62 and 365.54 mg/d, respectively). Daily manure H2S emission mass differed ($P < 0.01$) among dietary treatments (10.63, 15.16 and 21.10 mg/d for YS, C1, and QS respectively). In Exp 2 the addition of saponin extracts directly to manure did not affect any gaseous emissions measured. Average daily emission mass of CH_4, NH_3 and H_2S was 11.92 mg/d, 424.25 mg/d and 19.36 mg/d, respectively. Overall, the results of these experiments indicate that manure-derived gaseous emissions are altered by dietary inclusion of saponins rather than by direct application to manure.

Key Words: saponin extracts, air emissions, manure

780 Effect of manure source on ammonia emission on first day of application.

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Three sources of manure were evaluated for their effect on ammonia emission on day of application. Dairy slurry (DS) with large particle solids, dairy slurry with large particle solids removed (DSSR: 0.4 cm diameter × 0.7 cm on center screen), and anaerobically digested manure with large particle solids removed (ADSR) were applied to grass plots in 2010 and 2011. The DS and AD manures were applied to 1m x 1 m grass plots in replicate on 5 occasions in 2010 and 2011. The DSSR manure was applied on 4 occasions to 1 m × 1 m plots in 2011. Measurements of ammonia were obtained at hourly intervals from the air space inside a PVC cap dome (10 cm diameter × 10 cm height) to determine relative loss of ammonia from each manure source. Replicate domes were placed on each plot at hourly intervals for 6 to 10 min and then the concentration of ammonia was obtained in real time with a GasAlert hand-held meter with automated air pump. The day of application ammonia concentration for the combined years of 2010 and 2011 were different ($P < 0.05$): DS, 7.3 ppm, and ADSR, 5.4 ppm. Peak ammonia for the combined years of 2010 and 2011 ranged from 16.4 and 16.9 and was not different due to manure source. When DS, DSSR, and ADSR manure sources were compared in 2011, manure source significantly ($P < 0.05$) affected ammonia concentration with concentrations of DS — 11.0 ppm, DSSR, 8.8 ppm, and ADSR, 5.5 ppm, with all means different from each other. Peak ammonia was greatest ($P < 0.05$) for DS (24.9 ppm), with DSSR (19.3 ppm) and ADSR (17.5 ppm) the lowest, and not different from each other. Data indicated that the effect of anaerobic digestion and amount of solids impact the loss of ammonia from manure on the day of application.

Key Words: manure, ammonia

781 Partitioning of solids, nitrogen, and phosphorus in solids and liquid fractions of anaerobically digested dairy effluent.

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Data on the partition of solids, nitrogen, and phosphorus were collected at a commercial dairy that anaerobically digested (AD) manure (70% of

volume) and pre-consumer food wastes (30% of volume). Daily input into the AD averaged ~60,000 g/d as dairy manure and 30,000 g/d as pre-consumer food wastes (ruminant blood, egg waste, whey, fish stick byproduct, paper pulp waste, grease trap waste). The AD was a modified plug-flow design, operating under mesophilic conditions (23.5°C), with a 17 d retention time, and storage capacity of ~6,100,000 l. Data on flow of post AD effluent and solids were obtained by in-line flow meter (Siemens Magflo MAG 5000) and a stationary mixer wagon (NDE vertical feed mixer), respectively. Anaerobically digested effluent was ~3% solids. In 2008, data were collected when an Eys screw press liquid-solids separator was utilized. In 2011, data were collected when a DT 360 (Daritech) liquid-solids separator was utilized. Solids, nitrogen, and phosphorus separation from the effluent into solids was, mean and (standard deviation): Eys — solids 74% (8.5), nitrogen 13% (5.5), and phosphorus 21% (8.0): DT 360 — solids 21% (8.2), nitrogen 1.6% (0.63), and phosphorus 2.4% (0.97). Mean differences were observed for large particle solids removal from the AD dairy effluent. The majority of the nitrogen and phosphorus remained with the AD effluent after liquid-solids separation.

Key Words: anaerobically digested manure, solids, nitrogen

782 Inoculant volume of a mixed culture of rumen microorganisms on rate and extent of methanogenesis from processed dairy excrement for biofuel production by anaerobic digestion.

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The major limitation with anaerobic digestion of dairy waste is related to its initial rate of microbial activity and its concentration of volatile organic compounds as substrate for methanogenesis. Inoculating batch anaerobic digesters of dairy excrement with a viable mixed culture of rumen fluid at 30% of digester volume resulted in a several fold increase in methane production as compared with a non-viable (heat-killed) control. Practical application requires that a lower volume of inoculant be established. In vitro batch culture fermentations were conducted to test lower volumes of inoculant and different extracts of dairy excrement in a 3-way factorial designed experiment. Batch cultures with water extracts of fresh dairy excrement or liquid from a solid separator as substrate were inoculated with levels A (1%), B (5%), or C (10%) viable rumen fluid (V/V). Fermentations were conducted in duplicate along with representative blanks of each type of waste extraction and inoculation level. Fermentations were maintained for 0, 2, 4, 7, 9, 12, 14, and 16 d periods. Gas production, CO_2 and CH_4 concentrations, pH, free-ammonia, dry matter digestion, volatile fatty acid production, and gross energy digestion were measured. CH_4 volume averaged 11.4mL for B and 10.9mL for C inoculations, an increase of 176% and 175%, respectively, compared with inoculation A ($P < 0.01$). Differences in gas production were observed between the waste substrates as well. Liquid waste from a solid separator had 24% greater concentration of CH_4 than a fresh waste extract ($P < 0.01$), but total gas and CH_4 volume were 180% and 128% higher from fresh waste extract ($P < 0.01$). As the duration of fermentation was extended from 0 to 16 d the CH_4 volume increased by 200% ($P < 0.01$). Lower levels of viable rumen fluid are effective for inoculating dairy waste for bio-fuel production but require a longer fermentation.

Key Words: methane, anaerobic digestion, microbial inoculation

783 Effects of inorganic versus organic copper on nitrous oxide reductase activity in peat soil.

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Nitrous oxide (N_2O) is a potent greenhouse gas that contributes to global warming and stratospheric ozone destruction. Animal production emits approximately 1.5 Tg of N_2O annually and 51% of these emissions are associated with manure incorporation into soil. Nitrous oxide is mainly produced through the denitrification pathway. Nitrous oxide reductase (N_2OR) is the enzyme responsible for the reduction of N_2O to N_2 during denitrification. Nitrous oxide reductase uses copper (Cu) as its cofactor and its activity is compromised under conditions of Cu deficiency. The present study investigated organic (ORG) versus inorganic (INO) Cu at various concentrations (750, 550, 125, and 60 ug Cu/g soil) applied to soil, respectively, for their efficacy in affecting N_2OR activity. A control treatment (CON) containing soil and water, without added Cu, was also evaluated. The INO and ORG Cu treatments were dissolved in water and added to soil with low existing Cu concentrations in incubation vials. Treatment vials were anaerobically incubated to favor denitrification over a 24 h period. Gas samples were collected from the incubation vials every 8 h and analyzed for N_2O and N_2 concentrations, which were utilized to estimate N_2OR activity. The INO Cu versus CON did not affect N_2OR activity among different concentrations (0.11, 0.10, 0.04, 0.19, and 0.80 ug N_2O/g soil/h for INO 750, 550, 125, 60, and CON treatments, respectively) over sampling time ($P > 0.05$). However, N_2OR activity was higher for all ORG Cu treatments versus CON (11.42, 12.57, 2.67, 2.12, and 0.80 ug N_2O/g soil/h for ORG 750, 550, 125, 60, and CON, respectively) over the sampling time ($P < 0.05$), especially at the increasing Cu concentrations. These results highlight the importance of Cu form and concentration on N_2OR activity. Optimization of N_2OR activity could potentially decrease N_2O emissions associated with manure management in livestock production.

Key Words: organic Cu, inorganic Cu, nitrous oxide reductase

784 Nutrient removal with harvest of soybean forage and soybean seed produced with and without irrigation of dilute swine manure lagoon effluent.

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Nutrient management plans dictate the quantity of swine lagoon effluent and other manures applied to agricultural fields. Within a nutrient management plan, nutrient removal through crop harvest affects capacity for subsequent effluent application. A trial was conducted to compare nutrient removal with production of a forage-type soybean cultivar (soyF; Large Lad, Eagle Seed, Weiner, AR) harvested as forage and a standard cultivar (soyS; USG74A91, UniSouth Genetics, Dickson, TN) harvested as seed when produced with or without irrigation using dilute swine lagoon effluent. Twelve plots of 0.072 ha each planted on May 12, 2010, comprised 3 replications of the following treatments: 1) soyF non-irrigated, 2) soyF irrigated, 3) soyS non-irrigated, and 4) soyS irrigated. The irrigated plots received 6 applications of 2.84, 3.10, 2.54, 2.74, 4.52, 2.13 cm of effluent (0.005–0.022% N, 0.01–0.015% P, 0.02–0.03% K) via sprinkler irrigation from June 30 through August 8, when irrigation was terminated due to depleted effluent volume. Applications coincided with a drought season with mean rainfall of 2.11, 2.57 and 5.18 cm for June, July and August, respectively. The soyF plots were harvested with a plot forage harvester on August 12 and the soyS plots with a plot combine on October 19. Individual treatment means ± SEM (kg/ha) were: DM yield 4302, 8581, 1548, 2572 ± 664; N removal 116.9, 252.8, 95.8, 162.0, ± 20.8; P removal 14.2, 35.5, 10.3, 17.9 ± 2.8; K removal 114.8, 314.8, 34.1, 59.9 ± 22.9 for soyF non-irrigated, soyF irrigated, soyS non-irrigated and soyS irrigated treatments, respectively. There were crop-type by irrigation application interactions ($P < 0.05$) for DM yield, P removal and K removal with these responses being more pronounced when irrigation was applied to soyF than when applied to soyS. As expected more nutrients were removed with soyF than with

soyS harvest. However, under the conditions of this trial, crop removal of certain elements that influence nutrient management plans and effluent application rate were more responsive to effluent irrigation in soyF than in soyS production.

Key Words: effluent, soybean, nutrient removal

785 Effect of fibrous diets and inclusion level on the chemical composition and odors from pig slurry.

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Incorporation of high fiber ingredients into pig rations has the potential to reduce pollutants emitted from pig slurry tanks. A study was conducted to test whether diets containing 0, 80 and 160 g/kg of alfalfa hay, sunflower hulls or corn cobs influence the characteristics and odors from pig slurries. A total of 14 pigs weighing an average of 36 kg were kept in individual cages to allow the total collection of feces and urine. All pigs were fed ad libitum. Feces and urine were mixed in a 1:2.3 ratio (wt/wt), stored and fermented for 16 d in a temperature controlled room at 22 to 24 C. The slurry was sampled twice (on d 1 and on d 16) of the fermentation period and analyzed for pH, short chain fatty acids, chemical oxygen demand (COD) and nitrogen on a wet basis. All samples were tested for odor offensiveness using 18 trained panelists from the University of KwaZulu-Natal. A scale of 1 to 5 was used to rank the odor severity, where 1 = not offensive, 2 = mildly offensive, 3 = moderately offensive, 4 = strongly offensive and 5 = extremely offensive. Slurry pH and COD varied with fiber source ($P < 0.05$). After d 16, the COD for alfalfa hay, sunflower hulls and corn cobs were 369, 512 and 425 ± 34.2 mg of oxygen per liter. There was a significant interaction of fiber inclusion level and incubation period on COD and SCFA concentrations. Total SCFA concentration was higher at d 16 than d 1 ($P < 0.05$). Odor offensiveness varied due to fiber source ($P < 0.05$). Sunflower hulls and alfalfa diets were rated as less offensive (mean rank = 2.2) than corn cob diets (mean rank of 4.3). For all fiber sources, no differences ($P > 0.05$) were found between 80 and 160 g/kg. It was concluded that characteristics of pig slurries were influenced by fiber source and inclusion levels. The offensive odor from corn cobs suggests its considerable digestibility. More work still needs to be done to characterize other compounds from a large variety of locally available fiber sources that reduce water and air pollution from pig enterprises.

Key Words: short-chain fatty acids, slurry characteristics, odor offensiveness

Ruminant Nutrition: Beef Co-Products

786 Performance by feedlot cattle fed varying proportions and amounts of lime treated crop residues and distillers grains as substitutes for corn grain. A. L. Shreck*[1], C. J. Schneider[1], B. L. Nuttelman[1], D. B. Burken[1], G. E. Erickson[1], T. J. Klopfenstein[1], and M. J. Cecava[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]Archer Daniels Midland, Decatur, IL.*

The objective of this experiment was to displace graded amounts of dry-rolled corn (DRC) with varying ratios of distillers grains and lime-treated crop residues (DGCR). Linear and quadratic effects of DRC displacement within ratio of DGCR were tested. Sixty individually fed steers (Initial BW: 402 ± 31.3 kg) were assigned randomly to 10 treatments (6 steers/ treatment) and blocked (20 steers/block) based on initial BW. Treatments were 2 ratios of DGCR, 2 types of treated crop residue, and 3 DRC concentrations in the diet (10%, 25%, 40%; DM basis). The DGCR replaced corn and consisted of 2:1 or 3:1 ratios of modified distillers grains plus solubles (MDGS) and treated corn stover or a 3:1 ratio of MDGS and treated wheat straw. The control diet contained 35% MDGS, 5% untreated corn stover, and 56% DRC. All diets contained 4% supplement. Corn stover and wheat straw were ground (76 mm screen) and treated with 5% CaO (DM basis) at 50% DM and stored anaerobically. Increasing DRC quadratically increased ($P = 0.06$) DMI within the 3:1 straw diets. When comparing 3:1 treated stover and straw, DMI tended ($P = 0.10$) to interact across corn amount with DMI decreasing for treated stover and increasing for treated straw with increasing corn level. Carcass adjusted final BW tended ($P = 0.10$) to quadratically increase and G:F ($P = 0.06$) quadratically increased as corn amount increased in 3:1 stover diets. Increasing corn amount increased ($P = 0.07$) G:F in treated stover diets, regardless of ratio. Increasing corn level tended to increase ($P = 0.10$) ADG and increased ($P = 0.01$) 12th rib fat for 3:1 ratios. Cattle fed diets containing at least 25% corn and 3:1 ratios of distillers grains and lime-treated crop residues can achieve similar efficiency and carcass merit compared with cattle fed diets containing 5% roughage and 56% corn.

Key Words: alkaline treatment, corn, grain replacement

787 Comparing wet and dry distillers grains plus solubles for yearling finishing cattle. B. L. Nuttelman,* D. B. Burken, C. J. Schneider, G. E. Erickson, and T. J. Klopfenstein, *University of Nebraska-Lincoln, Lincoln.*

A finishing trial was conducted to compare the effects of drying distillers grains plus solubles (DGS) produced from the dry milling process. Yearling, crossbred steers (n = 171; 362 ± 30 kg) were utilized in a randomized complete block design, stratified within block, and then randomly assigned to one of 21 pens (8 or 9 steers/pen). Pens were assigned randomly to one of 3 treatments (7 replications/treatment) that consisted of: 1) corn-based control (CON); 2) wet distillers grains plus solubles (WDGS, 34.6% DM); and dried distillers grains plus solubles (DDGS, 88.2% DM). Distillers grains plus solubles were included at 35% of the diet DM and replaced a 1:1 blend (DM basis) of high-moisture and dry-rolled corn which was the same blend in CON. Grass hay and dry supplement were included at 7.5% and 5.0% of diet (DM), respectively in all diets. Additional fat was not added to CON, and therefore diets including DGS contained more fat than CON. All diets were formulated to contain a minimum of 13% CP. Steers were fed for 148 d. Final BW for WDGS and DDGS (679 and 675 kg, respectively) was greater than CON (646 kg; $P < 0.01$). Daily gain increased 0.23 and 0.20 kg/d for WDGS and DDGS, respectively when compared with CON (2.11, 2.08, and 1.88 kg, respectively; $P < 0.01$). Dry matter intake was not different ($P = 0.33$) between CON, WDGS, and DDGS (12.9, 13.1, and 13.3 kg/d, respectively). Cattle fed WDGS had greater G:F than DDGS and CON steers (0.162, 0.157, and 0.146, respectively; $P < 0.01$), and DDGS steers were more efficient than CON (i > $P < 0.01$). Cattle fed either distillers grains gained more, and thus had heavier HCW ($P < 0.01$). There were no differences for 12th rib fat, marbling score, or LM area ($P > 0.09$). Using G:F values, a 31.3 and 21.5% improvement above CON was calculated for WDGS and DDGS at 35% inclusion, respectively. Using the same calculations, WDGS was determined to have a 9.1% greater feeding value than DDGS. Similar to previous work, feeding DGS improves gain and efficiency compared with corn based diets, and WDGS has greater energy than DDGS.

Key Words: distillers grains, energy value, finishing cattle

788 Performance of cattle fed diets based on blended by-product pellets varying in rumen available energy and protein content. M. G. Zenobi*[1], P. Yu[1], D. A. Christensen[1], P. G. Jefferson[1,2], H. A. Lardner[1,2], and J. J. McKinnon[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

Two trials were conducted to evaluate the performance of growing cattle fed blended by-product pellets. Pellets were based on by-products from the oilseed and grain sectors and were formulated to be isonitrogenous (17.0% CP) and isocaloric (1.92 and 1.28 Mcal/kg NE_m and NE_g, respectively). In trial 1, 4 pellets were evaluated. The pellets were formulated to be either high starch (HS 45% DM basis) or high fat (HF 8.8% DM basis) and either low or high in soluble protein (LSP 27% of CP; HSP 37% of CP DM basis). In trial 2, only the 2 HF pellets were evaluated. In trial 1, 300 cross-bred steers (320 ± 19.6 kg, mean ± SD) were randomly assigned to one of 25 pens and fed one of 5 diets in a completely randomized block design. The control diet consisted of 46.9% forage and 53.1% barley-based concentrate. The 4 treatment diets consisted of 48.4% forage and 51.6% blended pellets (DM basis). All diets were formulated to 1.63 and 1.02 Mcal/kg NE_m and NE_g, respectively (DM basis). In trial 2, 180 cross-bred steers (326 ± 0.2 kg) were randomly assigned to one of 15 pens with each pen randomly assigned to one of 3 treatments in a completely randomized design. Treatments included a barley-based control and the 2 HF pellets from trial 1. In trial 1, no ($P = 0.36$) effect of treatment was observed on ADG, however, DMI was reduced ($P \leq 0.01$) with the HS LSP treatment and was highest ($P \leq 0.01$) for the HF HSP treatment. Gain:feed (G:F) was poorest ($P \leq 0.01$) for the HF HSP diet. In Trial 2, no effect of treatment was observed on ADG ($P = 0.80$) or DMI ($P = 0.06$), however cattle fed the barley-based control diet had the highest ($P \leq 0.01$) G:F ratio. Relative to the control diet, the calculated NE_g content (Mcal/kg DM) was 8.7% lower ($P \leq 0.01$) for the HF HSP treatment in trial 1 and 6.7% lower ($P \leq 0.01$) for both HF treatments in trial 2. The results indicate that blended by-product pellets can be a viable alternative for supplementing energy and protein in backgrounding diets. Caution needs to be exercised when feeding HF pellets due to poorer G:F ratios and potential negative impacts on cost of gain.

Key Words: blended by-product pellets, fat, growing cattle

789 Replacement of grazed forage and animal performance with distillers grains supplementation in a forage system.

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A beef systems study was conducted to determine optimal time within a forage system to supplement distillers grains, and feedlot performance relationship to supplementation. A completely randomized design with a 2 × 2 factorial arrangement was used. Spayed heifer calves (n = 203, BW = 205 ± 23 kg) grazed corn residue 138 d and bromegrass 29 d (WTR), native Sandhills range 128 d (SMR), and were finished on a common diet. Factorial treatments were 0.91-kg DM wet distillers grains with solubles (WDGS) (LO) or 2.3-kg DM WDGS (HI) supplement on corn residue, and modified distillers grains with solubles (MDGS) fed at 0.6% BW daily (SUP) or no MDGS (NO) during SMR. Available SMR grazing acres for SUP were 17% less than NO based on past research. Winter ADG was greater for HI cattle at 0.62 kg than LO at 0.31 kg ($P < 0.01$). Summer SUP ADG at 0.82 kg was greater than NO at 0.58 kg ($P < 0.01$). System gains included total WTR and SMR gains and were greatest among treatments for HI, SUP at 0.66 kg ($P < 0.01$). HI, NO and LO, SUP had a greater system ADG than LO, NO ($P < 0.01$). There were no differences in system ADG of HI, NO at 0.59 kg and LO, SUP at 0.57 kg ($P = 0.09$). Of all treatments, LO, NO had the lowest system gain at 0.47 kg ($P < 0.01$). There was no system gain interaction between WTR and SMR treatments ($P = 0.14$). Factorial treatments were maintained through finishing with 2 replications per treatment. Cattle were serially slaughtered and performance data adjusted to 1.32 cm BF. With SMR supplementation, feedlot ADG decreased ($P = 0.02$). Feedlot ADG for HI, NO and LO, NO were 1.8 kg and 1.7 kg, respectively, and for HI, SUP and LO, SUP were 1.6 kg and 1.5 kg, respectively. There were no significant DMI treatment differences. Summer SUP decreased G:F ($P = 0.005$) with HI, NO and LO, NO at 0.144 and 0.140, respectively, and HI, SUP and LO, SUP at 0.132 and 0.128, respectively. Higher WTR supplementation positively affected HCW ($P = 0.004$) with HI, NO and HI, SUP at 382.3 kg and 369.0 kg, respectively, and LO, SUP and LO, NO at 355.3 kg and 350.8 kg, respectively. Gains increased with higher WTR WDGS level and SMR MDGS supplementation, due to additional energy or undegradable intake protein supplied. System gains were highest for HI, SUP, intermediate for HI, NO and LO, SUP, and lowest for LO, NO. Winter supplementation increased HCW, and SMR supplementation decreased feedlot ADG and G:F, and no winter by summer treatment interactions were observed.

Key Words: beef cattle, distillers, supplement

790 Flint corn grain processing and increasing levels of citrus pulp in finishing diets for Nellore bulls.

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The effects of flint corn processing (steam flaking, 310g/l vs. grinding, 1.3 mm GMD) and the partial replacement of corn with citrus pulp (0, 25, 50 or 75%) in feedlot diets were evaluated. A total of 216 Nellore bulls (IBW 350 kg) were allotted to 40 pens and used in a randomized complete block design with a 2 × 4 factorial arrangement of treatments (SF100:CIT0; SF75:CIT25; SF50:CIT50; SF25:CIT75; GC100:CIT0; GC75:CIT25; GC50:CIT50; GC25:CIT75) for 103 d. The diets contained (% DM) 12% sugar cane bagasse and 88% concentrate. Data were analyzed using mixed procedure of SAS with pens as experimental units. For DMI, ADG, G/F and observed NE_g the effects of grain processing, the effects of citrus pulp inclusion in the diets and interactions were significant ($P < 0.01$). All the diets containing SFC presented less DMI than the GC75:CIT25 and the GC50:CIT50 diets. Citrus pulp had no effect on DMI of the SFC diets, however it increased DMI when it replaced up to 50% of the GC ($P < 0.01$). Inclusion of CIT decreased ADG in the SFC diets (1.80; 1.52; 1.70; 1.58 kg/head) and it increased ADG in the GC diets (1.60; 1.74; 1.85; 1.70 kg/head). The greatest G/F was observed for Nellore cattle fed the SF100:CIT0 diet followed by the SF50:CIT50 diet. Inclusion of citrus pulp decreased G/F of cattle fed SFC (0.222; 0.190; 0.200; 0.184) and had no effect for cattle fed GC diets (0.180; 0.176; 0.180; 0.186). Diet NE_g was greater for SFC diets (1.73; 1.51; 1.56; 1.45 Mcal/kg DM) than for GC diets (1.42; 1.37; 1.39; 1.44 Mcal/kg DM), with a negative effect of CIT in the SFC diets. Fat thickness was greater for GC than for SFC diets (4.4 mm vs. 5.0 mm). When CIT replaced up to 50% of corn in the diets fecal starch was less for SFC diets than for GC diets (2.0% vs. 9.3%). In conclusion, SFC increases diet NE_g for Nellore cattle fed high concentrate diets compared with ground corn. Citrus pulp decreases NE_g in SFC diets and has no negative effects on ground corn diets NE_g for Nellore cattle.

Key Words: citrus pulp, feedlot, grain processing

791 Evaluation of rumen metabolism and digestibility when treated crop residues are fed in cattle finishing diets.

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Five rumen fistulated steers were used in an incomplete 5 × 7 Latin square design. A 2 × 3 + 1 factorial arrangement of treatments was used. One factor was crop residue type (corn cobs, wheat straw, corn stover) and the other factor was degree of processing. For processing, residues were ground but not treated or ground and treated with 5% CaO (lime) at 50% moisture and stored anaerobically. All diets contained 40% wet distillers grains plus solubles and 4% supplement (DM basis). Residues replaced DRC at 25% of the diet (DM basis). The control diet contained 10% roughage (equal cobs, straw, and stover) and 46% DRC. An interaction ($P = 0.06$) was observed for acetate:propionate (C2:C3) ratio. Treatment of cobs (3.1 vs 2.6) and corn stover (2.9 vs 2.6) increased C2:C3 but treatment of wheat straw increased propionate which decreased C2:C3 (2.4 vs 2.6). No difference ($P > 0.10$) was observed for treated straw or stover compared with control (2.6) for C2:C3. An interaction was noted for average ruminal pH because compared with untreated forms, treated cobs (6.52 vs 6.38) and stover (6.23 vs 5.95) had greater pH but treated straw (5.81) had lower ($P = 0.08$) pH compared with untreated (6.05). Greater DM (73.7 vs 66.1%; $P = 0.001$), OM (77.0 vs 68.5%; $P = 0.001$), lipid (89.2 vs 85.2; $P = 0.02$) and NDF (66.8 vs 51.5%; $P < 0.001$) digestibility were noted when diets contained treated compared with untreated residues. However, no difference ($P > 0.10$) was observed between control and treated diets for DM (70.7 vs 73.7%) or OM (72.1 vs 76.9%) digestibility. Similar DMI was noted for treated and untreated ($P = 0.38$) diets but lower ($P = 0.001$) NDF intake was observed for treated diets (3.1 vs 3.5 kg/d), suggesting that CaO treatment partially solubilized NDF thereby decreasing measurable NDF intake. Results suggest that treated crop residues can substitute a portion of grain in feedlot diets and result in similar nutrient supply to the animal. The improvements in digestibility when treated residues are fed compared with untreated residues are related to fiber solubilization and improved fiber digestibility.

Key Words: alkaline treatment, crop residues, grain replacement

792 Effects of alternate feeding of dried distillers grains plus solubles on performance and body composition in gestating forage-fed beef cows.

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Forty-six nonlactating, gestating beef cows were used to examine effects of feeding either dried distiller′s grains plus solubles (DG) or grass hay on alternate days during mid-late gestation on intake, BW, ADG, G:F, and ultrasound carcass characteristics. Cows were arranged in a completely randomized design and dietary treatments included: 1) ad libitum hay daily (CON; n = 12); 2) hay and 0.4% BW DG daily (DG7; n = 12); 3) hay daily and 0.93% BW DG on Monday, Wednesday, and Friday (DG3; n = 11); and 4) hay only on Tuesday, Thursday, Saturday, and Sunday and 0.93% BW DG only on Monday, Wednesday, and Friday (DGA; n = 11). Cows were fed diets for 84 d with BW and carcass ultrasound data collected every 28 d. Feed intake was continuously monitored and intake data collected daily using the Insentec B. V. roughage intake control feeding system. Hay intake was greatest ($P < 0.01$) in CON (15.5 ± 1.0 kg/d) and least ($P < 0.01$) in DGA (10.6 ± 1.0 kg/d) with DG7 (13.6 ± 1.0 kg/d) and DG3 (12.7 ± 1.0 kg/d) being intermediate. By design DG intake was similar for DG7 (3.4 ± 0.1 kg/d), DG3 (3.3 ± 0.1 kg/d), and DGA (3.2 ± 0.1 kg/d). Total DMI was less ($P < 0.01$) for DGA compared with all other treatments. Body weight was similar ($P > 0.10$) among treatments at each weigh date, however a decrease ($P < 0.01$) in ADG was observed for CON (0.34 ± 0.06 kg/d) compared with all other treatments (0.73, 0.75, and 0.60 ± 0.06 kg/d for DG7, DG3, and DGA, respectively). Likewise, the G: F ratio was least ($P < 0.01$) for CON compared with all other treatments (0.02 ± 0.003, 0.04 ± 0.003, 0.05 ± 0.003, and 0.04 ± 0.003 kg of gain/kg of feed for CON, DG7, DG3, and DGA, respectively). Change in REA from d 1 to d 84 was greater ($P < 0.05$) in DG7 compared with all other treatments however there were no differences among treatments for intramuscular fat, rib fat, and rump fat throughout the trial. The feeding strategy DGA altered hay intake, total DMI, and REA, but did not alter other performance and carcass characteristics compared with other supplementation methods.

Key Words: beef cows, distillers grains, supplementation frequency

793 Dry-rolled or whole shell corn with or without wet corn gluten feed in receiving diets.

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With historically high grain and cattle prices, reducing ration costs while maintaining health and performance is important for attaining profitability. Previous research indicates the use of whole shell corn in receiving diets allows for cheaper processing costs and has the added benefit of slowing starch fermentation enough to limit incidence of grain-induced acidosis. Wet corn gluten feed (WCGF) is a byproduct that can aid in controlling bloat by providing energy in the form of fermentable fiber and protein. Our objective was to determine whether corn processing with or without WCGF had any effect on growth and performance. Two hundred 79 crossbred calves (230 kg) were randomly assigned to 24 pens. Pens were randomly allocated to treatment sequence in a 2 × 2 factorial completely randomized design. Treatments were a diet including 47% whole shelled corn (WSC), a diet including 29% whole shelled corn with 30% WCGF (BP WSC), a diet including 47% dry rolled corn (DRC), and a diet with 29% dry rolled corn with 30% WCGF (BP DRC). Diet percentages were recorded on a dry matter basis (DM). Data were analyzed using mixed models including the fixed effects of treatment and lot number while the random effects were lot × treatment, period, pen, and period × pen interaction. The addition of WGCF had a positive effect on ending weight; they were significantly higher than the WSC or DRC diets alone ($P = 0.03$). Daily gains for diets with WCGF were also higher ($P = 0.04$), thus making overall weight gain on the BP WSC and BP DRC significantly better ($P = 0.02$). There were no corn processing effects (all $P \geq 0.34$). There was an apparent interaction between digestive upsets that required treatment and the DRC diet ($P = 0.006$). However, this may be misleading due to the fact only 4 animals were treated for illness over the course of the study. Only one animal was treated for a digestive problem. There was no benefit seen to processing corn, but including WCGF at 30% (DM) increased gains and overall performance.

Key Words: receiving, whole shell corn, wet corn gluten

794 Effect of dried distillers grains with solubles on enteric methane emissions and nitrogen excretion from finishing beef cattle.

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The objectives of this study were to examine the effect of corn- or wheat-based dried distillers grains with solubles (WDDGS, CDDGS) on enteric CH_4 emissions from finishing beef cattle, and to determine if any observed reductions were a result of the fat content of CDDGS. Another objective of this study was to compare the effect of CDDGS or WDDGS on N excretion. The experiment was designed as a replicated 4 × 4 Latin square with 28-d periods using 16 ruminally fistulated crossbreed heifers (529.1 kg ± 41.1). The control diet contained 87% barley grain, 8% barley silage and 5% supplement (DM basis). Treatment diets were formulated by replacing 40% of barley grain DM with CDDGS, WDDGS, or WDDGS+oil. Corn oil was added to WDDGS (3.4% fat DM) to achieve the same level of fat as CDDGS (9.7% DM). All diets were fed as total mixed rations once daily ad libitum. Total collection of urine and feces was conducted between d 18 and 21. Enteric CH_4 was measured between d 25 and 28 using 4 environmental chambers. Feeding WDDGS increased ($P < 0.05$) CH_4 emissions as a percentage of gross energy intake (GEI) from 4.9 to 5.6% compared with the control. Heifers offered CDDGS (3.9% of GEI) or WDDGS+oil (4.2% of GEI) produced less ($P < 0.05$) CH_4 than heifers fed the control diet. Emissions between CDDGS and WDDGS+oil did not differ ($P > 0.15$). Excretion of N (as % of daily N intake) was greater ($P < 0.05$) for CDDGS, WDDGS and WDDGS+oil (82.5, 82.6 and 83.0%) compared with the control diet (73.8%). Results suggest that feeding CDDGS or WDDGS+oil can mitigate enteric CH_4 emissions in finishing beef cattle. However, the potential contribution of increased N excretion to heightened nitrous oxide emissions would have to be considered in a life cycle analysis of greenhouse gases arising from the feedlot.

Key Words: methane, beef cattle, dried distillers grains with solubles

795 Comparing the digestibility of wet and dry distillers grains plus solubles in cattle finishing diets.

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Twelve crossbred steers (525 ± 34 kg) were utilized in a 3-period crossover design to compare the digestion characteristics of wet and dry distillers grains plus solubles (DG) in finishing diets. Diets consisted of 40% of wet distillers grains plus solubles (WDGS, 34.1% DM) or dried distillers grains plus solubles (DDGS, 93.1% DM), or a corn control

(CON) containing no DG. Basal ingredients were dry-rolled corn, 7.5% alfalfa hay, and 5% dry supplement (DM basis) with DG replacing DRC. Molasses was included at 5% in the CON and DDGS diets to prevent sorting. Steers were adapted to diets for 14 d before the 5 d total fecal collection period. During the collection period, steers were individually tethered in stalls lined with rubber mats. Feces were collected and weighed daily at 0800 h and a composite was made by steer within collection period and analyzed to determine total tract nutrient digestibility. A duplicate sample was taken by day and dried for 48 h in a 60°C forced air oven to determine fecal DM output. There were no differences observed for DM or OM intake ($P > 0.15$). The CON and WDGS treatments had greater ($P < 0.03$) OM digestibility than DDGS diets (76.2, 73.0, and 67.3%, respectively), but were similar between CON and WDGS ($P = 0.22$). Diets containing DG had greater NDF intake compared with CON ($P < 0.01$). However, there were no differences for NDF digestibility between CON, WDGS, and DDGS (64.3, 62.0, and 58.4%, respectively; $P = 0.28$). Fat intake was greater for DG diets ($P < 0.01$), but fat digestibility was not different ($P = 0.46$) between treatments. Previous literature suggests animal performance will be improved when WDGS is included up to 40% compared with corn-based diets, and that drying DG negatively affects the feed efficiency relative to WDGS. Results from this study suggest OM digestibility is negatively affected when DG is dried to produce DDGS. However, OM digestibility for WDGS and corn-based diets are similar in this study and do not explain the improved performance in finishing diets containing WDGS.

Key Words: digestibility, dried distillers grains plus solubles, wet distillers grains plus solubles

796 The effects of titrating corn-based dried distillers grains plus solubles with sorghum-based wet distillers grains plus solubles on yearling heifers feedlot performance and carcass characteristics.

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This study compared performance and carcass effects of altering corn dried distillers grains plus solubles (DDGS) to sorghum-based wet distillers grains plus solubles (WDGS) ratios in a dry-rolled corn feedlot ration with 30% distillers grains plus solubles (DM basis). Yearling cross-bred heifers (n = 150; initial BW 383 ± 28 kg) were blocked by BW, implanted with Revalor H, stratified by hide color and randomized to treatment, and fed for 125 d. On d 98, 330 mg-hd^{-1}-d^{-1} of ractopamine hydrochloride (Optaflexx) was included into each treatment ration and fed the final 27 d of the finishing period. Combinations of distillers grains evaluated were: 30% DDGS (TRT1); 22.5% DDGS: 7.5% WDGS (TRT2); 15% DDGS:15%WDGS (TRT3); 7.5%DDGS:22.5%WDGS (TRT4); and 30% WDGS (TRT5). There were no differences ($P > 0.54$) among treatments in overall ADG, G:F, and DMI. Between Treatments 1 and 5, DMI increased 3.3% ($P = 0.05$) and G:F decreased 14.6% ($P = 0.03$) from 57 to 84 d. No other differences were detected in HCW, dressing percentage, marbling score, KPH or USDA Yield grade. Data suggest that when fed at 30% of the finishing diet DM, corn DDGS and sorghum WDGS can be blended or exchanged with no effect on finishing performance or carcass characteristics. These data would serve as a useful tool when formulating least cost dry-rolled corn based rations.

Key Words: beef heifers, carcass characteristics, distillers grains

797 Effects of increasing levels of distillers dried grains on intake and digestibility of moderate quality fescue hay.

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Ethanol production in the United States has increased more than 7-fold in the past decade, displacing nearly one-third of corn once used for livestock feed. Producers must find alternative feed sources, such as distillers dried grains plus solubles (DDGS). Including DDGS in dairy and finishing diets has been widely studied, but less information is available regarding the use of DDGS as a supplement for cattle consuming a forage-based diet. The purpose of this study was to determine the differences in voluntary intake and digestibility of moderate quality, long-stem fescue hay (9.5% CP, 72.3% NDF; DM-basis) by steers consuming increasing levels of DDGS (27.7% CP, 35.7% NDF; DM-basis). Four Hereford steers (384 ± 42.8 kg) were housed in individual pens (4 × 4 m) and randomly assigned to treatment blocks in a completely randomized, replicated 4 × 4 Latin square design. Steers were fed daily one of 4 levels of DDGS (0, 0.2, 0.4, or 0.8% of BW; DM-basis), denoted as control (CON), low (LOW), moderate (MOD) and high (HI). Steers were fed DDGS at 0800 and ad-libitum hay was offered at 0830. Steers had access to fresh water and salt at all times. Each pd consisted of a 10-d adaptation and a 7-d collection, during which hay intake, orts, and total fecal output were measured daily, followed by a 10-d washout. Data were analyzed using PROC Mixed, where the model included the fixed effects of treatment and pd and steer was included as a random variable. Period was the repeated measure and included steer nested within pd. Hay intake (kg DM or % of BW) did not differ ($P > 0.47$) between treatments. Total tract DM digestibility did not differ between CON and LOW steers but tended ($P = 0.09$) to be greater for MOD compared with LOW (56.48 vs. 51.11%, respectively). Digestibility did not differ between HI and MOD, but HI steers had greater ($P < 0.05$) DM digestibility (60.54%) compared with LOW and CON steers (51.11 and 51.98%, respectively). Digestibility of NDF did not differ between treatments. Increased DDGS did not affect hay intake; however, total tract digestibility of diet DM was improved as DDGS supplementation increased.

Key Words: DDGS, fescue hay, intake and digestibility

Ruminant Nutrition: Dairy Production IV

798 Sampling behavior of dairy cattle: Effects of spatial variation in feed quality on movements at the feed bunk. J. M. Huzzey,* J. A. Fregonesi, M. A. G. von Keyserlingk, and D. M. Weary, *University of British Columbia, Animal Welfare Program, Vancouver, BC, Canada.*

The factors affecting feed sampling behavior of cattle housed indoors are poorly understood. The objectives of this study were to measure the effects of spatial variation in feed quality on the feeding behavior of Holstein dairy heifers. Thirty-two heifers were housed in 4 groups of 8. Pens had 8 distinct feeding stations (FS). Three TMR qualities were used in the study: low energy (TMR-L), moderate energy (TMR-M), and high energy (TMR-H). During trial 1 (d 1 to 8), heifers were offered a uniform baseline diet (TMR-M to all 8 FS) interspaced with 2 uniform test diets on d 3 and 6 (TMR-L or TMR-H). During trial 2 (d 9 to 17) heifers were offered a non-uniform baseline diet (7 FS: TMR-L, 1 FS: TMR-H) interspaced with 3 uniform test diets on d 11, 14, and 17 (TMR-L, TMR-M, or TMR-H). Heifers were observed in pairs ($n = 16$) continuously for 15 min following fresh feed delivery each morning. Frequency of switches between FS and competitive displacements were recorded. Pair was considered the experimental unit. During trial 1 the average (±SE) number of FS switches per min when fed the uniform baseline diet was 0.68 ± 0.10; this was lower than when fed a TMR-L (1.34 ± 0.10; $P < 0.001$) and tended to be higher than when fed a TMR-H (0.44 ± 0.10; $P = 0.06$). Displacement frequency did not differ between dietary treatments in trial 1 ($P > 0.14$). During trial 2 the number of FS switches per min when fed the non-uniform baseline diet was 0.87 ± 0.09; this was lower than when fed a TMR-L (1.16 ± 0.09; $P = 0.01$) but higher compared with the TMR-M and TMR-H diets (0.56 and 0.38 ± 0.09, respectively; $P \leq 0.007$). Heifers engaged in more displacements per min when fed a non-uniform TMR (0.13 ± 0.03) than when fed TMR-M (0.06 ± 0.03; $P = 0.04$) or the TMR-L and TMR-H diets (0.07 ± 0.03 for both; $P \leq 0.11$). Dairy heifers appear to sample feed quality by changing feeding locations at the feed bunk; this sampling behavior is affected by variability in the energy density of the diet.

Key Words: sampling behavior, diet uniformity, agonistic interactions

799 Effect of precision feeding on performance, nutrient excretion, and feeding behavior of early lactation dairy cows. E. Maltz*[1,2], L. F. Barbosa[1], P. Bueno[1], L. Scagion[1], L. F. Greco[1], K. Kaniyamattam[1], A. de Vries[1], and J. E. P. Santos[1], [1]*University of Florida, Gainesville,* [2]*The Volcani Center, Bet Dagan, Israel.*

Objectives were to evaluate the effects of 2 feeding strategies on performance of early lactation cows. Fifty-eight Holstein cows at 21 DIM were randomly assigned to a control [$n = 29$; 16.2% CP, 1.64 Mcal of NE_L, 22% starch, and 19% forage NDF] or a precision diet [$n = 29$, 16.2% CP, 1.59 to 1.68 Mcal NE_L, 18 to 26% starch, and 16 to 22% forage NDF] that varied in the caloric density based on energy balance (EB) of cows. The TMR of precision cows were adjusted individually once a week according to the EB and DMI of the preceding week. The study lasted 16 wk, and nutrient digestibility, rumen fluid composition, microbial protein synthesis, and feeding behavior were evaluated. Data were analyzed with the GLIMMIX procedure of SAS. The mean diet NE_L was greater ($P < 0.01$) for precision than control cows (1.65 vs. 1.64 Mcal/kg) because of greater ($P < 0.01$) dietary concentrate (55.0 vs. 52.3%). Compared with controls, precision cows had similar DMI (24.3 kg/d), but NE_L intake tended ($P = 0.10$) to be greater (40.6 vs. 39.1 Mcal/d) because of greater caloric intake in the first 6 wk of the study. Yields of milk (45.2 vs. 41.9 kg/d), 3.5% FCM (44.0 vs. 40.8 kg/d) and milk protein (1.33 vs. 1.23 kg/d), and the feed conversion ratio (3.5% FCM/DMI; 1.82 vs. 1.74) were greater ($P < 0.05$) in precision compared with control cows. Precision cows produced more ($P < 0.05$) milk calories per kg of $BW^{0.75}$ (0.227 vs. 0.213 Mcal of NE_L/kg), although the proportion of consumed calories (82.3%) and N (37.4%) partitioned into milk did not differ between treatments. Digestibility of nutrients, composition of rumen fluid, rumen pH and microbial N synthesis remained mostly unaltered by treatments. Meal pattern differed, and precision cows consumed feed more sparsely throughout the day, spent more time ruminating lying, had similar meal length (36.3 min/meal) compared with control cows, but smaller ($P < 0.05$) meal size (3.33 vs. 3.64 kg/meal). Results indicate that allocating dietary resources according to individual needs of cows based on EB improves lactation performance compared with feeding a single TMR despite minor changes in caloric intake.

Key Words: dairy cow, feeding behavior, precision feeding

800 Concentrate levels and supplemental fat for grazing mid lactating cows. F. L. Macedo, S. F. Angolini, W. F. Angolini, C. T. dos Santos Dias, and F. A. P. Santos,* *University of São Paulo, Piracicaba, SP, Brazil.*

A grazing trial was conducted to evaluate the production response of mid lactating dairy cows to concentrate levels and supplemental fat. Twenty-two Holstein x Jersey cows were assigned to randomized blocks according to number of lactation (primiparous or multiparous), DIM (132 ± 60) and milk yield (20.9 kg $d^{-1} \pm 2.22$), in a 2x2 factorial arrangement. Treat ments were: 1) HS: High supplementation (1 kg of concentrate for every 2.5 kg of milk); 2) LS: Low supplementation (1 kg for every 5 kg of milk); 3) HSCS: HS with 2.78% of calcium salt (CS) of soybean oil (Megalac-E®); 4) LSCS:LS with 5.76% CS of soybean oil. Cows grazed fertilized Elephant grass pastures during 90 d. Concentrates were 15.2% CP (HS and HSCS) or 12% CP (LS and LSCS), based on fine ground corn. Data were analyzed using GLM procedure of SAS (1999) and effects were significant at P-value of < 0.05. Hand plucked samples of forage contained 18.6% CP and 54.4% NDF. Feeding HS decreased forage DMI (9.3 vs. 12.2 kg d^{-1}) with no changes in total DMI (16.5 vs. 15.2 kg d^{-1}). Fat supplementation had no effect on forage and total DMI ($P > 0.05$). There was an interaction for concentrate level and fat supplementation for milk yield ($P < 0.05$). Feeding HS increased milk yield (17.6 vs.14.2 kg d^{-1}) compared with LS when fat was not fed, but concentrate level had no effect when fat was fed (15.4 vs. 15.0 kg d^{-1}). Fat supplementation had a negative effect on milk yield when cows were fed with HS (17.6 vs. 15.4 kg d^{-1}) but not with LS (14.2 vs. 15.0 kg d^{-1}). Milk fat content was decreased ($P < 0.05$) by feeding either HS (3.53 vs. 3.60%) or fat (3.76 vs. 3.38%) with no interaction ($P > 0.05$). Content of milk protein, casein and lactose were not affected by treatments ($P > 0.05$) and MUN was decreased by feeding HS ($P < 0.05$). Plasma glucose was not affected ($P > 0.05$) by treatments but feeding HS decreased plasma NEFA ($P < 0.05$).

Key Words: calcium salts of soybean oil, grazing dairy cows, supplementation

801 Dry matter intake and behavior patterns of dairy cows fed diets combining pasture and total mixed ration.

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Nine Holstein cows (mean BW = 572 kg; SD = 76) fed a total mixed ration (TMR) were assigned to 3 3 × 3 latin squares (each with 10 d of adaptation followed by 10 d of sampling) to evaluate the effect of 0 (TMR0), 4 (TMR4) or 8 (TMR8) hours of daily access to fresh pasture on DMI and behavior patterns. Pasture (*Lolium multiflorum*; 22.1% CP, 24.0% ADF) was daily cut and offered ad libitum from 0800 h in individual stalls and TMR (16.8% CP, 16.4% ADF) was offered ad libitum during the remaining time. Daily DMI was measured for 7 consecutive days by weighing the amount of feed offered and refused. Behaviors (eating (EAT), ruminating (RUM), and others (OTH)) were recorded during one day using instantaneous sampling of each cow using 5 min scan sampling for 12 h after 0800 h. Mixed and general linear models were used to test main effects for traits with or without repeated measurements, respectively. Pasture DMI increased and TMR DMI decreased with time of access to pasture (TMR0 = 0 and 24.5 kg; TMR4 = 2.8 and 22.8 kg; TMR8 = 3.6 and 19.0 kg; SEM = 0.5 and 1.5, respectively) while total DMI intake was higher in TMR4 than TMR8 cows (25.6 vs 22.6 kg), but no differences were detected with TMR0 (24.5 kg; SEM = 1.6). Proportion of cows EAT (0.43; SEM = 0.03), RUM (0.25; SEM = 0.02) or OTH (0.31; SEM = 0.02) were not affected by treatments, but an effect of hour and treatment × hour were detected for these traits ($P < 0.01$). After hour 1, the proportion of cows EAT decreased and RUM and OTH increased in every treatment, but at hour 5 (after TMR4 cows were changed to TMR feeding), the proportion of TMR4 cows EAT was higher than in TMR0 and TMR8 cows (0.81, 0.46, 0.10, respectively) and RUM lower than in TMR0 and TMR8 cows (0.05, 0.20, 0.49, respectively). At hour 9 (after TMR8 cows were changed to TMR feeding) the proportion of TMR8 cows EAT was higher than in TMR0 and TMR4 cows (0.90, 0.42, 0.59, respectively) and RUM lower than in TMR0 and TMR4 cows (0.01, 0.27, 0.19, respectively). Time of access to fresh pasture influenced both DMI and behavior of TMR-fed dairy cows.

Key Words: pasture, total mixed ration

802 Supplemental fat for dairy calves fed accelerated milk replacer during mild cold stress.

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Sixty Holstein and Holstein-cross dairy calves (31 female and 29 male) fed accelerated milk replacer (MR) were used to determine response to increasing amounts of supplemental fat during mild cold stress. Calves (n = 20) were randomly assigned to one of 3 treatments; 1) Low fat (LF) (28:15 MR; 2) Medium fat (MF) (28:15 MR + 113 g/d commercial fat supplement (FAT) (60% fat); 3) High fat (HF); 28:15 MR + 227 g/d FAT. MF and HF calves received FAT d 1–21. All calves were fed LF d 22–49. MR was fed at 1.4% of birth body weight (BBW) d 1–10 and then 1.8% of BBW d 11–42 and 0.9% of BBW d 43–49 Weaned on d 49 and remained in hutches to d 56. MR was reconstituted to 13% solids. Calves were fed ad libitum a commercial starter grain (19.2% CP) and offered 4 L/d warm water. Calves were fed MR twice d at 0630 and 1730 in hutches bedded with straw. Starter intake (SI), MR intake (MRI), and ambient temperature (AT) were measured daily and body weight (BW), hip height (HH), and body length (BL) were measured weekly. Data were analyzed using PROC MIXED in SAS as a randomized design. Calf BBW averaged 42.0 ± 1.0 kg ($P = 0.41$), total serum protein averaged 5.8 ± 0.1 mg/dL, and birth AT averaged 5.0 ± 1.1°C. Average daily gain (ADG) was similar among treatments through 21 d and averaged 0.59, 0.76, and 0.68 ± 0.1 kg/d and through 56 d averaged 0.81, 0.84, 0.83 ± 0.1 kg/d for LF, MF and HF. Through 56 d SI averaged 1.1, 1.0, 0.9 ± 0.1 kg/d for LF, MF and HF and was higher ($P < 0.05$) for LF vs HF. Cumulative starter intake was similar among treatments on d 21, 42, and 56 but was 10.4 kg higher ($P < 0.05$) for LF vs. HF on d 49. Gain of HH on d 56 tended ($P = 0.09$) to be greater and d 49 BL gain tended ($P = 0.06$) to be greater for LF vs. HF. Gain:feed on d 56 ($P = 0.50$) averaged 0.81, 0.84 and 0.83 ± 0.02 for LF, MF and HF. Retrospective analysis showed calves with BBW <40.0 kg fed MF tended ($P = 0.08$) to have higher 21 d BW gain than LF. Calves with BBW >40.0 kg fed HF had greater ($P < 0.05$) 21d BW gain than MF with LF intermediate. Supplementing fat to nursery calves fed accelerated MR decreased SI through d 21 which had carryover effects on SI on d 49 but did not alter ADG, total gain or feed efficiency.

Key Words: accelerated milk replacer, supplemental fat, nursery calf

803 What do preweaned and weaned calves need in the diet: A high fiber content or a forage source?

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The objective of this study was to determine whether the improvement of the performance of young calves associated with the supplementation of chopped grass hay is due to an increase of the total NDF content of the consumed diet or to the provision of chopped grass hay. Sixty-three Holstein calves (9 ± 4.4 d old) were randomly distributed in 4 treatments resulting from the combination of 2 levels of NDF content of a pelleted starter and the supply or absence of forage provision: low NDF starter (18%) with or without chopped oat hay, and high NDF starter (27%) with or without chopped oat hay. All animals were fed the same milk replacer (21% CP, 19.2% fat) at the rate of 4 L/d at 15% DM from d 1 to 34, and 2 L/d at 15% DM from d 35 to 42 (weaning). The study finished 2 wk after weaning. Body weight was measured weekly, and individual calf starter and hay intake was recorded daily. On d 50, blood samples were obtained 2 h after the morning concentrate offer to determine serum glucose and insulin concentrations. On d 52, ruminal fluid samples were obtained via an esophageal tube, and pH was measured immediately. Data were analyzed with a mixed-effects model with repeated measures, except for pH values that had no repeated measures. During the preweaning period, starter intake was similar among treatments, but ADG tended ($P = 0.053$) to be greater in low NDF than in high NDF treatments (0.69 vs. 0.63 ± 0.020 kg/d, respectively). However, during the 2 wk after weaning, supplementation of forage improved ($P < 0.05$) concentrate intake and ADG without affecting the gain to feed ratio. Probably, the greater starter intake observed in forage-supplemented calves was mainly due to the greater ruminal pH found in forage-supplemented calves compared with forage-deprived calves (5.81 vs. 5.05 ± 0.063, respectively). On the other hand, the insulin to glucose ratio was greater ($P < 0.05$) in forage-supplemented compared with non-forage calves (6.53 vs. 4.24 ± 0.125 ng/L to mg/dL, respectively). In conclusion, a low NDF starter should be recommended during the preweaning period, and the provision of chopped hay is necessary right after weaning to improve calves performance.

Key Words: forage, NDF content, young calves

804 Fat and fatty acid sources affect growth and health of milk-fed calves.

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Fatty acid profiles of milk and milk replacer (MR) differ. Calf MR in the US are made from lard or tallow, which are low in short- and medium-chain fatty acids and linolenic acid. This 56-d trial compared a control MR containing 27% CP and formulated with 3 fat and fatty acid compositions. The 3 MR treatments were A) only lard totaling 17% fat, B) animal fat supplemented with butyrate, medium chain fatty acids, and linolenic acid using a commercial product (1.25% NeoTec4 MR, Provimi North America, Brookville, OH) totaling 17% fat, and C) milk fat totaling 33% fat. Holstein calves (24 female, 24 male; 41 ± 1 kg initial BW; 2 to 3 d of age) from a single farm were fed 660 g of DM from MR for 42 d and weaned. Starter (20% CP) and water were fed ad lib for 56 d. Calves were housed in a naturally ventilated nursery with added heat during the summer of 2011. Calves were in individual pens with straw bedding. Pen was the experimental unit. Data were analyzed as a completely randomized design with a 3 (MR treatment) by 2 (sex) factorial arrangement as a repeated measures mixed model. Pre-planned contrast statements of treatments A vs. B and A vs. C were used to separate means. There were no interactions of MR treatment by sex. Starter intake did not differ. Calf ADG and feed efficiency differed ($P < 0.05$; A < B, A < C). Pre-weaning days with scours differed ($P < 0.05$; A > B). Titers to bovine respiratory parainfluenza-3 and bovine virus diarrhea type 1 (vaccinations to these pathogens were on d 7 and 28) in serum samples taken on d 49, and 56 differed ($P < 0.05$; A < B). Concentrations of urea nitrogen and glucose in serum samples taken on d 7, 21, 28 differed ($P < 0.05$; A > B, A > C). The MR with lard was less optimal than the other 2 MR for baby calf growth and health.

Key Words: fat, fatty acids, dairy calf

805 Fatty acid profile and global gene expression in liver of calves supplemented with linoleic acid.

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Aim was to assess the fatty acid (FA) profile and global expression of genes in liver of calves fed increased linoleic acid (LA) during the first 30 d of life. Within 2 h of birth, bull calves (n = 31) were fed 4 L of good quality colostrum and assigned randomly to receive milk replacer (MR) with low (LLA, 0.56% LA) or high concentration of LA (HLA, 1.78% LA, DM basis) twice daily at 6.7 g of fat per kg of metabolic BW. Amounts fed were adjusted weekly. Liver biopsy was performed at 30 d of age. Microarray analysis (n = 9 per MR) was performed using GeneChip Bovine Genome Array from Affymetrix; transcriptome expression was analyzed by one-way ANOVA. The HLA treatment upregulated 236 genes whereas 265 genes were downregulated ($P < 0.05$, fold change ratio ≥1.3). KEGG pathway analyses were employed with WebGelstat database. Main upregulated biological pathways were focal adhesion, metabolic pathway, MAPK pathway, and PPAR α signaling. Some genes involved in these pathways were actinin α 2 (ACTN2), collagen type IV (COL4A4), acyl-CoA synthetase (ACSL6), prostaglandin D2 synthase (PTGDS), cytochrome P450 (CYP2E1), PPAR α (PPARA), filamin C (FLNC), and transforming growth factor B3 (TGFB3). The main downregulated biological pathways were metabolic pathways, T cell receptor signaling, Type II diabetes mellitus, and pentose phosphate pathway. Some genes related with these pathways were pyruvate kinase (PKLR), phospholipase (PLD1), phosphofructokinase (PFKM), 3-hydroxyisobutyate dehydrogenase (HIBADH), phosphoinositide 3-kinase (PIK3R3), and protein kinase C (PRKCQ). Liver FA were analyzed by gas-liquid chromatography. Total FA concentration of liver tissue was 8.5 vs. 7.6 g FA/100 g tissue (DM basis, LLA vs. HLA, $P < 0.02$). Calves fed HLA-MR had greater ($P < 0.01$) liver concentrations (g/100 g FA) of LA (22.1 vs. 15.9), PUFA (43.1 vs. 35.5), and n-3 FA (5.1 vs. 4.2). Calves fed LLA-MR had greater ($P < 0.02$) concentrations (g/100 g FA) of SFA (45.1 vs. 40.0) and MUFA (16.3 vs. 14.3). Supplementing LA increased LA content of liver and altered the expression of key genes involved in different hepatic metabolic processes.

Key Words: calves, linoleic acid, gene expression

806 Use of tail skin temperature as a proxy for core body temperature in neonatal Holstein male calves.

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Our objective was to determine if tail skin temperatures could be used as a proxy for core body temperature in neonatal Holstein male calves to have continuous measurements of body temperature over multiple days. A total of 79 calves were used in 3 measurement periods (7+ d each). Thermocron (Maxim Integrated Products, Inc., Sunnyvale, CA) were attached to the underside of the tail immediately proximal to the observable vein using expandable tape (Vetrap, 3M, St. Paul, MN). These calves were then used to compare core body temperature (as measured via rectal temperature, M700 digital thermometer, GLA Agricultural Electronics, San Luis Obispo, CA) and measured tail skin temperatures. Rectal temperatures were manually measured and recorded along with the clock time and date. These were then matched to the recorded skin temperature closest in time from individual Thermocrons (continuous recording every 10 min) and those data used in mixed model regression analysis. The final data set used 1178 paired observations coded to indicate day of trial, calf, and time of day (AM or PM). The model used had fixed terms for recorded tail temperature and day of trial. Time of day, calf and period were included as random terms. Day of trial was found to be non-significant and removed from the model. All other terms remained significant at $P < 0.05$. The final model adjusted for calf, period, and time of day. Rectal temperature (°C) was best predicted as tail temperature (°C) * 0.4964 ± 0.02551 + 19.9177 ± 0.9869. This equation has an R^2 of 0.6120, variance inflation factor of 2.57, and RMSPE of 0.68°C. Tail skin temperature is related to rectal temperature in neonatal male calves and can be used as a noninvasive proxy for core body temperature.

Key Words: calves, model, temperature

807 Body temperature of neonatal male Holstein calves is partially influenced by ambient temperature in the calf nursery.

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Neonatal mammals have limited ability to regulate their body temperature. This ability improves as the animal ages. However, even adult mammals ability to thermoregulate is known to be influenced by the ambient conditions. An experiment was designed to determine the extent that ambient temperatures influenced body temperature in neonatal male Holstein calves housed in a non-temperature controlled calf nursery. A total of 78 calves were used in 3 measurement periods (7+ d each). Each calf had Thermocron (Maxim Integrated Products, Inc., Sunnyvale, CA) attached to the underside of the tail immediately

proximal to the observable vein using expandable tape (Vetrap, 3M, St. Paul, MN). Calves were initially 2 d old and were monitored for 56 d. Ambient temperature was recorded using a Thermocron suspended inside the calf facility. Temperatures were recorded every 10 min and exhibited a circadian rhythm. All calves were housed in a single naturally ventilated barn with no added heat. Calves were housed in 1.2 × 2.4 m wire mesh stalls and bedded with straw. Calves were fed a common diet of milk replacer and ad libitum starter. Water was available at all times. Mixed model regressions were used to evaluate the relationship between ambient temperature and body temperature. Lag periods of 10 min from 0 to 120 min were calculated and used as potential regressors. Calf and trial were included in the model as random effects. Measurement time was modeled as a repeated term. Fixed terms were sequentially removed from the model until only significant terms remained and the variance inflation factor was less than 10 at which time the model was considered optimally parameterized. The accepted model included random terms of calf and trial in addition it includes terms for intercept, ambient temperature at the time of body temperature recording and ambient temperature 10, 20, 30, 40, 50, 100, and 120 min before body temperature reading. The model has log-likelihood R^2 of 0.32 and a variance inflation factor of 1.46. Body temperature in neonatal calves had a circadian rhythm and was partially related to ambient temperatures indicating that they may have troubles thermoregulating in periods of extreme temperature swings.

Key Words: calf, body temperature, ambient temperature

808 Jersey calf performance in response to high protein, high fat liquid feeds with varied fatty acid profiles.

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Most commercially available milk replacers (MR) use edible lard as the main fat source; it contains primarily long-chain fatty acids (LCFA). However, 10.8% of fatty acids (FA) in Jersey whole milk are medium-chain fatty acids (MCFA). Coconut oil (CO) is a rich source of MCFA. The objective was to determine whether altering the FA profile of MR with varying amounts of CO, to more closely match the FA profile typically found in whole milk from Jersey cows, would improve Jersey calf growth. This randomized complete block design trial was conducted at Waterman Dairy (Columbus, OH) from November, 2010 through August, 2011. Male (n = 18) and female (n = 32) Jersey calves were randomly assigned at birth to 1 of 4 liquid diets: pasteurized Jersey saleable whole milk (pSWM; 27.9% CP, 33.5% fat, DM basis); MR containing 100% of fat as edible lard (100:00; 29.3% CP, 29.1% fat); MR containing 20% of fat as CO (80:20; 28.2% CP, 28.0% fat); MR containing 40% of fat as CO (60:40; 28.2% CP, 28.3% fat). Calves were fed 2L of their respective liquid diet twice daily from 2d of age until 7wk of age, and once daily until weaning (8wk of age). Calves had ad libitum access to starter and water. Calf BW was recorded at birth and once weekly for 9 wk. Feed intake and scour days (number of days with fecal score > 2) were recorded daily. Hip height (HH) and wither height (WH) were taken at birth, 4, 7, and 9 wk. Average daily gain, BW, WH, and HH did not differ by treatment. Calves fed pSWM had a higher milk DMI than calves fed 80:20 (0.523 vs. 0.498 kg/d). There was no effect of CO on milk DMI. Grain DMI and total DMI did not differ among treatments. Calves fed pSWM had an increase in days with a fecal score >2 compared with calves fed 80:20 (4.24 vs. 2.00 d). Coconut oil had a quadratic effect on fecal score, with calves fed 100:00, 80:20, and 60:40 scouring 4.00, 2.00, and 3.63 d, respectively. In conclusion, DMI and ADG were similar among treatments. Differences among treatments in fecal scores implicate possible benefits of MCFA inclusion on calf health, presumably due to their known antimicrobial properties.

Key Words: Jersey calf, milk replacer, fatty acids

809 Methods of reducing milk replacer to prepare dairy calves for weaning when large amounts of milk replacer have been fed.

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Numerous trials and labs have reported that calves fed large amounts of milk replacer (MR) and weaned over 7 d (or less) have reduced ADG from depressed starter intake, lessened rumen development, and reduced post-weaning digestion. At least 3 laboratories have implemented 21 to 25 d weaning periods that ameliorated the ADG and intake problems. We compared different gradual weaning programs to have calves fully weaned after 42 d on MR. Measurements were made for 56 d. Calves were 2 to 3 d old Holstein male calves (44 ± 1.2 kg BW) sourced from a single farm and housed in individual 1.2 by 1.4 m pens within a naturally ventilated nursery. A textured 20% CP starter and water were fed free-choice. Trials were completely randomized designs using repeated measures with means separated using pre-planned contrasts. In Trial 1, a 27% CP, 17% fat MR fed at 0.66 kg DM/d for 42 d (LOW) was compared with the same MR fed at 0.88 kg/d for 21 d and reduced to 0.66 kg/d in one step for 21 d (HIGH), or a 22% CP, 27% fat MR fed at 0.79 kg/d for 21 d and changed to the 27% CP, 17% fat MR fed at 0.66 kg/d for 21 d before weaning (HIFAT). Calves fed HIGH had greater ($P < 0.05$) ADG and similar starter intake compared with calves fed LOW, while calves fed HIFAT had lower ($P < 0.05$) starter intake and ADG compared with calves fed LOW. In Trial 2, the same 27% CP, 17% fat MR was fed at 0.66 kg DM/d for 42 d (LOW), fed at 0.96 kg/d for 21 d and reduced to 0.66 kg/d in one step for 21 d (HIGH), or fed at 0.96 kg/d for 28 d and gradually reduced compared with HIGH over 14 d before weaning (HIGRAD). Calves fed both HIGH and HIGRAD had greater ($P < 0.05$) ADG and similar starter intake to calves fed LOW. Weaning calves over 14 to 21 d that had been fed MR at 0.88 kg DM or more did not result in reductions in ADG and starter intake. Treatment HIGH tested in both trials and published previously is relatively simple to implement.

Key Words: feeding rate, milk replacer, weaning

WSASAS Symposium: Ruminant Stress: Implications on Health and Performance of Ruminants

810 Effects of environment on fetal programming in ruminant livestock. S. W. Limesand,* D. T. Yates, A. R. Macko, and X. Chen, *University of Arizona, Tucson.*

Environmental heat stress reduces placental transfer of oxygen and nutrients to the fetus and can influence the set-points of metabolic pathways. Developmental adaptive responses to heat stress-induced placental insufficiency promote thrifty fetal metabolism and are necessary for in utero survival. However, thrifty metabolic programming can be detrimental after birth when sufficient nutrition and oxygen are available. The endocrine pancreas plays an important role in metabolic homeostasis even before birth by secreting insulin from β-cells in response to stimulation by nutrients, thus coordinating fetal growth with nutrient supply. Our goal is to understand the mechanisms by which developmental adaptations in β-cells occur in heat-stressed fetuses and determine how they manifest into less desirable production traits. We induce placental insufficiency and intrauterine growth restriction (IUGR) in fetal sheep by exposing the pregnant ewe to chronic heat stress during mid-gestation. This treatment results in fetal hypoxemia and hypoglycemia that progressively worsens throughout the third trimester. Glucose-stimulated insulin secretion (GSIS) in IUGR fetuses is also reduced by more than 80% compared with controls due to a 78% reduction in β-cell mass and less insulin per β-cell. However, β-cells isolated from IUGR fetuses secrete more insulin relative to total insulin content in vitro, indicating that stimulus-secretion coupling is greater than in control β-cells. In contrast, fetal sheep that are hypoglycemic only (produced by chronic maternal insulin infusion) exhibited a 45% reduction in GSIS in vivo as well as diminished insulin secretion from isolated islets. Together, these data demonstrate that hypoxemia is a major cause of developmental adaptations observed in β-cells after fetal heat stress. We are currently exploring elevated catecholamines as a mediating factor of hypoxemic effects. Plasma norepinephrine concentrations are negatively correlated with blood oxygen content and have been shown to inhibit insulin secretion. We have recently found that fetal islets chronically exposed to elevated norepinephrine in vivo exhibit enhanced insulin secretion after norepinephrine is removed, indicating that adaptive changes persist.

Key Words: intrauterine growth restriction, heat stress, pancreas

811 An evaluation of cold stress on ruminant nutritional requirements. B. Olson,* *Montana State University, Bozeman.*

In northern climates, cold may challenge a cow's ability to meet its energy/nutritional requirements during winter. For this reason, cattle are commonly fed 2 to 3 tons of hay per head, at high cost, to offset this perceived stressor, presumably because cold, often combined with wind, is thought to challenge a cow's thermal balance. At times, feeding hay meets a cow's direct physiological needs. Besides being fed hay during winter, cold temperatures can increase activity level, shivering, or metabolic rate, which require energy, or increase use of energy reserves, which reduces insulation. However, these are not long-term responses to cold stress. Alternatively, cattle in good body condition entering winter adjust behaviorally to maximize energy gain, primarily from the sun, and to minimize energy loss, primarily from wind. They also may reduce activity level under extreme conditions, and lower metabolic rate to conserve energy. Cattle that do not adjust, and subsequently produce a weak calf or do not rebreed are likely to be culled. Several studies indicate that the 1996 NRC model over-estimates maintenance requirements for beef cattle grazing winter range, presumably because the model does not account for the benefits of solar energy to help meet a cow's thermal balance, and their behavioral adjustments to winter conditions.

Key Words: cold, thermal, winter

812 An evaluation of temperament on performance and health of ruminants. R. F. Cooke,* *Oregon State University, EOARC, Burns.*

Temperament is defined as the fear-related behavioral responses of cattle when exposed to human handling. Our group evaluates cattle temperament using: 1) chute score; 1–5 scale that increases according to violent behavior during chute restraining, 2) exit velocity; speed of cattle exiting the chute, 3) exit score; dividing cattle according to exit velocity into quintiles and using a 1–5 scale (slowest to fastest quintiles), and 4) temperament score; average of chute and exit scores. To facilitate interpretation and dissemination of results, our group also assigns a final temperament type to cattle; adequate temperament (ADQ; temperament score ≤3) or aggressive temperament (AGR; temperament score >3). To understand the implications of temperament on beef production, our group recently evaluated the impacts of this trait on cattle productive, reproductive, and health parameters. As expected, AGR cattle had greater plasma cortisol vs. ADQ cattle during handling, independent of breed type (*Bos indicus* × *B. taurus*, $P < 0.01$; *B. taurus*, $P < 0.01$) or age (cows, $P < 0.01$; heifers, $P < 0.01$). In regards to reproduction, AGR females had reduced annual pregnancy rates vs. ADQ cohorts, independent of breed type (*B. indicus* × *B. taurus*, $P = 0.03$; *B. indicus*, $P = 0.05$). Moreover, *B. taurus* AGR cows had decreased pregnancy rate ($P = 0.03$), calving rate ($P = 0.04$), weaning rate ($P = 0.09$), and kg of calf weaned/cow exposed ($P = 0.08$) vs. ADQ cohorts. In regards to feeder cattle, AGR calves had reduced weaning BW ($P = 0.04$), heightened acute-phase protein response upon feedlot entry ($P \leq 0.05$), and reduced carcass weight ($P = 0.07$) vs. ADQ cohorts. Our group also reported that exposing *B. indicus* × *B. taurus* or *B. taurus* heifers to frequent human handling improved temperament ($P \leq 0.02$), reduced plasma cortisol ($P < 0.01$), and hastened puberty ($P \leq 0.02$). Similar benefits, however, were not observed in mature cows or feeder cattle. In conclusion, temperament affects productive, reproductive, and health parameters of beef cattle independent of breed type. Hence, strategies to improve herd temperament are imperative for optimal production efficiency of beef operations worldwide.

Key Words: cattle, production, temperament

813 Impact of weaning, transportation. and vaccination stress on beef cattle performance. J. D. Arthington,* *University of Florida, Range Cattle Research and Education Center, Ona.*

Stress is the result of an external or internal pressure which causes an organism to deviate from homeostasis. Professionals engaged in food animal production systems are certainly aware of the range of stressors affecting their animals; however, the repercussions of these events on nutrition and performance considerations are recently becoming better understood. This presentation will discuss research findings directed toward the acute phase protein (APP) reaction and performance of beef calves. Our research, and the work of others, has identified several instances where BW gain was negatively correlated to blood concentrations of APP. Although other studies have linked APP concentrations to instances of feedlot morbidity and/or disease, our research has focused on response variables collected from overtly healthy cattle being exposed to normal production stressors such as weaning, vaccination, transportation, and castration. Each of these practices will create an inflammatory reaction in cattle, the magnitude of which depends on a variety of factors which are currently not well understood. These can be both deliberate and non-deliberate in nature. Some common deliberate production practices are castration or the inclusion of an adjuvant within a vaccine. Production practices which may induce non-deliberate inflammatory responses include transportation, weaning, and commingling. Typically, deliberate production stressors are associated with some degree of tissue injury, whereas non-deliberate production stressors are linked to a disruption in social order, depression, or anxiety. Despite the source of stress, these inflammatory reactions tend to respond similarly in beef cattle and lead to the initiation of the APP reaction. The APP reaction begins with the production of pro-inflammatory proteins called cytokines (namely interleukin −1, interleukin-6, and tumor necrosis factor α). These cytokines are the initial instigators of the acute phase reaction, which orchestrates the subsequent production of APP and ultimately metabolism alterations affecting feed intake, nutrient utilization, and growth. These cytokines are highly pleiotropic and affect food animal performance both (1) directly, by decreasing circulating concentrations of insulin-like growth factor-1 via a reduction in hepatic cell sensitivity to growth hormone, and (2) indirectly, by stimulating the production of plasma proteins, thus diverting energy and nutrients away from BW gain and toward the production of inflammatory proteins and support of the immune system. In terms of total protein mass, the combination of immunoglobulin and the APP sum the majority of plasma protein mass observed following an acute phase inflammatory reaction. Our research group has specifically targeted 3 APP, including haptoglobin, ceruloplasmin, and fibrinogen. These proteins were selected due to their abundance in the blood of cattle responding to inflammatory signals, their acceptable stability during storage (i.e., freezing, thawing, and refreezing), and their relatively simple and cost-effective measurement in routine assay systems. The collective results of these studies implicate an important relationship between beef calf performance and the APP response to normal production stressors. An overreaching goal of these efforts is to seek modifications to beef production practices that help ameliorate the inflammatory response and thus improve beef cattle performance and well-being.

Key Words: stress, acute phase proteins, cattle

814 Impact of environmental stress on feedlot cattle.

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In the Midwest and Plains states, the heat waves of 1995, 1999, 2006, 2009, and 2010 were particularly severe with documented cattle losses approaching 5,000 head each year. However, during the summer of 2011, nearly 15,000 head of cattle perished across 5 states as a result of heat stress. The winters of 1992 to 93, 1996 to 97, 1997 to 98, 2006 to 07, and 2008 to 09 also caused hardship for cattle producers with some feedlots reporting losses in excess of 1,000 head. Up to 50% of the newborn calves were lost in many areas with over 75,000 head of cattle lost in the Northern Plains states during the 1996 to 97 and 2008 to 2009 winters. Late fall and early winter snowstorms in 1992, 1997, and 2006 resulted in the loss of over 25,000 head of feedlot cattle each year in the Central and Southern Plains of the United States. Economic losses from reduced performance of cattle experiencing severe environmental stress likely exceed losses associated from cattle death by 5- to 10-fold. Use of alternative supplementation programs may need to be considered for cattle challenged by adverse environmental conditions. Use of additional water for consumption and cooling, shade, and/or alternative management strategies need to be considered to help cattle cope with heat stress. During the winter, catastrophic losses typically occur during severe snowstorms, however early winter moisture combined with poor drying conditions may result in greater losses in performance and income due to muddy lot conditions and muddy cattle. Strategies need to be employed to minimize effects of mud, which is probably the single largest contributor to poor cattle performance in winter and spring. The above-mentioned weather events suggest that there are ample opportunities for cattle producers to minimize impact of environmental stress. Data will be presented regarding use of environmental models to determine benefits of sprinklers, shade and/or other mitigation techniques, which can reduce animal discomfort and address consumer concerns regarding welfare of animals housed outside. A greater understanding of cattle responses to weather challenges will be conveyed to caretakers to help animals cope with adverse climatic conditions.

Key Words: environmental stress, models, livestock management

Breeding and Genetics: Swine Breeding

815 Estimation of genetic parameters for birth weight, pre-weaning mortality and hot carcass weight in a crossbred population of pigs. M. Dufrasne*[1,2], I. Misztal[3], S. Tsuruta[3], J. Holl[4], K. A. Gray[4], and N. Gengler[1], [1]*Animal Science Unit, Gembloux Agro-Bio Tech, University of Liege, Gembloux, Belgium,* [2]*FRIA, Brussels, Belgium,* [3]*Department of Animal and Dairy Science, University of Georgia, Athens,* [4]*Smithfield Premium Genetics Group, Rose Hill, NC.*

Economically important traits, such as piglet mortality and growth potential, are both associated with birth weight (BRW) and therefore it is possible that BRW could be used as an early indicator for indirect selection for piglet survival and final weight. The aim of this study was to estimate genetic parameters for BRW, weaning mortality and growth traits in a commercial crossbred population of pigs to improve selection in a purebred terminal sire line. The edited data set consisted of 21,618 crossbred pigs from 262 purebred Duroc sires and 1,987 crossbred non-pedigreed Large White x Landrace dams. Traits analyzed were BRW, pre-weaning mortality (PWM) and hot carcass weight (HCW). All pigs had BRW and PWM records and 15,946 of these pigs had records for HCW. A multiple trait model with fixed effects of sex, dam parity and contemporary group, defined as month by year of birth, and random effects of sire, dam, litter and residual was utilized in the analysis. The mean BRW was 1.41 kg, the mean HCW was 93.4 kg and the percentage of PWM was 19.7%. PWM and HCW were nonlinear functions of BRW. PWM (HCW) were 75.51% (88.24 kg) for $BW < 0.7$ kg, 38.76% (91.71 kg) for $BW < 1.2$ kg and 11.75% (94.03 kg) for $BW > 1.4$ kg. The phenotypic correlations between BRW and HCW and between BRW and PWM were 0.11 and −0.28, respectively. Estimates of heritability and common litter effect were 0.19 and 0.11 for BRW, 0.04 and 0.06 for PWM, and 0.05 and 0.09 for HCW, respectively. Estimated genetic correlations were −0.75 between BRW and PWM, 0.49 between BRW and HCW, and −0.33 between PWM and HCW. Selection for increased birth weight in purebred terminal sire line may improve pre-weaning survival and final weight in the crossbred population.

Key Words: birth weight, genetic correlation, growth traits

816 Effect of within-year variation on growth performance and subsequent reproductive performance in gilts. C. R. G. Lewis*[1,2], K. L. Bunter[1], and S. Hermesch[1], [1]*Animal Genetics and Breeding Unit (AGBU), University of New England (UNE), Armidale, NSW, Australia,* [2]*PIC North America, Hendersonville, TN.*

Uniform performance is required for optimal production. This study aimed to examine within-year variation observed on gilts for production traits and their subsequent breeding performance. Data consisted of 5060 gilts from 3 breeds (Large White, Landrace and Duroc) and 3 herds in Australia over 15 years. Production traits were average daily again (ADG $\mu = 662$g/d) and backfat (BF $\mu = 10.9$mm) recorded at a live weight (WT) of 100kg. Reproduction traits were total born (TB $\mu = 10.6$), the number born alive (NBA $\mu = 9.76$), the number of stillbirths (SB $\mu = 0.83$) and farrowing age (FA $\mu = 384$) recorded in the first parity. General linear models were utilized to examine variation associated with month (12 levels, calendar month) at recording. Significant effects for all traits were herd, year, month, breed and the interaction between month and breed, which were fully cross-classified in these data. Farrowing age was fitted as a linear covariate for TB, NBA and SB, and TB was a linear covariate for SB. The production traits were also corrected for dam parity and birth litter size. Models for reproduction traits also included the animal's performance traits fitted within month. Least squares means (LSM) and associated P-values by breed, month and the month*breed interaction were assessed to examine differences in the within-year variation for traits and any possible breed (genetic) differences. The ranges in LSM for the effects of month were ADG = 50g/d, BF = 1.1mm, TB = 0.67, NBA = 0.72, SB = 0.23 and FA = 15.7d (min and max for all traits $P < 0.05$ difference). Growth rate was higher and BF was lower in cooler months. The differences between winter and summer were larger in magnitude for Duroc in comparison to the other 2 breeds. For reproduction traits, less TB were produced in cooler months (mated during the summer) and SB was higher for summer farrowings. Further analyses showed that if variation is generated in growth performance before breeding, then there is a differential effect on variation in the reproductive traits. Linear regressions of FA on ADG nested within month of farrowing resulted in ADG solutions of −0.35d/g in winter and −0.12d/g in summer. Quantifying the different sources of within-year variation and their interactions is of economic importance and could suggest paths for intervention strategies to increase uniformity in performance.

Key Words: gilts, variation, growth

817 Towards robust sows: Heat tolerance expressed in fecundity traits. S. Bloemhof*[1,2], E. Knol[1], E. van der Waaij[2], and I. Misztal[3], [1]*TOPIGS Research, Beuningen, the Netherlands,* [2]*Animal Breeding and Genomics Centre, Wageningen, the Netherlands,* [3]*Department of Animal and Dairy Science, University of Georgia, Athens, Georgia, United States of America.*

Globalization results in increased pork production, especially in warm climates such as Latin America and Asia. This requires a robust sow that is tolerant to environmental perturbations such as disease and heat tolerance, without compromising production. Objective of this study is to evaluate the effect of heat stress during the reproduction cycle of the sow on farrowing rate (FR) and litter size (LS). This as a start for genetic improvement of heat tolerance in sows and genetic selection for robust sows. Data included 22,750 observations on FR (0 or 1) and LS (1–25), on 5,024 sows. Sows of a purebred Yorkshire dam line were located on 16 farms in Spain and Portugal. Outside temperature data were available. Sows are exposed to heat stress when temperature exceeds the upper critical temperature (UCT). In a previous study the UCT for FR was estimated to be 19.2°C and for LS to be 21.7°C. Heat load can be calculated as temperature-UCT. To simplify the analysis, the effect of heat stress was studied as the effect of temperature or heat load per day on FR or LS; analyses included temperatures/heat loads from 28 d before until 75 d after insemination. Correlations were estimated between temperature/heat load and LS and FR for each day. Strongest correlation between temperature and FR was −0.09 on d 22 before insemination; −0.13 on d 16 before insemination in gilts, and −0.09 on d 18 before insemination in sows (parity > 1). Correlations increased marginally when estimated between FR and heat load instead of temperature. Heat load had the largest effect on FR on d 21 before insemination. Strongest correlation between temperature and LS was −0.04 on d 10 after insemination; −0.08 on d 10 after insemination in gilts. Correlations increased when estimated between LS and heat load instead of temperature. Heat load had the largest effect on LS on d 10 after insemination, intriguingly this is 2 d before implantation. In conclusion, gilts are more susceptible for heat stress than older sows. A genetic model for genetic improvement of heat tolerance in sows for LS and FR should include heat load instead of temperature as correlations between LS/FR were strongest with heat load.

Key Words: sows, fecundity, heat stress

818 A comparison of methods for predicting litter size in commercial pig lines. L. Tusell*[1], P. Perez[1], S. Forni[2], X. L. Wu[1], and D. Gianola[1], [1]*Department of Animal Sciences, University of Wisconsin, Madison,* [2]*Genus Plc, Hendersonville, TN.*

Genome-assisted evaluation requires statistical models capable of dealing with high-dimensional genotype data while yielding accurate predictions of merit of selection candidates. Various methods have been proposed for genome-enabled selection. Here, several procedures were compared with regard to their ability to predict phenotypes in 2 purebred pig lines and their cross. Data represented 2,598, 1,604 and 1,879 sows from 2 purebred and one crossbred line, respectively. Phenotype was the average number of piglets born, pre-corrected for systematic environmental effects. Genotypes were obtained using the Illumina PorcineSNP60 BeadChip. SNPs with minor allele frequency <0.05 and call rate >0.95 were excluded, yielding 46,855, 45,597 and 50,151 SNPs for the 2 purebred and crossbred lines, respectively. Missing genotypes were imputed from average allele frequencies at each locus. A 10-fold cross-validation assessed predictive ability of Bayesian Lasso, Bayesian Ridge Regression, Genomic BLUP, Reproducing Kernel Hilbert Spaces with kernel averaging, and a Radial Basis Function Neural Network using either the additive genomic relationship matrix (RBF-G) or principal component scores of the SNP matrix (RBF-UD) as inputs. Within line, methods yielded similar predictive ability, except for RBF models. The average correlation between observed and predicted phenotypes in testing sets (r) was higher in the crossbred line (0.27) than in purebred lines (0.19–0.23). RBF-G had the worst predictive ability in all lines: r = 0.10 and 0.17 in purebreds, and 0.21 in crossbreds. On the other hand, RBF-UD yielded the best predictive ability (r = 0.30) in crossbreds. This suggests that population structure affects predictive ability. When prediction was assessed in a large data set, principal component scores of the SNP matrix led to better predictive results, possibly because these scores are more informative than genomic relationships.

Key Words: genomic selection, neural networks, pigs

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SYMPOSIA AND ORAL SESSIONS

Animal Behavior and Well-Being: Pain and Discomfort in Farm Animals

819 Pain and discomfort in farm animals. S. T. Millman,* *Iowa State University, Veterinary Diagnostic and Production Animal Medicine, Ames.*

Animal pain is at the forefront of public concerns about animal welfare. In the field, animal caregivers and veterinarians must recognize species-specific and insult-specific responses to pain for timely diagnosis and treatment of ill and injured animals within the herd or flock. State animal protection laws typically prohibit “unnecessary pain and suffering,” and provide exemptions for customary livestock husbandry practices. However, defining what pain may be deemed “unnecessary” and which routine surgical procedures are “customary” is a contentious debate for the legal system and for livestock producers. Regional differences exist in terms of husbandry practices that are criticized, as well as the manner in which animal pain is addressed by animal producers, veterinarians, and policymakers. Differences in regulations and policies about painful husbandry procedures occur partly due to cultural reasons and public pressure, as well as understanding of animal welfare science, practical and economic constraints for implementation by producers and differences in data requirements for drug approval by regulatory agencies, especially for food producing species. Pain is defined by the International Association for the Study of Pain as “an unpleasant sensory and emotional experience associated with actual or potential tissue damage.” For both humans and animals, affective states such as pain can only be measured indirectly, and hence present challenges when designing experiments to gather empirical data. Whereas verbal self-reporting is the Gold Standard for pain assessment in humans, non-verbal procedures such as operant preference/avoidance tests are needed to enable animals to respond to our questions about their feelings of pain and distress. Interdisciplinary research teams, including animal scientists, biomedical scientists, agricultural engineers and applied ethologists, are developing novel and emerging techniques to facilitate scientific scrutiny of animal pain, to explore endogenous mechanisms of analgesia and to evaluate novel and currently available pain mitigating interventions. Understanding species-specific responses to pain and techniques to measure animal pain and distress in the laboratory or on farm, and efficacy of pain mitigating interventions are essential for development of socially acceptable husbandry guidelines, effective management of convalescent livestock and decision-making about humane endpoints, culling and euthanasia.

Key Words: pain, analgesia, animal welfare

820 The impact of housing and exercise on inflammatory molecules in the joints of open gilts. M. W. Orth,* J. M. Mapes, C. I. Robison, J. E. Link, and G. M. Hill, *Michigan State University, East Lansing.*

Osteoarthritis, a degenerative disease of articular cartilage, can contribute to the incidence of lameness in sows. Housed in gestation crates, sows spend much of their reproductive lives with limited mobility. Joint disuse may exacerbate joint degeneration. Degradation of articular cartilage produces an inflammatory process within the joint. The purpose of these studies was to determine if housing type and exercise affect the production of inflammatory molecules in joints. The objective was to measure concentrations of prostaglandin E2 (PGE2), interleukin-6 (IL-6), and leukotriene B4 (LTB4) in radioulnar joint synovial fluid. In Study 1, 16 Yorkshire × Landrace gilts, with an average BW of 125 kg, were housed in gestation crates (C, n = 8) or pens (P, n = 8) for 8 wk. Crates measured 0.6 m × 2.1 m and pens measured 2.4 × 3.0 m, with 4 animals per pen. In study 2, 18 gilts of the same breed cross (average BW of 114 kg) were housed in crates of the same dimensions. For 8 wk, 9 gilts ran 217 m, 5 d/wk (E), while the other 9 gilts remained in crates without exercise (NE). In both studies at the end of 8 wk sows were harvested and both forelimbs were collected from each gilt and placed on ice. Legs were cleaned of soft tissue while maintaining a closed radioulnar joint. Synovial fluid samples were collected via hypodermic needles, placed in microcentrifuge tubes, and stored at −80°C. Concentrations of PGE2, IL-6, and LTB4 were measured in the synovial fluid. There were no differences in PGE2, IL-6, or LTB4 concentrations between C and P gilts in Study 1. In Study 2 concentrations of IL-6 and LTB4 were not different between E and NE gilts. Non-exercised gilts had higher PGE2 concentrations than E gilts. Prostaglandin E2 is produced by articular cartilage as a result of trauma or degradation and inhibits collagen synthesis and activates matrix metalloproteinases. Therefore, higher concentrations of PGE2 in the joints of NE gilts over a period of time may be problematic. Even a short daily bout of exercise may reduce or prevent the production of inflammatory molecules in sedentary animals.

Key Words: inflammation, housing, exercise

821 Argon versus CO_2 gas induction of unconsciousness in piglets. L. J. Sadler*[1], T. M. Widowski[2], C. Wang[1], A. K. Johnson[1], and S. T. Millman[1], [1]*Iowa State University, Ames,* [2]*University of Guelph, Guelph, Ontario, Canada.*

The objective of this study was to compare efficacy of argon and CO_2 gases to induce unconsciousness and effects on piglet distress. Sixty-six 7-d-old piglets (BW 3.27 ± 0.24) from 11 litters were utilized. Three treatments were compared: 100% CO_2, 100% argon (ARG) and a control novel odor (peppermint: ODOR), supplied at 35% chamber volume exchange rate/min. Piglets were tested as pairs utilizing a modified Euthanex AgPro (Value-Added Science and Technology, Mason City, IA). Piglets were placed in the box and exposed to gas treatment until 30 s after loss of posture, at which time they were removed, checked for signs of sensibility (corneal reflex, pupil dilation and nose prick), and then placed in a pen until normal behavior resumed. ODOR piglets remained in the box for 14 min. Digital audio recordings were collected using a Marantz PMD 661 recorder and Crown PZM185 microphone during exposure to gas and analyzed with the STREMODO program for distress vocalizations. Individual piglets were weighed on d0 and d+1 relative to treatment and at weaning. Pupil dilation occurred in more ARG than CO_2 pigs (59% vs. 23%, $P = 0.02$), but there were no differences between gases for other signs of sensibility ($P > 0.1$). Piglets exposed to ARG took longer to lose posture ($P < 0.001$; 70 ± 8 vs. 214 ± 6, s) and to regain sensibility ($P = 0.03$; 371 ± 62 vs. 567 ± 64, s). ARG piglets performed more distress vocalizations while in the box compared with the other 2 treatments (ARG 8.8 ± 0.38, CO_2 0.34 ± 0.88 and ODOR 0.23 ± 0.25, % conscious time in which piglets were emitting a distress calls, $P < 0.001$). There were no ADG or weight differences between treatments. In conclusion, ARG to induce insensibility was more distressing for piglets than CO_2 based on number of distress calls, and increased latencies to loss of posture and return of sensibility.

Key Words: insensibility, distress, argon

822 Return to sensibility: Use of yohimbine (alpha 2-antagonistic reversal agent) for anesthetized sows.

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The objective of this study was to evaluate yohimbine efficacy as an anesthetic reversal agent for sows. A total of 12 mixed parity sows (233.6 ± 18.7 kg) were individually housed in pens. Sows were anesthetized using a combination of Xylazine (4.4 mg/kg), Ketamine (2.2 mg/kg), and Telazol (4.4 mg/kg) injected IM. Following a 20-min stabilization period, palpebral reflex was tested to confirm insensibility, and sows were injected with either S (0.1 mg/kg) or Y (0.1mg/kg) IM in the neck. Following anesthetization, 2 anesthesia reversal treatments were compared in a cross over design; TRT 1: sterile saline (S; n = 12) and TRT 2: yohimbine (Y; n = 12). A 3-point scale (0 = alert, 1 = diminished response, 2 = unresponsive) was used to score 5 sensibility responses every 10 min. including; human approach test (HAT), sow posture, palpebral reflex, jaw tone, and nose prick. Data were analyzed using PROC MIXED of SAS. For all sensibility parameters (mean ± SE), sows returned to sensibility faster when treated with Y compared with S; palpebral reflex (45.2 ± 10.7 vs. 115.3 ± 11.2 min) jaw tone (71.3 ± 23.2 vs. 271.8 ± 25.9 min) nose prick (73.9 ± 22.5 vs. 200.8 ± 23.5 min) HAT (187.2 ± 32.6 vs. 413.1 ± 33.8 min, $P < 0.001$), and sow posture (293.54 ± 35.5 vs. 458.3 ± 37.9 min), respectively. In addition, Y reduced overall recovery time by 172 min (289.9 ± 41.0 Y vs. 461.9 ± 42.4 S min, $P < 0.001$). In conclusion, Yohimbine is an effective reversal agent in sows. Yohimbine use reduced overall recovery time and reduced latency to regain sensibility. This drug may be a tool that veterinarians and researchers can use to ensure that sows recover from anesthesia with minimal complications more quickly. Yohimbine should be considered as an adjunct treatment when anesthetizing sows based on welfare benefits associated with faster return to sensibility and reduced recovery time.

Key Words: anesthesia, yohimbine, swine

823 Herd-level risk factors for hock injuries in US freestall herds.

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The aim was to investigate herd-level risk factors associated with the prevalence of hock injuries on Holstein herds in the northeastern United States (NE; n = 38) and California (CA; n = 38). One group of high production multiparous cows was monitored on each farm and data on housing, production, management, lying behavior and the condition of the hocks were collected. Focal cows (38 mean ± 3 SD), randomly selected from the assessment group, were evaluated for hock injuries on a scale of 1 to 5 (1 = healthy and 5 = evident swelling and severe lesion). Outcome variables were the (logit-transformed) proportion of cows having at least a minor hock injury (≥2) or moderate-to-severe injury (≥3). Univariable associations ($P \leq 0.05$) between predictors and outcome variables are presented. Prevalence of overall and moderate-to-severe injuries in the NE averaged (±SD) 80.7 ± 22.6 and 55.4 ± 27.6, respectively. The odds of either injury decreased with access to pasture (OR ≤0.17), deep bedding (OR ≤0.05), sand bedding (OR ≤0.06), bedding dry matter (%; OR ≤0.96), daily lying time (h/d; OR ≤0.51), lying bout duration (min; OR ≤0.93), and bedding hygiene (OR ≤0.25). The odds of these injuries increased with the number of lying bouts (OR ≥1.36), group variation in lying bouts (OR ≥1.80), brisket board height (cm; OR ≥1.09). Prevalence of overall and moderate-to-severe injuries in CA averaged (±SD) 56.7 ± 21.8 and 16.2 ± 17.1, respectively. The odds of overall hock injuries in CA decreased with daily lying time (h/d; OR = 0.52) and increased with stall stocking density (%; OR = 1.04). The odds of moderate-to-severe hock injuries decreased with herd milk production (OR = 0.72 for a 1,000-kg increase). These results suggest that improvement in barn design and management can decrease hock injuries.

Key Words: leg injury, animal welfare, barn design

824 Herd-level risk factors for lameness in US freestall herds.

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The objective was to identify herd-level risk factors for lameness in free stall housed Holstein herds in the northeastern United States (NE) and California (CA). Measures of productivity, management, housing, lying behavior and gait scores for the high producing group were collected in 40 farms in NE and 39 in CA. Predictors associated with the (logit-transformed) proportion of lame or severely lame cows at $P < 0.20$ were submitted to a multivariable general linear model and retained if $P < 0.05$. Prevalence of clinical lameness averaged (±SD) 30.8 ± 15.5% in CA and 54.8 ± 16.7% in NE; whereas, severe lameness averaged 3.6 ± 4.2% in CA and 8.2 ± 5.6% in NE. In the NE, clinical lameness decreased with herd size, deep bedding, and access to pasture, and increased with average herd lactation number and sawdust bedding. Severe lameness decreased with herd size, access to pasture, deep bedding, sand bedding, bedding hygiene and raising of heifers on farm. The final model for clinical lameness ($R^2 = 0.55$) included herd size (OR = 0.94, CI = 0.91–0.97, for a 100-cow increase), deep bedding (OR = 0.51, CI = 0.35–0.75) and average herd lactation number (OR = 2.45, CI = 1.49–4.00). The final model for severe lameness ($R^2 = 0.60$) included herd size (OR = 0.93, CI = 0.89–0.96, for a 100-cow increase) and deep bedding (OR = 0.35, CI = 0.23–0.53). In CA, clinical lameness decreased with herd size, water trough space per cow, bedding hygiene, and presence of rubber in the alley to the milking parlor, and increased with the variability of the lying bout duration. Severe lameness decreased with bedding hygiene, frequency of manure removal in the pen, and average frequency of lying bouts, and increased with average lactation number, average lying bout duration and variability of the lying bout duration. The final model for clinical lameness ($R^2 = 0.48$) included variability of the lying bout duration (min; OR = 1.06, CI = 1.03–1.09) and presence of rubber in the alley (OR = 0.54, CI = 0.35–0.81). The model for severe lameness ($R^2 = 0.42$) included variability of the lying bout duration (min; OR = 1.07, CI = 1.02–1.12) and average lactation number (OR = 3.33, CI = 1.58–7.01). In conclusion, changes in management factors may help decrease the prevalence of lameness on dairy farms.

Key Words: cow comfort, barn design, lying behavior

825 Differences in pain thresholds associated with active and healing digital dermatitis lesions in dairy cattle.

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Lameness is one of the primary animal welfare concerns in the dairy industry. Digital dermatitis, an infectious cause of lameness, is common in dairy cattle and appears to be painful. The pressure algometer is a tool that reliably quantifies pain responses in cattle and swine. The objective of this study was to determine pain thresholds associated with active and healing digital dermatitis lesions. Two hundred fourteen cases of digital dermatitis were enrolled in this trial, with a convenience sample (n = 129) re-examined either once or twice 3 to 12 d following treatment with tetracycline hydrochloride. Cows were restrained in a hydraulic lift table for hoof exams and lesion identification. Digital dermatitis lesions were classified as active, healing or healed. The 1 cm diameter tip of the pressure algometer was pressed against the lesion until the cow performed a leg withdrawal response, and the corresponding force was recorded in kg. Data were censored at 25kg, the maximum pressure recording limit for the device. Regression analysis of survival data, with robust sandwich variance estimates aggregated over cow, was used to distinguish pain associated with active, healing, or healed cases of digital dermatitis. Pain thresholds were significantly different between lesions that were classified as active, healing, or healed ($P < 0.0001$), with mean force (±SD) of 7.90kg (±9.45), 12.84kg (±10.49) and 25.0kg (±0) for active, healing and healed lesions, respectively. Contrast statements demonstrated that all 3-way comparisons were significantly different ($P < 0.001$). Measurement of pain thresholds using pressure algometry confirmed that digital dermatitis lesions are painful. Although pain is reduced during the healing stage relative to the initial active stages of disease, cattle remain twice as sensitive to pressure during healing versus when lesions are fully healed. These results indicate pain management should be considered when treating digital dermatitis, and pressure algometry could be used in future research to determine efficacy of pain management interventions for lameness in cattle.

Key Words: pain, digital dermatitis, lameness

826 Effects of anti-GnRF vaccine Bopriva and band castration on acute indicators of pain in feedlot beef cattle under North American management practices.

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Angus bulls (n = 60; 257 d of age; initial BW 358.8 ± 3.98 kg) were used to study the effect of an anti-GnRF vaccine and band castration on acute indicators of pain. Cattle were randomly assigned to 1 of 3 treatments: Bulls (C), band-castrated animals without pain mitigation (B), and animals administered an anti-GnRF vaccine Bopriva (I). Animals were randomly assigned to one of 6 pens and were fitted with a radio frequency ear tag so that individual animal feed intake could be recorded daily using an electronic feed bunk monitoring system. Two doses of Bopriva were administrated on d −35 and 0, and band-castration was performed on d 0. Visual analog scores (VAS) indicative of pain or discomfort were used to visually assess the behavioral responses of the bulls to the treatments on d −36, −35, −1, and 0 and salivary cortisol on d −35 and 0 as well as at −30, 0, 30, 60, 120, and 270 min post castration. Blood samples were collected on d 1, 2, 5, and 7 for determination of complete blood count (CBC). Data were analyzed using a mixed-effects model with castration, time and their interactions as main effects. No treatment differences in salivary cortisol or VAS ($P = 0.76$ and $P = 0.33$, respectively) were observed on d −35. However, on d 0, B cattle had greater ($P < 0.05$) salivary cortisol concentrations (4.6 ± 0.45 nmol/L) than C or I cattle (3.1 ± 0.45 and 3.3 ± 0.45 nmol/L, respectively). Also, VAS assessed on d 0, was 78.2 and 78.9% greater in B than C and I cattle, respectively. CBC did not differ ($P > 0.05$) between treatments on d 0, 1, and 2. However, on d 7, platelet concentration was greater ($P < 0.01$) in I than in C and B cattle. There was no indication that vaccination with Bopriva caused physiological or behavioral changes indicative of pain or discomfort. In contrast, band-castration resulted in elevated cortisol and VAS scores indicative of a pain response. Administration of Bopriva may be a welfare-friendly alternative to traditional castration methods for beef cattle.

Key Words: beef welfare, anti-GnRF vaccine, band castration

827 Effect of road transport and lairage on body temperature of feedlot steers.

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The effects of 6.5 h transport, location within truck trailer, and 16 h in lairage (LAR) following transport on the body temperature (TB) of 60 Angus steers (120 d grain-fed) were studied. Steer TB was obtained at 30 min intervals via transmitters surgically implanted 150 d before transport. Cattle were weighed and randomly allocated to a truck pen (10/pen) on loading. The truck had 3 upper deck (UD) pens (unshaded) and 3 lower deck (LD) pens (shaded). Ambient temperature (TA) and relative humidity (RH) were obtained every 30 min from loggers placed within each truck pen and at 4 lairage locations. During the trip TA was greater (29.7 ± 0.14°C;$P < 0.05$) on the UD compared with 28.5 ± 0.12°C on the LD. RH was lower ($P < 0.05$) on the UD compared with the LD at 31.8 ± 0.48% and 34.4 ± 0.41% respectively. At LAR mean TA and RH were was 24.4 ± 0.16°C and 52.4 ± 0.36% respectively. During loading TB increased from 39.4 ± 0.11°C to 40.2 ± 0.11°C. On commencement of travel TB of UD and LD cattle were 41.0 ± 0.08°C and 40. Nine ± 0.08°C ($P = 0.62$) respectively. Time series analysis was used to determine the effects of travel duration, time in LAR and location within truck on TB. Over the first 3 h of travel TB of LD cattle fell by 1.1 ± 0.7°C ($P < 0.01$) compared with 0.8 ± 0.7°C for UD cattle. Overall UD cattle TB (40.5 ± 0.11 C) were greater ($P < 0.01$) than LD cattle (40.0 ± 0.12°C). When the truck stopped for welfare checks (n = 4) TB of UD cattle increased by 0.5 to 1.1°C and 0.1 to 0.2°C for LD cattle. When travel re-commenced TB returned to the pre-stoppage values. On arrival at LAR the TB of UD and LD cattle were 40.1 ± 0.11 and 39.9 ± 0.11°C respectively ($P = 0.08$). During 16 h in LAR there were no differences between UD and LD cattle (mean TB = 39.3 ± 0.01°C; $P = 0.11$). Minimum TB (38.9 ± 0.11°C) occurred at 0300 h, and then increased gradually (39.4 ± 0.13°C) to 0900 h. The TB increase was likely due to human activity and animal movement within pens. Cattle previously on the UD were exposed to solar radiation and therefore had a greater heat load than those on the LD. However this did not appear to have any carry-over affects while the cattle were in LAR.

Key Words: transport, body temperature, steers

Forages and Pastures III

828 An electronic rising plate meter improves ability to accurately determine cool-season annual forage availability: I. Calibration.

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A key component of managing grazing enterprises and conducting grazing research is accurate and timely forage availability determination. Hand clipping quadrats is labor intensive, typically resulting in too few samples collected to accurately estimate paddock forage mass. An electronic rising plate meter (Jenquip ECO9, Feilding, New Zealand) can quickly produce immediate, objective estimates of forage availability. Our objective was to develop a set of equations to convert plate height to dry forage mass and determine the accuracy and precision of the plate meter estimated forage mass in cool-season annual forage. The plate meter was calibrated by observing the plate meter reading (settled plate-height, cm) centered on a 1,452 cm^2 quadrat and subsequently hand clipping the forage in the quadrat to ground level. Forage was bagged, weighed wet, dried for 72-h in a forced air oven at 50°C, and reweighed. Twenty such samples were collected on 14 to 28-d intervals (Oct 25, 2011 to Jan 19, 2012) at 2 locations (total data sets = 15, total samples n = 300). The data sets included measurements of wheat and rye, each grazed and ungrazed. Forage dry weight measured on individual quadrats (range 234 to 8,557 kg/ha) was regressed (PROC MIXED) on linear and quadratic centered plate height (plate height range 0 to 43 cm) with data set as a random effect. The analysis revealed that the quadratic term was not significant so it was removed. The random effects of data set tended to cluster into 2 groups that could be associated with time of year. Adding a season fixed effect with 2 levels, fall and spring (defined as before and after Jan 1, respectively) significantly improved the model fit. The equations were fall: 92.07 × plate height (cm) + 352 kg/ha, and spring: 154.82 × plate height (cm) + 699 kg/ha. The model had an r^2 of 81% in a simple linear regression with dummy variables for season. The limit of agreement was 0 ± 1,323 kg/ha at 95% confidence. This indicates that a single plate height is an unbiased estimator of forage mass that will be within 1,323 kg/ha of the clipped forage mass measurement 95% of the time. To reliably estimate mean forage mass in a paddock, several plate height measurements are needed.

Key Words: plate meter, forage mass

829 An electronic rising plate meter improves ability to accurately determine cool-season annual forage availability: II. Application.

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A key component of managing grazing enterprises and conducting grazing research is accurate and timely forage availability determination. An electronic rising plate meter (Jenquip ECO9, Feilding, New Zealand) can produce immediate estimates of forage availability quickly and objectively. The plate meter was calibrated (method described in a companion abstract), and the resulting equation had an r^2 of 81% in a simple linear regression. A single plate height forage mass estimate is imprecise but unbiased. Therefore, many plate height samples will improve the precision of the forage mass estimate in a paddock. Further, spatial variation of forage availability is a major component of the error of estimating forage mass. To characterize spatial variation, multiple plate heights were collected from random locations in paddocks in 2 data sets (data set 1: 90 plate heights in each of 10 paddocks of ungrazed wheat; data set 2: 60 plate heights in each of 12 paddocks of grazed rye). Coefficient of variation of plate heights within a paddock ranged from 23% to 45%. Confidence in the paddock estimates was increased by sampling more heights in each paddock and taking the means of forage mass estimates. For example, in an paddock with low estimated forage mass (1,043 kg/ha), collecting 5, 10, 30, or 60 random plate heights per paddock produced estimates of paddock forage mass with 95% confidence limits of 202, 142, 78, and 61 kg/ha, respectively. In an example paddock with high estimated forage mass (4,115 kg/ha), collecting 5, 10, 30, or 60 random plate heights per paddock produced estimates of paddock forage mass with 95% confidence limits of 792, 568, 356, and 226 kg/ha, respectively. Practitioners and researchers can use this relationship to optimize the number of plate height measurements for each enterprise or experiment.

Key Words: plate meter, forage mass

830 Evaluation of forage quality predictors in early- and late-maturing cultivars of annual ryegrass (*Lolium multiflorum* Lam.).

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Annual ryegrass (*Lolium multiflorum* Lam.) is a commonly utilized cool-season forage in the Southeast. Conventional laboratory predictors of forage quality (FQ) are based in large measure on the inverse relationship between cell wall constituents and digestibility with advancing forage maturity. However, total nonstructural carbohydrates (TNC) could have a more robust statistical relationship with digestibility than does fiber concentration in early-maturing cool-season annuals that exhibit significant growth with decreasing temperature and photoperiod. A field experiment was conducted to determine DM yield and FQ characteristics in an early-maturing Japanese (J) cultivar (Shiwasuaoba) and a conventional cultivar (Marshall; M) as influenced by planting date. Forty-eight plots were established at 2-wk planting-date (PD) intervals (8 plots/date) at the E.V. Smith Research Center in Tallassee, AL, from September through November 2008. The experimental design was a randomized complete block (n = 4) with split-plot restriction in which cultivars were subplots. Plots were harvested when forage canopy height reached 20 cm. Samples harvested from the first and second PD (PD1 and PD2, respectively) were analyzed for IVDMD and concentrations of NDF, ADF and TNC. Standard regression of TNC on IVDMD revealed adjusted r^2 values of 0.55, 0.18, 0.00 and 0.00 for M, and 0.00, 0.89, 0.19, and 0.00 for J from PD1 in successive regrowth harvests. For PD2, values for M were 0.00, 0.13, 0.79, and 0.00, and for J were 0.82, 0.70, 0.73, and 0.00. Standard regression of ADF on IVDMD from the same harvests revealed adjusted r^2 of 0.97, 0.59, 0.00, and 0.62 for M, and 0.00, 0.99, 0.99, and 0.85 for J from PD1. Harvests of M from PD2 had adjusted r^2 values of 0.39, 0.99, 0.80 and 0.76, and J had values of 0.91, 0.99, 0.95, and 0.00. Data are interpreted to mean that concentration of ADF was the superior predictor of forage quality across both cultivars and planting dates, but that concentration of TNC shows promise as a reliable predictor of FQ in early-season harvests of the early-maturing cultivar.

Key Words: annual ryegrass, total nonstructural carbohydrates, forage quality

831 Response of postpartum dairy cows to different grazing strategies: Effect of herbage allowance on milk and solids production. M. Sprunck[1,2], D. A. Mattiauda[1], G. Motta[1], M. Fajardo[1], and P. Chilibroste*[1], *[1]Facultad de Agronomía, Paysandú, Paysandú, Uruguay, [2]Agencia Nacional de Investigación e Innovación, Montevideo, Montevideo, Uruguay.*

The effect of contrasting herbage allowances on animal performance for early lactation Holstein dairy cows was under research. The experiment was carried out in autumn 2010 at the EEMAC, Research Station, Agronomy Faculty, Uruguay (30° S). Dairy cows (n = 36, LW = 572 ± 68 kg) were blocked by parity, expected calving date, LW and BCS, and randomly assigned to one of the following treatments: high (H: 14.5 kg DM day^{-1}/100 kg LW), medium (M: 9.6 kg DM day^{-1}/100 kg LW), and low (L: 8.3 kg DM day^{-1}/100 kg LW) herbage allowances (HA, n = 12 each). Grazed in individual plots of a 2nd year mix pasture (30% *Trifolium repens* and 70% *Festuca arundinacea*) between am and pm milking (7:30 to 14:30 h). After pm milking cows were supplemented with 8.5 kg DM of a TMR diet (CP = 171 ± 10 g/kg DM, NDF = 400 ± 20 g/kg DM). The chemical composition of herbage samples were: HHA (CP = 178 ± 34 g/kg DM, NDF = 449 ± 58 g/kg DM), MHA (CP = 170 ± 30 g/kg DM, NDF = 463 ± 62 g/kg DM) and LHA (CP = 169 ± 29 g/kg DM, NDF = 487 ± 69 g/kg DM). Dry matter intake from pasture was estimated with Diet Check approach (Heard, J. W. et al., 2004). The experimental design was randomized complete block. There were no significant differences in pasture DMI, but increased milk production and milk solids production (protein and fat, kg/cow/day) was observed for HHA and MHA treatment. This could be due to the lower NDF in the diet of these cows since herbage DMI did not differ between treatments. Increased of pasture allowance from low to medium and high herbage allowances per cow, increased milk solids production (protein and fat) resulting from a better quality of herbage intake.

Table 1. Measurements

	Herbage allowance			
Item	Low	Med	High	*P*-value
Milk (L/cow/day)	24.3	27.3	25.9	0.003
% Milk fat	3.74	3.62	3.8	0.137
% Milk protein	3.12	3.19	3.21	0.008
Milk fat (kg/cow/day)	0.902	0.993	0.985	0.039
Milk protein (kg/cow/day)	0.757	0.871	0.829	< 0.001
LW (kg)	551	549	540	0.681
Pasture DMI (kg/DM)	15.6	15.7	15.4	0.275

Key Words: early lactation, grazing, herbage allowance

832 The effects of time of allocation of a ryegrass-based pasture on animal performance, nitrogen utilization and grazing behavior from late-lactation dairy cows. R. E. Vibart,* D. Pacheco, K. Lowe, and B. A. Barrett, *AgResearch Ltd., Grasslands Research Centre, Palmerston North, New Zealand.*

The consumption of a more balanced fermentable carbon to nitrogen (N) ratio from herbage can potentially enhance herbage dry matter intake (HDMI), milk production, and N utilization by dairy cows, particularly those in late lactation. Eighty lactating cows (225 ± 3.3 DIM) were used to examine the effects of allocating a morning (0730 h, AM; 2 herds) vs. an afternoon (1530 h, PM; 2 herds) fresh pasture strip of a ryegrass (*Lolium perenne* L.)-based pasture on milk production, N utilization, and grazing behavior during 4 weeks in autumn (April, 2010). Cows grazed on the same pasture strip for a 24-h period, and were offered similar daily herbage DM allowance. Herbage composition differed among treatments. Herbage from the PM treatment had greater DM (22.7 vs. 19.9%; $P < 0.01$), organic matter (OM; 89.5 vs. 88.9%; $P < 0.01$) and water soluble carbohydrate concentrations (WSC; 10.9 vs. 7.6%; $P < 0.01$), primarily at the expense of crude protein (CP; 20.5 vs. 22.2%; $P < 0.01$) and neutral detergent fiber (NDF; 48.8 vs. 50.4%; $P < 0.05$). Estimates of HDMI did not differ among treatments; mean values (±SE) were 12.8 ± 0.64 kg/d. Although milk yield was similar among treatments, trends toward greater milk fat, milk protein, and milksolids (MS) yields were observed for cows on the PM treatment (684 vs. 627 g milk fat, 545 vs. 505 g milk protein, and 1228 vs. 1132 g MS/cow, respectively; $P < 0.10$). Estimates of urinary N excretion (g/d) did not differ among treatments; mean values (±SE) were 219.6 ± 6.9 g N/d. Initial HM available (kg DM/ha) and instantaneous HM disappearance rates (kg DM/ha and per h) did not differ among treatments, but fractional disappearance rates (0.56 vs. 0.74%/h for AM vs. PM treatments, respectively) differed among treatments ($P < 0.05$). Despite similar partitioning of N toward urine, given similar amounts of herbage allocation, a simple change in management practice such as allocating a fresh strip later in the day resulted in moderate increases in N captured in milk and MS yields in late-lactation dairy cows.

Key Words: grazing, herbage allocation, nitrogen utilization

833 Effect of stocking rate and cow lactation stage on nitrogen balance of grazing dairy cows considering two periods of supplementation at pasture. A. I. Roca-Fernandez,* D. Baez-Bernal, and A. Gonzalez-Rodriguez, *Agrarian Research Centre of Mabegondo, La Coruna, Galicia, Spain.*

To achieve high levels of efficiency from dairy systems is important to make the best use of nutrients for feeding cows by setting appropriate grazing management strategies on farms. For this, a balance between offer and demand has to be established at cow level. The aim of our study was to investigate the effect of stocking rate (SR), low (L, 3.9 cows/ha) vs. high (H, 5.2 cows/ha), and cow lactation stage (LS), early (E, 30 DIM) vs. middle (M, 135 DIM), on nitrogen (N) balance of grazing dairy cows. Seventy-two Holstein-Friesian cows were randomized in a block design with a 2 × 2 factorial arrangement of 4 treatments (LE, LM, HE, and HM). ΣN inputs (grass, silage, and concentrate) and ΣN outputs (milk and live weight) were evaluated in dairy cows grazing on rotationally perennial ryegrass-white clover swards. Two periods of supplementation at pasture, with (P1, March–April) vs. without (P2, May–August), were considered. Data were analyzed using PROC MIXED in SAS. Pasture and silage intake were higher ($P < 0.001$) in cows at the middle LS (15.9 ± 1.5 and 7.8 ± 0.8 kg of DM/cow per day) than in cows at the early LS (12.6 ± 0.2 and 6.2 ± 0.2 kg DM/cow per day) while concentrate intake was higher ($P < 0.001$) in cows at the early LS (4.1 ± 0.1 kg DM/cow per day) than in cows at the middle LS (1.5 ± 0.2 kg DM/cow per day). ΣN inputs were higher ($P < 0.001$) in cows at the early LS (189 ± 14 g N/cow per day) than in cows at the middle LS (163 ± 2 g N/cow per day). ΣN outputs were higher ($P < 0.001$) in cows at the early LS (121 ± 9 g N/cow per day) than in cows at the middle LS (105 ± 5 g N/cow per day). No differences were found between the 2 LS for N excretion. Supplements intake was higher ($P < 0.05$) in the high SR groups (10.4 ± 0.2 kg DM/cow per day) than in the low SR groups (9.2 ± 0.9 kg DM/cow per day). No differences were found between the 2 SR for ΣN inputs, ΣN outputs and N excretion. ΣN inputs were higher ($P < 0.001$) in the P1 (237 ± 8 g N/cow per day) than in the P2 (114 ± 19 g N/cow per day). ΣN outputs were higher ($P < 0.001$) in the P1 (140 ± 10 g N/cow per day) than in the P2 (86 ± 8 g N/cow per day). N excretion was higher ($P < 0.001$) in the P1 (479 ± 67 g N cow/

ha) than in the P2 (68 ± 24 g N cow ha-1). Increasing supplementation at pasture produced lower efficiency of N utilization by dairy cows.

Key Words: nitrogen efficiency, grazing dairy systems, supplements

834 Milk performance of two dairy cow genotypes (Holstein-Friesian vs. Normande) at two levels of supplementation (low vs. high) in long residence time grazing paddocks. A. I. Roca-Fernandez*[1,2], L. Delaby[3], S. Leurent[4], M. E. Lopez-Mosquera[2], and A. Gonzalez-Rodriguez[1], [1]*Agrarian Research Centre of Mabegondo, La Coruna, Galicia, Spain,* [2]*University of Santiago de Compostela, Lugo, Galicia, Spain,* [3]*INRA Agro-Campus Ouest UMRPL, Saint Gilles-Rennes, Bretagne, France,* [4]*INRA Experimental Farm Le Pin au Haras, Borculo-Exmes, Normandy, France.*

Grazing long residence time paddocks is a way to reduce management practices, fencing and labor in dairy farm conditions. Milk performance response of 2 dairy cow genotypes, Holstein-Friesian (H) vs. Normande (N), managed at 2 levels of concentrate supplementation at pasture, low (0 kg DM/cow per day) vs. high (4 kg DM/cow per day), was investigated during 9 years (2001–2009) at Le Pin au Haras (Normandy, France) experimental farm using the simplified rotational grazing system. Cows (n = 72) were randomly assigned in a block design with a 2 × 2 factorial arrangement of 4 grazing treatments (H0, H4, N0 and N4). Animals were rotationally grazing on 3 large paddocks (2.3 ha) with a mean residence time per paddock of 10 d. The aim of this research was to study the maximum of milk yield (MY max., at d 4) and the subsequent drop of milk (Dm, at d 10) reached in each long residence time grazing paddocks for both cow genotypes managed at both feeding regimens. Daily milk yield (MY) was recorded and every 10 d the MY max. and Dm were calculated. Data were analyzed using PROC MIXED in SAS. On average, milk production was higher ($P < 0.001$) in the Holstein-Friesian cows than in the Normande cows (7,452 ± 483 over 6,067 ± 358 kg/cow per year). The highest milk performance was reached by the H4 group (8,407 ± 285 kg/cow per year) and the lowest by the N0 group (5,401 ± 587 kg/cow per year) with the other 2 groups (H0, 6,497 ± 680 and N4, 6,733 ± 120 kg/cow per year) in between. Supplemented cows produced more milk ($P < 0.001$) than unsupplemented cows (7,570 ± 207 over 5,949 ± 634 kg/cow per year). The MY max. and Dm were higher ($P < 0.001$) in the Holstein-Friesian cows (25.5 ± 2.3 and −6.2 ± 0.6 kg/cow) than in the Normande cows (21.3 ± 1.6 and −4.7 ± 0.5 kg/cow). The group of cows feeding concentrate at pasture showed higher ($P < 0.001$) MY max. and lower ($P < 0.001$) Dm (25.6 ± 1.6 and −5.3 ± 0.2 kg/cow) than unsupplemented cows (21.2 ± 1.9 and −5.7 ± 0.4 kg/cow). The results indicate the importance of controlling the MY max. and the Dm reached in each long residence time grazing paddocks for both cow genotypes at both levels of supplementation. In each paddock, a cyclic 10 d grazing sequence was observed for MY response without affecting milk performance of cows over the whole lactation.

Key Words: dairy cow breeds, simplified rotational grazing system, milk peaks and drops

835 Effect of daily herbage allowance (low vs. high) and cow lactation stage (early vs. middle) on sward quality and milk performance of grazing dairy cows. A. I. Roca-Fernandez,* A. Gonzalez-Rodriguez, and O. P. Vazquez-Yañez, *Agrarian Research Centre of Mabegondo, La Coruna, Galicia, Spain.*

Sward structural characteristics have been shown to influence grass nutritive value, sward quality, pasture dry matter (DM) intake and milk performance of cows at different stage of lactation. The aim of this study was to investigate the effect of 2 daily herbage allowances (DHA), low (L, 25 kg DM cow^{-1} day^{-1}) vs. high (H, 30 kg DM cow^{-1} day^{-1}), on sward quality and milk performance of cows at 2 lactation stages (LS), early (E, 30 DIM) vs. middle (M, 135 DIM). Seventy-two Holstein-Friesian cows were randomized in a block design with a 2 × 2 factorial arrangement of 4 treatments (LE, LM, HE and HM). Animals grazed rotationally perennial ryegrass-white clover swards from March to August using variable stocking rates to impose the fixed DHA treatments. Sward quality was determined by NIRS System 6500. Daily milk yield (MY) was recorded by Alprow System and weekly milk composition was measured by MilkoScan FT6000. Data were analyzed using PROC MIXED in SAS. The low DHA treatments had more rotations ($P < 0.05$, +1 rotation), lower rotation length ($P < 0.05$, −3.7 d) and more grazing days ($P < 0.05$, +13 d) in comparison to the high DHA treatments (4 rotations, 31.4 d per rotation and 126 grazing days). The low DHA treatments showed lower pre- and post-grazing sward heights ($P < 0.05$, −2.1 and −1.0 cm) than the high DHA treatments (16.4 and 6.4 cm, respectively). The low DHA treatments presented lower ($P < 0.05$) DM content (18.4%), acid (ADF, 284 g kg^{-1} DM) and neutral detergent fiber (NDF, 509 g kg^{-1} DM) while higher ($P < 0.05$) crude protein (CP, 149 g kg^{-1} DM), water soluble carbohydrates (WSC, 167 g kg^{-1} DM) and digestibility in vitro of organic matter (747 g kg^{-1} DM) in comparison to the high DHA treatments (DM, 20.3%; ADF, 312 g kg^{-1} DM; NDF, 546 g kg^{-1} DM; CP, 131 g kg^{-1} DM; WSC, 149 g kg^{-1} DM; digestibility, 730 g kg^{-1} DM). There were differences on sward quality between rotations for both DHA treatments. The highest ($P < 0.05$) DM (26.2%) and fiber levels (ADF, 369 g kg^{-1} DM and NDF, 626 g kg^{-1} DM) and the lowest ($P < 0.05$) crude potein (CP, 106 g kg^{-1} DM), carbohydrates (WSC, 93 g kg^{-1} DM) and digestibility levels (678 g kg^{-1} DM) were found in the last rotation compared with the first rotation (DM, 16.4%; ADF, 231 g kg^{-1} DM; NDF, 433 g kg^{-1} DM; CP, 160 g kg^{-1} DM; WSC, 226 g kg^{-1} DM; digestibility, 803 g kg^{-1} DM) due to higher sward quality deterioration when grazing season advanced (from rotation 1 to 5) in both DHA treatments. Cows managed at the early LS showed higher ($P < 0.05$) MY (+5.3 kg cow^{-1} day^{-1}), with the lowest ($P < 0.05$) milk protein (−2.4 g kg^{-1}) and fat (−2.2 g kg^{-1}), than cows managed at the middle LS (19.5 kg cow^{-1} day^{-1}), with the highest ($P < 0.05$) milk protein (31.3 g kg^{-1}) and fat (39.1 g kg^{-1}). No differences were found on MY between both DHA treatments (L, 22.4 vs. H, 22.1 kg cow^{-1} day^{-1}), but higher ($P < 0.05$) milk protein (+0.9 g kg^{-1}) and fat (+1.0 g kg^{-1}) were observed in the low DHA treatments compared with the high DHA treatments (milk protein, 29.7 and fat, 37.5 g kg^{-1}). Decreasing DHA resulted in higher sward quality and milk protein and fat without penalizing MY.

Key Words: rotational grazing, grass nutritive value, pasture-based dairy system

836 Rearing of dairy heifers at pasture from temperate regions (Galicia, NW Spain). A. I. Roca-Fernandez,* A. Gonzalez-Rodriguez, and O. P. Vazquez-Yañez, *Agrarian Research Centre of Mabegondo, La Coruna, Galicia, Spain.*

To reduce rearing costs, some Galician dairy farmers have considered use of pasture as the main source of nutrients for heifers for 8 mo per year (5 mo, spring grazing + 3 mo, autumn grazing) and use of grass and maize silages to supplement heifers the remaining 4 mo. A study was carried at CIAM (NW Spain) experimental farm during 2 consecutive years to evaluate sward and animal responses of dairy heifers within different age and managed at different stocking rate. The aim of this research was to identify appropriate grazing management strategies capable of being implemented on farms for reaching acceptable daily body weight (BW) gains of dairy heifers. The trial involved spring-calving Holstein-Friesian heifers (n = 40) rotationally grazing perennial ryegrass and white clover pastures from March to July and supplemented with mixed silage (grass and maize), when grass production and/or sward quality was not appropriate to achieve desirable daily BW gains at pasture, due to summer drought in August and September and cold winter season in January and February. Sward variables related to grassland management as SR, herbage utilization and grass quality were determined and animal variables related to animal performance as BW, body condition score (BCS), rump height and daily BW gains were weekly controlled in 2 groups of dairy heifers at different age (young, 11 mo vs. old, 13 mo). Data were compared using Tukey′s test. On average SR was of 3.85 animals/ha, herbage utilization of 65%, sward crude protein content of 145 g/kg of DM and digestibility in vitro of organic matter of 783 g/kg of DM. Despite the seasonality observed in Galician grass production and quality across the year (higher grass nutritive value was found in spring grazing than in autumn grazing), daily BW gains in both dairy heifer groups ranged from 0.620 to 0.980 kg/d during the experimental period. Average daily BW gain at pasture was of 0.770 kg/d in both dairy heifer groups, with higher ($P > 0.05$) BW gains observed in young heifers (0.828 kg/d) than in old heifers (0.717 kg/d) due to young heifers were managed at lower SR ($P < 0.05$; 3.17 animals/ha) than old heifers (4.69 animals/ha). Average BCS in both dairy heifer groups was of 2.86 (over 5) reaching 440 kg of BW per animal with a rump height of 137 cm to insemination. Animals in both dairy heifer groups were inseminated within 15 mo of age while on pasture. Average pregnancy rate was of 80% and calving was programmed at 24 mo in both dairy heifer groups. Results from this trial show that rearing of dairy heifers at pasture is influenced by sward (SR) and animal (age) factors. Higher daily BW gains were observed in young heifers than in old heifers due to lower SR was applied in young heifers than in old heifers.

Key Words: dairy replacement, daily body weight gain, grazing system

837 Milk urea concentration test as a quick response of the energy/protein balance in dairy cattle ration. A. I. Roca-Fernandez,* A. Gonzalez-Rodriguez, and O. P. Vazquez-Yañez, *Agrarian Research Centre of Mabegondo, La Coruna, Galicia, Spain.*

When management decisions need to be taken at farm level, it is important to have an appropriate diagnosis tool as the milk urea concentration (MUC) test to get a quick response of the energy-protein balance in dairy cattle ration under different feeding conditions. The aim of this trial, carried out from March to August in 2007 at CIAM (NW Spain), was to investigate the MUC response on Holstein-Friesian dairy cows (n = 90) under 2 feeding regimens, grazing (G) vs. confinement (C), for milk production. Animals at different lactation stages, early (E) vs. late (L) calving cows, were randomly assigned to 3 treatments (GE, GL, and CE). Daily milk yield (MY) was recorded by Alprow System and weekly milk composition was measured by MilkoScan FT6000. Sward, silage and concentrate chemical composition were determined by NIRS System 6500. Data were analyzed using PROC MIXED in SAS. Silage and concentrate intake were higher ($P < 0.05$) in confined cows (9.3 ± 1.5 and 6.8 ± 1.2 kg DM/cow per day) compared with grazing cows (1.4 ± 1.0 and 2.3 ± 0.7 kg DM/cow per day). There were no differences ($P > 0.05$) between grazing treatments for pasture intake (GE, 13.6 ± 1.0 vs. GL, 13.0 ± 0.9 kg DM/cow per day) and grass crude protein content (GE, 133 ± 10 vs. GL, 146 ± 12 g/kg of DM). MY (25.6 ± 0.4 kg/cow per day) and body weight (644 ± 11 kg) were higher ($P < 0.05$) in confined cows compared with grazing cows with lower MY (GE, 24.3 ± 0.7 and GL, 18.4 ± 1.2 kg/cow per day) and body weight (GE, 569 ± 9 and GL, 601 ± 10 kg). The levels of MUC were higher ($P < 0.05$) in confined cows (CE, 251 ± 10 mg/kg) than in grazing cows (GE, 192 ± 9 and GL, 222 ± 8 mg/kg). Cows at E lactation stage showed the lowest ($P < 0.05$) values of MUC during the first month of lactation (GE, 141 ± 8 and CE, 107 ± 9 mg/kg) due to animals being in a negative energy balance situation attributed to the inability for ingesting sufficient amount of nutrients from grass and/or supplements (silage and concentrate). The highest levels ($P < 0.05$) of MUC in grazing cows were reached at 2 mo after calving (GE, 269 ± 5 and CE, 282 ± 6 mg/kg) when pastures contained highly degradable protein content and had high protein-energy ratio. The MUC test was an effective quick response diagnostic tool for detecting an imbalanced ration and correcting protein-energy levels in dairy cows at different lactation stage and feeding regimens.

Key Words: cow lactation stage, feeding regimens, milk urea content

838 Effect of calving date (spring vs. autumn) and parity (primiparous vs. multiparous) on milk performance of Holstein-Friesian grazing dairy cows from Galician conditions. A. I. Roca-Fernandez,* A. Gonzalez-Rodriguez, and O. P. Vazquez-Yañez, *Agrarian Research Centre of Mabegondo, La Coruna, Galicia, Spain.*

High inputs systems are currently applied by dairy farmers using higher productivity cows (9–10 t of milk/cow per year), with shorter life persistency (2–3 lactations), higher annual replacement (40–50%) and higher rates of concentrate (3–4 t/cow per year). Nevertheless, increase on inputs costs are now driving Galician farmers to thrust on grazing systems using lower productivity cows (6–7 t of milk/cow per year), with longer life persistency (5–6 lactations), lower annual replacement (20–25%) and lower rates of concentrate (1–2 t/cow per year). Questions about cow efficiency in terms of milk production according to calving date and parity are also in farmers minds when these 2 dairy systems are compared. The aim of our study was to evaluate the effect of calving date, spring (S, 23 ± 5 DIM) vs. autumn (A, 135 ± 7 DIM), and parity, primiparous (P, 1.2 ± 0.2 lactation) vs. multiparous (M, 2.9 ± 0.4), on milk performance response of Holstein-Friesian dairy cows on spring-summer grazing conditions. Animals (n = 72) were randomized in a block design with a 2 × 2 factorial arrangement of 4 treatments (SP, SM, AP and AM) grazing rotationally perennial ryegrass-white clover pastures. Sward chemical composition was measured by NIRS System 6500. Daily milk yield (MY) was recorded by Alprow System and weekly milk composition was determined by MilkoScan FT6000. Data were analyzed using PROC MIXED in SAS. The S groups were supplemented at pasture with 6 kg/cow per day of concentrate while the A groups only received 3 kg/cow per day of concentrate. The grazing season in 2009 was divided into 3 periods according to pasture quality: (1) March–April, (2) May–July, and (3) August–September. The S groups were yielding a 32% and 22% more milk ($P < 0.001$) than the A groups (AM, 24.8 ± 1.2 and AP, 22.3 ± 0.9 kg cow-1). The MY was a 18% and 12% higher ($P < 0.001$) in the M groups than in the P groups (SP, 26.7 ± 1.5 and AP, 21.9 ± 0.7 kg/cow). The highest ($P < 0.001$) milk peak was reached by the S groups (SM, 38.8 ± 2.1 and SP, 24.9 ± 1.7 kg/cow). MY and pasture quality were progressively decreasing accross grazing season advanced. Higher ($P < 0.001$) crude protein content (160 ± 6 g/kg of DM), water soluble carbohydrates (226 ± 8 g/kg of DM) and digestibility (803 ± 18 g/kg of DM) while lower neutral detergent fiber (433 ± 11 g/kg of DM) were observed in the (1) grazing period than in the (2) and (3). The lowest ($P < 0.001$) milk protein and the highest ($P < 0.001$) fat content were reached by the A groups. The results obtained from this trial point that calving date and parity are very important factors on dairy farms conditioning cow needs and milk performance at pasture. The group of spring calving multiparous cows showed the highest milk response on spring-summer grazing while the autumn calving primiparous cows showed the lowest milk response.

Key Words: dairy cattle, stage of lactation, pasture-based milk production systems

839 Effect of oilseed concentrate source (cottonseed vs. linseed) on milk composition and fatty acids profile of dairy cows (grazing vs. silage + grazing) from NW Spain humid region. A. I. Roca-Fernandez*[1], A. Gonzalez-Rodriguez[1], O. P. Vazquez-Yañez[1], and J. A. Fernández-Casado[2], [1]*Agrarian Research Centre of Mabegondo, La Coruna, Galicia, Spain,* [2]*Agrarian and Fitopathologic Laboratory of Galicia, La Coruna, Galicia, Spain.*

Diet of dairy cows influences milk composition and fatty acid (FA) profile. The highest concentrations of conjugated linoleic acid (CLA) and unsaturated fatty acids (UFA) are usually found in pasture-based milk production systems feeding lipid supplements. The objective of this study was to investigate the effect of forage source (G, grazing vs. S, silage+grazing) on milk composition and FA profile of autumn calving Holstein-Friesian cows supplemented with different oilseed concentrates (C, cottonseed vs. L, linseed). Four groups of cows (GC, GL, SC and SL) grazed separately in 4 farmlets at CIAM (NW Spain) from spring to summer in 2008. The G groups (GC, n = 12 and GL, n = 11) were all day grazing while the S groups (SC, n = 14 and SL, n = 13) were grazing half day and received 20 kg/cow per day of grass:maize (50:50) silage (33% DM). Daily milk yield (MY) was recorded by Alprow System and weekly milk composition was measured by MilkoScan FT6000 and FA profile by gas chromatography-mass spectrometry. Short (SCFA), medium (MCFA) and long chain FA (LCFA) were determined. Mono- (MUFA) and polyunsaturated (PUFA) were calculated. Data were analyzed using PROC MIXED in SAS. Average MY was higher ($P < 0.05$) in the G groups (GC, 22.3 and GL, 21.1 kg/cow per day) than in the S groups (SC, 20.9 and SL, 20.6 kg/cow per day). Milk protein was lower ($P < 0.001$) in the G groups (GC, 30.1 and GL, 31.3 g/kg) than in the S groups (SC, 32.3 and SL, 32.0 g/kg). Milk fat was lower ($P < 0.001$) in the G groups (GC, 35.7 and GL, 37.0 g/kg) than in the S groups (SC, 38.6 and SL, 39.9 g/kg). SCFA and MCFA were lower ($P < 0.001$) in the G groups (10.7 and 40.4 g/100 g of FA) than in the S groups (12.1 and 43.4 g/100 g of FA). LCFA were higher ($P < 0.001$) in the G groups (MUFA, 23.8 and PUFA, 3.7 g/100 g of FA) than in the S groups (MUFA, 21.5 and PUFA, 3.2 g/100 g of FA). CLA content was higher ($P < 0.001$) in the G groups (1.1 g/100 g of FA) than in the S groups (0.8 g/100 g of FA). LCFA and MUFA were higher ($P < 0.05$) in the cows feeding cottonseed concentrate (37.1 and 23.4 g/100 g of FA) than in the cows feeding linseed concentrate (35.2 and 21.5 g/100 g of FA). Farmers with high reliance on grazing and cottonseed concentrate would get higher LCFA and MUFA levels in milk fat.

Key Words: grazing dairy cattle, milk fatty acids composition, lipid feed supplements

Physiology and Endocrinology II

840 The physiology of heat stress: A shift in metabolic priorities at the systemic and cellular levels. R. P. Rhoads*[1] and L. H. Baumgard[2], [1]*Virginia Polytechnic Institute and State University, Blacksburg,* [2]*Iowa State University, Ames.*

Environmental heat stress (HS) undermines efficient animal production resulting in a significant financial burden to agricultural producers. The reduction in performance parameters, either lactation or lean tissue accretion, during HS has traditionally thought to result from the typical animal response of reduced nutrient intake during environmentally driven hyperthermia. Recently, this notion has been challenged with observations indicating heat-stressed animals may exploit 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 metabolism, stemming from coordinated interactions at whole-body and tissue specific levels. Such changes are characterized by increased basal and stimulated circulating insulin concentration in addition to the ostensible lack of basal adipose tissue mobilization coupled with a reduced responsiveness to lipolytic stimuli. Hepatic and skeletal muscle cellular bioenergetics also exhibits clear differences in carbohydrate production and use, respectively due to HS. The apparent dichotomy in intermediary metabolism between the 2 tissue types may stem from factors such as TCA cycle substrate flux and mitochondrial respiration. Thus, the HS response markedly alters post-absorptive carbohydrate, lipid and protein metabolism through coordinated changes in fuel supply and utilization across tissues in a manner that is distinct from commonly recognizable changes that occur in animals on a similar reduced plane of nutrition. Perhaps most intriguing is that the coordinated systemic, cellular and molecular changes appear conserved across physiological states and among different ruminant and monogastric species. Ultimately, these changes result in the reprioritization of fuel selection during HS, which may be important for whole-body metabolism and overall physiological adaptation to hyperthermia.

841 Single and double, fixed-time insemination of postpartum sows given intravaginal triptorelin gel. N. R. Augspurger*[1], M. E. Johnston[1], M. E. Swanson[2], and S. K. Webel[1], [1]*JBS United Inc., Sheridan, IN,* [2]*Pennatek LLC, Radnor, PA.*

The objective was to compare farrowing rates and litter sizes from 1 or 2 fixed-time inseminations of sows treated with 200 μg triptorelin gel (TG: OvuGel) at 96 h post-weaning with those of untreated sows inseminated daily while in estrus. Four hundred 3 weaned sows were blocked by genetic line (Ausgene, PIC), parity (parities 1–7; average parity 3.1), and previous lactation length (range 13 to 25 d; average length 19.4 d), and allocated to one of 4 treatments: 1) Controls (n = 102) inseminated the day they were observed in estrus and at 24 h intervals for the duration of estrus; 2) TG24 sows (n = 100) treated with TG 96 h post-weaning and inseminated once 24 ± 2 h post-TG; 3) TG30 sows (n = 101) treated with TG 96 h post-weaning and inseminated once 30 ± 2 h post-TG; and 4) TG24+30 sows (n = 100) treated with TG 96 h post-weaning and inseminated 24 and 30 h post-TG. The number of inseminations per sow allotted was 1.7, 1.0, 1.0, and 2.0 for treatments 1–4, respectively. Estrus was detected in 89%, 94%, 90%, and 88% of the sows in treatments 1–4, respectively. There was no effect of treatment on farrowing rate ($P = 0.743$). Farrowing rates were 83.3%, 81.0%, 77.2%, and 81.0% for treatments 1–4, respectively. Average number of pigs born alive was 11.1, 10.8, 10.7, and 11.0 for treatments 1–4, respectively ($P = 0.822$). Control sows were inseminated if detected in estrus, whereas sows assigned to TG treatment were inseminated at a fixed-time, regardless of estrus. The number of sows farrowed/number not in estrus was 0/11, 2/6, 5/10, and 4/12 for treatments 1–4, respectively. These data indicate that sows treated with TG 96 h after weaning and inseminated at a fixed-time, independent of estrus status, have farrowing rates and litter sizes comparable to sows inseminated multiple times during behavioral estrus. Furthermore, 2 fixed-time inseminations (24 and 30 h post-TG) did not improve sow performance over a single insemination given at either 24 or 30 h post-TG.

Key Words: sow, reproduction, OvuGel

842 Effects of glucuronic acid and *N*-acetylglucosamine supplementation on the in vitro maturation and fertilization of pig oocytes. A. Mello,* K. Dalton, and B. D. Whitaker, *The University of Findlay, Findlay, OH.*

Increasing the perivitelline space (PVS) surrounding pig oocytes could improve the cortical reaction and decrease the incidence of polyspermic penetration during in vitro fertilization (IVF). Oocytes were supplemented during the last 24 h of maturation with 0.01 mM of PVS components, glucuronic acid or *N*-acetylglucosamine (GlcNAc) and then subject to IVF and subsequent embryonic development. Oocytes (n = 300) were evaluated for zona pellucida and PVS thickness after maturation in addition to the presence of cortical granules using the intensity of fluorescence. Fertilization characteristics were evaluated 12 h after IVF and rates of embryonic cleavage and blastocyst development were observed at 48 h and 144 h after IVF, respectively. There were no significant differences in zona pellucida thicknesses or fluorescent intensities of cortical granules; however, unsupplemented oocytes had a significantly thinner ($P < 0.05$) PVS (10.28 ± 0.86 μm) compared with the glucuronic acid (16.44 ± 0.87 μm) and GlcNAc (15.14 ± 1.20 μm) supplemented oocytes. Oocytes supplemented with glucuronic acid had a significantly less ($P < 0.05$) incidence of polyspermic penetration (15.00 ± 6.88%) compared with unsupplemented (30.00 ± 8.07%) and GlcNAc supplemented oocytes (40.00 ± 7.93). Oocytes supplemented with GlcNAc had significantly less ($P < 0.05$) male pronuclear development (60.00 ± 4.03%) compared with unsupplemented (70.00 ± 4.77%) and glucuronic acid supplemented oocytes (75.00 ± 5.07%). No significant differences in embryo cleavage rates at 48 h after IVF were seen but oocytes supplemented with glucuronic acid had a significantly higher ($P < 0.05$) percentage of blastocysts at 144 h after IVF (40.82 ± 6.29%) compared with the unsupplemented oocytes (21.74 ± 6.49%) and the GlcNAc supplemented oocytes (19.15 ± 6.42%). 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: cortical granule, polyspermy, IVF

843 Litter characteristics and thermoregulatory behavior of first parity sows exposed to a controlled heat stress (HS) during gestation. M. C. Lucy*[1], T. J. Safranski[1], J. N. Rhoades[1], J. W. Ross[2], N. K. Gabler[2], R. P. Rhoads[3], and L. H. Baumgard[2], [1]*University of Missouri, Columbia,* [2]*Iowa State University, Ames,* [3]*Virginia Tech, Blacksburg.*

First parity sows suffer from seasonal infertility that is associated with HS. The objective was to test the effects of HS on thermal regulation during gestation and assess carryover effects after farrowing in first parity sows. Nulliparous gilts (n = 23) were brought into environmental chambers, inseminated and assigned to one of 2 ambient temperature treatments [HS, n = 12 (27 to 37°C; relative humidity, RH 85 to 55%) or TN, n = 11 (15 to 20°C; RH 60 to 50%)] that were applied during gestation. Rectal, ear and shoulder temperatures (RT, ET, and ST) and respiration rate [RR; breaths per minute (BPM)] were collected (0900 and 1500h). Piglets and placentas were weighed after farrowing. There was an effect of treatment ($P < 0.001$) on RT (38.4 ± 0.1 vs 38.1 ± 0.1°C), ET (35.9 ± 0.1 vs 29.6 ± 0.1°C), ST (35.8 ± 0.1 vs 29.1 ± 0.1°C), and RR (58 ± 2 vs 30 ± 2 BPM) in gestation (HS vs TN). Sows were moved to a thermoneutral farrowing room (23°C) during the last wk of gestation. Gestation was shorter ($P < 0.05$) for HS (115.7 ± 0.5 d) compared with TN (117.4 ± 0.5 d). The number of live born (11.5 ± 0.8), still born (0.3 ± 0.1), and mummies (0.4 ± 0.2) per litter were similar for HS and TN. There was an effect of treatment on birth weight ($P < 0.01$) and placental weight ($P < 0.10$) because HS sows had lighter piglets (1180 ± 50 vs 1409 ± 53 g) and lighter placenta (224 ± 12 vs 255 ± 13 g) compared with TN. The piglet weight difference (HS vs TN) was maintained for wk 1 (2171 ± 109 vs 2761 ± 113 g; $P < 0.001$) and wk 2 (3809 ± 205 vs 4488 ± 205 g; $P < 0.05$) but not at weaning (4824 ± 205 vs 5259 ± 214 g; $P > 0.10$). The RT, ET, and ST (respectively) increased ($P < 0.001$; 38.2 ± 0.1 to 39.5 ± 0.1°C, 31.8 ± 0.3 to 35.0 ± 0.3°C, 30.2 ± 0.3 to 33.8 ± 0.3°C; d −5 to d 10) after farrowing (during lactation). There was a carry-over effect of gestational HS on RT in farrowing (non-HS conditions) because HS sows had a greater increase in RT after farrowing (39.8 ± 0.1 vs 39.2 ± 0.1°C on d 2; $P < 0.001$). In summary, gestational HS shortened gestation and reduced piglet birth and placenta weight. There were carry-over effects of gestational HS on sow thermoregulation during lactation. This project was supported by USDA NIFA 2011–67003–30007.

Key Words: sow, heat stress

844 Comparison between conventional sex-sorted semen and a higher dose\ lower concentration sex-sorted semen on conception rates and calf gender ratio.

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The objective of this study was to compare conception rates and gender ratios among Jersey heifers and lactating cows inseminated with conventional (Low Dose High Sort [LDHS]) or High Dose Low Sort (HDLS) sex-sorted semen. Study subjects consisted of nulliparous heifers and lactating cows that received their first service after a 50-d voluntary waiting period (VWP). Females were allocated systematically to each treatment group. Subjects that failed to conceive were rebred to the same sire and type of sex-sorted semen for up to 2 additional services. Females that were not pregnant after 3 breeding attempts were censored. A total of 1,879 services were performed on 1,029 eligible females (LDHS; n = 499, HDLS; n = 530). Experiment groups were comparable at enrollment with respect to age at first AI among heifers ($P = 0.45$) and DIM at first AI for multiparous cows ($P = 0.53$). Nulliparous heifers bred to HDLS had a 17% higher risk of conceiving compared with LDHS (HR = 1.17; $P = 0.12$); cows had a 22% higher risk of conception to HDLS (HR = 1.22; $P = 0.05$). Insemination to HDLS resulted in fewer female calves compared with LDHS (77.4% vs. 88.4%, $P < 0.01$). The odds ratio for a female calf born to a dam inseminated to HDLS compared with LDHS was 0.44 ($P < 0.01$). The use of HDLS sex-sorted semen resulted in a minimal improvement in the instantaneous risk for pregnancy. Furthermore, the use of HDLS resulted in 11% less females compared with LDHS which may be explained by the lower gender bias in HDLS compared with LDHS. Nevertheless, the reduction in proportion of pregnancies with female calves may be cost-effective given the simpler processing technique required to sort semen into HDLS compared with LDHS.

Key Words: sex-sorted semen, sperm dose, conception rate

845 Effect of a post-weaning high-energy diet on age at puberty, testicular characteristics, and semen production in Holstein bulls.

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We previously reported that feeding Holstein bulls a high energy (HE) diet beginning at 58 d of age increased LH secretion at 125 d, increased testosterone concentration from 181 to 210 d, and increased scrotal circumference (SC) from 147 to 230 d. In the present experiment, the impact of this diet on age at puberty and on testicular measurements, seminiferous tubule diameter, and semen production in mature bulls is reported. From 58 to 230 ± 0.3 d of age, calves received either a high energy diet (HE, n = 8; 2.2 Mcal/kg NEm and 1.37 Mcal/kg NEg, targeted ADG 1.5 kg/d) or a control diet (n = 7; 1.70 Mcal/kg NEm and 1.09 Mcal/kg NEg, targeted ADG 0.75 kg/d). Thereafter, bulls were fed a similar diet. Beginning at 241 ± 5 d of age, semen collection was attempted and continued every 14 d using a teaser animal and artificial vagina until each bull attained puberty. Puberty was defined as the day an ejaculate containing 50×10^6 spermatozoa with 10% motility was obtained. Ages of bulls during these collections ranged from 233 to 396 d. SC was measured on d 262, 305, 332, and 367. To assess mature semen production, semen was collected thrice weekly during the 4 weeks before slaughter at 580 ± 18 d of age. Epididymal and testicular measurements were collected after slaughter, and seminiferous tubule diameter was measured using fixed and stained sections of testes. Age at puberty did not differ between treatments (310 ± 35 d), but SC was greater ($P < 0.05$) in the HE treatment during the puberty assessment period. As mature bulls, sperm production did not differ between treatments in the collections preceding slaughter. However, testis weight (318.0 ± 13.5 vs. 267.5 ± 14.4 g), epididymal weight (31.6 ± 1.1 vs. 28.0 ± 1.2 g), and testis volume (305.0 ± 11.9 vs. 244.9 ± 12.9 cm^3) were all greater ($P < 0.05$) in the HE treatment. Seminiferous tubule diameter did not differ between treatments (252.23 ± 2.44 μm). These data suggest that a HE diet initiated at 2 mo of age increased testis size, but did not accelerate puberty, increase sperm production, or increase seminiferous tubule diameter.

Key Words: bull, diet, testes

846 Oviductal protein and ovarian hormone concentrations during the first five days of the estrous cycle in first and third estrous ewe lambs and mature ewes.

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The objectives of this study were to determine if ampullary (AMP) and isthmic (IST) protein concentrations patterns, and progesterone (P4) and estradiol (E2) concentrations patterns differ over the first 5 d of the estrous cycle among first (pubertal; FE) and third estrous (TE) ewe lambs and mature ewes (ME). Crossbred, spring-born ewe lambs (n = 40) and mature (4- to 6-yr-old; n = 20) were assigned randomly at estrus to treatments arranged in a 3 (cycle type; CT) x 5 (day of cycle) factorial (n = 4 ewes per treatment). Observation of estrus occurred twice daily with the aid of mature, epididymectomized rams beginning in October. Each ewe was bi-laterally salpingectomized on either Day 0 (estrus), 1, 2, 3 or 4 after estrus. A jugular blood sample was collected from each ewe immediately before surgery on these days. Right and left AMP and IST segments were flushed with 4 and 2 mL of Delbecco's PBS (pH = 7.2), respectively. PMSF was added to a final concentration of 10 mM to each flushing and flushings were flash frozen in liquid N2. Protein in flushings was assayed using the BCA method (Pierce, Rockford, IL). Serum samples were assayed for P4 and E2 concentrations by RIA. There was an interaction ($P < 0.01$) between CT and day of cycle for AMP and IST protein concentrations. These interactions were caused by greater ($P < 0.05$) protein concentrations in the AMP and IST of ME than in FE ewes on Day 2 and lower ($P < 0.05$) concentrations in ME than in FE ewes on Day 4. There was an interaction ($P < 0.01$) between CT and day of cycle for P4 and E2 concentrations and P4:E2 ratios. P4 increased ($P < 0.05$) more rapidly from D 2 to 4 in ME than in FE and TE ewes. E2 increased ($P < 0.05$) from D 2 to 3 more rapidly in ME than in FE and TE ewes; whereas, E2 deceased ($P < 0.05$) from D 3 to 4 in ME and TE ewes, while E2 increased ($P < 0.05$) from D 2 to 4 in FE ewes. P4:E2 ratios increased ($P < 0.05$) from D 2 to 4 in ME and TE ewes than in FE ewes. In conclusion, concentration patterns of AMP and IST protein and ovarian steroid hormones during the first 5 d of the estrous cycle differ between FE and ME ewes. These results indicate the possibility that reduced fertility in ewe lambs at their first estrus may be caused by an inappropriate protein milieu in the AMP and IST that may be detrimental to normal early embryonic development.

Key Words: oviductal protein, ovarian steroids, ewe lambs

847 Effect of phytoestrogens on basal and GnRH-induced gonadotropin secretion from ovine pituitary cells in culture.

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The objective of our study was to assess the effect of dietary phytoestrogens (PEs) on basal and stimulated gonadotropin secretion. We used ovine pituitary cells in culture to assess the effect of PEs on basal and GnRH agonist-induced LH and FSH secretion. Pituitary tissue was collected from wether lambs, enzymatically dispersed and aliquots of the resulting cell suspension were used to seed 24 well culture plates. After attachment, media containing vehicle, 50 or 5000 pM estradiol (E2), or increasing concentrations (1, 10, 100, or 1000 nM) of PE (coumestrol [CM] or zearalenone [ZR]) was added to 4 replicate wells. Each experiment was duplicated. Media was collected after treatment with E2 or PE for 48 h and basal FSH secretion was determined by RIA. The effect of estrogen on gonadotrope responsiveness was also assessed by incubating cells with E2 or PE for 12 h followed by addition of a GnRH agonist (Des-Gly^{10}, D-Ala^{6} GnRH ethylamide [GnRH-A] at 0.1, 1, 10, 100, 1000 pM) and incubation for 6 h. Data were analyzed using linear mixed model procedures. For basal secretion, fixed effects were treatment (TRT) and experiment (EXP). Random effect was plate (PL). For GnRH-A induced LH secretion, fixed effects were TRT, GnRH-A, and TRT:GnRH-A. Random effects were EXP, EXP:GnRH-A, PL, and PL:GnRH-A. Our data indicate that 100 nM CM and ZR decreased ($P < 0.001$) basal FSH secretion by 40%. Treatments with 50 pM E2 or 100 nM CM or ZR increased ($P < 0.01$) the sensitivity of the response to GnRH-A by 27-fold. The effects of E2 and PE on basal and agonist-induced gonadotropin secretion were blocked ($P < 0.01$) by the estrogen receptor (ER) antagonist ICI 182,780. To examine the role of specific ER isoforms in the PE-induced effects, we incubated cells with ERα or β agonists (propyl pyrazole triol [PPT] and diarylpropionitrile [DPN], respectively) and assessed basal and GnRH-A induced responses. PPT was 10–100 times more effective than DPN in decreasing basal FSH secretion and increasing GnRH-A induced LH secretion ($P < 0.01$). Overall, these data demonstrate that PEs mimic E2 and affect gonadotrope function in a manner that is likely mediated by ERα.

Key Words: phytoestrogen, gonadotropin, estrogen receptor

848 Effect of acidic pH on uterine response to interferon-τ.

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Low uterine pH associated with high blood urea and dietary protein, can reduce fertility in dairy cows. The objective was to determine the effects of acidic pH on protein expression of the endometrial cells of the bovine uteri in response to interferon-τ (IFN-τ).Using bovine endometrial (BEND) cells as a model, the experiment was designed to determine the effects of acidic pH on the production of 2 IFN tau stimulated proteins, ISG15 and Mx1. Dimethadione (DMD), a weak non-metabolizable acid, was used to decrease culture medium pH. Bovine endometrial cells were cultured in media containing 0 (pH = 7.3 ± 0.05), 10 (pH = 7.2 ± 0.05), 15 (pH = 7.0 ± 0.05), or 20 (pH = 6.8 ± 0.05) mM DMD and subsequently challenged with 0 or 10,000 antiviral units of recombinant IFN-τ and were incubated for 24 h. Once harvested, BEND cells were lysed and the lysate was analyzed for protein content. Protein was separated by SDS-PAGE and subjected to Western blot analysis and immunoblotting to assess the production of Mx1 and ISG15. DMD decreased ($P < 0.01$) the pH of the culture media. Based on optical density, IFN-τ increased ($P < 0.01$) Mx1 and ISG15 production regardless of DMD treatment after 24 h. There was effect of DMD ($P < 0.01$) and DMD by IFN-τ interaction ($P < 0.01$) on both Mx1 and ISG15. The 15 and 20 mM DMD reduced ($P < 0.01$) IFN-τ-induced Mx1 expression, whereas 20 mM DMD reduced ($P < 0.01$) ISG15 expression in response to IFN-τ indicating that acid pH abrogated BEND cell Mx1 and ISG15 production in response to IFN-τ. These results show that acidic pH disrupted IFN-τ-stimulated Mx1 or ISG15 production, and it may indicate that high dietary protein may compromise fertility by inducing lower pH in uterine secretions altering proteins essential for pregnancy.

Key Words: pH, interferon-τ, bovine endometrial cells

Symposium: Reproductive Immune Interactions

849 Maternal immunological adjustments to pregnancy in ruminants and possible implications for postpartum uterine health. P. J. Hansen,* *University of Florida, Gainesville.*

It is an oft-stated maxim that pregnancy represents a natural allograft because the conceptus inherits paternal histocompatibility genes that encode proteins recognized as foreign by the dam. Despite this fact, there is little evidence that immunological rejection or dysregulation is an important cause of pregnancy loss or retarded fetal development in livestock. The one exception may be for conceptuses produced by somatic cell nuclear cloning since increased trophoblast expression of major histocompatibility complex class I proteins and accumulation of CD3+ T lymphocytes in endometrium have been reported for cloned pregnancies. Experiments with rodents and livestock indicate that there are a multitude of mechanisms to prevent immune rejection of the conceptus. Some of these mechanisms are played out at the level of the conceptus (for example, reduced antigenicity of the trophoblast) whereas others involve regulation of maternal immune responses, largely in the endometrium, under the control of maternal or conceptus derived regulatory molecules. There is some evidence in rodents for a temporary maternal anergy toward conceptus antigens. There is also non-specific immunosuppression mediated by regulatory T cells, gamma-delta T cells, M2 macrophages, and the corpus luteum and placenta (via secretion of progesterone). It may be that the prolonged period of local immunosuppression in the endometrium during pregnancy renders the female less able to prevent establishment of microbial infections after parturition. Little is known about the restoration of immunocompetence in the uterus after parturition although some populations of immunoregulatory cells, such as gamma-delta T cells in sheep, are largely cleared in the first week postpartum. Understanding regulation of endometrial immune function during pregnancy and the consequences for postpartum immune function may lead to novel strategies to reduce microbial infections of the uterus during the postpartum period.

Key Words: pregnancy, immunology, postpartum

Ruminant Nutrition: General Ruminant Nutrition

850 Effects of crude glycerol supplementation on in vitro ruminal fermentation and Merino ewes performance. S. J. Meale*[1], S. Ding[1], T. A. McAllister[2], R. D. Bush[1], D. Palmer[1], and A. V. Chaves[1], *[1]Faculty of Veterinary Science, University of Sydney, Sydney, NSW, Australia, [2]Lethbridge Research Center, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.*

The increasing availability of crude glycerol from the biodiesel industry has led to an interest in its use as an energy source in ruminant diets. However, its effects on ruminal fermentation patterns and CH_4 production are unclear and there are no reports on the effect of its inclusion in the diet on wool production or growth in Merino sheep. Thus, the objectives of this study were to determine the effects of increasing levels of crude glycerol on in vitro ruminal fermentation and CH_4 production and DMI, ADG, wool growth and quality in Merino ewes. Crude glycerol replaced whole wheat (DM basis) in the diet at levels of 0, 6 and 12% DM, in both in vitro and in vivo studies. In exp. 1, diets were dried and ground through a 1-mm screen and incubated twice for 24 h. Buffer and rumen liquor were mixed 3:1 and gas production and CH_4 concentration was measured after 6, 12 and 24 h of incubation with pH and IVDMD measured at 24 h. Data from both the in vivo and in vitro experiments were analyzed using the MIXED procedure of SAS. Cumulative gas (mL/g DM) and CH_4 production (mg/g DM) were similar ($P > 0.05$) among dietary treatments. In vitro DMD (%) increased ($P < 0.01$) and pH showed a tendency ($P = 0.07$) to decline, with increasing concentrations of crude glycerol. In exp. 2, 39 Merino ewes were randomly assigned to the 3 treatments (n = 13 ewes/treatment). Diets were available continuously for a 10 wk period through the use of automatic feeders. Ewes were weighed every 7 d. Wool yield was determined on mid-side patches of 100 cm cm^2 shorn at d 0 and d 70. Dye-bands were used to determine wool growth. Intake, ADG and G:F were similar among treatments ($P > 0.05$). Neither wool yield nor length were affected by diet ($P > 0.05$). Yet, spinning fineness declined ($P < 0.05$) in ewes fed 6% DM crude glycerol and fiber diameter (μm) showed a tendency ($P = 0.06$) to decline following the supplementation of crude glycerol. This indicates the potential for crude glycerol to be included in the diets of Merino sheep at up to 12% DM with the potential to marginally improve wool quality.

Key Words: Merino ewes, methane, wool production

851 Process development and nutritional evaluation of a supplemental byproduct feed for cattle from expired grocery foods. M. A. Froetschel*[1], C. L. Ross[1], and L. E. Brewer[2], *[1]The University of Georgia, Athens, [2]Viridiun LLC, Cumming, GA.*

An ensiling experiment and a feeding/digestibility trial were conducted in response to a commercial effort to recycle outdated vegetable foods from large scale grocery stores into cattle feed. A representative mixture of vegetable, fruit and bakery refuse from several Atlanta grocery stores was processed into a homogeneous slurry. Pre-ensiled grocery byproduct (GBP) was 5.06 pH and contained 20.8% DM, 85% predicted TDN, 53.7% WSC, 23.5% NDF 14.5% ash, 12.3% CP, 11.9% fat and 17.7% lactic and 2.3% acetic acid. GBP was ensiled in 8L lab silos with pre-ensiling treatments to increase its DM content including 0, 8, 16 and 24% additions of citrus pulp and 2 levels of oven drying (5 replications / treatment). After 8 wk of anaerobic storage all GBP mixtures were effectively preserved and stable for 72 h of aerobic exposure. Ensiled GBP (100%) was 3.96 in pH, 20.6% DM,80.1% predicted TDN, 1.7% WSC, 37.6% NDF, 13.8% ash, 14.3% CP, 11.6% fat and 18.6% lactic and 2.7% acetic acid. In the feeding trial, 8 yearling Holstein steers (267 kg BW, SD = 29 kg) were fed increasing dietary concentrations of the GBP (commercially processed as Readi-Blend, Viridiun LLC) in a replicated 4 × 4 Latin Square designed experiment. Steers were fed 0, 18, 36 and 54% ensiled GBP (DM basis) as part of a total mixed ration (TMR) substituted for a control TMR. The control TMR on a DM basis was 68% wheat silage and 32% concentrate (81% soyhulls, 9.5% soybean meal and 9.5% ground corn). The TMR rations averaged 35.9, 30.7, 26.8, and 23.8% DM with increasing supplemental GPB. Steers were fed rations daily to provide 1.2 times their previous day intake with chromic oxide included as a digestibility marker. Individual intakes were measured daily and BW was determined at wk intervals. Overall, steers exhibited 1.25 kg ADG during the 8 wk feeding trial. DM intake of rations, expressed as a percent of BW, was 2.12, 2.31, 2.23 and 2.07 (SE = 0.05) and increased in a quadratic manner ($P < 0.01$), respectively, with incremental levels of GBP. Supplemental GPB appears to be palatable and digestible as it increased DM intake 5 to 9% ($P < 0.01$), when included at 18 to 36% (DM basis) in a TMR that was very high in moisture content. Commercially processed ensiled GBP is an effective concentrate feed supplement for growing cattle.

Key Words: cattle feed, grocery byproduct, nutritive value

852 Biometrics of digestive tube of kids suckled up to 90 days fed different sources of goat milk replacers. L. S. Knupp, M. I. Marcondes,* M. M. S. Santos, N. O. Souza, L. M. Carvalho, M. A. S. Novaes, J. V. F. Souza, and C. M. Veloso, *Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

The organs of animals have different development rates; their maximum rates occur at different ages and body weight. The development rates of each organ can be influenced by plane of nutrition. This work aimed to evaluate the biometrics of the digestive tract of goats suckled up to 90 d with different sources of goat milk replacers. Twenty-four Saanen (12) and Alpine Brown (12) kids were randomly assigned to treatments and were slaughtered at 90 d. The animals were fed with coast-cross hay and starter, both ad libitum, and one liter of milk, or replacer, per day. The treatments were goat milk (GM), cow milk (CM), fermented cow colostrum (FC) and lactal - commercial milk replacer (LAC). The organs were separated and weighed with and without digesta. The parameters analyzed were: Rumen, omasum, abomasum, small and large intestine. Data were analyzed using a complete randomized design, using the initial weight as a covariate. When occurred difference between treatments, the Tukey test was applied to evaluate the least squares means, using a significance level of 5%. The animals treated with CM had greater rumen weight ($P < 0.05$) than the ones fed with GM and FC (0.414 vs. 0.311 and 0.308, respectively), likely due to greater starter and hay intake. Omasum, abomasum and large intestine were not affected by applied diets and their mean weights were 0.026; 0.105 and 0.256, respectively. The small intestine in animals treated with CM, were greater than those fed FC (0.490 vs. 0.334; $P < 0.05$). In conclusion, cow milk and lactal provided the best development of the digestive tract, especially for the rumen. Supported by CNPq/INCT-CA.

Key Words: abomasum, omasum, rumen

853 Evaluation of a prototype galactooligosaccharide supplement in milk replacer for neonatal calves.

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Digestive disorders are common during the first few weeks of life of the newborn calf, particularly under non-optimal sanitary conditions and immune status. Strategies to improve gut health and alleviate intestinal upsets during this period are required. Non-digestible oligosaccharides with good fermentation potential may function as prebiotics that modulate growth and activity of beneficial microbial populations, which results in enhanced gut health and function. Galactooligosaccharides (GOS) have demonstrated such prebiotic potential. In this study, the effect of GOS supplementation on intestinal health, development, function, and integrity as well as performance of dairy calves was evaluated under intensified feeding conditions. Eighty purchased male calves were assigned either to a control commercial milk replacer or to the same diet enriched with GOS (ca. 3% of DM). After 2 and 4 wk, 8 calves per treatment were slaughtered. Organ size was determined and samples of rumen, duodenum, jejunum, ileum, and colon were collected for in vitro nutrient transport, permeability, and histology analysis. The remaining 48 calves continued on trial to wk 8. Body growth, nutrient intake, and fecal and respiratory scores were measured throughout the trial. Calves on the control treatment showed significantly greater growth, nutrient intake, lower fecal scores and had fewer days with elevated fecal scores than GOS-supplemented calves. Size of digestive organs, nutrient transport, and epithelial permeability were not affected by treatment. Although digesta VFA concentrations were greater for control, intestinal villi height and width and crypt depth were greater in calves receiving GOS. Although total hydrolyzed monosaccharide content was similar between diets, lactose content of the GOS-supplemented diet was much lower than the control diet (19.7% vs. 43.6%), which may have limited growth. In conclusion, the GOS-supplemented milk replacer had a laxative effect and supported slightly lower performance while promoting greater intestinal epithelial growth.

Key Words: prebiotics, galactooligosaccharides, gut

854 Remote monitoring of individual animal mineral supplement intake by range cattle.

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Individual animal intake and behavior associated with mineral supplementation of cattle on rangelands is largely undocumented. Our objective was to develop instrumentation to remotely obtain such information. We designed and constructed a solar powered high precision load cell and continuous (every 0.25 s) data acquisition system, configured to a standard range mineral feeder. The system was field tested in November 2010 and October 2011 at the V Bar V Ranch in central Arizona. Load cell precision varied with temperature and wind. Wind speed (kph) ranged from 0 to 23 and averaged 14 ± 0.3 in 2010. Corresponding values were 0 to 32 and 11 ± 0.4 respectively, in 2011. Temperature (°C) ranged from −7 to 4 and averaged −2 ± 0.9 in 2010. Corresponding values were −1 to 11 and 2 ± 1.1 respectively, in 2011. In pre-dawn hours when ambient conditions were relatively consistent, baseline variation of the load cells was ± 2 g. This value increased to ± 17 g during mid day. Individual cow identification was accomplished via time-stamped, motion activated digital photography. Feeding bouts were classified by predetermined acute weight change thresholds and matched to a cow by visual inspection of images. Duration of feeding bouts (min) ranged from 1 to 16 and averaged 3 ± 0.4 in 2010, and 1 to 21 and 4 ± 0.4 respectively, in 2011 ($P > 0.1$). Mineral intake (g/feeding bout) ranged from 1 to 679 and averaged 109 ± 16.0 in 2010, and 2 to 1598 and 226 ± 25.4 respectively, in 2011 ($P < 0.05$). Measured total daily intake (g/cow) ranged from 1 to 1009 and averaged 190 ± 26.0 in 2010, and 2 to 1009 and 218 ± 48.6 respectively, in 2011 ($P < 0.05$). Intake rate (g/min) ranged from 1 to 182 and averaged 45 ± 5.2 in 2010, and 1 to 446 and 82 ± 8.0 respectively, in 2011 ($P < 0.05$). Correlation of the classification protocol was tested between 2 independent observers. For discrete (n = 5) bouts, $r^2 = 0.95$, SE = 5.3 ($P < 0.05$), and for multiple animal (n = 7) bouts, $r^2 = 0.75$, SE = 18.0 ($P < 0.05$). This system, as tested, is capable of providing individual animal intake of mineral supplement under rangeland management conditions.

Key Words: individual animal intake, mineral supplement, remote measurement

855 Effect of corn processing on growth performance and fecal nutrient composition in dairy bull calves fed whole or steam-flaked corn diets from pre-weaning to 8 weeks post-weaning.

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A study was conducted to investigate the effect of corn processing growth performance and fecal nutrient concentrations in dairy bull calves fed from 8 weeks pre-weaning to 8 weeks post-weaning. Sixteen individually housed dairy bull calves (8 Holstein and 8 Jersey; average initial BW = 34.2 ± 8.13 kg) were separated within breed into 1 of 2 treatments: diets (starter and growing) containing either steam-flaked (SF) or whole (WC) corn. Body weights were collected on arrival, at weaning, and at study completion. Feed intakes were recorded daily. Fecal samples were collected every 7 d from 8 weeks before weaning through 8 weeks post-weaning when the first steer reached feedlot weight (125 kg). Samples were dried at 100°C until dry and ground in a Wiley mill to pass through a 1 mm screen. Ground samples were analyzed for all or part of the following: DM, ADF and NDF (Ankom 200 fiber digester, Ankom, Macedon, NY), CP (TC400; Leco Corp., St. Joseph, MI), and starch. Starch analysis was performed using an amyloglucosidase colorimetric assay. Data were analyzed as a complete random design using the mixed procedure of SAS (Cary, NC) with animal as the experiment unit and week from weaning as the repeated measures. Growth performance, including BW (initial, weaning, and final), ADG (pre- and post-wean), pre-wean DMI, and feed efficiency were similar ($P > 0.10$) across treatments, with SF animals tending ($P < 0.10$) to have higher overall DMI and lower post-wean G:F compared with WC animals. Post-weaning DMI was greater ($P < 0.05$) for SF calves versus WC calves. Pre-weaning fecal components were similar for both groups ($P > 0.10$). Fecal NDF and ADF were higher ($P < 0.01$) and starch content was lower ($P < 0.01$) in the SF group post-weaning versus the WC group. We conclude that corn processing does not affect dairy calf performance through 8 weeks post-weaning. However, fecal starch concentrations between whole and steam-flaked corn begins to diverge once the dairy calf has been weaned.

Key Words: corn processing, dairy calf, fecal nutrient

856 Effects of short-term feed restriction on ruminal function.

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This study was conducted to evaluate whether the severity of short-term feed restriction (FR) affects ruminal function. Eighteen ruminally cannulated heifers were blocked by BW and randomly assigned to 1 of 3 treatments differing in the severity of FR; 75, 50, or 25% of ad libitum intake relative to the baseline period. Each heifer was exposed to 14 d for adaptation, 5 d for baseline, 5 d of FR, and 3 wk of recovery (R1, R2, and R3). Heifers were fed the same diet (60% forage: 40% concentrate) throughout the study and were fed ad libitum during the baseline and recovery periods. Water was available at all times. Ruminal pH and DMI were measured daily and absorptive function was evaluated using the temporarily isolated and washed reticulo-rumen technique. There was a treatment × period interaction for DMI ($P < 0.01$) with lowest values for 25% (2.65 kg/d), intermediate for 50% (5.3 kg/d), and greatest for 75% (8.2 kg/d) during FR, but differences were not observed among treatments within other periods. Treatment × period interactions were also detected for nadir ($P < 0.01$), mean ($P < 0.01$) and maximum ($P < 0.01$) ruminal pH. Generally, heifers fed 25% increased pH to a greater extent during FR but decreased to a greater extent during R1 when compared with those fed 50 and 75%. The area ($P < 0.01$) that pH <5.5 was smaller during FR (0.4 pH × min/d) and greater during R1 (80.4 pH × min/d) than baseline (24.2 pH × min/d), but R2 and R3 (44.9 and 36.2 pH × min/d, respectively) did not differ from baseline. The absolute rate (mmol/h) for acetate absorption ($P < 0.01$) was greater during baseline (332.1 mmol/h) than FR (253.5 mmol/h) with the rate being faster in R3 relative to FR; however, the rates did not differ between R1 (320.0 mmol/h) and R3 (343.8 mmol/h). Absolute rates for propionate and butyrate absorption (period effect, $P \leq 0.04$) also followed a similar pattern as for acetate, except that baseline and FR values did not differ. The results of this study indicate that 5-d FR increases the risk for ruminal acidosis, regardless of the severity of FR imposed, which may be linked to negative carry-over effects of FR on acetate absorption.

Key Words: feed restriction, ruminal pH, short-chain fatty acid absorption

857 Identifying improbable feed samples using a multivariate procedure.

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Individual feed analyses can be in error and unrepresentative of a feed population. Erroneous feed samples within a feed summary will decrease the accuracy of summarized nutrient statistics and may reduce ration formulation accuracy. Our objective was to implement a robust multivariate procedure for identification of improbable samples and to create an accurate database summarizing nutrient means, SD, and covariances of feeds. The covariance of nutrients is critical for understanding complex nutrient variation and the NRC (2001) feed library does not provide covariances. The procedure examines 3 statistics; individual nutrient concentrations of a single sample, the covariance of a single sample, and the joint covariance of multiple samples. The SAS (version 9.3) procedures were univariate, principal component analysis (PCA), and two-stage clustering (TSC), respectively. Specific removal criteria were: nutrient concentrations > 3.5 SD from the mean, PCA scores > 3.5 SD from the mean PCA, and concurrent global peaks of pseudo F-statistic and pseudo T-Square. The proposed procedure results in minimal statistic changes (<1%) when applied to a simulated normal population free of outliers. Adding simulated erroneous samples greatly affected the covariance in some situations and application of the procedure removed problematic samples and resulted in similar statistics of interest compared with the normal population. The procedure was applied to 133,677 corn silage samples and 18,237 samples were removed (83% of the removed samples by PCA and TSC). After removal of improbable samples, the ash with lignin correlation decreased from 0.65 to 0.30, SD changes ranged from 0.02 to 1.04 units, and minor changes of the means were observed. Correlations of −0.31 (NDF with lignin), −0.37 (NDF with starch) and −0.29 (NDF with CP) were observed in the removed outlier clusters compared with correlations of 0.70, −0.88, and 0.18 in the proposed corn silage population, respectively. Evaluating multiple nutrients of a feed sample using a multivariate procedure is more robust compared with examining one nutrient and is important for obtaining accurate covariance estimates.

Key Words: covariance, multivariate

858 Application of meta-analysis to build new feed unit systems for ruminants based on absorbed nutrients and animal responses in France.

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A steering group is now working in France to update the Feed energy, protein systems for cattle, sheep and goat by 2013. A major goal of this project is to simply model the main digestive events to predict the absorbed flows of VFA, amino acids, glucose and fatty acids. For cattle, a large database (2156 treatments, 818 experiments) was built from the literature to develop the updated systems. The attention is first focused on the fermentable organic matter (FOM) in the rumen, which is the key to predict productions of microbial protein, volatile fatty acids and gas. FOM (54.4 ± 11.0%dry matter, DM) is predicted from diet digestible OM (DOM = 63.8 ± 8.1%DM) minus the digestible fractions in the intestines of starch, protein, fatty acids and NDF (FOM = DOM –DST –DPR – DFA –DNDF). DOM is corrected for digestive interactions due to levels of dry matter intake, % of concentrate and the rumen protein balance (duodenal CP-ingested CP). Fractions DST (8.2 ± 5.5%DM) and DPR (5.5 ± 1.8%DM) are predicted from in sacco data, DFA (3.4 ± 1.2%DM) and DNDF (3.5 ± 2.3%DM) are predicted from regressions issued from meta-analysis. A second point focusing the interest is the prediction of the microbial growth efficiency (MGE = 25.6 ± 8.6 gNm/kg of TDOMr) which is influenced by the fractional outflow rates of particles (MGE = 21.3 + 1.06 kp%/h, n = 215, nexp = 87, RMSE = 2.2) and liquids (MGE = 22.9 + 0.22 kl%/h, n = 297, nexp = 117, RMSE = 2.3). A third point of interest is the rumen undegradable protein (RUP) which are predicted from the in sacco effective degradability of N (EDN) corrected for actual transit (RUP%DM = CP%DM*(1 - EDN), n = 318, nexp = 124, RMSE = 0.94% DM). Afterward, the major empirical responses of digestion were integrated into a simple mechanistic model of the rumen with an optimization procedure to determine the optimal values of some less known parameters of digestion. The further step of the project is the updating animal requirements and their multiple responses to diet (efficiency, outflows of N, P and CH_4, composition of products…) to absorbed nutrients according to their nutritional and physiological status.

Key Words: feed unit, meta-analysis, ruminants

859 Sampling sites and inserting depth of oral stomach tube affects the fermentation parameters of ruminal fluid collected in dairy cows.

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Six rumen-fistulated dairy cows (BW = 604 ± 36 kg; milk yield = 15 ± 2.4 kg) were used in 2 trials to validate the technique for collection of ruminal fluid by a Geishauser oral stomach tube (OST). Trial 1 was conducted to compare the difference of ruminal fermentation parameters among rumen sites (cranial dorsal, cranial ventral, central, ventral, caudal dorsal and caudal ventral). Ruminal fluid was collected at 5 to 6 h after morning feeding for 3 consecutive days through rumen cannula (RC). The samples were analyzed for pH, volatile fatty acids (VFA), ammonia N, sodium, potassium, calcium, chloride, and phosphorus concentrations. Variables of ruminal fluid collected were analyzed using the mixed procedure of SAS. Compared with central or ventral rumen, cranial dorsal rumen had higher pH, ammonia and sodium concentrations, and lower VFA concentrations ($P < 0.05$), indicating that sampling site was one main factor contributing to the difference of ruminal fermentation parameters for samples collected via OST and RC. In trial 2, the fermentation parameters of ruminal fluid collected via OST at 2 inserting depth (180 or 200 cm) were compared with those of ruminal fluid collected via RC (ventral sac). When OST was inserted at a depth of 180 cm, the OST head was located in the cranial dorsal (atrium) of the rumen. Ruminal fluid collected via OST had higher pH and sodium concentration, and lower VFA, potassium, calcium and phosphorus concentrations than that collected via RC ($P < 0.05$). However, when OST was inserted at a depth of 200 cm, OST head could reach to the central rumen through the front rumen pillar. No differences were found in pH, VFA, ammonia, and ion concentrations between samples collected via 2 methods ($P > 0.05$). These results indicated that the OST should be inserted to reach the central rumen to obtain representative rumen fluid samples.

Key Words: oral stomach tube, fermentation parameters, dairy cows

860 Comparison of nutrient composition and in vitro digestion characteristics of spent mushroom soybean (*Pleurotus* spp.) substrate and soybean straw. J. P. Gafigi[1], M. Mutimura[2], and S. Uwituze*[1], [1]*National University of Rwanda, Faculty of Agriculture, Department of Animal Productions, Butare, Rwanda,* [2]*Rwanda Agriculture Board, Kigali, Rwanda.*

Landholdings in Rwanda are small with over 60% of households cultivating less than 0.7 ha. This has resulted in low animal productivity; hence the search for alternative animal feeds is encouraged in Rwanda. A study to compare nutritive values and in vitro digestibility characteristics of spent mushroom soybean substrates (SMS) and soybean straw (SBS) as potential animal feeds was conducted. Samples of SMS and SBS were analyzed for DM, OM, CP, P, Ca, NDF, and ADF. In vitro fermentation medium consisted of 1:2 ruminal fluid: McDougall′s buffer and the experiment was a completely randomized design. Each sample (0.2 g, DM basis) was put in a gas syringe and there were 3 replicates per substrate. Syringes containing samples with 30 mL of fermentation medium and 2 blanks were incubated in a water bath at 39°C for 72 h. Readings of gas volumes were recorded every 2 h. Gas accumulated within 24 h of incubation was used to calculate metabolizable energy (ME), OMD, and digestible crude protein (dCP). Data for in vitro gas production, ME, OMD, and kinetic coefficients of fermentation were statistically analyzed using PROC Nonlinear Model of SAS (9.3. Inc.). Results showed that SMS contained less ($P < 0.05$) OM, NDF, and ADF (91.7, 58.4, and 34.5% DM, respectively) compared with SBS (95.4, 74.2, and 59.79% DM for OM, NDF, and ADF, respectively), but SMS had higher ($P < 0.05$) CP (7.8% DM) than SBS (6.1% DM). SMS had less ($P < 0.05$) gas production than SBS over 72 h of incubation. SMS had less ME ($P < 0.05$) compared with SBS (1.39 vs. 1.53 Mcal/kg of DM), but more dCP ($P < 0.05$) than SBS (40.8 vs. 25.0 g/kg DM). SBS had greater ($P < 0.05$) portions classified as slow degradable, effective degradable and potential degradable than SMS. SBS required more time ($P < 0.05$) to be degraded in vitro than SMS, but both substrates had similar ($P > 0.05$) degradation rates. SMS had a high CP content but had less in vitro gas production. The low gas production might be attributable to *Pleurotus* spp., which contains complex compounds such as polyphenols and flavonides that are hardly degraded by ruminal microbes. Soybean straw is likely a better feedstuff than SMS based on its greater potential degradable portion, which is a good indicator of better quality feeds.

Key Words: digestibility, mushroom byproduct, soybean byproduct

Ruminant Nutrition Symposium: Update on Nutrient Requirements for Ruminants

861 Revising protein requirements of calves and heifers. T. M. Hill*[1], H. G. Bateman II[1], J. M. Aldrich[1], and A. J. Heinrichs[2], *[1]Nurture Research Center, Provimi North America, Brookville, OH, [2]Department of Animal Science, Penn State University, University Park.*

Research published since the dairy NRC (2001) relating to protein needs of calves and heifers was reviewed and compared with requirements from NRC (2001). The experiments used varied intakes or concentrations of CP or varied fraction or fractions of CP in the diet relative to an energy measure. Animal requirements were reviewed in 4 categories to identify advances in understanding of nutritional requirements since publication of NRC (2001). Categories included 1) calves less than 2 mo of age fed milk and starter, 2) calves to approximately 4 mo of age fed starter with limited forage, 3) pre-breeding age heifers, and 4) post-breeding age heifers. For calves in category 1, data estimating optimum ratios of amino acids for the milk-fed calf were identified. For calves in categories 1 and 2, data estimating optimum ratios of CP to ME were identified. For heifers in category 3, optimum diet CP:ME appeared similar to NRC (2001) but other differences existed. No experiments found tested the 70% RDP of CP recommendation for calves in category 3, however, approximately 65% RDP supported more typical dairy heifer ADG than lower amounts. Few differences from NRC (2001) were found for heifers in category 4. Precision or limit-feeding vs. more conventional ad lib fed programs appears to offer utility to save costs and reduce nutrient and fecal outputs with dietary adjustments to maintain protein intake relative to energy and DMI. The presentation will cite the literature since NRC (2001) found in the search. The new literature includes experiments measuring growth, rumen and whole animal metabolism, digestibility, tissue harvest, blood chemistries, and hormones. The focus will be on change in protein fraction consumed relative to growth and metabolism in calves and heifers with differences and similarities to recommendations from NRC (2001) highlighted.

Key Words: calves, heifers, protein

862 Revising energy requirements of dairy breed calves and heifers. M. E. Van Amburgh,* *Cornell University, Ithaca, NY.*

Work conducted over the last 15 years has provided a wealth of data on the maintenance and growth requirements of dairy calves and heifers. The data provide new insights and refines our ability to describe tissue requirements for energy, protein, amino acids, fatty acids and minerals for growth. Re-evaluation of the 2001 Dairy NRC maintenance requirements for calves (Diaz et al., 2001; Tikofsky et al., 2001; Blome et al., 2003) indicated the maintenance requirement is accurate for calves up to approximately 100 kg BW. Data from harvest studies have provided information that allows us to refine the efficiencies of energy and protein utilization for growth before weaning and post-weaning. For example, the 2001 NRC calf model uses an efficiency of metabolizable energy to net energy of 0.69 (Toullec, 1989) whereas a re-evaluation indicates a value of 0.60 for lighter, leaner calves. This partial efficiency is not fixed and is a function of body fat deposited by calves which is dependent on rate of growth, stage of maturity and before weaning, the amount of fat calories consumed above maintenance. Joost et al., (2007) and Tikofsky et al. (2001) directly and indirectly demonstrated that fat deposition does not come from carbohydrates in milk fed calves and Mills et al. (2010) showed that fatty acid profile impacts fat deposition. Tissue samples from various studies were used to update the values for amino acid composition (g/100 g of CP): methionine, 1.79; lysine, 6.26; histidine, 2.41; phenylalanine 3.65; tryptophan, 1.18; threonine, 3.83; leucine, 6.96; isoleucine, 2.94; valine, 4.28; and arginine, 6.75 and provides the opportunity to better formulate pre-weaned calf diets. Data now exist to describe the apparent energy supply to the animal from pre-weaning to full rumen function and this had been lacking from growth models and will be discussed. The study by Meyer (2005) from birth to 350 kg BW provides the ability to assess application of the mature body weight and target growth system implemented by the 2001 NRC. Evaluations of the current net energy equations indicate a 35% bias in energy required when mature body size is not accounted for.

Key Words: calves, heifers, nutrient requirements

863 Protein and amino acids for growth. E. C. Titgemeyer,* *Kansas State University, Manhattan.*

The Beef NRC (1996) predicts that all AA are used by cattle for growth with equal efficiency and that the efficiency decreases linearly with BW up to 300 kg. More recent data from Holstein steers (BW 132 to 228 kg) indicate that different AA are used for growth with different efficiencies. Efficiency of AA use for whole- body protein deposition (increase in AA deposition divided by the increase in AA supply) averaged 26% for Met (11 trials), 38% for Leu (4 trials), and 64% for His (2 trials). Efficiencies of Met and Leu utilization for growth were less than predicted by NRC. Energy supplementation improves efficiency of AA utilization. Analysis of data from 11 trials demonstrated that efficiency of Met use increases with supplemental energy but decreases with BW [Efficiency = 0.465 + 0.082 supplemental GE (Mcal) - 0.0028 BW (kg)]. Improvements in Leu utilization in response to energy supplementation appear somewhat less than for Met. Improvements in AA use in response to energy supply were similar when energy was provided as glucose, fat, or VFA, so energy source is not as important a factor as energy level. Supplementation of excesses of other AA improved efficiency of use of Met, Leu, and His; this may be due in part to energy provided as AA. Increases in ruminal ammonia absorption did not affect efficiency of Met use, but improved utilization of Leu. Efficiency of Met use was improved when Gly was supplemented, and this may be due to modulation of sulfur-AA metabolism. Despite the over-estimation by NRC of efficiency of AA utilization for growth, predicted total (maintenance plus growth) AA requirements in some situations are reasonable, reflecting that maintenance requirements are less than predicted by NRC or that AA are used for growth at much greater efficiencies when AA supplies are well below the requirement for maximal protein deposition. It is unknown if growth promotants impact efficiency of AA use. NRC (1996) provides a useful framework for estimating AA requirements of growing cattle, but modifications to predicted efficiencies and maintenance requirements areneeded to improve accuracy of the estimates.

Key Words: amino acids, cattle, utilization

864 Update on protein and amino acid requirements for lactating dairy cows. H. Lapierre*[1], L. Doepel[2], and D. R. Ouellet[1], *[1]Dairy and Swine R&D Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [2]Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada.*

The Nutrient Requirements of Dairy Cattle (NRC, 2001) states that "current knowledge (on AA) is too limited to put forth a model that

quantifies AA requirements for dairy cattle." A decade later, have we gained enough information to move forward? This presentation assumes that 1) requirements (rqt) should be expressed as metabolizable protein (MP) and not CP; 2) for simplicity, MP rqt cover only maintenance and milk; that is, MP rqt = endogenous urine (EnU) + scurf + metabolic fecal protein (MFP) + milk; 3) duodenal endogenous proteins are not part of rqt (unlike NRC, 2001). To estimate total MP rqt, first the type and amount of proteins exported out of the cow need to be estimated and then divided by an efficiency of utilization of MP supply to synthesize these proteins or end products. From 217 treatments (Doepel et al., 2004 JDS 87:1279), MP rqt for EnU and scurf averaged only 6 and 1% of MP rqt (NRC, 2001): current estimations based on Swanson (1977. JDS 60:1583) can probably be kept. Our efforts focus on the greater contributors to MP rqt: milk and MFP. Milk protein is certainly an easy assessment, acknowledging that true protein needs to be used. Conversely, MFP is a challenging measurement. Estimations from Swanson (1977) are currently used by most models, but with different interpretations (e.g., NRC, 2001 vs. CNCPS v 6.1). Furthermore, this estimation of fecal protein excretion is not divided by an efficiency factor, unlike all the other functions, probably because it includes more than excreted proteins synthesized from AA. We therefore propose to use values of endogenous loss estimated in dairy cows using an isotopic dilution method (e.g., Ouellet et al., 2010 JDS 93:4252). Once the protein rqt is estimated for each function, AA composition for the function is needed to determine AA rqt. An update of milk AA composition, based on true protein output, is proposed. Similarly, estimation of the AA composition of endogenous loss is proposed to replace the currently used composition (whole empty body weight). In addition, based on measurements of liver and mammary AA uptake, it is proposed that the efficiency of utilization 1) varies with AA supply; 2) differs among AA; 3) is the same across the different functions. These refinements should improve estimations of protein rqt for dairy cows.

Key Words: amino acid, dairy cow, protein

Teaching/Undergraduate and Graduate Education Symposium: Online Education for a Hands-On Career: The good, the bad and the ugly of online education in animal sciences

865 Making the world your stage through best practices in distance education. E. Sewell[1], B. Parr*[1], and D. Mulvaney[2], *[1]College of Education, Auburn University, Auburn, AL, [2]Animal Sciences, Auburn University, Auburn, AL.*

Opportunities for students to participate in courses via distance education (DE) are becoming increasingly prominent in many tertiary education institutions. Those with enrollment of 10,000 or more students typically offer some distance delivered course work. Online graduate degree programs are slowly emerging in the agriculture sectors. What are some best practices for DE? Through DE classrooms, students can participate in valuable education experiences that fit around their schedule and location. Video cameras and computer technologies are employed to take students out of the normal classroom and put them in places such as active business and industry to give students a first-hand understanding of the concepts being covered. Class videos may be supplemented with PowerPoint presentations through course capture software. For example, Panopto allows instructors to have slides transition while a video is playing enabling students to simultaneously watch video and PowerPoints. Classroom capture can be used both as an off-line recorder for asynchronous videos as well as on-line for streaming classes in real time. Complimentary videos are posted via YouTube that help promote class discussions on web-based learning management systems. Communication can use text messages, social networks and video chat. Platforms are set up to enable communication with students, other instructors, and administrators using methods and tools that are already familiar and effective for them. The secret to simulating the face-to-face experience has been the frequent exposure of students to simply recorded videos of their classmates and the professor via CMS. Discussions through DE can virtually be face-to-face via video chat functions. Typewritten responses to discussion board topics may be completely replaced with the easy video capture available through CMS. Instructional videos in technical subject areas; for example, animal science can be recorded up-close and viewed and reviewed often by students, eliminating the need to "move in close" so everyone can see. Integrating sound teaching practices with technology serves as a foundation for best practices of developing a DE course and program.

Key Words: teaching and learning, distance education

866 Real and perceived barriers to distance education in animal sciences and other disciplines. K. Boland*[1], B. Parr[1], and D. Mulvaney[2], *[1]College of Education, Auburn University, Auburn, AL, [2]Animal Sciences, Auburn University, Auburn, AL.*

Providing distance education (DE) courses, while not new, has become an increasingly popular approach to serve diverse populations of learners. Despite the movement toward more DE courses in tertiary institutions, many refrain from developing DE courses due to numerous barriers involved in developing these courses, curricula and programs. We test a hypothesis that DE has not received universal respect in the animal sciences community because of a diverse number and seriousness of perceived problems to be presented here. Using a rank analysis within a multi-component, qualitative/Delphi survey, animal science faculty and administrators were asked to identify which barriers were most likely impediments toward advancement of DE development in the discipline to gain insight into the perception of which barriers are most problematic. Reasons that institutions presently did not offer courses via DE included: time constraints of faculty, costs or lack of funding; equipment and technology limitations, technical knowledge/technical support, demand for distance education, lack of recognition for faculty, pedagogical issues and concerns, administrative issues, lack of adequate compensation/ administrative appreciation for faculty's time and efforts, lack of faculty rewards or incentives, lack of ability to teach skills requiring "hands on" instruction, concerns about faculty workload, lack of time and support from administration to develop course and materials, lack of time and support from administration to learn technologies, lack of personal contact between instructor and student, concerns about course quality, equipment failures/costs of maintaining equipment, lack of faculty commitment to spend time to master the use of technologies, and lack of nonverbal communication between instructor and student. Analysis of the real and perceived barriers for developing DE options in animal sciences should enable faculty and administrators to overcome them and adapt to pedagogies, curricula, and learning systems that meet increasing expectation and demand for dynamic blended, mobile learning environments.

Key Words: distance education, barriers

867 Engaging the new biology: Integrating quantitative genetics and genomics in animal breeding graduate learning. R. M. Lewis* and B. B. Lockee, *Virginia Tech, Blacksburg.*

Over the past 25 years in land-grant institutions, focus on quantitative areas of genetics, particularly animal breeding, has reduced sharply as programs focused new hires in molecular genetics. Many faculty members with expertise in quantitative genetics are in the later stages of their careers. Thus, at a time when integrating genomic information with quantitative genetics is imperative, our capacity to train professionals with such expertise is at risk. One means to redress this situation is through across-institutional collaboration. Beginning in fall 2007, 4 universities joined efforts to develop a multi-state curriculum in animal breeding and quantitative genetics through distance-delivery. Thus far, 147 graduate students from 32 institutions have enrolled in 8 one-credit online courses, completing a total of 444 credit hours. Recently, an expanded consortium of 7 universities has formed to extend that curriculum further. Its aim is to train students with the skills to integrate advances in animal genomics with the agricultural systems emerging from our "New Biology for the 21st Century." Courses are being offered using programmatic tools in distance-delivery complemented by on-site summer short courses. The curriculum will consider 5 areas: core (prerequisite) knowledge, applications, quantitative genetics, statistical methods, and interface with molecular genetics. Educational backgrounds and aims differ among students enrolled. Therefore, the program is designed to be comprehensive, offering both breadth and depth of coverage, and to combine theory with application to solve real-world problems. The curriculum will be integrated into AG*IDEA, a national consortium of universities offering programs and courses in agriculture disciplines online. Beyond providing an infrastructure, that partnership will increase the accessibility of the curriculum nationally. The outcome will be more students pursuing and completing a postsecondary degree in quantitative aspects of genetics, with advanced skills and knowledge directly applicable to the agricultural workplace.

Key Words: distance delivery, genetics, graduate education

868 Service learning: Hands-on opportunities for on-line courses. O. U. Bolden-Tiller*[1], L. G. Martin[2], and I. Everett[1], [1]*Tuskegee University, Tuskegee Institute, AL,* [2]*Auburn University, Auburn, AL.*

Service learning can draw the most disengaged individuals into meaningful school experiences that deepen understanding and nurture practical effectiveness. We hypothesize that students enrolled in courses, including online courses, can gain skills and knowledge by participating in service learning. The objective of the current study was to ascertain knowledge gained through service learning in an introductory course in animal sciences. The service learning project (SLP) consisted of students selecting the animal species of their choice and developing an activity/fact sheet and interactive presentation geared toward 3- to 5-yr-olds. Following their participation in the SLP, 65 students enrolled in an introductory animal science class during fall 2011 completed a survey consisting of quantitative items, primarily on a Likert scale (0 = strongly disagree; 5 = strongly agree), aimed to gauge what and how these students learned, particularly in comparison to other teaching styles, such as lecture. Overall, students enjoyed the assignment, indicating that they learned more than in a lecture setting (3.57/5) and that they learned something new through the service learning project (4.24/5). Participants also indicated that they learned something beyond the assigned topic (3.35/5) and looked forward to participating in additional SLP (4.48/5). Interestingly, there was a significant difference ($P < 0.05$) in "what service learning meant" to each participant, ranging from teaching (43), learning and then teaching about what one has learned (14) and community service (7) to a class requirement (1). Our findings suggest that although students found service learning beneficial, consistent with previous findings, there were mixed results and inconsistent findings of student outcomes that seek to assess what and how service-learning students learned as well as how their learning compared with that within other pedagogical contexts, suggesting that a more rigorous assessment tool should be used to document and assess student learning in service-learning courses.

Key Words: animal sciences, service learning, distance education

869 Student learning in undergraduate animal breeding courses is improved through play of an online genetic simulation game. 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.*

The need to develop genetic simulation tools that provide undergraduate students an opportunity to apply course concepts in practice has long been recognized by educators in animal breeding. CyberSheep is an online genetic simulation tool developed at Virginia Tech, in which students manage a flock of sheep within a cooperative breeding scheme. The aim of CyberSheep is to provide a virtual lab where students can observe the consequences of their culling and breeding decisions in real time, benefiting their understanding of animal breeding concepts. Undergraduate students at the University of Wyoming and North Carolina State University were anonymously evaluated before and after playing CyberSheep to determine its contribution to their learning. Students were asked to evaluate their level of understanding of fundamental concepts used in CyberSheep including inbreeding, estimated breeding values, evaluating genetic merit of breeding stock, management of a lethal recessive allele, and cooperative breeding generally. Survey scores were analyzed using the GLM procedure of SAS. Play of CyberSheep corresponded with clear improvement ($P < 0.05$) in student understanding of cooperative breeding schemes, recessive allele management, and evaluation of genetic merit. Based on a 5-point scale, students rated their initial understanding of these 3 concepts at 3.1, 3.6, and 3.6, respectively, coinciding with a moderate level of understanding. Their scores rose ($P \leq 0.007$) to 3.6, 4.0, and 3.9, respectively, in the final survey indicating an improvement in their understanding of these same concepts with the use of CyberSheep. In general, students were satisfied with what they learned from CyberSheep with a score of 3.8, and found the simulation to be "fun" and a "worthwhile experience" with an average score of 3.5 and 3.6 for each criterion, respectively. It was concluded that the use of CyberSheep benefited animal breeding students in their understanding of fundamental concepts taught in animal breeding courses.

Key Words: animal breeding, education, genetic simulation

Author Index

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