RUMINANT NUTRITION III

1779 (W238) Prevalence of subclinical ketosis detected by near infra-red analysis of BHB in DHI milk samples. D. E. Santschi*, R. K. Moore and D. M. Lefebvre, *Valacta, Ste-Anne-de-Bellevue, QC, Canada*

Subclinical ketosis is a common early lactation disorder. Herd prevalence is often unknown because there are no specific clinical symptoms and because individual testing of dairy cows can be costly and time consuming. Since October 2011, Valacta (Dairy Centre of Expertise, Quebec and Atlantic Canada) offers routine infra-red testing of β-hydroxybutyrate (BHB) in DHI milk samples. Over 293,000 milk samples from fresh cows (DIM 5-35) from 4179 dairy herds have been analyzed for BHB concentration (199,003 multiparous and 94,036 primiparous cows). Based on a previously published trial comparing blood and milk BHB concentrations, thresholds 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). Overall incidence of subclinical ketosis (POS and SUSPECT) was 24.7% over the first 5 weeks of lactation. Incidence for DIM 5 to 35 was 21.5% and 26.6% for primiparous and multiparous cows, respectively. Distribution of incidence in relation to DIM was different between primiparous and multiparous cows. Highest incidence for primiparous cows (33.7%) was in the first week postpartum but in the third week for multiparous cows (33.5%). By DIM 35, incidence declined to 13.1% and 17.9% for primiparous and multiparous cows, respectively. Among herds with at least 10 cows analyzed for BHB ($n = 3560$), within herd prevalence of ketosis for the 10th, 25th, 50th, 75th and 90th percentile were 11, 17, 24, 33 and 43% respectively. Ketosis prevalence was affected by month of calving ($P < 0.001$). Highest incidence was observed for cows calving in May-June and October-November whereas lowest incidence was observed for cows calving in August and September. Ketosis prevalence was also affected by breed ($P < 0.001$). Prevalence for Ayrshire ($n = 12,443$), Brown Swiss ($n = 1814$), Holstein ($n = 271,367$) and Jersey ($n = 6554$) cows was 24.4, 22.7, 24.7 and 34.6%, respectively. Milk BHB concentration was negatively correlated with milk Fat:Protein ratio (R = -0.39; $P < 0.001$) and the correlation was affected by breed. Correlations between milk BHB and Fat:Protein ratio were -0.34, -0.35, -0.39 and -0.32 for Ayrshire, Brown Swiss, Holstein and Jersey cows, respectively ($P < 0.001$). Results indicate subclinical ketosis incidence varies greatly among dairy herds and is influenced by breed and season. Monitoring of subclinical ketosis prevalence is important as a first step towards greater transition success.

Key Words: ketosis, dairy cow, DHI

1780 (W239) Role of treatment soybean meal with pistachio extract on total tract nutrients digestibility of Holstein bulls. A. Jolazadeh[1], M. Dehghan banadaky*[2], K. Rezayazdi[3] and N. Vahdani[4], [1]*University of Tehran, Karaj, Iran,* [2]*Department of Animal Science, Faculty of Agriculture, University of Tehran, karaj, Iran,* [3]*Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* [4]*university of Tehran, karaj, Iran*

This experiment was conducted to study the effects of treatment soybean meal (SBM) with pistachio extract on total tract nutrients digestibility of Holstein bulls. The sun dried pistachio hulls were grounded through a 0.5 mm screen and soaked in water (1 pistachio: 10 water). Filtered extract was concentrated by heating at 95℃. SBM was treated with pistachio concentrated extract (PCE) containing 11.14% total phenol and 7.13% total tannin/DM of extract. Twenty-eight Holstein bulls (average initial weight 256 ± 63kg) were assigned randomly to one of four treatments with seven replicates in a completely randomized design for 94 days. Bulls were fed 70% concentrate diets and had free access to balanced total mixed ration (TMR) and fresh water. All bulls were individually fed and 10 d before the start of the experiment were adapted to the experimental diets. Treatments included: 1; control (SBM without PCE) 2; SBM with 5% PEC 3; SBM with 10% PEC and 4; SBM treated with 15% (kg PEC/100kg DM SBM). Total-tract apparent digestibility of DM, organic matter (OM), CP, NDF and EE were determined using acid-insoluble ash as a marker. There was no effect ($P < 0.05$) of tannin supplementation on total tract nutrient digestibility such as: DM, OM, CP, EE and NDF. These results suggested that high levels of PCE can be used in diet without any adverse effects on total tract nutrient digestibility in bulls.

Key Words: nutrients digestibility, pistachios hulls, tannin

1781 (W240) Effect of polyherbal supplementation as feed additive on milk production and composition in lactating goats. K. Rezayazdi*[1], F. Mirzaei[2] and M. Hosseinabadi[3], [1]*Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* [2]*Animal Science Research Institute, Karaj, Iran,* [3]*University of Tehran, Karaj, Iran*

The objective of this study was to evaluate the effect of adding a dried mixture of 7 herbal plants including thyme, mint, oregano, cumin, camel thorn, garlic and eucalyptus as a natural additive to the ration on milk production and composition in lactating goats. Because previously other researchers had studied about effects of these herbal plants on animals indivisually.Twenty goats (21 DIM, 2–3 years old, average BW 34.45 kg) were used in a completely randomized design with 2 treatments for a 40 day trial. Treatments were (1) control

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ration (basal diet), (2) control ration + 250 mg kg⁻¹ BW per d of a mixture of herbal plants. Animals were pen fed and all of data were analyzed with PROC MIXED procedure of SAS. Average milk production at the start of the experiment was similar in both groups (900 g/d). Milk production data and milk samples were collected every 10 day and milk composition was determined. The results showed that milk production (1073 and 1031 g/day for treatment 1 and 2, respectively) was not affected by addition of herbal plant mixture. Milk fat (2.76 and 2.79% for treatments 1 and 2, respectively), milk protein (2.76 and 2.79%) and milk lactose (5.44 and 5.40%) were not significantly different. It is concluded that herbal plant mixture were used in this study had no significant effect on milk production and composition in dairy goats.

Key Words: herbal plants, milk production and composition, dairy goats

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1782 (W241) Changes of protozoal diversity in response to forage and protein of diets in the rumen of dairy cows. J. Zhang, D. Bu*, S. Zhao and J. Wang, *State Key Laboratory of Animal Science, Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing, China*

The present study was conducted to investigate the changes of quantity and diversity of rumen protozoa in dairy cows fed with different forage and protein diets. Forty-eight healthy Chinese Holstein dairy cows were utilized in randomized block design, and the sixteen cows in every group had similar body conditions. The treatments were as follows: MF (forage sources: alfalfa hay and corn silage; protein sources: soybean meal and miscellaneous meals), CSA (forage sources: corn stover; protein sources: soybean meal and miscellaneous meals), CSB (forage sources: corn stover; protein sources: miscellaneous meals). Rumen fluid was collected via a stomach tube before and after morning feeding on 31, 61, and 91 d of experiment. Microbial DNA in rumen fluid sampled on 91 d was extracted by a CTAB plus bead beating method. The 18S rRNA gene sequences were trimmed and imported to MOTHUR for OTU analysis at 98% identity level. Results showed that the number of protozoa was not different among three groups based on microscopic counting and qPCR. Totally, 726 clones were obtained from three groups. There were 61 OTUs in three groups, 20 OTUs in CSA, 20 OTUs in CSB and 22 OTUs in MF. The three groups shared 10 OTUs, while CSA, CSB and MF had 6, 5 and 7 unique OTUs respectively. Compared with CSA (54.0), MF (46.2) and CSB (30.1) had lower species richness of protozoa based on ACE index. Compared with CSA (0.25), MF (0.11) and CSB (0.23) had higher diversity of protozoa based on Simpson index. Taxonomy analysis showed that *Dasytricha* (54.8%), *Entodinium* (16.4%), *Eudiplodinium* (14.2%), *Diplodinium* (7.7%) and *Isotricha* (3.3%) were the predominant genera in the rumen fluid. In different forage groups, *Diplodinium dentatum, Epi-*

dinium caudatum, Eudiplodinium maggii were only found in CSA, while *Isotricha intestinalis, Ophryoscolex purkynjei* were only found in MF. But in different protein groups, there was no apparently changed protozoal species. In conclusion, different sources of forage and protein in diets had no significant effect on the number of rum. However, feeding corn stover can result in higher protozoal abundance, and feeding soybean meal can lead to lower protozoal diversity.

Key Words: protozoa; diversity; forages.

1783 (W242) Pyrosequencing-based profiling of bacterial 16S rRNA genes identifies the unique Proteobacteria attached to the rumen epithelium of bovines. S. Zhao, J. Wang* and D. Bu, *State Key Laboratory of Animal Science, Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing, China*

The objective of this research is to characterize the unique bacterial community attached to the rumen epithelium in both dairy cows and beef cattle. The rumen content and rumen epithelium samples were collected from four Chinese Holstein dairy cows and five Australian beef cattle when the animals were slaughtered. The microbial DNA was extracted from rumen content and epithelium using CTAB plus bead beating method. Community compositions of bacterial 16S rRNA genes from content and wall were examined using a tag-encoded amplicon pyrosequencing assay with bacterial-targeting universal primers 8F and 533R. The sequencing was performed with Roche 454 GS FLX instrument. The platform QIIME was used for reads trimming and OTU analysis. The reads sharing more than 97% identity were clustered into OTUs. The results showed that 158 729 trimmed sequences with the length of 300-560 bp were kept. After OTU picking, 2735 OTUs were formed, and the average reads counts per sample was 7280. The bacterial species richness from epithelium was significantly lower ($P < 0.01$) than that from content according to Chao1 index, and bacterial α diversity from epithelium was also significantly lower ($P < 0.01$) than that from content according to Shannon index. The PCoA analysis revealed that epimural bacterial community was distinctly different from that in content, which implied some unique bacterial community attached to the epithelium of bovine. To further find out what the unique community was, taxonomy and significance test were carried out. While the *Fimicutes* (~42%) and *Bacteroidetes* (~20%) were the predominant abundant bacteria on epithelium, significant higher ($P < 0.01$) abundance of *Proteobacteria* (~26%) were present on epithelium than that in content (~3%). *Hylemonella, Desulfobulbus, Campylobacter* and unclassified *Neisseriaceae* were the predominant bacteria attached to epithelium compared to the content in both dairy cows and beef. These unique bacteria were microaerophilic (except for *Desulfobulbus*), and all of them were able to hydrolyze urea, which could further certify

the function of oxygen scavenging and urea hydrolysis for bacteria community attached to epithelium.

Key Words: rumen epithelium, bacterial community, pyrosequencing

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1784 (W243) Genetic diversity of dipeptidyl peptidase IV from anaerobic bacterial cultivation in vitro **in dairy cow.** J. W. Zhao[*1], J. Q. Wang[2], S. G. Zhao[2] and D. P. Bu[2], *[1]College of Animal Science and Technology of Inner Mongolia University for the Nationalities, Tongliao, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

The objective of this experiment was to reveal the genetic diversity of dipeptidyl peptidase IV (DPP-IV) gene from anaerobic bacterial cultivation in vitro and the influence of monensin to bacteria containing DPP-IV gene. There were two groups: one group substrate was casein (P), the other group substrate was casein with monensin added (M). Each group had three duplicated samples. Anaerobic culture was done after inoculating with rumen fluid. And then anaerobic bacterium was collected after 12 h culture and its DNA was extracted. DPP-IV gene library was established through PCR. Samples were detected by quantitative real-time PCR. Sixty-six sequence of DPP-IV gene were obtained from picking clones. The results of BLASTP analysis showed these sequences matched with *Prevotella ruminicola*, *Prevotella marshii* and *Paraprevotella xylaniphila*. Twenty-three operational taxonomic units (OTU) were found by Mothur software analysis, and OTU9 might be a DPP-IV gene of protein degradation bacteria sensitising to monensin. Quantitative analysis showed that the copy number of DPP-IV gene in P group was significantly higher than that of M group ($P < 0.01$). These results suggested that monensin affected the amount of bacteria containing DPP-IV gene.

Key Words: anaerobic bacterial cultivation in vitro, dipeptidyl peptidases IV, genetic diversity

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1785 (W244) Effects of test weight, precision processing and processing index on in situ ruminal digestibility of barley grain in beef heifers. Y. Zhao[1,2], S. Yan[2], Z. He[1,3], U. Anele[1], M. L. Swift[4], T. A. McAllister[5] and W. Yang[*1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China, [3]Key Laboratory for Agro-Ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, The Chinese Academy of Sciences, Changsha, China, [4]Alberta Agriculture and Rural Development, Lethbridge, AB, Canada, [5]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

The objective of this study was to evaluate the effects of test weight (TW; g/L), precision processing (PP) and processing index (PI) of barley grain on kinetics of in situ ruminal digestion. The study was designed as a 2×2×2 factorial arrangement with treatments: TW (low vs. high), PP (control vs. PP) and PI (75 vs. 85%). Ten barley samples with 5 low (574 g/L) and 5 high (632 g/L) TW were either dry-rolled with single roller setting (control) or sieved into small and large kernels, then dry-rolled based on kernel size of each fraction (i.e., PP). Each sample was dry-rolled moderately or coarsely with PI of 75 or 85%, which was calculated as TW after rolling/TW before rolling × 100%. Three beef heifers (650 ± 25 kg BW) fitted with rumen cannulas and fed diet consisting of 70% barley silage and 30% barley grain concentrate were used for in situ incubation. Kinetics of DM digestibility in situ after 0, 3, 6, 12, 24, and 48 h of incubation was estimated using the model: $y = a+b (1-e^{-ct})$. Effective ruminal degradability (ED) of DM was estimated using equation $ED = a + bc/(c + k)$ with k = 6%/h. There was no interaction between TW and PI on kinetic parameters, however, there was interaction between TW and PP on ED of DM ($P < 0.01$), and between PP and PI on potential degradable fraction, b ($P < 0.01$) and rate of degradation, c ($P < 0.04$). Overall, the TW of barley grain did not affect the kinetic parameters except that the ED was greater ($P < 0.01$) with high (43.4%) than low (41.8%) TW in control, but not in PP (low vs. high TW; 44.5 vs. 44.1%). Compared to control, PP reduced ($P < 0.01$) soluble fraction a (PP vs. control; 3.0 vs. 4.6%) and the b (73.6 vs. 75.4%), but increased ($P < 0.01$) the c (7.8 vs. 6.4%/h) and ED (44.3 vs. 42.6%). Decreasing PI from 85 to 75% considerably increased ($P < 0.01$) kinetics parameters, a (3.0 vs. 4.5%), b (71.7 vs. 77.3%), c (5.7 vs. 8.6%/h), and ED (37.2 vs. 49.7%). These results indicated that manipulating processing method such as PP and PI could effectively alter ruminal digestion kinetics of barley grain, whereas the effect of varying TW is limited.

Key Words: barley grain processing, in situ DM digestibility, beef heifers

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1786 (W245) Longitudinal shifts in the rumen bacterial communities of dairy cows during the transition period.

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The transition period in dairy cows refers to the period three weeks prior to calving to three weeks post-calving and is critical for sustained milk production and animal health. We evaluated the rumen microbial dynamics in primiparous and multiparous cows during their transition period. In the current study, ten animals from primiparous ($n = 5$) and multiparous groups ($n = 5$) were randomly selected based on the freshening date (expected date for parturition). Each animal was sampled for rumen contents by stomach tube, two hours after feeding, at four time points i.e., three weeks prior to the anticipated freshening date (S1), soon after the animal freshened (S2), four weeks (S3) and eight weeks (S4) into lactation. Both groups received the same dry cow ration (CP-14.65%; NDF-43.66%; Starch-21.9%) prior to calving and the same lactating cow ration (CP-17.21%; NDF-33.14%; Starch-27.19%) post calving. The genomic DNA form rumen samples was extracted and amplified using the primers BSF8 (27F) and BSR357 annealing to the V1-V2 region of the 16S rDNA bacterial gene. The amplicon libraries were sequenced on a 454 Jr Roche platform and analyzed for bacterial diversity using QIIME. A total of forty bacterial communities were analyzed that involved annotations of 100,000 reads, which were assigned to 15,861 operational taxonomic units (OTU). Bacterial community comparisons were based on the Uni-Frac distance metric which revealed that both study group and study day had an independent effect on the community compositions ($P < 0.05$; Permanova test). The most abundant phyla observed were *Bacteroidetes* and *Firmicutes* across all communities. As the cows transitioned into lactation, the ratio of *Bacteroidetes* to *Firmicutes* increased from 6:1 to 12:1 ($P < 0.05$; Mann-Whitney U test) and this ratio was higher in primiparous than in multiparous animals ($P < 0.05$). This study elucidated distinct shifts in the rumen microbiome confounded by dietary and physiological changes in both primiparous and multiparous dairy cows in their transition period. However, validating these results using more animals per lactation group is warranted.

Key Words: dairy cows, transition period, rumen bacteria, pyrosequencing, 16S pyrotags

1787 (W246) Effects of assumptions on estimating energetic efficiencies in lactating dairy cows.

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Theoretical estimates of efficiencies of metabolic and physiological processes have proven useful in teaching undergraduate and graduate courses in animal metabolism and bioenergetics. To maintain accurate numbers, new understandings have been applied to various biochemical pathways in ruminants. Further understanding of the mammalian ATP synthase, costs of membrane transport, electron transport, and oxidative phosphorylation have improved the accuracy of estimated theoretical efficiencies of energy metabolism. Advances include identifying the costs of: 1) the malate-aspartate shuttle for transporting protons and electrons into the mitochondria, 2) pyruvate transport into the mitochondria, and 3) counter transport of ATP and GTP out of the mitochondria with the concomitant cost of transporting ADP, GDP, and inorganic phosphorous into the mitochondria. As currently accepted, electron transport results in 10 and 6 protons pumped from the matrix to the intermitochondrial space when the electrons are derived from NADH + H$^+$ and FADH$_2$, respectively. The discovery that bovine heart ATP synthase requires the flow of 8 protons from the intermitochondrial membrane space into the mitochondrial matrix through the ATP synthase to produce 3 ATP is critical to estimating energetic efficiency in mammalians. Consequently, 2.7 ATP are produced from each NADH + H$^+$ formed in the mitochondria, 2.5 ATP from each NADH + H$^+$ formed in the cytosol, and 1.6 ATP from each mitochondrial FADH$_2$ when each is coupled to oxidative phosphorylation. Mitochondrial GTP formed in the TCA cycle is equivalent to 0.7 ATP when GTP is transported out of the mitochondria. Energy available from ATP hydrolysis varies from 32 to 52 kJ/mole of ATP with an average of 42 kJ/mol. Using these data, theoretical efficiencies and net ATP production/cost were calculated and compared to those of Baldwin [*Journal of dairy science* **51**(1): 104-111. (1968)] (Table 1787). These values demonstrate the importance of applying current research and ideas to create accurate values of theoretically estimated metabolic and physiological pathways.

Key Words: energy, metabolism, ATP

Table 1787. Theoretically estimated efficiencies and net ATP production/cost for various biochemical pathways

Pathway	Current		Baldwin, 1968	
	ATP Produced	Efficiency	ATP Produced	Efficiency
Propionate to glucose	-4.7	-	-4	-
Glucose to CO_2 and H_2O	32.9	49%	38	56%
2 Propionate to CO_2 and H_2O	28.2	38%	34	46%
Fat turnover	45.7	36%	-17	-
Milk lactose synthesis	-	76%	-	78%
Milk protein synthesis (100 g)	-	77%	-	82%
Milk fat synthesis	-	71%	-	72%
Total milk synthesis	-	75%	-	76%

1788 (W247) Nutrient supply estimations errors when using free ruminal bacteria as reference sample.

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The chemical composition of bacteria associated with solid (SAB) and liquid (LAB) rumen-digesta phases was studied to confirm errors when LAB is used as reference sample to estimate nutrient supply from SAB (González et al., 2012). Three rumen and duodenum cannulated wethers were fed three isoproteic diets for three successive periods. Diets included protein concentrates (sunflower meal and spring pea) untreated or treated with malic or ortophosphoric acid and heat supplied in this order. Diets were formulated with 45% oat (avena sativa) hay and 55% concentrate (fresh matter basis; 30% corn grain, 30% barley grain, 15% sunflower meal, 22% spring pea, 3% minerals and vitamins) and offered daily at 45 g/kg BW0.75 in six identical meals. Bacterial samples (SAB and LAB) were isolated after 12 d of continuous intraruminal infusion of $(15NH4)2SO4$ (25 mg 15N/d). Results were compared by variance analysis considering wethers (as blocks) and diets in the model. Compared with SAB, LAB showed consistently lower contents (g/kg DM) of OM (780 vs. 693; $P < 0.001$), starch- glucose (33.4 vs. 19.9; $P = 0.013$), and total lipids (221 vs. 113; $P < 0.001$), but greater CP content (402 vs. 429; $P = 0.007$) and 15N enrichment (atoms %: 0.0585 vs. 0.0817; $P = 0.005$). Present data fitted well with the relationship predicting SAB 15N enrichment from the same LAB value reported in the previously cited study (variation coefficient of the mean prediction error = 13.0%). The mean ratio 15N-SAB/15N-LAB allows establishing CP supply from synthesized SAB is under evaluated by 25.6% when LAB is used as reference. This under evaluation was even greater for starch-glucose (44.2%) and lipids (61.9%) supply. These under evaluations were close to those previously reported by González et al., 2012. Taking into consideration that SAB is the main microbial source of nutrient supply, these errors should be factored in when attempting to improve ruminant nutrition. Predictions using 15N as marker are useful for correcting errors associated with the traditional use of LAB as reference sample, and therefore to obtain a more accurate estimate of microbial nutrient supply to the ruminant.

Key Words: rumen bacteria, chemical composition, 15N enrichment

1789 (W248) Evaluation of the Nordic dairy cow model Karoline in predicting methane emissions.

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Models are widely used to predict methane (CH_4) emissions, and are used to develop mitigation options and policies. In the current study, the performance of the Nordic dairy cow model Karoline was evaluated in predicting CH_4 emissions. Karoline is a dynamic, deterministic and mechanistic simulation model describing the digestion and metabolism of nutrients, and production in a dairy cow. The model was evaluated against observed data from studies reporting CH_4 emissions from respiration chamber studies. The dataset included a total of 184 treatment means from 31 published papers. The dietary and animal characteristics used for the model evaluation represent the typical range of diets fed to dairy cattle. When analyzed with a fixed regression analysis, there was a good relationship between predicted and observed CH_4 emissions measured from respiration chamber studies ($R^2 = 0.93$) with a small root mean square error of prediction (RMSPE = 10.1% of the observed mean). The mean bias was small but statistically significant, and there was no slope bias. Most of the error was due to random bias (96.4%), whereas the contributions of mean and slope bias were small (3.4 and 0.2%, respectively). By considering study as the random effect in the model (mixed model regression analysis), the fit improved to $R^2 = 0.98$ and RMSPE decreased to 6.1% of the observed mean. The influence of some input variables such as total DM intake, dietary concentrations of CP, NDF and ether extract, and OM digestibility (OMD) on the residuals (observed– predicted) of CH_4 emissions were not significant. The residuals of both CH_4 emissions and OMD were significantly related to each other, indicating the Karoline model requires accurate estimates of digestion kinetic parameters as input variables. It is concluded that the Nordic dairy cow model Karoline is a useful tool in predicting CH_4 emissions and understanding the system behavior. The model can also be used in developing mitigation strategies for the national inventories of CH_4 emissions.

Key Words: Karoline model; methane emissions; mechanistic model

1790 (W249) Effects of different feeding frequencies on rumen tissue histology and cell proliferation of feedlot cattle.

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This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different feeding frequencies on rumen tissue histology and cell proliferation of rumen papillae of feedlot cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 48 18-mo-old yearling Nellore bulls (358.2 ± 19.4 kg) were fed in individual pens for 94-d according to the following treatments: 1) feeding one time daily (1x; 0800), 2) feeding two times daily (2x; 0800 and 1400), 3) feeding three times daily (3x; 0800, 1100 and 1400), and 4) feeding four times daily (4x; 0800, 1100, 1400 and 1700). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 60% to 86% of diet DM. The finishing diet contained: 67.0% cracked corn grain, 14.0% sugarcane bagasse, 9.0% soybean hulls, 5.5% soybean meal, 4.0% supplement containing 30% of urea, and 0.5% limestone (DM basis). At harvest, a 1-cm^2 fragment of each rumen was collected from ventral sac for histological assessment. Histological sections were stained with hematoxylin and eosin, embedded in paraffin wax, and sectioned. Morphometric measurements, such as papillae surface area, papillae height, papillae width, keratinized layer thickness, and mitotic index, were determined in four papillae per animal using computer-aided light microscope image analysis. In addition, cell proliferation was determined by immunohistochemistry technique using the monoclonal mouse anti-proliferating cell nuclear antigen. Orthogonal contrasts were used to assess linear, quadratic, and cubic relationship between feeding frequency and the dependent variable. Feeding frequency did not affect ($P > 0.10$) papillae width, keratinized layer thickness, and cell proliferation. However, as feeding frequency increased, papillae surface area in cm^2 (1x = 1.11; 2x = 1.11; 3x = 1.29; 4x = 1.22), papillae height in mm (1x = 2.85; 2x = 2.79; 3x = 3.29; 4x = 3.14), and mitotic index, as % of basal cells (1x = 9:12; 2x = 10.60; 3x = 12.85; 4x = 12.63) linearly increased ($P < 0.05$). Papillae surface area and papillae height were also affected ($P = 0.01$) cubically as feeding frequency increased. Thus, increasing feeding frequencies affected rumen tissue histology variables. In a practical way, feeding yearling Nellore bulls three times daily seems to be the most feasible option.

Key Words: mitosis, Nellore, papillae

1791 (W250) Survey of nutritional recommendations used by dairy cattle nutritionists in Brazil in 2013.

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This survey was designed to describe the nutritional recommendations and management practices adopted by Brazilian dairy cattle nutritionists in 2013. Forty-three nutritionists responsible for about 960 dairy farms, completed the survey within 1-mo, which was available online (www.surveymonkey.com) and consisted of 77 questions. The level of grains included in lactation diets recommended by 22 (55.0%) participants ranged from 31% to 50%, but 8 (20.0%) nutritionists recommended diets with 51% to 60%, and 10 (25.0%) used less than 31% grains. Likewise, the level of concentrate included in lactation diets recommended by 18 (43.9%) participants ranged from 41% to 50%, but 11 (26.8%) nutritionists recommended diets with 51% to 60%, and 12 (29.3%) used less than 31% concentrate. Corn was the primary source of grain used in lactation diets ($n = 37$; 97.4%). With respect to the energy unit used to formulate lactation diets, 40.5% ($n = 15$) nutritionists used TDN, followed by the NFC (29.7%; $n = 11$). The main source of information for feed energy values was the NRC (73.2%, $n = 30$), followed by CPM-Dairy (17.1%, $n = 7$). The typical range of roughage inclusion in finishing diets was 50.5%, and corn silage was the primary roughage source, being used by 30 nutritionists (79.0%). Moreover, the average recommended concentrations of NDF were 35.4%. Also, NDF was the fiber analysis method of choice by 29 of the nutritionists (76.3%), whereas physically effective NDF was cited by 7 (18.4%) of the respondents. Regarding coproduct use in lactation diets, citrus pulp pellets was the primary coproduct included in lactation diets, being used by 20 (51.3%) of the nutritionists. Use of whole cottonseed was reported by 8 (20.5%) nutritionists, whereas soybean hulls was reported by 7 (17.9%) of the respondents. When asked about feeding frequency, most of the clients served by the nutritionists surveyed typically feed twice daily (70.7%; $n = 29$), whereas 10 participants (24.4%) reported that their clients feed cows three times daily. This study presents a part of an overview of the practices and management recommendations currently applied by dairy cattle nutritionists from all regions in Brazil. Also, this survey may help to identify and solve problems in Brazilian dairy cattle operations, and moreover, these data may facilitate the design of industry-oriented research.

Key Words: Brazil, dairy, survey

1792 (W251) Effects of type of base forage on the Beta-carotene content of milk and blood plasma in lactating Holstein cows. H. C. Leicester[*1,2] and L. J. Erasmus[2], *[1]UC Davis, Davis, [2]University of Pretoria, Pretoria, South Africa*

It is well established that β-carotene has a positive effect on fertility of dairy cattle (Arechiga et al., 1998; J. Dairy Sci. 81, 390-402). The aim of this project was to determine the β-carotene content and variability of the main forage fed, blood plasma and milk of lactating Holstein cows managed in three typical South African production systems which differ in the base forage. These were pasture based systems (S1), predominantly corn silage based total mixed ration (TMR) systems (S2), and predominantly hay and alfalfa based TMR systems (S3). Within each system, 10 farms were selected based on their management and diet similarity within system and, from each farm, 20 cows where selected which had > 60 days in milk and were in lactation 2 or higher. The 20 cows/farm were chosen randomly from cows meeting these criteria. From each farm, a representative sample of the main forage, plasma samples from the 20 cows and a 2 liter bulk tank milk sample were collected. All samples were analyzed for β-carotene. The β-Carotene analyses of the predominant forages in each system revealed values of; S1; 20.9 ± 6.78 mg/Kg, S2; 3.1 ± 2.59 mg/Kg and S3; 22.4 ± 15.05 mg/Kg. Mean plasma β-Carotene of S1 cows was 5.5 ± 2.39 mg/L and this differed ($P < 0.05$) from S3 with values of 3.0 ± 0.66 mg/L, which tended ($P < 0.10$) to differ from S2 at 1.7 ± 0.06 mg/L. Bulk milk tank samples had β-Carotene levels of S1 (15.4 ± 7.40 mg/L), S2 (2.3 ± 0.43 mg/L) and S3 (4.1 ± 2.30 mg/L). While no guidelines exist for adequacy of β-Carotene levels in milk, plasma β-Carotene levels of < 1.5 mg/L is defined as 'deficient', 1.5 to 3.5 is 'marginal' and levels > 3.5 are 'optimal' (Schweigert and Immig, 2007; Int. Dairy Topics, 6,4). On this basis, S1 cows had 'optimal' plasma β-Carotene levels whereas S2 and S3 cows had 'marginal' β-Carotene levels, which suggests that dietary β-Carotene supplementation is required. However the wide variation in the β-Carotene levels of the base forages, both among and within systems, suggests that dietary β-Carotene supplementation should not be based solely on system, but should include β-Carotene analysis of the base forage.

Key Words: fertility production ICheck

1793 (W252) Effect of acute exposure to ergot alkaloids on short-chain fatty acid absorption and barrier function of isolated bovine ruminal epithelium. A. P. Foote[*1], G. B. Penner[2], M. E. Walpole[2], J. L. Klotz[3], L. P. Bush[4] and D. L. Harmon[4], *[1]USDA, ARS, US Meat Animal Research Center, Clay Center, NE, [2]University of Saskatchewan, Saskatoon, SK, Canada, [3]USDA-ARS, FAPRU, Lexington, KY, [4]University of Kentucky, Lexington*

Ergot alkaloids present in endophyte-infected tall fescue are the causative agents for fescue toxicosis in cattle. Ergot alkaloids have been shown to cause a reduction in blood flow to the rumen epithelium as well as a decrease in short-chain fatty acid (SCFA) absorption from the washed rumen of steers. It is possible that ergot alkaloids could negatively impact SCFA transport pathways and the barrier function of the rumen epithelium. An experiment was conducted to determine if acute exposure to an endophyte-infected tall fescue seed extract (EXT) would affect total, passive, or facilitated acetate and butyrate flux across the isolated bovine rumen epithelium as well as the barrier function measured by inulin flux and tissue conductance (G_t). Flux of ergovaline across the ruminal epithelium was also evaluated. Ruminal tissue from the caudal dorsal sac of Holstein steers ($n = 6$), fed a common diet, was collected and isolated shortly after slaughter and mounted between two halves of Ussing chambers under voltage clamp conditions. In vitro treatments included vehicle control (0.4% methanol), Low EXT (50 ng ergovaline/mL), and High EXT (250 ng ergovaline/mL). Results indicate that there was no effect of an acute exposure to ergot alkaloids on total, passive, or facilitated flux of acetate or butyrate across the isolate bovine rumen epithelium ($P > 0.51$). Inulin flux ($P = 0.16$) and G_t ($P > 0.17$) also were not affected by EXT treatment, indicating no alteration in barrier function due to acute ergot alkaloid exposure. Based on ergovaline concentrations measured in the serosal buffer of the High EXT treatment, the flux rate is approximately 0.25– 0.44 ng/(cm^2 · h). These data indicate that specific pathways for SCFA absorption and barrier function of the ruminal epithelium are not affected by acute exposure to an extract of tall fescue seed at the concentrations tested. Ergovaline has the potential to cross the rumen epithelium of cattle which could contribute to the reduced foregut blood flow seen in previous experiments and lead to reduced growth rates of cattle.

Key Words: ergot alkaloids, ergovaline absorption, fescue toxicosis

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1794 (W253) Evaluation of the CNCPS v6.5 for predicting metabolizable energy and protein allowable milk in sugarcane based diets.

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Sugarcane is a high energy yielding crop, and is an alternative feed for dairy cows in tropical regions. This experiment evaluated the sensitivity of CNCPSv6.5 for predicting milk yield in sugarcane based diets. Data for evaluation were obtained from 13 published experiments, representing 50 treatments. Metabolizable energy (ME) and protein (MP) allowable milk were predicted based on reported DMI and diet composition. An algorithm was used to adjust the nutrient composition of individual ingredients from commercial laboratory databases when feed chemistry data were incomplete. The correlation coefficients between observed and predicted milk yield were based on BLUP (R^2_{BLUP}) and model predictions using the mean study effect (R^2_{MP}). When milk yield was predicted based on the first limiting nutrient, either ME or MP, the correlation coefficient generated with R^2_{BLUP} was 0.985 and with R^2_{MP} was 0.81. With ME predicted milk yield, the R^2_{BLUP} correlation coefficient was 0.989 and for R^2_{MP} it was 0.81, and when the predictor was MP they were 0.92 and 0.67, respectively. The Bayesian Information Criterion was 219 for MP or ME, 110 for ME, and 127 for MP. The Mean Square Prediction Error (MSPE) using MP to predict milk yield was 5.4, and it was 10.8 when ME or MP or ME were predictors. When the MSPE was partitioned, 0.22%, 0.01% and 3.6% of the error was due to mean bias for the MP or ME, ME, or MP predicted milk yield, respectively, 35.41%, 32.94% and 30.72% was due to systematic bias, and 64.37%, 67.05% and 65.68% was due to random variation. Concordance Correlation Coefficients were computed to account for the accuracy and precision of the predictions, values were: 0.79 for MP or ME, 0.83 for ME, and 0.75 for MP. Using CNCPSv.6.5 to predict milk yield responses in sugarcane based diets was reliable. In the available data sets, the prediction of ME allowable milk yield was better than MP and this most likely reflects differences in actual rates of digestion and library values along with ingredient bias.

Key Words: dairy cattle, model evaluation, tropical feed

1795 (W254) Effects of different feeding frequencies on DMI variation and selective consumption by feedlot cattle.

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This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different feeding frequencies on DMI variation and selective consumption (sorting) of diets by Nellore cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 48 18-mo-old yearling Nellore bulls (358.2 ± 19.4 kg) were fed in individual pens for 94-d according to the following treatments: 1) feeding one time daily (1x; 0800), 2) feeding two times daily (2x; 0800 and 1400), 3) feeding three times daily (3x; 0800, 1100 and 1400), and 4) feeding four times daily (4x; 0800, 1100, 1400 and 1700). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 60% to 86% of diet DM. The finishing diet contained: 67.0% cracked corn grain, 14.0% sugarcane bagasse, 9.0% soybean hulls, 5.5% soybean meal, 4.0% supplement containing 30% of urea, and 0.5% limestone (DM basis). The DMI variation was calculated for each individual yearling bull as the difference in intake, expressed as % of variation, between consecutive days throughout the study. Samples of orts and diets were collected on days 12 and 51 of the study for particle size distribution determination, which was performed by sieving using the Penn State Particle Size Separator and reported on as-fed basis. Values equal to 1.0 indicate no sorting, < 1.0 show selective refusals, and > 1.0 indicate preferential consumption. Orthogonal contrasts were used to assess linear, quadratic, and cubic relationship between feeding frequency and the dependent variable. During the period of adaptation, DMI variation was affected ($P < 0.01$) cubically as feeding frequency increased (1x = 16.1%; 2x = 23.2%; 3x = 14.4%; 4x = 15.9%), however, feeding frequency did not affect ($P > 0.10$) DMI variation during the finishing period. Feeding frequency only affected particle sorting during the adaptation period, in which as feeding frequency increased, sorting for screen 3 (diagonal opening = 1.18 mm) was affected ($P < 0.01$) quadratically (1x = 0.993; 2x = 0.995; 3x = 0.999; 4x = 0.985). Thus, based on the results of this study, feeding frequency affects DMI variation and diet sorting only during the adaptation period. Cattle fed three times daily presented lower DMI variation and lesser extent of sorting.

Key Words: fluctuation, Nellore, sorting

1796 (W255) Evaluation of mineral excretion of lactating Holstein dairy cows supplemented with copper, manganese and zinc in organic and inorganic forms.

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Forms of minerals, organic and inorganic, impact the amount of mineral available for intestinal absorption. However, in the ruminant, when inorganic minerals dissociate they can associate with feed components decreasing their availability for intestinal absorption. The objective of this study was to evaluate the impact of level of feeding organic and inorganic forms of Cu, Mn and Zn (Bioplex Cu, Mn, and Zn; Alltech, Inc.) on mineral fecal excretion of lactating dairy cows on a commercial dairy. Fifty lactating Holstein dairy cows (70 DIM) were randomly assigned to five treatments: Control, Organic75, Organic100, Organic125, and Inorganics ($CuSO_4 \cdot 5H_2O$, $MnSO_4 \cdot H_2O$ and $ZnSO4 \cdot H_2O$) (Table 1796). Therefore control cows received only the levels of minerals present in the TMR based on NRC. Minerals were given by daily dosing individual cows with an oral solution of the mineral treatment for 28 d (24 d for adaptation, and 4 d of sample collection). Fecal samples were collected rectally twice a day (am and pm), combined for a 24h sample and sent for analysis of mineral content and composition. For 11 d, Cr was supplemented (10g/d) with minerals to estimate total fecal output. Statistical analysis was performed in R (version 2.15.1) using ANOVA. No differences were observed for fecal output (kg/d) ($P = 0.35$) and manganese excretion (g/d) ($P = 0.23$) among treatments. Copper and zinc excretion levels did differ among treatments ($P < 0.001$). Averages (g/d) for copper excretion were 0.48, 0.66, 0.68, 0.76 and 0.58 for Control, Organic75, Organic100, Organic125 and Inorganic, respectively; and averages for zinc excretion were 2.70, 3.21, 3.04, 3.42, 2.78 for Control, Organic75, Organic100, Organic125 and Inorganic, respectively. Greatest concentrations of mineral excretion were observed in cows supplemented with 25% above NRC requirement levels of Bioplex Cu and Zn while lowest levels of mineral excretion were observed in cows dosed with control and Inorganics. In conclusion, this study shows that mineral form only affects copper and zinc excretion. However, treatment comparisons are not corrected for contributions of minerals from other dietary components (DMI), so conclusions on levels of mineral fecal excretion may change when considering apparent absorption.

Key Words: minerals, fecal excretion, dairy cattle

Table 1796. Levels of minerals supplemented on top of TMR (control diet) for each treatment

	Control	Organic75	Organic100	Organic125	Inorganics
			(mg/d)		
Mn	354.00	125.07	166.76	208.45	166.76
Cu	472.00	215.07	286.76	358.45	286.76
Zn	1409.00	375.88	501.18	626.48	501.18

1797 (W256) Evaluation of milk yield and composition of F1 Holstein x Gir lactating cows supplemented with rumen-protected choline during the transition period.

R. C. D. Souza[*1], R. C. Souza[1], A. B. D. Pereira[2], R. F. Cota[1], T. A. Torres[1], I. B. Fortes[1] and G. V. Fonseca[3], [1]PUC Minas, Betim, Brazil, [2]University of New Hampshire, Durham, [3]PUC, Betim, Brazil

The use of rumen-protected choline (RPC) is a strategy to improve fat metabolism in the liver and reduce the prejudicial effects of negative energy balance in dairy cows during the peripartum. The objective of this study was to evaluate milk yield and composition of cows supplemented with RPC during the transition period (from 21 d pre-partum until 21 d post-partum). Thirty two lactating F1 Holstein x Gir cows (16 multiparous and 16 primiparous) were blocked by parity and randomly assigned to one of two dietary treatments: no addition of RPC (NC) and addition of 60 g of RPC (AC; To-plac Transition, Nutrifarma, Taió, PR, Brazil). Diets contained 60% forage as corn silage and were isonitrogenous and isocaloric according to the NRC (2001) model. Supplementation of RPC was done from 21 d before expected parturition until 21 d post-partum. The experiment was analyzed as a randomized complete block design using the MIXED procedure for SAS and least square means were reported according to the tukey post-hoc test. Milk production was lower for multiparous cows in the NC diet (32.2 kg/d) compared to the AC diet (34.4 kg/d, $P < 0.05$), but no effect was observed for primiparous animals. A difference between treatments was observed for milk fat yield for multiparous cows (0.88 kg/d and 1.17 kg/d for NC and AC, respectively, $P < 0.05$) and primiparous cows (1.02 kg/d and 1.17 kg/d for NC and AC, respectively, $P < 0.05$) and somatic cells count for multiparous cows (401 x 10^3 cells and 258 x 10^3 cells for NC and AC, respectively, $P < 0.05$) but not for primiparous cows (143 cells/mL and 93.8 cells/mL for NC and AC, respectively, $P > 0.05$). Also, no difference was found between treatments and parity level for milk fat percentage, milk protein or milk solids non-fat. Rumen protected choline supplementation to F1 Holstein x Gir multiparous cows improved milk production and milk fat yield. Effect on primiparous cows was observed only on milk fat yield.

Key Words: rumen protected choline, milk yield, milk composition.

1798 (W257) Effects of supplemental bupleurum extract on blood material metabolism in heat-stressed dairy cows. X. Sun*, *Ministry of Agriculture-Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China*

This study investigated the effect of bupleurum extract (BE) on blood material metabolism of lactating dairy cows under heat stress. Forty lactating Chinese Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to four groups and were individually fed a basal diet with 0, 0.25, 0.5, or 1.0 g BE/kg DM. The experiment lasted 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21, 42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. Supplementation of BE decreased urea nitrogen (BUN) contents (5.65, 5.58, 5.81 vs 5.95 mmol/L, $P < 0.05$), but increased blood total protein (80.97, 81.08, 81.00 vs 77.22 g/L, $P < 0.05$) level. Cows fed 0.25 or 0.5 g/kg BE increased albumin content (38.61, 37.53 vs 36.18 g/L, $P < 0.05$) compared with control cows, but BE supplementation had no effects ($P > 0.05$) on blood glucose (GLU), nonesterified fatty (NEFA), total triglyceride (TG), low density liporotein cholesterin (LDL-C) and high density liporotein cholesterin (HDL-C). Sodium (Na) (136.63, 134.72, 136.05 vs 137.90 mmol/L; $P < 0.01$) and phosphorus (P) (1.94, 1.96, 1.81 vs 2.13 mmol/L; $P = 0.05$) concentrations in serum were decreased by BE supplementation, while potassium (K) (3.80, 3.83, 3.90 vs 3.48 mmol/L; $P < 0.01$) and calcium (Ca) (2.56, 2.59, 2.66 mmol/L; $P < 0.01$) concentrations were decerased than in controls, but BE supplementation had no effect ($P > 0.05$) on serum magnesium (Mg) concentration. Serum chlorine (Cl) concentration was increased in cows fed 0.5 g/kg BE (148.01 vs 140.79 mmol/L; $P < 0.05$) compared with control cows, and tended to be higher (144.08 vs 140.79 mmol/L; $P < 0.1$) in cows fed 0.25 g/kg BE, but was not affected in cows fed 1.0 g/kg BE. These findings suggest that BE supplementation could improved the protein metabolism and maintain the balance of electrolyte concentration.

Key Words: bupleurum extract; heat stress; blood material metabolism

1799 (W258) Evaluation of the updated version of CNCPS (v6.5). A. Foskolos*[1], E. A. Collao-Saenz[2], D. A. Ross[1], R. J. Higgs[1] and M. E. Van Amburgh[1], *[1]Cornell University, Ithaca, NY, [2]Universidade Federal de Goiás, Jatai-GO, Brazil*

The first version of The Cornell Net Carbohydrate and Protein System (CNCPS) was released in 1991, and since then it has been continuously under evolution. Our objectives are to describe the latest updates of the model resulting in version 6.5 and to evaluate model predictions against both literature and on-farm data. Degradation rates of protein and carbohydrate fractions were modified to meet new fractionation schemes, updated amino acid (AA) profiles on a whole feed basis were made and a combined efficiency of essential AA use was adopted representing an improved understanding of AA metabolism. Three different datasets were developed to evaluate lysine (Lys) and methionine (Met) requirements (AA dataset), rumen N balance (rumen dataset) and metabolizable energy (ME) and protein (MP) allowable (lactation dataset). In total 96 peer-reviewed studies with 367 treatments and 15 regional farms with 50 different diets were included. The AA dataset was used to estimate the concentration of Lys and Met that maximizes milk protein yield and content according to the broken line model with plateau: results suggested concentrations of 7.00 and 2.60%MP for Lys and Met, respectively for maximal protein yield and 6.77 and 2.85%MP for Lys and Met, respectively for maximal protein content. Proposed concentrations are slightly higher for Lys and 11-18% higher for Met compared with CNCPSv6.0 which can be attributed to changes in the AA profile of feeds. The ability of the model to predict post-ruminal flows of N and milk yield was assessed using the correlation coefficient based on the BLUP (R^2_{BLUP}) or model predictions using a mean study effect (R^2_{MP}) and the concordance correlation coefficients (CCC) to simultaneously account for accuracy and precision. The model predicted accurate and precise post-ruminal flows of rumen degraded and undegraded N (RDN and RUN, respectively; $R^2_{BLUP} = 0.98$ and 0.92 and CCC = 0.88 and 0.80 for RDN and RUN, respectively), bacterial N ($R^2_{BLUP} = 0.97$; CCC = 0.84) and provided a uniform offset of non-ammonia N that is robust with little bias ($R^2_{BLUP} = 0.98$; CCC = 0.92). For the lactation dataset, the model predicted accurate and precise milk yield according to the first limiting nutrient (MP or ME) with a $R^2_{BLUP} = 0.95$, $R^2_{MP} = 0.78$ and CCC = 0.83. Results suggest a significant improvement of the model due to current updates.

Key Words: CNCPS, evaluation, dairy cattle

1800 (W259) Effects of bupleurum extract on performance and health status in heat-stressed late lactation dairy cows. B. Shi[1,2], N. Zheng[1], J. Cheng[1,2], L. Min[1], C. Yin[1] and J. Wang*[1,3], *[1]Ministry of Agriculture- Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

This study was conducted to investigate the effects of bupleurum extract (BE) on performance and health status in heat-stressed Chinese Holstein dairy cows. Forty lactating cows (days in milk = 207.98 ± 12.2; average milk yield = 30.96 ±

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3.96 kg/d; parity = 1.96 ± 1.07) were randomly assigned to 1 of 4 treatments according to a completely randomized block design. Cows were individually housed in pens and fed ad libitum three times daily. Treatments consisted of 0, 0.5, 2.5 or 5% BE of dry matter (CG, LG, MG or HG).The experiment lasted for 11 weeks in hot summer. Ambient temperature and relative humidity were recorded daily (0600, 1400, and 2200). Milk yields, dry matter intake (DMI), respiration rates (RR) and rectal temperatures (RT) were recorded twice a week and milk samples were collected twice a week. Blood was collected in evacuated tubes via caudal venipuncture at 0, 3, 6, 9, 11 week. Data were analyzed by repeated measures using Proc Mixed procedure of SAS 9.2. During the experiment, average temperature-humidity index were 76.8 ± 6.3, 82 ± 6.54 and 78.3 ± 6.1 respectively at 0600h, 1400h and 2200h. There was no treatment effect on RR, RT, DMI and milk yield, while the values of DMI (19.41, 19.04, 18.61 vs. 19.19 kg/d) tended to decrease with increasing dose. Milk urea nitrogen in MG was lower (12.06 vs. 12.92 mg/dL, $P < 0.05$) than that in CG, while contents of milk fat, milk protein, lactose, total solids and somatic cell counts were not significantly affected ($P > 0.05$). The mean corpuscular hemoglobin in HG was lower than that in CG (16.56 vs. 16.98 pg, $P < 0.05$). The Mean corpuscular hemoglobin concentration (346.35, 347.81, 344.87 vs. 351.28 g/L, $P < 0.05$) was decreased due to BE supplementation. No significant difference in the number of leukocytes, red blood cell count, hematocrit, lymphocytes, mean corpuscular volume, mean platelet volume and red blood cell distribution width were detected among groups. There was no treatment effect on glutamic-pyruvic transaminase, glutamic oxalacetic transaminase, globulin, albumin, total protein and alkaline phosphatase. These results indicate that BE supplemented with high dose of 5% had no negative effect on the performance and health status in heat stressed late lactation dairy cows, and 5% is safety dose.

Key Words: bupleurum extract, performance, health status

1801 (W260) Estimation of NDF pool in the rumen of cattle using fecal excretion and diet characteristics.
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The objective of this work was to estimate ruminal pool of NDF in cattle from the fecal excretion of fiber and diet characteristics using a meta-analytical approach. The dataset was compiled from 60 experiments with lactating cows and growing cattle carried out in Europe and Brazil, totaling 227 treatment means. The dataset was analyzed using linear mixed models according to meta-analysis techniques. The variation among experiments was considered as a random effect in the models. An unstructured (co)variance matrix was used. The evaluation of the effect of animal category was accomplished on intercept and slopes through a "dummy" variable D (i.e. binary variable),where D = 0 for lactating dairy cows and D = 1 for growing cattle. All analyses were performed using the MIXED procedure of SAS 9.2.Different models were adjusted considering two different units for NDF pool (pNDF): kg and g/kg BW. The independent variables were selected based on biological relevance and also on estimates of partial Pearson's correlation with the dependent variable. In this way, the independent variables were: fecal excretion of NDF (fNDF), representing the undigested fiber pool; dietary NDF content (dNDF), representing the dietary input of fiber; and the ratio between dietary iNDF (indigestible NDF) and dNDF (iNDF/dNDF), representing the quality of dietary fiber.The adjusted models were: pNDF (kg) = 2.95 -2.75 × D + 1.217 ×fNDF(kg)– 0.08034 × fNDF^2 (kg) + 0.003×dNDF(g/kg DM)– 1.606 × (iNDF/dNDF), R^2 = 0.95, s_{XY} = 0.54, where D = 0 for lactating cows and D = 1 for growing cattle; and pNDF (g/kg BW) = 5.20– 3.62 × D + 1.067 × fNDF (g/kg BW)– 0.03324 × fNDF^2 (g/kg BW) + 0.005 × dNDF (g/kg DM)– 2.809 × (iNDF/dNDF), R^2 = 0.93, s_{XY} = 0.94. All terms were found significant ($P < 0.05$) and there was no lack of fit for both models ($P > 0.63$). The meta-analysis results brought into evidence that NDF rumen pool can be estimated from fecal and diet characteristics avoiding the utilization of invasive techniques.

Key Words: meta-analysis, mixed models, ruminal evacuation

1802 (W261) Performance and carcass traits of immunocastrated Nellore cattle fed to β-agonists.
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Beta-adrenergic agonists (βAA) have been used to improve performance and carcass traits of feedlot cattle. The use of non-castrated males for meat production is a common practice because they grow fast, use energy more efficiently and produce leaner and high-yielding carcasses. This work was developed to evaluate the effect of βAA and immunocastration on the performance of feedlot finished Nellore cattle. Ninety-six males (409 ± 50 kg LW; 20 mo old) were divided in two groups and half of them received two doses of immunocastration vaccine (Bopriva) within 30 days interval. Animals were fed for 70 days a common diet containing 76% concentrate and 24% roughage (corn silage). Following they were split in 3 groups (n = 32) and fed 30 more days one of the follow-

ing treatments: control diet without βAA (CON); control diet plus 80mg/d zilpaterol hydrochloride (Zilmax) (ZIL); control diet plus 300mg/d of ractopamine hydrochloride (Optaflexx) (RAC). Individual DMI, ADG and F:G were recorded. Data was analyzed as complete block randomized design in a 2x3 factorial arrangement. No interaction was observed between sex condition and treatments. There was no difference in DMI (9.1 kg/d) but non-castrated males were heavier (551 vs 520 kg; $P = 0.0004$), tended to have a greater ADG (1.21 vs 1.06 kg/d; $P = 0.1084$) and F:G ratio (132 vs 115 g of DMI/kg ADG; $P = 0.1102$) than immunocastrated, respectively. Immunocastrated animals had smaller hot carcass weight (HCW; 304 vs 323 kg; $P = 0.0006$) without difference in dressing percentage (DP; 58.5%). Animals fed ZIL showed highest ADG and F:G ratio (1.39 kg/d and 156 g of DMI/kg ADG, respectively; $P < 0.05$). CON treatment showed the smallest ADG and F:G ratio (0.89 kg/d and 94 g of DMI/kg ADG, respectively; $P < 0.05$). Treatment RAC showed intermediate results (ADG 1.1 kg/d and F:G 122 g of DMI/kg ADG, respectively; $P < 0.0001$) compared to ZIL and CON. There was no effect of treatment on final BW, DMI and HCW. Animals fed βAA showed heavier carcasses (313 kg RAC; 320 kg ZIL) than CON (308 kg) resulting in a higher DP for ZIL (59.1%) when compared to RAC (58.3%; $P = 0.0351$) and CON (58%; $P = 0.0048$), respectively. Non-castrated animals have better feedlot performance and βAA improves animal efficiency in feedlot.

Key Words: feedlot, growth, ruminant nutrition

SAS 9.2. Compared with control cows, cows fed nicotinamide had higher contents of insulin (0.37 vs 0.34 ng/mL; $P = 0.03$), triiodotyronine (1.43 vs 1.27 ng/mL; $P = 0.03$) and leptin (2.74 vs 2.25 ng/mL; $P = 0.02$). Nicotinamide supplementation had the tendency to increase the thyroxine (29.02 vs 27.57 ng/mL; $P = 0.08$) and heat shock protein 70 (3.06 vs 2.29 ng/mL; $P = 0.10$), but had no effect ($P > 0.05$) on the contents of glucagon, insulin-like growth factor-1, growth hormone, prolactin and neuropeptide in blood. Cows fed nicotinamide had the tendency to elevate the activity of superoxide dismutase (10.29 vs 9.63 U/mL; $P = 0.07$), but had no effects ($P > 0.05$) on the activity of glutathione peroxidase, the levels of total antioxidant capacity and malondialdehyde. The contents of immunoglobulin (Ig) A (238.83 vs 160.38 μg/mL; $P = 0.01$), IgG (34.90 vs 21.54 μg/mL; $P = 0.03$), interleukin-4 (IL-4) (91.23 vs 77.19 pg/mL; $P = 0.04$) and IL-6 (138.81 vs 97.79 μg/mL; $P = 0.01$) were increased, and the ratio of CD4^{+}/CD8^{+} were higher tendency (1.47 vs 1.16; $P = 0.10$) in cows fed 8g/d nicotinamide than in controls, while the levels of IgM, tumor necrosis factor-α, lymphocytes and the proportion of CD4^{+} and CD8^{+} T lymphocytes had no difference ($P > 0.05$) compared with the control. These results indicate that nicotinamide supplementation helps to alleviate the hormone metabolism disorder, improve antioxidant activity, and enhance the immune function in heat-stressed dairy cows.

Key Words: nicotinamide, dairy cows, blood metabolism

1803 (W262) Effects of nicotinamide on hormone levels, antioxidant status and immune function of cows in heat stressed dairy cows. J. Cheng[1,2,3], N. Zheng[1,3,4], X. Sun[1,2,3], D. P. Bu[3], L. Pan[3] and J. Wang[*1,3,4], [1]*Ministry of Agriculture- Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China,* [2]*College of Animal Science and Technology, Anhui Agricultural University, Hefei, China,* [3]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [4]*Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

The experiment was conducted to investigate the effects of nicotinamide on the blood hormone levels, antioxidant status and immune function of heat-stressed dairy cows. Twenty healthy early lactation Holstein cows (78.8 ± 11.0 DIM, 37.7 ± 1.8 kg of milk/d, 1.7 ± 0.4 parity) were randomly arranged to control and nicotinamide supplementation group. Cows were fed basic diet in control group and basic diet plus 8 g/d nicotinamide in nicotinamide group for 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21, 42, and 56. Data were analyzed by MIXED model procedure of

1804 (W263) Effects of supplemental bupleurum extract on blood material metabolism in heat-stressed dairy cows. X. Sun[1,2,3], N. Zheng[1,3,4], J. Cheng[1,2,3], D. P. Bu[3], L. Pan[3] and J. Wang[*1,3,4], [1]*Ministry of Agriculture- Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China,* [2]*College of Animal Science and Technology, Anhui Agricultural University, Hefei, China,* [3]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [4]*Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

This study investigated the effect of bupleurum chinense DC. extract (BE) on blood metabolism of lactating dairy cows under heat stress. Forty lactating Chinese Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to four groups and were individually fed a basic diet(CP = 17.2%, NDF = 53.4%) with 0, 0.25, 0.5, or 1.0 g BE/kg DM, respectively. The experiment lasted 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Dry matter intake was recorded twice a week. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21, 42, and 63. Data were analyzed by MIXED model

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procedure of SAS 9.2. Supplementation of BE increased dry matter intake (20.80, 21.61, 22.13 vs 20.91 kg/d, P = 0.02) and blood total protein (80.97, 81.08, 81.00 vs 77.22 g/L, P = 0.03) level, but decreased urea nitrogen (BUN) contents (5.65, 5.58, 5.81 vs 5.95 mmol/L, P = 0.04). Cows fed 0.25 or 0.5 g/kg BE increased albumin content (38.61, 37.53 vs 36.18 g/L, P = 0.01) compared with control cows, but BE supplementation had no effects (P > 0.05) on blood glucose (GLU), nonesterified fatty (NEFA), total triglyceride (TG), low density liporotein cholesterin (LDL-C) and high density liporotein cholesterin (HDL-C). Sodium (Na) (136.63, 134.72, 136.05 vs 137.90 mmol/L, P < 0.01) and phosphorus (P) (1.94, 1.96, 1.81 vs 2.13 mmol/L, P = 0.05) concentrations in serum were decreased by BE supplementation, while potassium (K) (3.80, 3.83, 3.90 vs 3.48 mmol/L, P < 0.01) and calcium (Ca) (2.56, 2.59, 2.66 vs 2.46 mmol/L, P < 0.01) concentrations were decerased than in controls, but BE supplementation had no effect (P > 0.05) on serum magnesium (Mg) concentration. Serum chlorine (Cl) concentration was increased in cows fed 0.5 g/kg BE (148.01 vs 140.79 mmol/L, P = 0.04) compared with control cows, and tended to be higher (144.08 vs 140.79 mmol/L, P = 0.08) in cows fed 0.25 g/kg BE, but was not affected in cows fed 1.0 g/kg BE. These findings suggest that BE supplementation could improved the protein metabolism and maintain the balance of electrolyte concentration.

Key Words: bupleurum extract; dairy cows; blood metabolism

1805 (W264) Effects of nicotinamide on blood material metabolism of dairy cows under heat stress.

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The experiment was conducted to determine the effects of nicotinamide on the metabolism of carbohydrate, lipid, protein and the mineral of serum in heat-stressed cows under hot environment. Twenty healthy early lactation holstein cows (78.8 ± 11 DIM, 37.7 ± 1.8 kg of milk/d, 1.7 ± 0.4 parity) were randomly assigned to control and nicotinamide supplementation group. Cows were individually fed basic diet (CP = 17.2%,NDF = 53.4%) in control group and fed basic diet plus 8 g/d nicotinamide in nicotinamide group. The trial lasted 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Feed intake was recorded twice a week. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21,

42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. There was no significant difference in dry matter intake between treatments (20.60 vs 20.71 kg/d; P > 0.05). The concentrations of nonestesterifiedfattyacid (221.25 vs 250.08 uEq/L; P = 0.03), total triglyceride (0.13 vs 0.15 mmol/L; P = 0.03), total cholesterol (5.79 vs 6.57 mmol/L; P = 0.04), and low density lipoprotein cholesterol (1.43 vs 1.76 mmol/L; P = 0.04) were decreased significantly by nicotinamide supplementation. Nicotinamide supplementation had the tendency to decrease β-hydroxybutyricacid level (0.66 vs 0.76 mmol/L; P = 0.10), but had no effect (P > 0.05) on the levels of serum glucose, total protein, albumin and urea nitrogen. Compared with control group, the levels of sodion (139.59 vs 137.90 mmol/L; P = 0.03) and chloridion ion (148.72 vs 139.75 mmol/L; P = 0.05) in serum were increased significantly by nicotinamide supplementation, but there was no difference (P > 0.05) in the levels of serum kalium, magnesium, phosphonium between the two groups. These findings suggest that nicotinamide supplementation can improved the lipid metabolism and maintain electrolyte balance of cows under heat stress.

Key Words: nicotinamide; dairy cow; blood metabolism

1806 (W265) Supplementation of selenium plus vitamin E vs. canola oil in the diet of feedlot cattle: which one can improve nutritional quality of meat modifying gene expression?

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The metabolic conversion of dietary components is a control mechanism for gene expression, so the present study aimed to evaluate the effects of selenium (Se), vitamin E and canola oil on the expression of antioxidant and lipogenic genes. Forty-eight Nellore bulls at calan gate allocated in the Department of Animal Science USP-FZEA-Brazil were divided into four groups: Control(C): basal diet (30% forage- corn silage- and 70% concentrate, dry matter according to the nutrient requirements recommended by NRC,1996); Se+Vit E: addition of 2.5mg Se+500 IU vitamin E; Canola: addition of 3% canola oil; Se+Vit E+Canola: addition of 3% canola oil+2.5mg Se+500 IU of vitamin E(/kg DM, always). After 12 weeks, the animals were slaughtered at the Abattoir-School Campus and liver samples collected. Total RNA was extracted using RNeasy Tissue Kit (Qiagen), measured at 260 and 280nm, analyzed by agarose gel. RNA was converted into cDNA using DNase I and High Capacity RNA-to-cDNA kit and it was used for determination of gene expression by RT-qPCR using Taqman probes, 18S as endogenous control (Applied Biosys-

Table 1806. Gene expression

GENE	C	Se+Vit E	Canola	Se+Vit E +Canola	Pr > F	C1	C2	C3
NRF2	1.1661	1.8295	0.8032	1.121	0.0525	0.7904	0.5756	0.0079
GPX-1	1.1209	1.6099	0.8125	1.1594	0.08	0.783	0.8467	0.0109
GPX-4	1.3153	2.6565	1.1741	1.0114	0.0265	0.553	0.1032	0.0118
SCD	1.4732	2.3247	1.0792	2.674	0.0568	0.289	0.0751	0.0572
HMG-CoA-R	1.1911	1.4905	0.2459	0.9522	0.0633	0.4948	0.811	0.0096

tems) and calculated by Pfaffl's equation. The data were analyzed by Mixed SAS 2009 and contrasts used were: control vs. other (C1); Se+Vit E and Canola vs. Se+Vit E+Canola (C2); Se+Vit E vs. Canola (C3). The results are in Table 1806. The supplementation with Se+Vit E and Canola didn't show effects when compared to the control (C1), but differences were observed between Se+Vit E and Canola (C3), which had opposite effects. Se+Vit E induced expression of cytoprotectives genes (NRF2, GPXs, GSS) and increased the expression of responsible gene for the synthesis of CLAs (SCD) encouraging studies to improve nutritional quality of meat, but caution is needed because it can induce the synthesis of cholesterol through the expression of the gene HMG-CoA-R. Although Canola didn't increase the expression SCD gene, canola oil reduced the expression of HMG-CoA-R gene.

Key Words: antioxidants, bovine, cholesterol.

1807 (W266) Effects of feeding a corn straw or mixed forage diet on immune function in dairy cows.

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It has been demonstrated in previous researches that dietary nutrients affect immune function through their regulations on producing and activating immune factors. This study was conducted to evaluate the effects of feeding a corn straw or mixed forage diet on immunity of lactating cows by analysing compositions of serum immunoglobulins (Igs), cytokines, inflammation factors and plasma lymphocyte subsets. Twenty primiparous, lactating and ruminally fistulated Holstein cows were used in this study. Cows were randomly assigned to high forage diet (HF, forage: concentrate = 60: 40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (LF, forage: concentrate = 40: 60) with corn straw as the forage source. This experiment lasted for 2 months, and blood samples were obtained via jugular vein before morning feeding at the last day of the trial period. Plasma lymphocyte subsets were determined by flow cytometry and other indexes were measured with ELISA kits. Data were analyzed using the PROC MIXED procedure of SAS 9.1. The results showed that levels of serum IgA (37.81 and 39.77 ng/mL), secretory IgA (sIgA) (1.55 and 1.59 ng/mL), interleukin-2 (IL-2) (132.55 and 137.96 ng/L), IL-4 (33.53 and 35.22 ng/L), IL-6 (8.27 and 8.53 ng/L), IL-10 (37.65 and 39.47 ng/L), IL-12 (31.57 and 33.66 ng/L), interferon-α (IFN-α) (16.71 and 16.94 ng/L), IFN-γ (865.44 and 851.58 ng/L), tumor necrosis factor-α (TNF-α) (199.49 and 206.46 ng/L), prostaglandin E$_2$ (PGE$_2$) (152.86 and 160.95 ng/L) and plasma CD4^{+} lymphocyte subset (27.88 and 30.54%), CD8^{+} lymphocyte subset (21.02 and 22.25%) and CD4^{+}/CD8^{+} ratio (1.57 and 1.57) were not affected by experimental treatments ($P > 0.05$), and cows in LF group tended to have higher serum IgE (498.55 and 469.64 ng/mL, $P = 0.09$), IgM (195.01 and 182.75 ng/mL, $P = 0.09$) and insulin-like growth factors-1 (IGF-1) (15.14 and 13.78 μg/L, $P = 0.06$) concentrations than those in HF group, while serum IgG (16.57 and 17.46 μg/mL, $P = 0.09$) level tended to be higher in HF group ($P < 0.10$). The results of this study indicated that different dietary systems had no effect on immunity in lactating cows.

Key Words: diet system, dairy cow, immunity

1808 (W267) Fatty acid composition of milk from cows supplemented with canola oil.

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The objective of this study was to evaluate the inclusion of canola oil in the diet of dairy cows on the fatty acid (FA) composition of milk. Eighteen lactating Holstein cows were distributed in 6 contemporary 3 x 3 Latin Square, 3 periods and 3 treatments: T1 = control diet (without oil), T2 = inclusion of 3% canola oil and T3 = 6% inclusion of canola oil in the diet (dry matter). The cows were individually fed. The experiment was conducted during three periods of 21 days, with 14 days for adaptation and seven days to collections. The milk samples were collected to determine the fatty acid composition on the last day of each experimental period. Identification and quantification of fatty acid were done by gas chromatograph (column of 100 meters using hydrogen carrier gas). The results were analyzed using the MIXED procedure of SAS (2001). The effects of treatments were analyzed using two orthogonal polynomial contrasts: linear (L) and quadratic (Q), the significance

Table 1808. Fatty acid composition (g/100g total FA) of milk from cows fed canola oil

Fatty acid composition	Inclusion of canola oil (%)				P	
	0	3	6	SEM	L	Q
Saturated	64.91	55.29	51.42	1.25	< 0.0001	= 0.033
Y = 63.97(1.11)– 2.1958(0.1677)X						
Unsaturated	34.48	43.53	47.52	0.98	< 0.0001	= 0.0049
Y = 35.4756(1.1284) + 2.1664(0.1748)X						
Omega-3	0.20	0.39	0.43	0.02	< 0.0001	= 0.0008
Y = 0.2286(0.0268) + 0.03369(0.005927)X						
Omega-6	1.98	2.08	2.11	0.05	0.273ns*	0.728ns
Omega-6/Omega-3	11.51	5.52	5.33	0.06	< 0.0001	= 0.0002
Y = 10.49(0.6779)– 1.055(0.1728)X						
Thrombogenicity	2.92	1.99	1.74	0.09	< 0.0001	= 0.001
Y = 2.78(0.10)– 0.1948(0.02030)X						
Atherogenicity	2.43	1.52	1.25	0.09	< 0.0001	= 0.0002
Y = 2.32(0.096)– 0.1952(0.01845)X						

ns = not significant.

declared at P ≤ 0.05. The inclusion of 6% of canola oil in the diet increased 53.49% of milk omega-3 concentration and reduced 53.69% of omega-6/omega-3 ratio, in compare with the control treatment. The thrombogenicity (capacity to promote heart attacks and strokes) and atherogenicity (capacity to promote atherosclerosis) decreased linearly ($P < 0.0001$) with the inclusion of canola oil in the diet (Table 1808). In conclusion, canola oil alters the fatty acid composition of milk, resulting in healthier milk with nutraceutical properties.

Key Words: omega-3, dairy, nutraceutical, health

1809 (W268) Effects of a corn straw or mixed forage diet on bovine milk fatty acid biosynthesis. M. Zhao[1], D. P. Bu[1], J. Q. Wang*[1], X. Q. Zhou[1,2], Y. Zhang[1] and P. Sun[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Northeast Agricultural University, Harbin, China*

The study was designed to investigate the effects of different forage types on milk fatty acid (FA) profile. Thirty two dairy cows were divided into group MF (alfalfa and corn silage as forage source) and group CS (corn stover as forage source). The whole experiment lasted for 15 wk (2-wk adaptation and 13-wk experimental period) following 2-wk covariate period (a total of 17-wk). Milk fat content and fatty acid profile were measured. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. The results showed that milk fat content in group MF was higher than group CS, but no difference was observed (4.46 vs 4.38%, $P > 0.05$). The proportion of milk saturated fatty acid (SFA) was significantly higher in group MF (74.77 vs 69.93%). However, unsaturated fatty acid (UFA) in group CS was higher than group MF (25.23 vs 30.07%). Unlike polysaturated fatty acid (PUFA), proportion of monounsaturated fatty acid (MUFA) in group CS exhibited significantly higher level mainly due to the large proportion of *cis*-9 C18:1 (MUFA, 21.62 vs 26.51%). Feeding the MF

diet significantly increased short- and medium-chain fatty acid (SMCFA) proportion but decreased long-chain fatty acid proportion in group MF (SMCFA, 47.38 vs 41.02%; LCFA, 52.62 vs 58.98%). Therefore, corn stover as forage source in the diet could increase the proportion of UFA but decrease the proportion of SMCFA in milk.

Key Words: alfalfa, corn silage, corn stover

1810 (W269) Influence of forage level and corn processing method on feeding behavior of Nellore bulls. M. Caetano[1,2], A. R. Cabral[3], G. B. Feltrin[1], R. S. Goulart[4], S. Luz e Silva[3], P. R. Leme[3] and D. P. D. Lanna*[1], [1]*University of Sao Paulo/ESALQ, Piracicaba, Brazil, [2]University of Adelaide, Roseworthy, Australia, [3]University of Sao Paulo/ FZEA, Pirassununga, Brazil, [4]MSD Saúde Animal, Sao Paulo, Brazil*

The objective of this study was to investigate the influence of neutral detergent fiber from forage (NDFf) levels and corn processing methods (CPM) on feeding behavior of finishing *Bos indicus* cattle fed high-concentrate corn-based diets. Forty Nellore bulls (388.1 ± 25.8 kg) were used in a randomized complete block design in a 4 x 2 factorial arrangement. Four levels of NDFf (3, 8, 13, and 18% sugarcane silage DM basis) were evaluated for two CPM: high moisture corn (HMC) and finely ground dry corn (FGC). Animals were fed ad libitum for 81 d, with diets delivered twice daily in individual pens. Sugarcane silage contained 64.0% NDF and 10.8 mm of mean particle size, all diets had 8% of whole linted cottonseed and the geometric particle sizes were 1.30 and 5.84 mm for FGC and HMC, respectively. Feeding behavior was evaluated twice (24 h each period) with fixed intervals of five min. Activities evaluated were eating, drinking, ruminating (R), chewing (C) and idling (min/d). Intake (IN), rumination (RU) and total chewing rate (TCR) were calculated (min/kg of DM). Number of meals (NM), interval between meals (IR) and meal duration

(MD) were estimated (min). The first derivative was solved of a 2nd order polynomial to determine optimal NDFf level. Animals fed HMC had 12.6% lower DMI ($P < 0.01$) and 6.1% lower ME intake (MEI; $P = 0.04$) compared to those fed FGC, but the IN was 21.6% greater for HMC than FGC ($P < 0.01$). There was a quadratic effect of NDFf on DMI ($P < 0.01$), MEI ($P < 0.01$) and IN ($P < 0.01$), with 10.8, 11.4 and 10.0% NDFf yielding the highest intakes, respectively. These NDFf levels to achieve maximum DMI and MEI are greater than recommendations in literature. Interactions between CPM and NDFf were observed for R ($P < 0.01$) and C ($P < 0.01$), however, when the RU and TCR were calculated, linear effects of NDFf were found for both. Increasing NDFf level increases the RU ($P < 0.01$) and TCR ($P < 0.01$). The HMC increases NM ($P < 0.01$) and decreases IR ($P < 0.01$) and MD ($P < 0.01$) when compared to FGC. Increasing NDFf level increased linearly the MD ($P < 0.01$). In conclusion, zebu cattle required around 11% NDFf to maximize DMI and MEI. The HMC increased the NM (min) and the IN (min/kg of DM).

Key Words: behavior, feedlot, zebu

1811 (W270) Evaluation of a hand-held meter to detect subclinical ketosis in dairy cows.

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TNN is a new hand-held meter for detecting subclinical ketosis of dairy cows by determining blood β-hydroxybutyrate (BHBA). The objective of this study was to evaluate the performance of this new cowside test by comparing BHBA results obtained using the hand-held meter with those results made with a laboratory method and comparing the accuracy between diagnostic performance using blood and using milk and urine. 275 blood samples and 97 urine samples and 85 milk samples from clinically healthy Holstein cows between 1 and 58 days post-calving were analysed. The correlation coefficients for BHBA with TNN versus laboratory methods were 0.92. Based on Bland-Altman plot, agreement between two methods was good for BHBA. In this study, the TNN test had sensitivities of 75 and 88% at 1.2 and 1.4 mmol of BHBA/L of whole blood, respectively. Specificities were 97 and 99%, respectively. Compared with TNN the sensitivities and specificities of urine test and milk test were lower. The sensitivities and specificities were 57 and 80% for milk tests, respectively, and 71 and 94% for urine tests, respectively, when 1.2mmol/L of blood was defined as the threshold. Raising the threshold of laboratory method to 1.4mmol/L, The sensitivities and specificities were 75 and 79% for milk tests, respectively, and 75 and 93% for urine tests, respectively. We conclude that TNN is a useful tool to diagnose subclinical ketosis and blood tests are better methods than urine tests and milk tests due to higher sensitivity and specificity.

1812 (W271) Effects of rumen protected choline supplementation on milk yield and plasma metabolites in dairy cows fed hay based diets.

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Most of studies on the effect of rumen protected choline (RPC) supplementation in dairy cows have been done using silage based diets. Accordingly, the aim of the study was to evaluate the effect of RPC supplementation in early lactating dairy cow receiving hay-based diet. For this purpose 12 Italian Holstein multiparous cows, in the first month of lactation (28 DIM), were divided into two experimental groups: control group (CTR) receiving no choline, and RPC group receiving 20 g/day of choline in rumen protected form (Balchem Inc., New Hampton, NY). Diets contained 50% hay (alfalfa and Meadow Hay), and 50% concentrates. Cows were housed at the Animal Production and Research of the Università degli Studi di Milano, fed in a Roughage Intake Control feeding system, and milked twice a day. The experiment lasted 9 weeks. Dry matter intake and milk yield were measured daily. Plasma was collected on week 1, 2, 3, 5, and 9 of the experimental period and analyzed for glucose, cholesterol, triglycerides, nonesterified fatty acids, betaidrossibutirrate and urea N. Before statistical analysis, daily measurements for DMI and milk yield were condensed to weekly means. Data were analysed as a completely randomized design by Proc MIXED procedure of SAS using treatment and time as fixed factors and cow within treatment as a random factor. The REPEATED statement was used for variables measured over time. Through the 9 weeks, treatment did not affect DMI (22.7 vs. 23.5 kg/d in CTR and RPC respectively) and milk yield (28.2 vs. 29.4 kg/d). Dietary treatment did not affect the metabolic profile of experimental cows, except for plasma glucose concentrations that tended ($P = .010$) to be higher in RPC cows than those of CRT (61.08 vs. 56.75 mg/dL). In this study RPC supplementation did not reveal any alterations in milk yield and serum metabolites in dairy cow receiving a hay-based diet, even though an exhaustive comparison with silage-based diet, merit further investigations.

Key Words: choline, hay based diet, milk yield

1813 (W272) Liver metabolism of Holstein cows is altered by nutrient supply but not by lipopolysaccharide in vitro. M. Garcia*, B. J. Bequette and K. M. Moyes, *Department of Animal and Avian Sciences, University of Maryland, College Park*

Recent work suggests liver function is reduced during inflammation. To our knowledge, no studies have examined whether increased amino acid or propionate supply improves hepatic function during inflammation and how this is altered by stage of lactation. The objective of the current study was to characterize the effect of nutrient supply and lipopolysaccharide (LPS) challenge on hepatic intermediate metabolism for cows in early and mid-lactation by employing gas chromatography–mass spectrometry (GC-MS) and stable isotope tracer ($[^{13}C_3]$ pyruvate). Liver samples were collected via biopsy from healthy early ($n = 6$, < 21 DIM) and mid-lactation ($n = 6$, < 110 DIM) Holstein cows. Liver slices were incubated for 2 h at 37°C in 3 mL of Krebs-Ringer bicarbonate buffer containing 2 mM of a 50:50 mix of labeled and unlabeled $[^{13}C_3]$pyruvate with addition of either phosphate buffered saline (control), 2 mM propionate, or 2 mM amino acids, with or without addition of LPS (200 ng/mL). Krebs cycle intermediates were determined by GC-MS by monitoring alanine, aspartate, and glutamate, which are in metabolic equilibrium with Krebs cycle intermediates. Data were analyzed as a randomized block design in a 3×2×2 factorial arrangement. Significance was declared at $P < 0.05$. Overall, LPS challenge had minimal effects on intermediary metabolism. Regardless of nutrient supply, the ^{13}C kinetics demonstrated that the liver of early lactation cows exhibits higher relative activity of phosphoenolpyruvate carboxykinase (PEPCK), a tendency for greater flux of pyruvate to oxaloacetate ($P = 0.07$, 82 vs. 74%), and a lower relative activity of pyruvate dehydrogenase (PDH) compared to pyruvate carboxylase (PC) when compared to cows in mid-lactation. Regardless of stage of lactation, propionate and amino acids increased the proportion of acetyl-CoA derived from pyruvate (13 and 10%, respectively) compared to control (7%), with no difference in the flux of oxaloacetate that derived from pyruvate. Moreover, propionate increased the relative activity of PDH compared to PC. In conclusion, results suggest that the LPS endotoxin exposure in vitro does not impair liver metabolic function and that cows in early lactation had a greater gluconeogenic capacity than cows in mid-lactation.

Key Words: cows, liver, nutrient flux

1814 (W273) Effect of postruminal infusion of fructose on hepatic steatosis. K. E. Boesche*, J. E. Sibray, S. L. Koser and S. S. Donkin, *Purdue University, West Lafayette, IN*

Periparturient dairy cattle are prone to metabolic disease and frequently experience hepatic steatosis. A more complete understanding of the development and impact of hepatic steatosis has been hampered by the lack of a predictable and convenient steatosis induction model. Intensive fructose consumption in both rats and humans rapidly results in hepatic steatosis and insulin resistance, but the impacts of fructose on hepatic steatosis in dairy cattle are unknown. The objective of this study was to examine the effects of postruminal fructose supply on accumulation of liver triglycerides (TG) and other parameters of fatty liver disease in lactating dairy cattle. Eighteen multiparous late-lactation (241.7 ± 28.5 d in milk) Holstein cattle were assigned to either control (CON), postruminal fructose infusion (INF), or a pair-fed (PAIR) group. INF cows were previously fitted with rumen cannulae and received 1000 g/d D-fructose for 7 d as a 16.67% w/v fructose solution delivered postruminally. Fructose dose averaged 1.47 g ± 0.11/kg body weight (BW) and was delivered over a 23 h period. Amount of feed offered to PAIR group was matched to the previous 24 h intake of INF cows to account for any potential impact of fructose infusion on voluntary feed intake. CON group was fed ad libitum. There were no differences ($P > 0.1$) between groups in BW or body condition score before or after the infusion period. Milk production decreased (26.2, 23.1, 23.3 ± 0.79 kg for CON, INF, PAIR, respectively; $P < 0.05$) in both INF and PAIR groups during infusion period and was accompanied by decreased feed intake (23.5, 20.1, 19.4 ± 1.21 kg/d dry matter intake; $P < 0.05$). Plasma TG levels were not significantly different ($P > 0.1$) before, during, or after fructose infusion, but were numerically lower in INF, compared to PAIR, after infusion. Liver TG levels did not differ ($P > 0.1$) by group before or after infusion. Plasma fructose levels tended to remain high (602.9, 485.8 ± 44.60 µM for INF, PAIR, respectively; $P < 0.1$) in INF group after infusion period. Plasma glucose levels did not differ ($P > 0.1$) by group, nor did serum nonesterified fatty acid levels ($P > 0.1$). Data do not support the use of 7 d postruminal infusion of D-fructose at 1000 g/d as a model to study hepatic steatosis in lactating dairy cattle.

Key Words: fructose, hepatic steatosis, postruminal infusion

1815 (W274) Effects of rare earth-chitosan chelate on liver and kidney parameters in lactating dairy cows. J. Li[1,2], J. Q. Wang[1], P. Sun[1], F. D. Li[2] and D. P. Bu*[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China*

Rare earth-chitosan chelate (RECC) formed by β-NH$_2$ and rare earth ions with glucosamine molecule (1,4)-OH on the glycosidic bond, have been used as a new chelating ligand feed additives to promote efõcient feed utilization in ruminants and improve animal productivity while reducing the need for

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antibiotics and chemical additives. Numerous reports have indicated that suitable amount of RECC mixtures in the diet increase not only the liveweight gain of livestock and poultry but also milk and egg production. The objective of this study was to determine the effect of different proportion of rare earth-chitosan chelate (RECC) on hepatic and renal function of lactating dairy cows. Forty-eight lactating Holstein dairy cows (DIM = 130 ± 5, average milk yield = 33.2 ± 5.1 kg/d) were randomly assigned to 4 treatments ($n = 12$) with addition of RECC (0 (control), 0.15%, 0.75%, and 1.5%, respectively) in diets. The experiment lasted for 9wk with the first week for adaptation. Blood was collected in evacuated tubes via caudal venipuncture at 0, 2, 4, 6, 8 week and the tubes with blood samples were centrifuged at $3500 \times g$ for 15 min to obtain serum, which was separated into several aliquots and stored at $-80°C$ in an ultra-low-temperature freezer until further analysis. Data were analyzed by mixed or GLM procedure of SAS software. No significant differences ($P > 0.05$) were found for the activity of glutamic-pyruvic transaminase (ALT) and glutamic oxalacetic transaminase (AST), total protein (TP), albumin (ALB), globulin (GLB), Uric Acid (UA) and urea nitrogen(UREA) in all the dietary treatments. Compared with control, there were no difference ($P > 0.05$) in total bile acid (TBA) and creatinine (CRE) between 0.15% RECC and 0.75% RECC treatments, while increased ($P < 0.05$) when the RECC adding dose up to 1.5%. Feeding 0.15% or 1.5% RECC resulted in higher total bilirubin(TBIL)(5.77, 6.05 umol/L vs. 4.89, 4.89 umol/L) and indirect bilirubin (DBIL) (2.30, 2.54 umol/L vs. 2.00, 1.93 umol/L) vs. control and 0.75% RECC group ($P < 0.01$). These results suggested that the adding doses of RECC in dietary did not affect the activity of ALT and AST, while TBA, CRE, TBIL and DBIL were significantly increased in 0.15% RECC. So it was concluded that adding 1.5% RECC in dietary has a negative effect on the function of liver and kidney in dairy cows.

Key Words: dairy cows, liver and kidney parameters, rare earth-chitosan chelate

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1816 (W275) Supplementation of *Aspergillus oryzae* α-amylase on ruminal volatile fatty acid distribution and digestive tract gene expression in beef steers fed a steam-flaked corn based finishing diet. B. N. Gordon[1], S. W. Hahm[*1], J. J. Wagner[1], J. S. Jennings[2], H. Han[1] and T. E. Engle[1], [1]*Colorado State University, Fort Collins, [2]Texas A&M AgriLife Research, Amarillo*

The objective of this study was to investigate the impact of *Aspergillus oryzae* α-amylase (AAM) supplementation on rumen VFA profile and relative abundance of mRNA associated with nutrient absorption in ruminal and duodenal tissue from beef steers. Nine crossbred steers (average BW 622 ± 50 kg), with rumen and duodenal fistulas were housed in individual stations and fed a high concentrate finishing diet twice daily for 8 d. Treatments included CON (corn meal; $n = 5$) and AAM (750 fungal α-amylase units/g; $n = 4$). Dietary treatment supplements were applied as a top dress (3 g of α-amylase or corn meal into 150 g of dried distiller's grains (DDG) for the AM feeding and 2 g of α-amylase or corn meal into 100 g of DDG for PM feeding). On d 5, rumen fluid samples were obtained every 4 h for 24 h and analyzed for VFA concentration. On d 9, rumen papillae and duodenal mucosal tissue samples were collected. Total tissue RNA was extracted for real-time PCR analysis. Sodium/potassium ATPase pump α1, glucose transporter 2 and 5, putative anion transporter, isoform1, sodium/hydrogen antiporter isoforms1, 2 and 3, 3-hydroxy 3-methylglutaryl coenzyme A synthase isoform2, down regulated in adenoma, monocarboxylate co-transporter isoform1, and glyceraldehyde-3-phosphate dehydrogenase mRNA were tested. Relative expression (fold change) of mRNA in ruminal and duodenal tissues were analyzed using PROC GLM and VFA distribution was analyzed as a randomized block design with repeated measures using the MIXED procedure of SAS. Concentrations of VFA and the acetate to propionate ratio were similar across treatments. However, acetate:propionate ratio and butyrate molar percentage were numerically greater ($P = 0.17$) in AAM steers compared to controls. Genes tested were not significantly changed by AAM supplementation in the rumen or duodenum. However, genes involved in nutrient absorption were numerically decreased in the rumen and increased in the duodenum in the AAM supplemented steers compared to the controls.

Key Words: duodenum, fungal α-amylase, gene, rumen, steer, volatile fatty acids

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1817 (W276) Effects of rumen-protected choline during the transition period on nonesterified fatty acids and β-hydroxybutyrate concentrations in periparturient dairy cattle. I. M. Lima[1], R. A. Silva[1], C. H. Ramires[1], S. L. Viechnieski[2] and R. D. Almeida[*1], [1]*Universidade Federal do Paraná, Curitiba- Paraná, Brazil, [2]StarMilk Farm, Céu Azul- Paraná, Brazil*

The effects of rumen-protected choline (RPC) on nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHBA) concentrations, body condition score (BCS), and milk fat to protein ratio (FPR) were evaluated in periparturient dairy cows. Pregnant Holstein cows ($n = 106$) and heifers ($n = 52$) in a commercial farm in Southern Brazil were blocked by parity and expected day of calving and randomly assigned to 2 treatments. Cows in the first treatment were supplemented with rumen-protected choline (RPC; Reashure, Balchem Corp.), whereas cows in the second treatment were not supplemented (CON). All animals were housed together in transition pens, and RPC cows were individually top-dressed 60 g/d RPC to provide 17.3 g of choline while restrained in feedline head-locks from 21 d before to 28 d after calving. The CON diets

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were top-dressed with 60 g/d of corn meal. Four blood samples were collected from each animal (7 d before calving, at calving, 7 and 14 d after calving). Data was analyzed using MIXED procedure of SAS with a model containing the effects of block, treatment, time, and treatment*time interaction as fixed effects, prepartum BCS as a covariable, and cow within treatment as a random effect. Body condition score did not differ ($P > 0.05$) between RPC and CON cows in all three observations (21 d before calving, at calving, and 28 d after calving). Multiparous cows showed greater ($P < 0.01$) NEFA and BHBA concentrations than primiparous ones; 0.361 ± 0.017 mmo/L vs. 0.294 ± 0.023 mmol/L; and 0.646 ± 0.019 mmo/L vs. 0.562 ± 0.024 mmol/L, respectively. Concentrations of NEFA peaked ($P < 0.01$) at calving; 0.473 ± 0.021 mmo/L, whereas BHBA concentrations peaked ($P < 0.01$) at 14 d after calving; 0.724 ± 0.044 mmol/L. Nonesterified fatty acids concentrations did not differ ($P > 0.05$) between RPC and CON cows; 0.355 ± 0.017 mmol/L vs. 0.324 ± 0.017 mmol/L. Similarly, BHBA concentrations did not differ ($P > 0.05$) between treatments; 0.633 ± 0.020 mmol/L vs. 0.606 ± 0.020 mmol/L, respectively for RPC and CON cows. Finally no milk FPR differences ($P > 0.05$) were observed between RPC and CON cows in the first test-day after calving; 1.30 vs. 1.34. In the particular conditions of this on-farm trial with very modest lipid mobilization (3.35 BCS at 21 d before calving and 3.10 BCS at 28 d after calving) no benefits on RPC supplementation were detected.

Key Words: choline, dairy cows, ketosis

1818 (W277) Effects of replacing alfalfa hay and corn silage with corn straw in diets on main hormones in blood of dairy cows. X. Q. Zhou[1,2], D. P. Bu[2], Y. D. Zhang[2], M. Zhao[2], P. Sun[2] and J. Q. Wang[*1,2], [1]Heilongjiang Bayi Agricultural University, Daqing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China

To study the effects of replacing alfalfa hay and corn silage with corn straw in diets on main hormones related to metabolism in blood of Holstein cows, Twenty-four firstborn and healthy Holstein lactating dairy cows with similar DIM (55 ± 27 d) and body weight (520 ± 25 kg) were randomly divided into 2 groups. Diets contained similar concentrate mixtures with the same forage-to-concentrate ratio of 36:64 (dry matter basis). Different forage sources were then added: 17.30% alfalfa hay and 18.77% corn silage (MF); 36.07% corn straw (CS). The preliminary experiment lasted for 2 wks followed by a 60-day former experiment. The blood samples on d 61 were collected and evaluated the concentrations of insulin (INS), growth hormone (GH), leptin (LEP),cortisol (COR), insulin-like growth factor-1(IGF-1) and prolactin (PRL) in serum. Compared with the MF group, the concentrations of IGF-1 (384.31 vs 311.73%, $P < 0.01$) and LEP (3.67 vs

3.12%, $P < 0.05$) in CS group were significantly increased, but the concentrations of PRL (175.51 vs 230.37%, $P < 0.05$) was decreased. No difference was observed in other hormones ($P > 0.05$). Results showed that under the condition of the same concentrate, different forages can greatly affect concentrations of some hormones in the blood which closely relate to the changes of body's immune and production performance.

Key Words: corn straw, dairy cows, hormones

1819 (W278) Body condition score at calving alters the hepatic transcriptome in grazing dairy cattle. H. Akbar[1], Z. Zhou[*1], K. Macdonald[2], K. E. Schütz[3], G. Verkerk[2], J. R. Webster[3], S. L. Rodriguez Zas[1], J. R. Roche[2] and J. J. Loor[1], [1]University of Illinois, Urbana, [2]DairyNZ, Hamilton, New Zealand, [3]AgResearch, Hamilton, New Zealand

The objective of this study was to use transcriptomics and bioinformatics to evaluate changes in hepatic gene expression profiles in cows managed to achieve a high (H, 5.5 BCS), medium (M, 4.5 BCS), or low (L, 3.5 BCS) BCS (10-point scale). Target BCS at calving were achieved by managing feed allowance before dry off. Post-calving cows were allocated pasture and pasture silage. Liver from 10 cows per BCS group was biopsied on wk 1, 3, and 5 relative to parturition. A whole-transcriptome bovine microarray (Agilent) was used. An ANOVA with repeated measures using PROC MIXED resulted in 5888 DEG due to the main effect of BCS and 327 differentially expressed genes (DEG; False Discovery Rate < 0.05) due to BCS × wk. Bioinformatics analysis was performed with the Dynamic Impact Approach (DIA), focusing on pathways from the KEGG database. The BCS × wk DEG, analysis of most-impacted pathways revealed marked differences on wk 1 for H vs. L and M vs. L; 'fatty acid biosynthesis', 'biosynthesis of unsaturated fatty acids', 'ascorbate and aldarate metabolism', and 'steroid biosynthesis' were among the top 5 highly-impacted pathways when comparing H vs. L and L vs. M. All were highly-inhibited in H vs. L, but highly-activated in L vs. M. The degree of impact on pathways was quite low when comparing H vs. M on wk 1 and there were few differences in pathway flux (i.e. little change in activation/inhibition). Remarkably, on wk 3, pathways in L vs. M remained activated but signaling pathways such as NOD-like receptor, p53 signaling, and RIG-I-like receptor were among the most-impacted. The most-impacted pathways in H vs. L on wk 3 were, for the most part, the same as those observed on wk 1. 'Fatty acid biosynthesis' on wk 3 was the most-impacted pathway and markedly inhibited in H vs. M. Data from wk 5 indicate a lesser effect of BCS at calving on the transcriptome because impact values, regardless of BCS, were substantially lower than those in wk 1 and 3. However, it is noteworthy that the 'sulfur relay system' pathway, key for post-transcriptional RNA modifications in mammals, was the most impacted and inhibited pathway in H vs. M. Preliminary bioinformatics anal-

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yses underscored the role of BCS at calving on liver function through alterations of the molecular phenotype and indicate a likely optimum BCS between 4.5 and 5.5.

1821 (W280) The mRNA expression of the classical genes of enzymes involved in milk fatty acid synthesis does not explain milk fat depression in dairy cows. A. Siurana*, D. Gallardo and S. Calsamiglia, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain*

Feeding polyunsaturated fatty acids (PUFA) to dairy cows results in milk fat depression (MFD) in some, but not all cows. The objective of this research was to compare the mRNA expression of enzymes involved in fatty acid (FA) synthesis in the mammary gland of cows resistant or sensitive to MFD resulting from feeding PUFA. Four cows were selected from a dairy farm after a switch from a control diet to a linseed-rich diet: two were resistant to MFD and had high milk fat content before and after the change (R-MFD); and two were sensitive to MFD and milk fat content decreased after the change into the linseed diet (S-MFD). Fresh milk samples were collected from each cow the week before and two weeks after the diet change, and analyzed for milk fat content, milk FA profile and transcriptional profiling of mRNA by Illumina RNA-sequencing technology. The study focused on the enzymes reported to be involved in MFD: acetyl-CoA carboxylase (ACACA), fatty acid synthase (FASN), glycerol-3-phosphate acyltransferase (GPAT), acylglycerol-3-phosphate acyltransferase (AGPAT), stearoyl-CoA desaturase (SCD1), fatty acid binding protein (FABP), lipoprotein lipase (LPL), sterol regulatory element binding protein (SREBP1) and spot 14 (S14). When S-MFD cows were fed linseed, milk fat decreased from 3.56 to 2.54%, the unsaturated:saturated FA ratio increased from 41/59 to 45/55 and short- and medium-chain FA proportion (C4 to C14 and 50% C16; SMFA) decreased from 33.9 to 32.8%, as expected, but there were no significant changes in the mRNA expression of the genes tested. When R-MFD cows were fed linseed, milk fat unexpectedly increased from 4.06 to 4.36%, the unsaturated:saturated FA ratio increased from 35/65 to 39/61,

1820 (W279) Short term feed restriction increases afternoon but not morning milk fat concentration in lactating dairy cows. A. M. Abdelatty*[1,2], M. E. Iwaniuk[2], A. E. Weidman[2], B. B. Teter[2], M. A. Tony[1], F. F. Mohammad[1] and R. A. Erdman[2], *[1]Cairo University, Cairo, Egypt, [2]University of Maryland, College Park*

The elevated milk fat concentration exhibited by cows during the early periparturient period is related to the degree of body tissue mobilization. We hypothesized that feed restriction could be used as tool to study temporal changes in milk composition. Our objective was to test the effect of short-term feed restriction on milk fat concentration. Ten multiparous Holstein cows (100 + 17 DIM) were used in the 21 d study. During d 1 to 14, all cows were allowed ad libitum access to a total mixed ration that was formulated to meet 2001 NRC nutrient requirements for 40 kg/d milk production and this period was used as covariate in the ANOVA. Treatments (Trt) consisted of either ad libitum (AL) or restricted (RES) feeding during d 15 to 18 where RES cows were fed 60% of their d 1 to 14 ad libitum intakes. All cows returned to ad libitum feeding on d 19 to 21. Cows were milked twice daily at 0630 and 1630 h and fed once daily at 0900 h. Milk production and composition were measured at each milking on d 13 to 21. As expected, milking time influenced milk production and composition ($P < 0.001$) for fat and protein. While feed restriction decreased ($P < 0.001$) milk production, but not milk protein and fat percent. There were treatment by milking time interactions for milk fat ($P < 0.001$) and protein ($P = 0.008$) percent which were increased at the 1630 h but not the 0630 h milking. A day by treatment by milking time interaction ($P < 0.02$) was observed for milk fat which showed the greatest elevation at the 1630 h milking on d 16. These results demonstrate that feed restriction can be used to study temporal changes in milk composition.

Table 1820.

Milking: Treatment	0630 h		1600 h			$P =$		
	AL	RES	AL	RES	SEM	Time	Trt	Trt*Time
Milk, kg	21.6	19.2	18.8	15.2	0.72	0.007	0.001	0.014
Milk protein, %	2.88	2.87	2.73	2.87	0.058	0.001	0.392	0.001
Milk other solids, %	5.66	5.54	5.54	5.54	0.028	0.073	0.065	0.008
Milk Fat %								
Day 15	2.98	2.69	4.32	4.10	0.24	0.001	0.274	0.001
Day 16	2.96	2.89	4.30	5.86				
Day 17	2.96	2.87	4.20	4.94				
Day 18	3.00	2.89	4.16	5.10				
Days 19 to 21	3.03	2.86	4.12	3.89	0.13	0.001	0.232	0.742

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SMFA proportion did not change (average of 31.4%) and only the expression of ACACA decreased and that of AGPAT6 and FABP3 increased. The unexpected over expression of AGPAT6 and FABP3 transcripts in R-MFD cows may be potential candidate genes involved in the MFD-resistance. Other genes that may also be involved need to be identified.

Key Words: milk fat depression, mRNA expression, extruded linseed.

1822 (W281) Effects of niacin supplementation and forage type on milk, digestibility, blood parameters and body temperature in lactating dairy cows. R. B. Standish*, P. S. Erickson, N. L. Whitehouse, B. J. Isenberg, E. M. Barron, J. Y. Buckley and A. M. Pike, *University of New Hampshire, Durham*

This experiment evaluated the effect of niacin combined with either corn silage (CS) or grass silage (GS) based diets on apparent total tract nutrient digestibility, milk yield and composition, body temperature, and blood parameters. Four ruminally-cannulated Holstein cows were used in a 4 x 4 Latin square design with a 2 x 2 factorial arrangement of treatments with 28-d periods. Treatments were CS or GS based diets without or with 12 g niacin/d. One primiparous and three multiparous late lactation cows (225 ± 12 d in milk) were used. One cow was removed during the third period due to unrelated causes. Each period, dry matter intake (DMI) and milk production were recorded (d 19-28), and samples of blood (1300h, d 28), milk (0630 and 1730 h for 2 d), feeds (0545 and 1745 h on d 19-28), feces, and body temperature (both at 2-h intervals on d 26-28) were taken. Serum was analyzed for glucose and non-esterified fatty acids. Feed and feces were analyzed for acid insoluble ash, and digestibility was determined for dry matter (DM), organic matter (OM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), starch, fat, and hemicellulose (NDF-ADF). Data were analyzed using the mixed procedure of SAS. Orthogonal comparisons were used to evaluate main effects and interactions. Repeated measures were used to analyze body temperature and means were separated using Tukey's test. Intake of DM was greater ($P = 0.01$) for cows fed CS than for cows fed GS (29.01 and 24.09 kg/d, respectively). Digestibility of NDF was greater ($P = 0.002$) for cows fed GS than for cows fed CS (63.7 and 45.8%, respectively). Digestibilities of DM, OM, ADF, CP, and starch were similar among treatments. Hemicellulose digestibility was greater ($P = 0.002$) for cows fed GS versus cows fed CS (82.2 and 53.1%, respectively) because cows fed GS had lower DMI. Fat digestibility was greater ($P = 0.02$) for cows fed CS versus cows fed GS (93.0 and 82.4%, respectively). Milk yield was less for cows fed GS versus CS (20.0 and 29.9 kg/d, respectively). Fat (0.77 and 1.07 kg) and protein yields (0.61 and 0.96 kg) were less for cows fed GS versus CS ($P = 0.02$ and 0.04, respectively). Body temperature tended ($P = 0.08$) to be lower for cows fed GS and niacin (37.7°C) versus cows fed only CS (38°C). Niacin did not improve any parameter except for lowered body temperature.

Key Words: niacin corn silage grass silage

1823 (W282) Differences in hepatic transcriptional regulatory networks due to body condition score at calving in grazing dairy cattle. H. Akbar[1], Z. Zhou[*1], K. Macdonald[2], K. E. Schütz[3], G. Verkerk[2], J. R. Webster[3], S. L. Rodriguez Zas[1], J. R. Roche[2] and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]DairyNZ, Hamilton, New Zealand, [3]AgResearch, Hamilton, New Zealand*

Despite recent progress in nutrigenomics of peripartal dairy cattle, many components of transcriptional regulation in hepatic networks remain unknown. The objective of this study was to use gene network analysis on hepatic microarray data to identify transcription regulators (TR) and their target genes. Holstein-Friesian cows managed to achieve a high (H, 5.5 BCS), medium (M, 4.5 BCS), or low (L, 3.5 BCS) BCS (10-point scale) were used. Target BCS at calving were achieved by managing feed allowance before dry off. Post-calving, cows were allocated pasture and pasture silage (predominantly perennial ryegrass). Liver from 10 cows per BCS group was biopsied on wk 1, 3, and 5 postpartum. A whole-transcriptome bovine microarray (Agilent) was used. An ANOVA with repeated measures using PROC MIXED resulted in 5888 differentially-expressed genes (DEG) due to main effect of BCS (False Discovery Rate < 0.05) and 327 differentially expressed genes due to BCS × wk. TF network analysis was performed with Ingenuity Pathway Analysis (IPA). The network analysis uncovered TP53 as a central hub regulating a large spectrum of genes altered by BCS. Expression of TP53 was overall greater in H vs. M and L vs. M, but lower in H vs L. Other important TR altered by BCS were CTNNB1, SREBF1, RXRA, STAT1, NFKBIA and YWHAH. Among DEG with a BCS × wk effect due to H vs. M or L vs. M on wk 1, HNF4A was among 10 TR uncovered to have the greatest number of targets. Unlike wk 1, out of 9 TR identified in wk 3, the expression of MYC was downregulated in H vs. L but this TR had the greatest number of targets. Similarly, MYC had the greatest number of targets in L vs. M on wk 3 but was upregulated. Contrary to wk 1, on wk 5 the expression of MYC was upregulated in H vs. L and FOXP3 was identified as an important TR. Expression of FOXP3 on wk 5 was downregulated in H vs. M but among 16 TR identified it had the greatest number of targets. It is noteworthy that TP53, MYC, and FOXP3 are key controllers of cell proliferation/apoptosis in non-ruminant tissues/cells. Although HNF4A also is related with liver development, it has broader functions in terms of controlling expression of metabolic genes. Preliminary interpretation suggests an important role of a few TR in the control of liver function.

Key Words: gene networks, bioinformatics, systems biology

1824 (W283) Effects of a corn straw or mixed forage diet on mammary gland function and its endocrine regulation in early lactation dairy cows. T. Qin[1], H. Y. Wang[1], D. P. Bu[*2] and H. B. Zhu[1], *[1]Embryo Biotechnology and Reproduction Laboratory, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

The forage system is critical to lactation performance in dairy cows. The objective of this study was to evaluate the effects of two different forage patterns on the mammary gland and the endocrine regulation of its functions. Twelve multiparous, early-lactation Holstein cows were randomly assigned to high forage diet (MF, forage: concentrate = 60: 40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (CS, forage: concentrate = 40: 60) with corn straw as the forage source. Body weight (BW), body condition score (BCS) and dry matter intake (DMI) of each cow were recorded. Milk yield were recorded daily,and milk compositions and somatic cell count (SCC) were detected. Blood samples were collected weekly, and mammary biopsies were taken on 16 days postpartum. Data were analyzed using the PROC MIXED procedure of SAS 9.1. From the 6-wk of lactation, cows fed MF diet produced more milk (23.05 and 18.24 kg/d; $P < 0.05$), and tended to produce more milk fat (1.08 and 0.81kg/d; $P = 0.07$) and protein (0.69 and 0.59kg/d; $P = 0.10$) compared with cows fed CS diet. In CS group, the milk SCC were greater than those in MF group (Somatic cell score: -5.25 and -6.88; $P = 0.02$). There were no differences in BW, BCS and DMI ($P > 0.05$). Compared to MF cows, insulin like growth factor-I (IGF-1) in blood (70.21 and 50.49 ng/mL; $P < 0.05$) and *IGF-1R* expression in mammary (1.86 ± 0.15 and 1.45 ± 0.11; $P = 0.02$) were lesser in CS group. Mean concentrations of serum BHBA (1.64 vs 0.51 mmol/L; $P < 0.0001$) and NEFA (832.3 vs 309.0 μEq/L; $P < 0.01$) in MF cows peaked in week 2 after calving, and greater than CS group. The secretory activity of mammary epithelial cells (MEC) and the rate of mammary cell proliferation in both groups had no significant difference ($P > 0.05$),but the rate of cell apoptosis in CS group were greater relative to the MF group (1429 ± 103 and 679 ± 128 counts/mm^2; $P = 0.003$). The results indicated that lactation performance of dairy cows were affected by forage patterns, which was closely related to their endocrine regulation in dairy cows.

Key Words: forage sources,mammary gland function,endocrine regulation

1825 (W284) Milk fatty acid profile of dairy cows grazing a tropical pasture supplemented with sources of rumen protected fat. J. D. Souza[*1], F. Batistel[2], C. Sitta[1] and F. A. P. Santos[2], *[1]University of Sao Paulo, Piracicaba, Brazil, [2]University of São Paulo, Piracicaba, Brazil*

The objective of this experiment was to investigate the effects of supplementation of early lactation dairy cows grazing a tropical pasture with diets containing calcium salts of palm oil (CSPO) or calcium salts of soybean oil (CSSO) on milk fatty acid profile. Twenty-seven cows (15 ± 3 DIM) were used in a randomized block design and subjected to the following treatments: a) control (no fat); b) 400 g CSSO cow^{-1} d^{-1}; c) 400 g CSPO cow^{-1} d^{-1}. Cows grazed paddocks of *Pennisetum purpureum* and received 8 kg cow^{-1} d^{-1} (DM) of concentrate twice daily. Treatment periods were 90 d in length and milk samples were taken at 30, 60 and 90 d of experimental period for milk fatty acid analysis by gas chromatography. Data were analyzed as repeated measures using a mixed model with block as random effect and means were compared by Tukey test. The CSSO increased C18:2 cis-9 trans-12, CLA cis-9 trans-11 and CLA trans-10 cis-12 in the milk fat compared with control and CSPO. Both fat sources increased C18:3 cis-9 cis-12 cis-15 in the milk fat. The *de novo* synthesis was reduced by both fat sources and the CSPO increased mixed fatty acids (C16 + C16:1), due to greater incorporation of C16 from the diet. The preformed fatty acids were increased by CSSO supplementation. The CSSO decreased total saturated fatty acids, and increased MUFA and PUFA compared to control and CSPO. Overall, both sources of fat changed the milk fatty acid profile, and CSSO increased unsaturated fatty acid whereas CSPO increased saturated fatty acids.

Key Words: palm oil, soybean oil, tropical pasture

Table 1825. Milk fatty acid profile of grazing dairy cows supplemented with fat

g/100g of fat	Control	CSSO	CSPO	SEM	*P*-value
C18:2 cis-9 trans-12	1.66[c]	2.07[a]	1.92[b]	0.09	0.002
C18:3 cis-9 cis-12 cis-15	0.33[b]	0.43[a]	0.39[a]	0.02	0.07
CLA cis-9 trans-11	0.66[b]	0.86[a]	0.69[b]	0.05	0.005
CLA trans-10 cis-12	0.02[b]	0.09[a]	0.019[b]	0.003	0.0001
De novo	25.6[a]	20.8[b]	21.4[b]	0.99	0.005
Mixed	30.7[b]	30.2[b]	33.9[a]	1.4	0.04
Preformed	43.7[b]	49.0[a]	44.7[b]	2.2	0.04
Total of saturated	66.9[a]	61.5[b]	64.1[a]	1.76	0.01
Total of MUFA	28.9[b]	33.6[a]	31.6[ab]	1.3	0.04
Total of PUFA	4.2[b]	4.9[a]	4.3[b]	0.24	0.02

1826 (W285) Evaluating daily variation in body weight, milk production, and rumination activity on a commercial dairy with robotic milking.

R. W. Bender*, D. E. Cook, T. L. Chandler, H. M. White and D. K. Combs, *Department of Dairy Science University of Wisconsin, Madison*

Emerging technologies allow commercial dairy producers to collect a wide array of individual cow data on a daily basis, with the potential to profoundly influence managerial and nutritional decision-making on a pen basis. The objective of this study was to utilize daily body weights, rumination activity, and milk production data from lactating dairy cows to evaluate random variation that exists on a commercial dairy. Data were obtained from a commercial robotic dairy farm in Melrose, WI via the Lely T4C herd management system for either a whole year (daily body weights and daily milk production) or one week (rumination). Data from approximately 500 cows in seven pens (1 pen per robot, approximately 70 cows per pen) was utilized. Cows were assigned to a pen post-calving and remained there until dry off. All data is presented as mean ± standard deviation. On this dairy, milk production averaged 37.4 kg, with a standard deviation of 1.0 kg among days within a pen, 14.4 kg among individual cows within a pen, and 21.2 kg among days within individual cows. Body weight averaged 689.2 kg, with a standard deviation of 4.5 kg among days within a pen, 75.6 kg among individual cows within a pen, and 34.6 kg among days within individual cows. Rumination (min per day) averaged 461.1 min, with a standard deviation of 6.1 min among days within a pen, 128.0 min among individual cows within a pen, and 43.6 min among days within individual cows. A statistical power calculation would suggest that with 7 pens and 95% confidence, a difference of 1.5 kg mean milk production, 6.5 kg mean body weight, or 8.0 min mean rumination time could be deemed statistically significant from day to day within this herd. Understanding the magnitude of the variability among these parameters could be a powerful tool to monitor pen level changes over a short period of time and implement immediate managerial modifications.

Key Words: body weight, milk production, rumination

1827 (W286) Peroxisome proliferator activated receptor-γ controls lipogenic gene networks in goat mammary epithelial cells.

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In non-ruminants, peroxisome proliferator-activated receptor-γ (*PPARG*) plays a crucial role in fatty acid (FA) metabolism through the regulation of lipogenic gene expression. However, whether or how *PPARG* regulates the activity of mammary lipogenic genes in ruminant mammary cells remains largely unknown. This study explored the potential role of *PPARG* in regulating mRNA expression of lipogenic genes in lactating goat primary mammary epithelial cells (GMEC). Adenoviral transfection of the *PPARG* response element into GMEC was used in this study. The *PPARG* agonist rosiglitazone (ROSI) was used to study gene expression changes in response to PPARG activation. Expression of 39 genes involved in milk fat synthesis plus 3 internal control genes was measured using qPCR. Data from triplicate cultures were log-transformed and statistically analyzed using the GLM of SAS. The multiple comparisons were corrected using Tukey's test and significance set at $P < 0.05$. Over-expression of *PPARG* without (Ad-PPARG+DMSO) or with (Ad-PPARG+ROSI) ROSI markedly upregulated ($P = 0.0001$) the expression of *PPARG* compared with the control (Ad-GFP (Green fluorescent protein)+DMSO) and ROSI (Ad-GFP+ROSI) treatments. Over-expression of *PPARG* without ROSI up-regulated ($P < 0.05$) the expression of some lipogenic enzymes (*ACSS2, ACSL1, SCD, DGAT1, FADS1, GPAM, LPIN1*), transcription regulators (*LXRα, MLXIPL, PPARG, PPARGC1B),* and components of the circadian CLOCK network (*CRY1, CRY2*). After ROSI treatment of PPARG-overexpressing GMEC there was a further and marked increase ($P < 0.05$) in the mRNA expression of lipogenic enzymes (*FASN, ACSS2, GPAM, LPIN1, ACSL1, SCD*), transcription regulators (*LXRα, PPARG, SREBF1, PPARGC1B*), and components of the circadian CLOCK network (*CLOCK, CRY1, CRY2*). It was noteworthy that expression of *RXRα*, a partner of *PPARG*, was down-regulated in PPARG-overexpressing GMEC with or without ROSI treatment. These results provide direct evidence that *PPARG* plays a crucial role in regulating fatty acid metabolism in goat mammary cells and underscore the importance of *PPARG* in the mammary gland during lactation.

Key Words: PPAR, nutrigenomics, milk fa synthesis

1828 (W287) Effects of ergot alkaloid exposure on serotonin receptor mRNA in the smooth muscle of the bovine gastrointestinal tract.

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Various serotonin (5HT) receptor subtypes have been located in the gastrointestinal tract and some are associated with gut motility. Cattle exposed to ergot alkaloids through consumption of contaminated feedstuffs have demonstrated signs (e.g.-increased rumen DM content and total content) that suggest a reduction in gut motility. Ergot alkaloids have been shown to interact with biogenic amine receptors and specifically serotonin receptors. Therefore, the objective of this study was to evaluate the effect of dietary exposure to ergot alkaloids has on the expression of 5HT receptor subtypes 5HTR2A (NM_001001157.1) and 5HTR4 (NM_001010485.1) in the smooth muscle of the reticulum, rumen, omasum, abomasum, duodenum, jejunum, ileum, cecum and colon of cattle. Ruminally cannulated Angus steers ($n = 12$; BW = 547 ± 31 kg)

were paired by weight and randomly assigned to 6 blocks. Steers were fed alfalfa cubes at $1.5 \times NE_m$ and were ruminally dosed daily with 1 kg of either endophyte-infected (E+; 4.45 ppm ergovaline) or endophyte-free (E-) tall fescue seed for 21 d prior to slaughter. On d 22 steers were slaughtered and samples of smooth muscle from the different sites of the gastrointestinal tract were sampled, rinsed, homogenized in Tri-reagent, and total RNA was isolated. Semi-quantitative real-time PCR was conducted using SYBR green and glyceraldehyde 3-phosphate dehydrogenase (NM_001034034.2) as a reference gene. Resultant data were analyzed using mixed models of SAS. There was no interaction of sampling location by seed treatment for either gene evaluated. For 5HTR4 only the main effect of sampling location was significant ($P < 0.001$) with ileum and jejunum having the greatest amount of transcript ($P < 0.05$) followed by the colon and duodenum ($P < 0.05$). The remaining tissue sites did not differ. Expression of 5HTR2A in E- steers was greater ($P = 0.04$) than E+ steers with lower relative quantities of 5HTR2A in E+ steers for all tissue sampling locations except the abomasum ($P = 0.054$). The enteric 5HTR2A receptor is associated with smooth muscle contraction and the observed decrease in expression in E+ treated steers suggests that ergot alkaloids may play a role in negatively affecting gut motility. Future work will explore the effects alkaloids might have on genes that encode for the G proteins and other downstream signal transduction proteins associated with these 5HT receptors.

Key Words: bovine, ergot alkaloids, serotonin receptor

1829 (W288) Effect of mineral supplementation on lactational performance in early-lactating dairy cows fed a high-concentrate diet. A. R. Alfonso-Avila[*1], E. Charbonneau[1], P. Y. Chouinard[1], G. Tremblay[2] and R. Gervais[1], [1]*Université Laval, Québec, QC, Canada,* [2]*Agriculture and Agri-Food Canada, Soils and Crops Research and Development Centre, Quebec, QC, Canada*

Previous studies reported an increase in milk fat synthesis when lactating dairy cows were fed diets with higher dietary cation-anion difference (DCAD) or K, supplied as K_2CO_3. This study investigated the effects of DCAD, cation source, and buffering capacity of the mineral supplement on lactational performance of early-lactating dairy cows fed a high concentrate diet. Ten primiparous and 25 multiparous Holstein cows averaging 38 ± 13 DIM were distributed according to a randomized block design (7 blocks) for 5 wk, including a 1-wk pretreatment collection period, used as a covariate. Treatments consisted of C) a basal diet formulated to contain 40% forage (60% corn silage) and 60% concentrate (16% CP, 47% non-fibrous carbohydrates, 29% NDF, DCAD +65 mEq/kg) as control; K1) C + 1.8% K_2CO_3 (DCAD: +326); K2) C + 2.6% $KHCO_3$ (DCAD: +324); K3) C + 1.9% KCl (DCAD +64); and Na) C + 1.4% Na_2CO_3 (+322). Orthogonal contrasts

were used to assess the effects of K_2CO_3 (C vs. K1), buffering capacity (K1 vs. K2), DCAD (K1 vs. K3), and cation type (K1 vs. Na). Treatment period was 28 d with the last 5 d used for data and sample collection. The selected comparisons detected no effect of treatments on DMI (24.1 ± 1.2 kg/d; $P > 0.14$) and milk yield (36.8 ± 1.8 kg/d; $P > 0.12$). Blood K^+ concentration was higher in cows fed K1 (3.99 mmol/L) as compared with C (3.75; $P < 0.01$), K2 (3.79; $P = 0.02$), and Na (3.68; $P < 0.01$), whereas no difference was observed with cows fed K3 (3.89; $P = 0.20$). Blood Cl^- concentration was lower in cows fed K1 (106.1 mmol/L) as compared with Na (108.3; $P = 0.01$). However, no difference was observed in blood Na^+ concentration of cows fed K1 and Na (139.9 ± 0.4 mmol/L; $P = 0.18$). As compared with Na, cows fed K1 had a higher milk protein content (3.12 vs 2.93%; $P = 0.04$) but a similar milk protein yield (1087 ± 67 g/d; $P = 0.56$). Milk fat percentage was higher in cows fed K1 compared with C (4.03 vs 3.26%; $P = 0.02$), whereas milk fat yield (1305 ± 134 g/d; $P = 0.21$) or 4% fat corrected milk (34.0 ± 2.6 kg/d; $P = 0.61$) were not affected. As opposed to previously published results, under conditions of the current experiment, increasing DCAD or K^+ concentration in a high concentrate diet did not improve milk fat yield in early lactating cows.

Key Words: DCAD, potassium carbonate, milk fat synthesis

1830 (W289) Mineral profile, inmunoglobulins and antioxidant activity in culls cows fed DDGS. A. Flores-Mariñelarena[*1], E. Acosta Sánchez[1], G. Corral-Flores[1], C. Rodríguez-Muela[1], J. A. Ramírez-Godínez[1], J. Dominguez-Viveros[1], A. Anchondo-Garay[1] and H. Ramírez-Garduño[2], [1]*Universidad Autónoma de Chihuahua, Chihuahua, Mexico,* [2]*INIFAP, Chihuahua, Mexico*

The objective was to evaluate the effect of four levels of Distillery Dry Grains (DDGS) in the diet of cull beef cows on body weight (BW) and average daily gain (ADG) every 15 d and the mineral profile (Zn, Mn and Cu) and immunoglobulins in blood serum, and the antioxidant activity (AA) in blood plasma (d 0 and d60). Thirty five mature cows of different genotypes with an average live weight of 350 ± 40 kg were randomly divided into four treatments with different levels of DDGS: T1 (Control, 0%, $n = 9$), T2 (5.7%, $n = 9$), T3 (11,23%, $n = 8$) and T4 (16.45%, $n = 9$). A completely randomized design with treatment and time of sampling as fixed effects was used. Data was analyzed with the GLM of SAS. For the multiple comparisons of means a Tukey's test was used. The BW and ADG were similar ($P > 0.05$) between treatments. Serum levels of Zn, Cu, and Mn between treatments did not differ ($P > 0.05$). During the feeding period the serum levels of Zn and Cu were similar ($P > 0.05$). However, levels of Mn were higher ($P < 0.05$) at d 0 than at d 60 (1.69 $\pm$ 0.11 µmol/L vs 1.36 $\pm$ 0.11 µmol/L, respectively). The AA

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and immunoglobulins were similar ($P > 0.05$) between treatments at d 60, but were different ($P < 0.05$) at d 0 (5.74 ± 0.32 g *100 mL [1]) vs d 60 (8.12 ± 0.33 g *100 mL [1]) of the feeding period. It was concluded that the inclusion of DDG's in the diet of cull beef cows did not affect the ADG, the mineral profile and the AA. However, Mn concentration was reduced and immunoglobulin increased during the 60 d feeding period.

Key Words: cull cows, antioxidant activity, mineral profile, immunoglobulin

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1831 (W290) Metabolic characteristics and truly metabolizable protein supply to dairy cattle from new cool-season forage corn varieties in western Canada. S. Abeysekara, D. A. Christensen, N. A. Khan, X. Huang* and P. Yu, *University of Saskatchewan, Saskatoon, SK, Canada*

The objectives of the present study were to quantitatively evaluate the metabolic characteristics of protein in the rumen and intestine of dairy cattle and to estimate the content of truly metabolizable protein (MP) in newly developed cool-season forage corn varieties. Six new corn cultivars, including 3 Pioneer (PNR) and 3 Hyland (HL), coded as PNR-7443R, PNR-P7213R, PNR-7535R, HL-SR06, HL-SR22, HL-BAX-XOS-RR, were evaluated in the present study. The metabolic characteristics, MP supply to dairy cattle, and energy synchronization properties were modeled by the DVE/OEB system and the NRC-2001 model. The parameters evaluated were (1) potential microbial protein (MCP) synthesis in the rumen from available degraded protein and energy (2) truly absorbable rumen synthesized microbial protein (AMCP) (3) truly absorbable rumen undegraded feed protein (ARUP) (4) truly absorbed rumen endogenous protein and (5) total truly MP (6) the degraded protein balance (DPB). Both models estimated significant ($P < 0.05$) differences in contents of MCP synthesized from rumen degraded protein (RDP) and ARUP among the cultivars. The NRC-2001 model estimated significant ($P < 0.05$) differences in total truly MP and DPB among the cultivars. According to NRC-2001 model, the contents AMCP, ARUP and total truly MP contents were higher ($P < 0.05$) for cultivar HL-SR06, resulting in the lowest ($P < 0.05$) DPB. Cultivar, HL-SR06 also had the highest rumen available N/kg of organic matter (OM) and high hourly effective degradability ratios among the corn cultivars. However, none of the cultivars reached the optimal target hourly effective degradability ratio (25 g N g/kg OM), demonstrating N deficiency in the rumen. Hyland-SR06 had the highest contents of MCP synthesized from RDP, ARUP and total truly MP. However, regardless of the differences among cultivars, forage corn based rations of dairy cows needs to be balanced with a high protein containing concentrate to improve the rumen degradable protein deficit.

Key Words: corn, protein metabolic characteristics, protein evaluation system

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1832 (W291) Hepatic expression of genes associated with glutathione and fatty acid metabolism during the peripartal period reveal beneficial effects of MetaSmart and Smartamine M supplementation on health status in dairy cows. J. S. Osorio[1], P. Ji[2], J. K. Drackley[3], D. N. Luchini[4] and J. J. Loor*[3], *[1]University of Illinois, Champaign, [2]William H. Miner Agricultural Research Institute, Chazy, NY, [3]University of Illinois, Urbana, [4]Adisseo S.A.S., Alpharetta, GA.*

Fifty-seven multiparous Holstein cows were fed a control diet (CON, $n = 24$; 1.49 Mcal/kg DM prepartum and 1.75 Mcal/kg DM postpartum), CON plus MetaSmart (MS, $n = 15$; Adisseo France S.A.S.), or CON plus Smartamine M (SM, $n = 18$; Adisseo France S.A.S.). Treatments began on -21 days in milk (DIM) and continued through 30 DIM. MetaSmart (0.19% of DM) and SM (0.07% of DM) were top-dressed on the CON diet. Liver samples ($n = 8$-9/treatment) collected at -10, 7, and 21 DIM were used for real-time qPCR of genes associated with metabolism of Met, glutathione, fatty acid, and gluconeogenesis as well as inflammation, oxidative stress, hepatokines, growth hormone signaling, and DNA methylation. Data were analyzed using the MIXED procedure of SAS with the preplanned contrast CON vs. MS+SM. Expression of Met adenosyltransferase 1A (*MAT1A*) increased ($P = 0.001$) over time (-10 vs 21 d) in Met-supplemented cows while it decreased ($P = 0.002$) in CON cows. Glutathione metabolism-related genes such as glutathione reductase (*GSR*; $P = 0.02$) and glutathione synthase (*GSS*; $P = 0.004$) had lower expression at 21 DIM in Met-supplemented cows, while glutamate-cysteine ligase catalytic tended (*GCLC*; $P = 0.07$) to have a similar pattern as *GSR* and *GSS*. Expression of 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (*HMGCS2*) was lower ($P = 0.02$) in Met-supplemented cows at 21 DIM. *HMGCS2* is highly corelated with ketogenesis. Expression of peroxisome proliferator-activated receptor α (*PPARA*; $P = 0.04$) and phosphoenolpyruvate carboxykinase 1 (*PCK1*; $P = 0.03$) was greater in Met-supplemented cows, while a trend ($P = 0.06$) was observed for the hepatokine fibroblast growth factor 21 (*FGF21*). Increased expression of *MAT1A* over time in Met-supplemented cows coupled with greater *PPARA* expression is suggestive that Met, a methyl donor, might have promoted the activation of *PPARA* via S-adenosylmethionine by reducing DNA methylation of the PPARA promoter region. The role of the *PPARA-FGF21* axis as an activator of gluconeogenesis was underscored by the concomitant upregulation of *PCK1* in Met-supplemented cows. Postpartal down-regulation of *HMGCS2* in Met-supplemented cows could be related with a lower production of ketones bodies, which agrees with the trend ($P = 0.15$) observed in the overall group ($n = 57$) suggesting a lower predisposition to developing ketosis. The parallel down-regulation of *GSR*, *GSS*, and *GCLC* at 21 d might indicate a lower requirement for the antioxidant activity of glutathione in Met-supplemented cows.

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1833 (W292) Feed intake and feeding behavior of lactating dairy cows were affected by dietary fatty acid profile. H. Khalilvandi-Behroozyar[1], M. Dehghan Banadaky*[2], M. Ghaffarzadeh[3] and K. Rezayazdi[2], [1]*Department of Animal Science, Urmia University, Urmia, Iran, [2]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [3]Chemistry and Chemical Engineering Research Center of Iran, Tehran, Iran*

There are quite rare data regarding effects of dietary fatty acid profile on feeding and chewing behavior. The aim of this study was to evaluate the milk fatty acid profile in early lactating dairy cows supplemented with protected unsaturated fatty acids sources and prilled source of palm fatty acids. Twenty four multiparous Iranian Holstein cows individually were assigned to diets with different fatty acid profiles and supplemented through 30 days before expect calving date to 50 days in milk. Dietary treatments consisted of (1) Prilled Pam fatty acids (PO) [Energizer RP10 , 2 & 2.25% DM in pre- and postpartum, respectively]; (2) Ca-salts of sunflower oil (SO) [Persia Fat- SO]; (3) Ca-salts of fish oil (FO) [Persia Fat- FO] and (4) equal amounts of Persia Fat- FO & Persia Fat- SO. Calcium salts were supplemented as 2.2 and 2.5% of dietary DM in pre- and postpartum period, respectively. All rations contained identical forage and concentrate components. Feeding behavior was continuously monitored for 5 consecutive days in 15, 30 and 45 days in milk using video recordings. Data were analyzed using PROC MIXED of SAS 9.1 with repeated measures in time function. Dry matter intake for PO was less than Persia Fat with different FA profiles (20.17 vs. 23.56, 22.25 and 2.53, for treatments 1 to 4, respectively, $P < 0.05$). Supplementation of palm fatty acids decreased meal number, meal length and time to consume 1 kg of DM or NDF, but amount of feed intake in each meal was not affected. Time interval between meals was numerically increased ($P > 0.05$) by supplementation of PO (2.74 vs. 2.28, 2.51 and 2.53, for treatments 1 to 4, respectively).The PO treatment increased time spent ruminating in each bout, but increased rumination bout intervals. Total number of rumination bouts was not affected by fat supplement type. Total rumination time (660.48 min vs. 587.86, 584.8 and 73.75, for treatments 1 to 4, respectively) and rumination per kg of DM (32.74 min vs. 24.95, 26.28 and 25.47, for treatments 1 to 4, respectively) and NDF (102.39 min vs. 78.02, 82.21 and 79.62, for treatments 1 to 4, respectively) were increased for PO than PUFA supplemented cows. We conclude that saturated fat supplement suppress DMI via increase time spend to consume or rumination feed.

Key Words: palm oil, PUFA, rumination

1834 (W293) Whole cottonseed and vitamin E in diets for Nellore cattle finished in feedlot: Performance traits and Feed conversion. A. M. Ferrinho*[1], F. Baldi[2], B. M. Toda[1], F. B. Mendonça[1], B. L. Utembergue[1], R. R. Germano[1], A. S. C. Pereira[1], P. R. Leme[1] and S. L. Silva[1], [1]*Universidade de São Paulo, Pirassununga, Brazil, [2]Universidade Estadual Paulista "Júlio de Mesquita Filho"- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil*

This study aimed to evaluate the daily live weight gain, live weight evolution, feed efficiency (ratio live weight gain/dry matter intake), hot and cold carcass weight and carcass yield of bulls finished in feedlot feeding. A total of 54 bulls were confined, with approximately 350 kg initial weight, average age of 24 months, in a randomized blocks design with factorial arrangement of treatments (3 x 3), totaling 9 treatments with 6 animals in each treatment. The animals were fed three diets: 1) control without cottonseed (CTL), 2) containing cottonseed at 30% of DM (CAR) and 3) diet containing cottonseed at 30% of DM and 500 IU vitamin E/kg of DM (VITE). The diets used were composed of different concentrates, including dry corn grain, citrus pulp, sugarcane bagasse raw and soybean meal with forage concentrate ratio of 86:14 and an average of 55% CP in the three diets The animals were kept in pens, three to three, and fed once a day, for 83, 104 and 111 days and slaughtered. For feed conversion and carcass weight, the the fixed effects of treatment, slaughter period and the interaction between them, and the block random effect were included in the model. For repeated measured traits, the fixed effects of treatment, weighing period and the interaction between them, and the block random effect were included in the model. The data were submitted to an analysis of variance using the proc mixed command (SAS statistical program) applying a significance level of 5%. The interaction between treatment x slaughter period was significant ($P < 0.05$) for feed conversion where animals fed the VITE and CAR diets and slaughtered at 111 days showed better feed conversion efficiency with averages of 4.68 kg DM and 4.94 kg DM respectively. The interaction treatment x slaughter period was also significant ($P < 0.05$) for live weight evolution ($P < 0.01$). The mean daily live weight gains were 4.10 kg, 3.74 kg and 0.6 kg for CAR, VITE and CTL respectively. There was a significant effect of diets containing whole cottonseed (CAR and VITE) on hot and cold carcass weight compared to the diet without whole cottonseed ($P < 0.01$), while for carcass yield, animals slaughtered at 111 days showed higher (56,33%) than animals slaughtered before ($P < 0.05$). The animals fed diets with cottonseed have better performance for live weight gain, feed conversion and carcass weight.

Key Words: cottonseed, feed efficiency, daily live gain

1835 (W294) Effect of chitosan and lipid source combination on energy intake and milk yield and composition of dairy cows. T. A. Del Valle[*1], V. C. Galvão[1], F. C. R. D. Santos[1], E. F. Jesus[2], A. G. B. V. B. Costa[1], C. E. C. Consentini[1], G. F. D. Almeida[1], G. F. Cabral[3], F. Zanferari[1] and F. P. Rennó[1], *[1]School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, Brazil, [2]School of Agricultural and Veterinary Sciences of UNESP, Jaboticabal, Brazil, [3]School of Animal Science and Food Engineering of University of São Paulo, Pirassunga, Brazil*

The aim of this study was to evaluate the effects of chitosan and soybean oil in the dairy cow's diets, on energy intake and milk yield. Twenty-four Holstein averaging 174.7 ± 53.1 DIM, were randomly assigned in six Latin Square design with a two by two factorial arrangement of treatments. The diets contained chitosan (150 mg.kg^{-1} of body weight) and/or soybean oil (3.3% of the diet DM). Each experiment period had a 14 d adaptation period and an seven for collection data. Sampling of milk was done on days 16, 17 and 18 of each period to evaluate the composition. The net energy intake (NEI), energy requirement for maintenance (NE$_m$) and lactation (NE$_L$) were obtained from the equations of NRC (2001). NEI was decrease with the use of chitosan in the diets without supplementation of soybean oil, but has no difference between diets containing soybean oil as well as the dry matter intake. The NE$_L$ was decrease by addition of soybean oil in the diet, regardless of the addition of chitosan. This occurred due to the reduction of on average 5.0 g.kg^{-1} the synthesis of fat in milk of animals fed soybean oil. Although the animals receiving chitosan and soybean oil had less milk yield (31.26 kg) compared with animals receiving only the soybean oil (32.86 kg) and in this diet decrease fat concentration was only 3.7g. kg^{-1}, making fat corrected milk unchanged. Milk yield did not differ between cows fed chitosan diet (33.87 kg) and control diet (32.85 kg).The net energy balance was decrease on chitosan diet (2.97 Mcal) compared with control diet (5.33 Mcal) and was not influenced by the addition of chitosan on diets containing soybean oil (5.0 Mcal). The efficiency of use of energy, measured by the ration between the NE$_L$ and digestibility energy intake, was decrease by the addition of chitosan in diets with soybean oil and increased in diets without oil. Chitosan increases energy efficiency in dairy cows, provided that the diet has a low level of ether extract.

Key Words: fat, feed additive, milk energy

1836 (W295) Plasma urea concentration of beef heifers fed with different lipid sources and frequency supplementation. M. C. A. Santana[*1], V. C. Modesto[2], G. T. Pereira[2], R. A. Reis[2], G. M. P. Melo[2], H. J. U. Costa[2], T. T. Berchielli[2] and L. P. L. Moreira[2], *[1]Emater, Goiânia, Brazil, [2]UNESP, Jaboticabal, Brazil*

This research aims to evaluate urea plasma responses under different lipid sources and supplementation frequencies. The experiment was conducted throughout a 4-mo period during the dry season. The experiment was completely random, using a 3×2 factorial arrangement (3 supplements and 2 supplementation frequencies). The supplements were derived from 3 different sources, soybean grains, soybean oil and protected fat (Megalac-E), the 2 supplement frequencies were (D) daily or 3 days of week (Monday, Wednesday and Friday) called "alternate" (A). In the 4-mo experimental period, August–November, blood samples were taken from the jugular vein four hour after the morning feeding. Subsequently, these samples were centrifuged and stored until the urea blood level was evaluated. In all treatments, no urea levels differences were observed in August and September ($P > 0.05$). The Megalac–E that was supplied daily presented a higher urea plasma level in comparison to the alternate supplement of soybean oil in October ($P < 0.05$).The animals that were given soybean oil supplements daily showed lower urea plasma concentration values ($P < 0.05$) in November by treatments and periods. Overall, this data indicated that the urea blood level can be influenced according to the feeding strategy during the dry season.

Key Words: soybean grains, soybean oil, protect fat

Table 1836. Plasma urea concentration of heifers supplemented with different lipid sources at two different frequencies (mg/dL)

	D-SG	A-SG	D-SO	A-SO	D-ML	A-ML
August	27.5[Aa]	26.8[Aa]	27.6[Aa]	26.7[Aa]	27.8[Aa]	26.2[Aa]
September	21.1[Aa]	21.1[Aa]	29.9[Aa]	21.6[Aa]	26.1[Aa]	28.6[Aa]
October	24.8[ABa]	23.0[ABa]	28.9[ABa]	17.9[Ba]	32.3[Aa]	25.0[ABa]
November	24.4[ABa]	28.0[Aa]	13.5[Bb]	23.5[ABa]	21.9[ABa]	22.3[ABa]

Lowercase in columns and capital letters in rows differ (P < 0.05).
D = daily; A = alternately; SG = Soybean grain; SO = Soybean oil; ML = Megalac-E

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1837 (W296) Effects of selenium supply, maternal plane of nutrition, and physiological stage on nitrogen flow, microbial efficiency, and metabolizable protein in primiparous ewes.

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Primiparous Rambouillet ewes ($n = 84$, age = 240 ± 17 d, BW = 52.1 ± 6.2 kg) were allocated to $2 \times 3 \times 2$ factorial arrangement to evaluate dietary Se (adequate Se [11.5 µg/kg BW] or high Se [77.0 µg/kg BW]), nutritional plane (60% [restricted], 100% [control], or 140% [high]), and physiological stage at necropsy (parturition or d 20 of lactation) effects on nitrogen digestion and microbial CP production. At parturition, lambs were removed from all ewes and 42 ewes ($n = 7$ per treatment) were necropsied. Remaining ewes were transitioned to a common lactation diet to meet NRC requirements and machine milked for 20 d. Differences between treatments were determined by the GLM procedure in SAS. No three way interactions were present ($P > 0.10$), but many 2-way interactions were found ($P < 0.05$). Selenium did not influence N intake ($P = 0.23$). Nitrogen intake increased with plane of nutrition during gestation and lactation ($P < 0.001$; 13.3 vs. 20.2 vs. 31.4 ± 0.6 g during pregnancy and 40.4 vs. 41.6 vs. 42.2 ± 0.5 g during lactation for restricted, control, and high ewes, respectively). Microbial efficiency of ewes on restricted diets (7.0 ± 1.04 g microbial nitrogen/kg truly fermented) was decreased compared with control and high ewes (13.4 and 14.9 ± 1.04 g microbial nitrogen/kg truly fermented) but these differences were gone after 20 d of lactation ($P > 0.15$). Supranutritional Se supply and restricted and adequate nutrient planes increased microbial efficiency regardless of physiological stage ($P = 0.04$). Selenium supplementation increased ($P = 0.04$) total tract N digestion during gestation (69.3 and $71.4 \pm 1.0\%$, respectively) but decreased N digestion during lactation (74.7 and $72.9 \pm 0.9\%$, respectively). Ruminal N digestion was greater ($P = 0.01$) during gestation in restricted ewes compared with control or high ewes (59.1 vs. 44.9 and $39.9 \pm 2.8\%$, respectively); however, post-ruminal N digestion was less ($P = 0.02$) in restricted ewes compared with control and high nutritional planes (13.1 vs. 26.1 and $28.1 \pm 2.8\%$, respectively). Metabolizable protein increased ($P < 0.001$) during gestation with increasing nutritional intake but did not differ during lactation. Nutritional plane and Se supplementation had different effects on nitrogen digestion and microbial efficiency but those effects were dependent on physiologic stage.

Key Words: ewes, microbial efficiency, selenium

1838 (W297) Effect of prototype sequestering agents on performance and milk aflatoxin M1 concentrations of dairy cows fed aflatoxin B1-contaminated diets.

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This study examined if 3 in-feed mycotoxin-sequestering agents could reduce milk aflatoxin M_1 (AFM$_1$) concentration and improve the performance and immunological responses of dairy cattle fed diets contaminated with aflatoxin B_1 (AFB$_1$). Fifteen lactating cows were used in a 5×5 Latin square design with four 28-d periods and 3 replicate squares. Treatments included a Control diet (C), a toxin (T) diet containing 75 ug of AFB$_1$/kg of TMR DM and 3 diets containing T and one of three prototype sequestering agents (S1, S2, and S3). The AFB$_1$ was mixed with corn and molasses and dosed in gelatin capsules orally to cows before the TMR was fed on d 21 to 25. Milk was sampled twice daily on d 20 to 28 and plasma was sampled on d 20 and 25. The statistical model contained effects of diet, period, square, appropriate interactions and cow nested within square. Feeding T increased the milk AFM$_1$ concentration beyond the FDA safety threshold (0.5 ug/kg) and values were greater ($P < 0.001$) than those in cows fed C. Sequestering agents (S1, S2 and S3) did not reduce the transfer of AFB$_1$ to AFM$_1$. Feeding T reduced ($P = 0.03$) milk fat (0.93 vs. 1.05 kg/d) and protein (0.78 vs. 0.89 kg/d) yield and tended ($P = 0.09$) to reduce milk fat (3.74 vs. 3.84%) and protein (3.12 vs. 3.24%) concentrations compared to C. Feeding sequestering agents prevented these reductions in yields and concentrations of milk components except that S3 reduced milk fat yield. Cows fed S3 had lower ($P = 0.01$) DMI and greater ($P = 0.01$) feed efficiency (FCM/DMI; 1.34 vs. 1.12) than those fed C. Feeding T instead of C reduced ($P < 0.05$) red blood cell counts and hemoglobin concentration. Plasma acid-soluble protein concentration and monocyte counts were lower ($P < 0.05$) in cows fed S1, S2 and S3 compared to those fed T reflecting attenuation of the immunological challenge posed by feeding AFB$_1$. Sequestering agents had no effect on milk AFM$_1$ concentration but prevented adverse effects of AFB$_1$ on milk component yields and concentrations and immunological response indices

Key Words: milk, mycotoxin, sequestering agents

1839 (W298) Blood glucose concentrations and deposition of muscular and subcutaneous fat tissues of Nellore young bulls finished in pasture supplemented with crude glycerin. E. San Vito*, J. F. Lage, L. Maneck Delevatti, E. E. Dalanttonia, L. R. Simonetti, M. B. Abra and T. T. Berchielli, *Universidade Estadual Paulista Júlio de Mesquita Filho- UNESP, Jaboticabal, Brazil*

This trial aimed to evaluate the effects of feeding crude glycerin (CG)- 80% of glycerol- included as a substitute to corn grain in supplements of young bulls finished in pasture on rainy season on deposition of muscular and subcutaneous fat tissues and blood glucose concentration. The longissimus muscle area (LMA), rib fat thickness between the 12 and 13 ribs (RFT) and subcutaneous fat thickness in the region P8 (P8) were evaluated. Fifty Nellore young bulls with initial shrunk body weight of 427 ± 15.76 kg were randomly assigned to five treatments consisted of increasing crude glycerin concentration in the supplement: 0, 7, 14, 21, and 28% of dry matter. The CG used was derived from soybean biodiesel production. Animals were distributed in 10 paddocks of *Brachiaria brizantha* cv. Xaraés, with 1.8 ha each (2 paddocks per treatment). The animals were supplemented daily in a proportion of 300 g/100kg of BW. The supplement control was constituted of corn grain, soybean meal, urea, gluten meal and mineralized salt, containing 370 g/kg DM of CG. The measurements were done in the beginning of the experiment and in each 28 d, by ultrasound (Model Aloka 500, linear carcass probe with 17.2 cm and frequency of 3.5 MHz), to evaluate the deposition of muscular and subcutaneous fat tissues. Blood was collected in vacutainer tubes from the tail vein after 16 h withdrawal period from feed and water. 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 no statistical significance (P>0.05) among the treatments, and the final average values observed were: 71.5 cm $<$ su$P>2</$su$P>$ to LMA, 4.4 mm to P8 and 3.7 mm to RFT. The gain observed in the variables (initial value– final value) LMA, P8 and RFT were 13.3 cm $<$ su$P>2</$su$P>$ 1.7 mm and 1.3 mm, respectively. CG inclusion did not affect the blood glucose concentrations (P>0.05), however the values showed a quadratic effect (P = 0.020), with the highest concentration (81.8 mg/dL) in the level of 14% inclusion of crude glycerin. Addition of crude glycerin in supplement (28% of DM) does not affect the deposition of muscular and subcutaneous fat tissues or blood glucose concentrations of Nellore young bulls finished in pasture on rainy season.

Key Words: beef cattle, glycerol, pasture

1840 (W299) Effect of propolis on plasma metabolites and hematocrit of Holstein calves. P. Peravian*[1], K. Rezayazdi[2] and G. Nehzati[3], *[1]University of Tehran, Tehran, Iran, [2]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [3]University of Tehran, Karaj, Iran*

The object of this study was to investigate the effect of propolis powder on the plasma metabolites and hematocrit of suckling calves. Propolis in this experiment was come from Taleghan vicinity (near Tehran). 40 Holstein female calves with 41 ± 1 kg of body weight from 14 to 65 d of old were used in a completely randomized design with 4 treatments and 10 replicates in each treatment. Treatments were 1) Control (without Monensin in starter and without propolis in milk), 2) Starter without Monensin and 500ppm soluble propolis powder in milk, 3) Starter without Monensin and 1000ppm soluble propolis powder in milk and 4) Monensin in starter and without propolis in milk. Starter was formulated according to NRC 2001 (21.6% CP and 2.89 ME (mcal/kg)). Calves received 6 L/d of milk replacer (milk protein based, 22% CP, 19% EE) for the 6 wk. Blood sample were collected every 14 d (3hours after feeding), then transferred to laboratory and hematocrit (platelets, hemoglobin, red blood cell, white blood cell, lymphocyte) were measured. Blood samples centrifuged and plasma separated from blood to measure metabolites (total protein, albumin, Immunoglobulin G). Results showed that mean concentration of Platelets (3.06, 4.95, 3.18, 5.63 *10^5/ml) and Lymphocytes (69.50, 72.25, 75.25, 71.75%) were not affected by treatments. Hemoglobin (11.12, 8.8, 10.15, 9.6 g/dl) red blood cell (11.28, 8.07, 10.19, 10.28 *10^6/ml) for treatments 1–4 respectively were not affected by treatments. For white blood cell (50.75, 60.75, 71.50, 52.25 *10^3/ml for treatment 1–4 respectively) there was a tendency to be affected by treatments (P = 0.06). Mean concentration of Total Protein (10.94, 11.31, 11.68, 11.54 g/dl) had a trend to significance (P = 0.09). Albumin (6.13, 5.63, 6.13, 5.66 g/dl) and Immunoglobulin G (1.91, 1.73, 2.00, 1.47(g/dl) for treatment 1–4 respectively) significantly affected by treatments (P < 0.05). It is concluded that 1000 ppm propolis in compare of Monensin has potential to improve immune responses through its effect on the WBC, Albumin and IgG of Holstein female calves.

Key Words: propolis, Holstein female calves, immune responses

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1841 (W300) Effects of maternal plane of nutrition, selenium supply, and physiological stage on digestibility and ruminal fermentation in ewes.
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Objectives were to investigate effects of nutritional plane and Se supply during gestation on digestibility and ruminal fermentation at parturition and early lactation. Primiparous Rambouillet ewes ($n = 84$, age $= 240 \pm 17$ d, BW $= 52.1 \pm 6.2$ kg) were allocated to $2 \times 3 \times 2$ factorial arrangement of treatments. Factors included dietary Se (adequate Se [11.5 µg/kg BW] or high Se [77.0 µg/kg BW]), nutritional plane (60% [restricted], 100% [control], or 140% [high]), and physiological stage at necropsy (parturition or d 20 of lactation). At parturition, lambs were removed from all ewes and 42 ewes ($n = 7$ per treatment) were necropsied. Remaining ewes were transitioned to a common diet, which met lactation requirements, and mechanically milked for 20 d. Three way interactions were not present ($P > 0.10$). As expected, DMI was altered by both nutritional plane and physiological stage. In pregnancy and lactation, DMI increased with plane of nutrition ($P < 0.001$; 500 vs. 755 vs. 1183 and 1173 vs. 1237 vs. 1295 ± 19 g for restricted, control, and high ewes during pregnancy and lactation, respectively). Neither DMI nor total OM digestion were altered by Se supply. Total OM digestion was greater ($P = 0.03$) in restricted compared with high ewes during both gestation (75.8 and 67.0 ± 1.2%, respectively) and lactation (68.4 and 64.8 ± 1.2%, respectively). Both apparent ($P < 0.01$) and true ($P = 0.04$) ruminal OM digestion was greater in restricted (60.7 ± 1.42%) vs. control and high ewes (56.4 and 54.4 ± 1.42%, respectively). Ewes fed high Se during gestation had greater ($P = 0.03$) apparent and true ruminal OM digestion during gestation but were not different at d 20 of lactation. Ruminal acetate proportions were lower ($P = 0.03$) and the ratio of acetate + butyrate over propionate tended ($P = 0.09$) to be greater in high Se vs. adequate Se fed ewes. Ewes fed restricted diets had greater acetate ($P < 0.001$), lower propionate proportions ($P < 0.001$), and lower total VFA concentrations ($P < 0.01$). Ewes at parturition had greater total VFA ($P < 0.001$) than ewes during lactation. These data indicate that maternal plane of nutrition, Se supply, and physiological stage all impact digestion and ruminal fermentation which will influence circulating nutrients available for fetal growth and milk production.

Key Words: digestibility, ewes, selenium

1842 (W301) Effect of reduced energy density of close-up diet on dry matter intake, milk yield and energy balance in multiparous Holstein cows.
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The objective of this study was to determine the effect of reduced energy density of close-up diet on DMI, milk yield and energy balance (EB) in multiparous Holstein cows which were fed for ad libitum intake. Thirty-nine dry cows were blocked and assigned randomly into 1 of 3 energy concentrations (6.8, 6.2, 5.4 MJ of NE_L/kg; 14.0% CP) diets to meet 100% (100NRC; $n = 13$), 90% (90NRC; $n = 13$), 80% (80NRC; $n = 13$) of the NRC (2001) dietary NE_L recommendation, respectively, from 21 d before expected day of calving. After parturition, all cows were fed the same lactation diet to 70 d in milk (DIM). Data were analyzed by SPSS with repeated measures procedure or One-Way ANOVA procedure. The DMI (14.3, 13.6, 12.6 kg/d; $P = 0.009$) and NE_L intake (NEI, 97.1, 83.3, 68.6 MJ/d; $P < 0.001$) prepartum were significantly different for 100NRC, 90NRC and 80NRC groups. In the last 24 h before calving, the 80NRC group consumed 1.3 kg and 0.7 kg more diet (DM) than the 100NRC and 90NRC groups ($P > 0.05$), respectively, but the NEI was very similar among the 3 treatments. During the first 4 wk postpartum, the DMI and NEI for the 80NRC group were numerically greater than those for the 100NRC ($P > 0.05$). The milk yields of 90NRC and 80NRC groups were numerically greater than 100NRC from 1 to 10 wk (36.6, 38.6, 38.7 kg/d; $P > 0.05$), but the 4% fat-corrected milk yields (45.4, 45.7, 45.4 kg/d; $P > 0.05$) were very similar due to the significantly higher milk fat content for 100NRC. The energy consumption for 100NRC, 90NRC and 80NRC were 149.8%, 126.2% and 101.1% of their calculated energy requirements prepartum, and 72.7%, 73.1% and 75.2% during the first 4 wk postpartum, respectively. In conclusion, the low energy density prepartum diet was effective in controlling NEI prepartum, and was beneficial in increasing DMI, whilst alleviating negative EB postpartum.

Key Words: dietary energy density, dry matter intake, milk yield

1843 (W302) Effects of lysolecithin on milk fat synthesis and milk fatty acid profile of cows fed diets differing in fiber and unsaturated fatty acid concentration.
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Thirteen multiparous Holstein cows (> 70 DIM) were used in a crossover design that tested the effect of lysolecithin under diets differing in fermentability and polyunsaturated fatty acid (FA) concentration. Experimental periods were 20 d and

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included two 10 d phases. During phase 1, a standard fiber and low fat diet was fed (32% NDF, no added oil) and during phase 2 a lower NDF higher oil diet was fed (30.5% NDF and 2% oil from whole soybeans and soybean oil). A 14 d washout period between experimental periods allowed milk fat recovery. Treatments were control and lysolecithin (10 g/d/cow of LYSOFORTE[brand], Kemin Industries, Des Moines, IA) extended in a ground corn carrier. Milk was sampled on d 0, 5, and 10 of each phase for determination of fat and protein concentration and FA profile. There was no effect of treatment or treatment by time interaction for DMI or milk yield, however on d 5 of phase 2 lysolecithin tended to decrease DMI ($P < 0.10$). There was a treatment by time interaction for milk fat concentration and yield ($P < 0.05$). Milk fat concentration was higher in lysolecithin on d 5 of phase 1, but decreased progressively in both treatments during phase 2. Milk fat yield was not different among treatments during phase 1, but was lower in lysolecithin on d 5 and tended to be lower on d 10 of phase 2 ($P < 0.10$). There was no effect of treatment or treatment by time interactions for milk protein concentration or yield. No treatment by time interactions were detected for the concentrations of milk de novo (< 16 C) or preformed (> 16 C) FA. Concentrations of de novo FA decreased, but preformed FA increased during phase 2 ($P < 0.001$) and no treatment differences were detected at any time point. There was an effect of time, but no treatment by time interactions for milk *trans* FA isomers ($P < 0.05$). Briefly, *trans* 11 C18:1 and *cis*-9, *trans*-11 conjugated linoleic acid (CLA) decreased progressively during phase 2 as *trans* 10 C18:1 and *trans*-10, *cis*-12 CLA increased progressively. Lysolecithin increased milk fat concentration when feeding a higher fiber and lower fat diet, but decreased milk fat yield when feeding a lower fiber and higher fat diet, although biohydrogenation pathways were not modified.

Key Words: dairy cows, lysolecithin, milk fat depression

1844 (W303) Effects of fescue toxicosis induced by endophyte-infected tall fescue seed on forestomach epithelial gene expression in Angus steers.

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A previous report demonstrated that steers exposed to an endophyte-infected tall fescue seed extract had altered rumen epithelial blood flow and decreased ruminal flux of VFA. Thus, this study was conducted to determine whether there are differences in gene expression related to VFA absorption between steers dosed with endophyte-infected (E+; 4.45 mg ergovaline/kg) or endophyte-free (E-) tall fescue seed. Twelve ruminally cannulated Angus steers (BW = 547 ± 9 kg) were stratified based on BW and randomly allocated to 6 blocks. The steers were fed alfalfa cubes at 1.5 x NE_m and dosed (1

kg/d) with ground tall fescue seed via rumen cannula once daily for 21 d. On d 22, the steers were slaughtered and tissue samples were immediately collected from rumen, reticulum, omasum, and abomasum. Samples were rinsed extensively with ice-cold physiological saline to remove residual feed and contents before separating epithelia from the underlying tissue. Thereafter, samples of epithelial tissue (1 g) were immediately homogenized with TRI-reagent. The expression levels of monocarboxylate transporter 1, 2, and 4 (MCT1, MCT2, and MCT4, respectively), sodium hydrogen exchanger 1, 2, and 3 (NHE1, NHE2, and NHE3, respectively), putative anion transporter 1 (PAT1), downregulated in adenoma (DRA), anion exchanger 2 (AE2), sodium bicarbonate cotransporter 1 (NBC1), 3-hydroxy 3-methylglutaryl coenzyme A synthase 2 (HMGCS2), and sodium potassium ATPase pump 1 (ATP1) were measured using SYBR-Green and abundances were quantified by qPCR using glyceraldehyde-3-phosphate dehydrogenase as the control gene. The levels of MCT1 and MCT4 expression were lower ($P < 0.05$) in the rumen tissue of steers dosed with E+ seed, whereas MCT2 was not different. The expression of NHE2 was lower ($P < 0.05$) for E+ steers, whereas NHE1 and NHE3 were not affected by seed in the rumen epithelium. The levels of DRA and AE2 expression were lower ($P < 0.05$) for E+ steers in the rumen epithelium, whereas PAT1, NBC1, HMGCS2 and ATP1 were not affected by seed treatment. Expression of these genes in reticulum, omasum, and abomasum epithelia, were not affected ($P > 0.05$) by seed treatment. These data indicate that endophyte-infected tall fescue seed may contribute to depression of ruminal VFA absorption in a dissociated state (pH > 5.8) by the depression of MCT1 and MCT4 in the rumen associated with NHE2, DRA and AE2. Consequently, this may contribute to decreased gain associated with fescue toxicosis in cattle.

Key Words: VFA transporter, gene expression, tall fescue

1845 (W304) Replacement of soybean meal by high energy cottonseed meal in diets of dairy cows: milk production and ovarian follicular dynamics.

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Supply of high biological value protein is key to reproductive and productive performance, however the cost is high. The aim of this study was to evaluate replacement of soybean meal by high energy cottonseed meal like protein source in dairy cows diets on productive and reproductive parameters. Five Girolanda cows with average body weight of 530 kg, distributed in 5x5 Latin square were used (5 levels of substitution of soybean meal by high energy cottonseed meal: 0% (FA0), 15% (FA15), 30% (FA30), 45% (FA40) and 60% (FA60) and 5 periods). Each period lasted 18 d. Milk production (MP) and

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Table 1845. Milk production (MP, kg/day), body score condition (BSC, 1–5), number of recruited follicles (NRF), dominant follicle diameter (DFD, mm), and corpus luteum diameter (CLD, mm) of Girolanda cows feeding with diets with substitution of soybean meal by high energy cottonseed meal

Treatment	MP	BSC	NFR	FMD	CLD
FA0	14.4 ± 0.2[a]	2.9 ± 0.03	25.69 ± 1.22	15.10 ± 0.39	20.60 ± 0.7
FA15	12.4 ± 04[c]	2.9 ± 0.07	26.08 ± 1.31	17.90 ± 0.64	21.15 ± 0.7
FA30	14.6 ± 03[a]	2.9 ± 0.05	26.83 ± 1.12	16.90 ± 0.33	21.85 ± 0.6
FA40	14.5 ± 0.2[a]	2.9 ± 0.03	25.89 ± 1.28	14.90 ± 0.34	21.10 ± 0.9
FA60	13.7 ± 04[b]	2.9 ± 0.07	26.08 ± 1.01	18.30 ± 0.32	20.40 ± 1.0
P	< 0.0001	0.3002	0.8133	0.1039	0.6781

FA: diet without substitution; FA15 replacement 15% of soybean meal by high energy cottonseed meal; FA30 replacement 30% of soybean meal by high energy cottonseed meal; FA40 replacement 40% of soybean meal by high energy cottonseed meal; FA60: replacement 60% of soybean meal by high energy cottonseed meal; *P*: significance level
A, b, c…different letters in same column indicate differences by Tukey test

body score condition (BSC) were evaluated on the 18th day and ovarian evaluations (number of recruited follicles (NRF), dominant follicle diameter (DFD), and corpus luteum diameter (CLD)) were conducted from 7 to 18th day of supplementation by trans-rectal ultrasonography. Data were analyzed by Tukey test with 5%of significance level. Replacement of protein source (replacement of soybean meal by high energy cottonseed meal) do not influenced (*P* > 0.05) body score condition, number of recruited follicles, dominant follicle diameter, and corpus luteum diameter. However, could reduce milk production in higher and lower replacements levels (Table 1845). The replacement of soybean meal by high energy cottonseed meal as protein source at level of 30 or 40% is feasible because not alters reproductive and productive performance, and promotes reduced diet cost.

Key Words: protein sources, follicles, girolando

1846 (W305) Supplements with chelated mineral for cows Nellore: Growth performance, oocyte quality and oxidative stress. T. D. P. Trindade, L. K. Hatamoto-Zervoudakis*, C. Pasa, J. T. Zervoudakis, P. P. Tsuneda, F. M. Wingert and A. L. Cândida de Resende Fraga, *Federal University of Mato Grosso, Cuiaba, Brazil*

Nutrition has a major influence on reproductive performance (expression of estrus, follicular development, quality of gametes, ovulation rate, uterine environment, embryo development, maintenance of pregnancy, etc.). Chelated minerals may provided potential benefits to reproduction, enhancing mineral absorption and retention in animal tissues, improved functioning of dependent enzyme systems of minerals (antioxidant systems), best performance (higher daily weight gain, feed conversion, lower mortality, greater production of meat, eggs and milk). The objective of this study was to evaluated oocyte quality and production traits in Nelore cows grazing supplemented with copper, zinc and selenium in chelated form. 24 multiparous Nelore cows were used, with 36 mo of average age, 395 kg of body weight and body condition score of 4.8. Animals were divided into 2 groups: control group (CG, animals supplemented with inorganic mineral) and Supplemented Group (SG, animals supplemented with zinc, copper and selenium in chelated form). Each group was raised in a paddock of *Brachiaria brizantha* cv. Marandu, receiving 1 kg of supplement/animal/day. Every 2 wk the animals were weighed and body condition score (BCS) was evaluated. During experimental period (99 d), two aspirations (59 and 99 d of supplementation) were performed. Oocytes were assessed as viable and non-viable and follicular fluid levels of oxidative stress was measured by TBARS concentration. The experiment was a completely randomized design and data analyzed by ANOVA with a significance level of 5%. Chelated minerals supplementation did not affect (*P* > 0.05) total number of oocytes retrieved (*P* = 0.5028), numbers of viable oocytes (*P* = 0.1449), and body weight (*P* = 0.3587). The use of chelated minerals provided greater BCS at the end of experiment (*P* = 0.0500, 5.27 ± 0.14 versus 4.83 ± 0.17) and higher gain in body condition score (*P* = 0.0178, 0.82 ± 0.18 versus. 0.25 ± 0.13). Animals supplemented with chelated minerals showed less oxidative stress in follicular fluid (0.05 ± 0.01 versus 0.09 ± 0.02, *P* = 0.047). Oral supplementation with minerals zinc, copper and selenium in chelated form at used levels, improved body condition score and reduced oxidative stress in follicular fluid of Nelore cows at pasture during dry- water transition.

Key Words: Body score condition, chelate, oxidative stress

1847 (W306) Contribution of a chelated trace mineral supplement as a methionine source for dairy cows. M. O. Caldeira[*1], R. O. Rodrigues[1], M. R. Waldron[1,2] and G. I. Zanton[3], *[1]University of Missouri, Columbia, [2]Nutrition Professionals, Inc., Chilton, WI, [3]Novus International, Inc., St. Charles, MO*

This experiment sought to determine whether the methionine contained in a trace mineral supplement made a meaningful contribution toward meeting the methionine requirement of the dairy cow. Four multiparous ruminally-cannulated lactating Holstein dairy cows were used in 4 × 4 Latin square design with 7-d periods. Treatments were administered at a rate of 0.08 g of 2-hydroxy-4-methylthio-butanoic acid (HMTBa)/kg of BW on d 0 of each experimental period: 1) HMTBa chelated to Zn, 80% HMTBa, dosed ruminally (MIN; Minitrex Zn, Novus International, St. Charles, MO, USA), 2) Ca-salt of HMTBa,

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84% HMTBa, dosed ruminally (MHA; MHA feed supplement, Novus International), 3) HMTBa free acid, 88% HMTBa, dosed ruminally (ALR; Alimet, Novus International), and 4) HMTBa free acid, 88% HMTBa, dosed post-ruminally (APR; Alimet Novus International). Approximately 5 kg of rumen mat contents from each animal were removed through the cannula, mixed with the appropriate treatment dose, and replaced in the rumen. For post-ruminal treatment, a 50cc syringe was placed in the omasal canal, and contents were expelled into the abomasum; all other animals received a post-ruminal infusion of water. Blood samples were collected regularly through each experimental period. Feed was restricted for 30 min before treatment administration, following which, animals were fed for ad libitum consumption. Data were analyzed using MIXED procedure of SAS, using averaged pre-infusion measurements as covariates. Plasma concentrations of methionine did not differ between MIN, MHA, and ALR treatments; however, APR resulted in a greater ($P < 0.001$) concentration of plasma methionine compared with other treatments. A treatment x time interaction ($P < 0.001$) was observed for plasma methionine, in which APR increased at 1.5 h after infusion, reaching peak at 3 h ($P < 0.001$), and leveling with other treatments at 12 h ($P > 0.10$). Greater plasma concentrations of HMTBa ($P < 0.001$) were found in APR than in MIN, MHA and ALR; however, these did not differ between each other ($P > 0.10$). There was a treatment x time interaction ($P < 0.001$) for HMTBa; APR peaked at 1.5 h after infusion ($P < 0.001$), declined sharply until 9 h when lower concentrations of HMTBa were observed compared with other treatments ($P \leq 0.05$). After 12 h, HMTBa treatments no longer differed ($P > 0.10$). In conclusion, the availability of methionine in plasma did not differ between treatments administered ruminally; however, significant increases were observed when treatments were administered post-ruminally. These results suggest that MIN may be used to contribute toward the methionine requirement for dairy cows.

Key Words: HMTBa, rumen, supplementation

1848 (W307) Effect of the supplementation of plant extracts, vitamins and their associations on feedlot performance and carcass traits of Nellore cattle.
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Fifty-six Nellore (*Bos indicus*) young bulls of +360 kg initial weight and +20 mo of age were used to evaluate the effect of the supplementation of vegetable extract, A, D and E vitamins and their associations on the feedlot performance (finishing phase) and carcass characteristics. Animals were maintained in individual pens for 105 d (21 and 84 d, for adaptation and trial period, respectively). Animals were individually weighed, and blocked by initial body weight. Pens within a block were randomly assigned to one of four treatments: (C) Control diet including A, D and E vitamin; (V) Control diet plus 50% A, D and E vitamin; (E) Diet including 0.14% (DM basis) of plant extracts; (A) Diet with association of these two additives (50% A, D and E vitamin + 0.14% (DM basis) of plant extract). The treatments provided the same diet for all animals (85 and 15%, for concentrate and forage, respectively), varying only the inclusion of the different additives. Further, all treatments received monensin (30 mg/kg of concentrate). Feed offered was monitored daily as well as feed refusals were collected and weighed to determine daily dry matter intake (DMI) and feed efficiency (F:G). Animals were weighed every 28 d after 16 h feed withdrawal for calculating average daily gain (ADG). No effects of treatments ($P > 0.10$) were observed for DMI (9.69, 10.28, 10.03, 9.98 kg/day for diets C, V, E, A, respectively), ADG (1.60, 1.66, 1.64, 1.64 kg/day for diets C, V, E, A, respectively), and F:G (0.17, 0.16, 0.16, 0.16 for diets C, V, E, A, respectively). Back fat thickness, LM area, hot carcass weight, cold carcass weight, and cooling losses were not affected by treatments ($P > 0.10$). In conclusion, supplementation of plant extracts, vitamins and their association did not produces additional benefits on the feedlot performance or carcass traits of Nellore cattle. Supported by CAPES/NUTRON.

Key Words: plant extract, feedlot performance, carcass, Nellore

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1849 (W308) Body condition score assessment in a grazing Jersey herd in Costa Rica.
A. Saborío-Montero* and J. M. Sánchez, *Centro de Investigaciones en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San José, Costa Rica*

The aim of this research was to carry out a body condition score (BCS) observational study in a commercial grazing Jersey herd in Costa Rica (9°55' N, 83°51' W, 2350 m of altitude). The study comprised 5864 BCS records from 122 cows (29 primiparous and 93 multiparous) over a 16 mo period. Cows were scored weekly by the same person from ninth wk prepartum to 43th wk postpartum. The 1 to 5 points scale was used (1 = emaciated, 5 = obese). Animals feeding practices were based on intensive grazing of 30 d regrowth kikuyu (*Kikuyuocloa clandestina*) (14.8% DM, 23.4% CP, 54.0% NDF, 25.7% ADF, 1.4 Mcal/kg NE_L (3x), 2.2% Lignin) and supplementation of a balanced concentrate according to physiological stage. During the close up period animals were fed 4 kg of concentrate daily (14% CP, 1.7 Mcal/kg NE_L(1x), 35% Starch, 0.2% Ca), and during lactation 1 kg of concentrate (18.6% CP, 1.9 Mcal/kg

NE$_L$, 48% Starch, 1.0% Ca)/2.5 to 3 kg of milk. Primiparous and multiparous cows BCS at calving was 4 points (95% CI: 3.80–4.22 points) and 3.8 points (95% CI: 3.71–3.94 points), respectively. BCS nadir after calving differed ($P < 0.05$) between primiparous (3.1 points, 95% CI: 2.97–3.23 points) and multiparous cows (2.9 points, 95% CI: 2.76–2.96 points). When stratifying BCS at calving into values ≤ 3.25, 3.50 to 4.00 and ≥ 4.25 points, differences ($P < 0.01$) were found in nadir extreme values within primiparous or multiparous groups of cows. Values were 2.63, 2.94 and 3.29 points for primiparous and 2.27, 2.78 and 3.20 points for multiparous, respectively. Likewise, the average BCS change differed ($P < 0.01$) between extreme values in the same group, showing -0.25, -0.81 and -1.19 points for primiparous and -0.71, -0.93 and -1.21 points for multiparous cows in the same order. BCS at calving in primiparous cows was correlated with nadir ($r = 0.65$, $P < 0.001$) and BCS change ($r = -0.76$, $P < 0.001$). Similarly, BCS at calving in multiparous cows was correlated with nadir ($r = 0.62$, $P < 0.001$) and BCS change ($r = -0.55$, $P < 0.001$). Cows that calved with higher BCS, lost more BCS postcalving, but remained at a greater BCS at nadir and the whole lactation. Results suggest that BCS at calving could be used as a partial indicator of BCS nadir and BCS change from calving to nadir; which has important implications on production and fertility of cows. However more research should be done to extend these findings to wider populations.

Key Words: BCS, Body condition score, grazing Jersey cows

1850 (W309) Intake and nutrient digestibility of growing Nellore heifers and steers fed two levels of calcium and phosphorus. L. F. Costa e Silva[*1], T. E. Engle[1], P. P. Rotta[1], S. C. Valadares Filho[2], R. D. Valadares[3], F. A. S. Silva[3] and E. C. Martins[3], *[1]Colorado State University, Fort Collins, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal De Vicosa, Vicosa, Brazil.*

An experiment was conducted to evaluate intake and nutrient digestibility of Nellore heifers and steers fed two levels of calcium and phosphorus. Thirty two Nellore heifers and eighteen Nellore steers were used. Four animals from each gender were used as baseline reference animals and slaughtered at the beginning of the experiment. Four animals from each gender were fed at maintenance (MAIN) and 10 steers and 24 heifers were assigned to the ad libitum (ADLIB) group. The ADLIB heifers were further divided into four groups. Treatments were: 1) Ca and P fed at requirements (CaPR) with a 50:50 of roughage:concentrate (R:C) diet; 2) CaPR with at 70:30 R:C diet; 3) 43% of the Ca and 80% of the P requirement (CaPL) with a 50:50 R:C diet; and 4) CaPL with a 70:30 R:C diet. The ADLIB steers in this experiment were fed CaPR. Half of the steers and the heifers were slaughtered at d 50 and the other

animals were slaughtered a d 100 of the feeding period while all MAIN animals were slaughtered at d 100. Total feces and urine were collected from all animals 72 h before slaughter. Dry matter digestibility and apparent absorption and retention of Ca and P were similar across Ca and P treatments. Final body weight and, consequently, average daily gain was higher ($P < 0.05$) in heifers receiving the high concentrate diet compared to the low concentrate diet while the levels of Ca and P did not affected ($P > 0.05$) the performance. Under the conditions of this experiment, the level of dietary Ca and P can be reduced in the diet and not impact intake, digestibility or performance of growing Nellore heifers and steers.

Key Words: minerals, sugarcane, performance

1851 (W310) Ration composition in Wisconsin dairy herds: Factors affecting fertility. A. H. Souza[*1], P. D. Carvalho[2], C. M. Drake[3], R. D. Shaver[2] and M. C. Wiltbank[2], *[1]University of California Cooperative Extension, Tulare, [2]University of Wisconsin, Madison, [3]University of California, Davis*

The aim of this study was to determine whether composition of total mixed ration (TMR) diets influence reproductive efficiency of dairy farms in Wisconsin. Dairy producers and nutrition consultants from all herds agreed to provide a single snapshot of their complete TMR-ration information used in the post-fresh and high-milk production pens. The nutritional information included all ingredients and nutrient composition of all mixes used, as well as a herd backup that contained accurate production, health and reproductive records with archive files with previous 12 mo. The final database included data from 49 free-stall Holstein-dairy herds in WI (DC305 $n = 44$ and PCDart $n = 5$). Size of herds enrolled in the data collection varied from 143 to 2717 lactating cows (average 719.6 ± 77.2), were milked 2 ($n = 6$) or 3 ($n = 43$) times per day, with average production per cow of 39.0 ± 1.3 Kg/day, and average DMI of 25.1 ± 0.5 Kg/day. Records from PCDart herds were absorbed into DC305 and calculations of reproductive parameters such as conception rate at first AI (CR1AI), overall conception rate (CR), and interval from calving to conception (ICC) were performed with the same standardized command in DC305 to summarize performance records from the previous 12 mo. Statistical analyses were performed with the proc MEANS, proc CORR, and proc MIXED of SAS (version 9.3). There was a great variation in diet composition, with CP varying from 16.0 to 18.7%, RDP from 9.1 to 12.3%, NDF from 24.9 to 35.1%, NFC from 31.7 to 46.6%, Starch 20.1 to 30.8%, and Fat from 3.1 to 6.7%. Milk production level was not associated with CR1AI, CR, or ICC ($P > 0.10$). However, greater DMI tended to be associated with lower CR1AI ($r = -0.25$, $P = 0.10$) and lower CR ($r = -0.25$, $P = 0.11$). Diet CP and RDP did not seem to affect CR1AI, CR, or ICC ($P > 0.10$). Similarly, Fat content did not influenced fertility parameters ($P > 0.10$). Interestingly,

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percentage of NDF was positively associated with CR1AI (r = 0.36, P = 0.01). In addition, greater energy content in the diet measured as NFC, NFC-intake, or Starch were all detrimental to CR1AI (NFC: r = -0.54, P < 0.01; NFCi: r = -0.42, P < 0.01; Starch: r = -0.37, P = 0.03), and CR (NFC: r = -0.51, P < 0.01; NFCi: r = -0.44, P < 0.01; Starch: r = -0.21, P = 0.20). In conclusion, although diets should be balanced to meet milk production requirements, maximizing digestible fiber and lowering highly fermentable energy contents should improve fertility of high producing cows.

Key Words: dairy cows, diet composition, fertility

1852 (W311) Milk quality from dairy farms divided in five levels of production. L. L. Cardoso, M. I. Marcondes*, G. A. T. Ferreira, V. L. N. Brandao, A. S. Trece and A. S. Trece, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*

This study aimed to characterize the physicochemical properties of milk from different production scales. A databank with 21,917 analyses, from January 2005 to December 2012, of 409 producers was used. Milk samples were collected twice a month and placed directly into milk cooling tanks. The properties were divided according to monthly average of daily milk yield in the following levels: 10 to 100 L of milk per day (N = 7858); 100 to 200 L (N = 6494), 200 to 500 L (N = 5085), 500 to 1000 L (N = 1725), 1000 to 5000 L (N = 755). Years and months were analyzed in a completely randomized split-plot design repeated in a time scheme, with years as plots and months as sub-plots. Within the reported period, 11.32% of the samples were from producers who account for 44.25% of production. Moreover, the great majority of the samples (88.68%) are from producers representing 55.75% of the supplied milk. An urgent need of improvement in management of total bacterial count (TBC) was observed throughout the year, and only August and September presented results below 100,000 CFU/mL. Somatic cell count (SCC), decreases in dry period, where June is the month with the lowest rate, and there is an increase in this SCC in the rainy season. This characterization is important so the industry can establish a protocol for mastitis control and mammary gland health throughout the year. No significant difference was found when correlating levels of production and SCC. However, TBC was affected by levels of production (P < 0.05), which mean that greater producers, in general, have a better management of this item. Protein was not affected by production levels (P > 0.05), and it increases in early dry period, with a subsequent decrease until the beginning of the rainy season. For small producers (up to 500 L, including the first three levels) June had the highest fat production. The data obtained in the study shows that dairy farming in the region is predominantly developed in small properties. However, higher volumes are produced by fewer producers. The quality of milk produced deserves attention from the entire production chain of milk, and it still presents problems as high TBC, high SCC and low total solids, requiring more efficient management techniques.

Key Words: fat, milk, protein

1853 (W312) MasterGraze silage for growing Holstein heifers. D. L. Gadeken[*1], K. Koone[2], S. harris[2], M. kirk[3] and D. Casper[1], *[1]South Dakota State University, Brookings, [2]Masters Choice, Anna, IL, [3]masters Choice, Anna, IL*

MasterGraze (MG) is a new corn silage hybrid that is a grazing corn. The MasterGraze hybrid will develop grain, but harvest is recommended before grain development which results in a plant that is high in sugar and crude protein (CP). Thus, the unique nutritional attributes of MG makes it an attractive forage source for dairy heifers. Twelve growing Holstein heifers weighing 220.1 ± 28.8 kg were assigned to 1 of 2 treatments varying in type of corn silage. The Control (C) ration consisted of conventional corn silage (Dekalb) and the MG ration consisted of MG corn silage. Corn silages were fed at 38.6% (DM basis) with 19.6% alfalfa hay and 41.8% grain mix. The experimental grain mixes consisted of ground shelled corn, soybean meal, urea, minerals and vitamins that were formulated for each corn silage's nutritional profile. The rations were formulated to be 16% CP (DM basis) and meet or exceed all nutrient requirements for a growing Holstein heifer. Due to a limited amount of MG silage, the experiment was conducted for 5 wk. Animals were trained and fed using the Calan feeding door system to determine daily DM intake. All heifers were fed the C corn silage during the training period and measurements were taken for 1 wk to be used as a covariate. Covariate adjusted average body weights (251.5 and 242.7 kg for C and MG, respectively) were similar (P < 0.24) for heifers fed both corn silages. Average dairy gains (1.22 and 1.16 kg/d) were similar for heifers fed both corn silages. Dry matter intakes were similar but, numerically lower for heifers fed MG (6.49 and 4.99 kg/d). Feed conversions were similar (0.23 and 0.34 kg gain/kg feed), but numerically greater for heifers fed MG. The limited animal numbers in this study prevented finding significant differences between treatments, however, the feed costs savings are approximately $0.09/heifer/d feeding growing dairy heifers MG corn silage given the same performance based on ration formulation. Given the numerical differences in DM intakes and feed conversions, the cost advantages are greater than $0.09/heifer/d with MG.

Key Words: vorn dilage, fairy heifers, MasterGraze

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1854 (W313) Transcriptome profiling of milk in dairy cows fed linseed. A. Siurana*, D. Gallardo and S. Calsamiglia, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra 08193, Spain*

Feeding linseed to dairy cows results in milk fat depression (MFD), but there is a wide range of sensitivity, with some cows not showing any reduction in milk fat, while others having a strong MFD. The objective of this study was to compare the mRNA expression of transcripts expressed in pelleted milk cells in cows resistant or sensitive to MFD. Four cows were selected from a dairy farm after a switch from a control diet to a linseed-rich diet: two were resistant to MFD and had high milk fat content before (4.06%) and after the change (4.36%) (R-MFD); and two were sensitive to MFD and milk fat content decreased after the change into the linseed diet (3.56 to 2.54%, S-MFD). Fresh milk samples were collected from each cow the week before and 2 wk after the diet change, and transcriptional profiling of mRNA was analyzed by Illumina RNA-sequencing technology. A total of 24,880 transcripts were tested. When S-MFD were fed linseed, 54 transcripts increased mRNA expression by 3 to 23 fold, and 9 transcripts decreased mRNA expression by 3 to fivefold compared with the same cows fed the control diet. When R-MFD cows were fed linseed, 306 transcripts increased mRNA expression by 2 to 12 fold and 544 transcripts decreased mRNA expression by 2 to ninefold compared with the same cows fed the control diet. The largest differences were observed between R-MFD and S-MFD cows when fed linseed, where the R-MFD cows increased mRNA expression of 668 transcripts by 2 to 20 fold and decreased mRNA expression of 1161 transcripts by 2 to 81 fold compared with S-MFD cows. When cows were fed the control diet, the R-MFD cows increased mRNA expression of 156 transcripts by 2 to 23 fold and decreased mRNA expression of 740 transcripts by 2 to 42 fold compared with S-MFD cows. When R-MFD cows were compared with S-MFD cows regardless of the diet fed, 91 mRNA transcripts were expressed more, and 460 transcripts were expressed less in R-MFD compared with S-MFD cows. As an example, the gene of the fatty acid binding protein 7 increased mRNA expression by 19 (in the linseed diet) and 20 (in the control) fold in R-MFD compared with S-MFD cows. This preliminary study show the potential of Illumina RNA-sequencing technique to find new candidate genes implicated in MFD.

Key Words: RNA-sequencing, milk fat depression, linseed

1855 (W314) Feeding diets inducing milk fat depression to heat-stressed dairy cows on performance, energy partitioning, and antioxidant status. S. Kargar[1], M. Khorvash[1], G. R. Ghorbani[1] and D. J. Schingoethe*[2], *[1]Isfahan University of Technology, Isfahan, Iran, [2]South Dakota State University, Brookings, SD*

Effects of grain source and dietary oil supplement on production performance, energy balance, metabolic heat production, and markers of liver function of heat-stressed lactating dairy cows were evaluated using eight multiparous Holstein cows (77.0 d in milk) in a duplicated 4×4 Latin square design with a 2×2 factorial arrangement of treatments. Experimental diets contained either ground barley or ground corn supplemented with either fish oil or soybean oil at 2% of dietary dry matter. Rectal temperature showed no change (averaging 38.9°C) regardless of diet but respiration rate tended ($P = 0.08$) to be decrease in cows fed fish oil as compared to cows fed soybean oil (58.4 vs. 62.5 breath/min). Dry matter intake tended ($P = 0.09$) to be greater for barley- vs. corn-based diets (23.2 vs. 22.3 kg/d), but was reduced for the fish oil compared to soybean oil supplemented diets (21.1 vs. 24.3 kg/d; $P < 0.001$) which was negatively correlated with plasma concentrations of alkaline phosphatase ($r = -0.45$; $P \leq 0.01$) and malondialdehyde ($r = -0.26$; $P < 0.15$). Actual milk yield and energy-corrected milk yield were not affected by grain source whereas feeding fish oil decreased milk yield as compared to soybean oil. Due to lesser dry matter intake, metabolic heat production was decreased in cows fed fish oil relative to cows fed soybean oil. Although feeding fish oil vs. soybean oil reduced net energy for both maintenance and lactation, net energy balance remained unchanged across treatments. However, back fat thickness positively changed (+4.0 mm) in cows fed corn- but not barley-based diets that were supplemented with fish oil vs. soybean oil ($P = 0.10$). There was an interaction between dietary grain source and oil supplement on in vitro indicators of plasma lipoperoxidation including basal and maximum conjugated dienes and calculated area under the curve which were greater in corn-based diets supplemented with fish oil vs. soybean oil. In vivo plasma lipoperoxidation estimated by the plasma level of the major lipoperoxidation product (malondialdehyde) was greater in cows fed fish oil vs. soybean oil which substantiated increased susceptibility of plasma lipoperoxidation in respective cows. Overall, results from current experiment suggest that in cows fed diets supplemented with soybean- vs. fish-oil biosynthesis in the mammary gland was prioritized over anabolism and oxidation in peripheral adipose and muscle tissues regardless of type of grain used.

Key Words: Milk fat depression, Heat stress, Dairy cow

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1856 (W315) Altering ewe nutrition in late gestation; the impact on lamb performance. F. McGovern[*1], F. Campion[1], T. Sweeney[2], S. Fair[3], S. Lott[2] and T. M. Boland[1], *[1]School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, [2]College of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland, [3]Department of Life Sciences, University of Limerick, Limerick, Ireland*

Exposing the fetus to adverse conditions in-utero may result in developmental adaptations to the postnatal, structural and physiological growth of the animal. Maternal nutritional status is one of the primary extrinsic factors, contributing to the programming of fetal nutrient availability and nutrient partitioning throughout gestation. Altering the level of nutrition received by the ewe has been shown to affect fetal growth, influencing birth weight, postnatal growth and metabolism, and reproductive function. The objective of this study was to examine the effects of offering ewes 80% (R), 100% (M), or 120% (E) of recommended metabolisable energy (ME) requirements from d 105 of gestation to parturition on subsequent ewe and lamb performance. In a randomized complete block design study, sixty twin bearing ewes were allocated to one of three dietary treatments (n = 20). Energy requirements were calculated individually for each ewe and amended according to specific treatment allocation. Ewe liveweight and body condition score (BCS) were recorded throughout the study. Within 1 h of birth, the birth weight, lambing difficulty and skeletal measurements were recorded from all lambs. Ewes were hand milked at 1, 10, and 18 h post-partum and lamb colostrum intake recorded. Lamb live weight was recorded intermittently from birth to slaughter and subsequent average daily gain (ADG) calculated. Restricting the metabolisable energy offered (R) to the ewe in late gestation resulted in a decline in ewe body weight ($P < 0.05$) and BCS ($P < 0.01$) at 24 h post-partum when compared to ewes offered the excess energy diet (E). Combined litter weight, colostrum yield at 1 h post-partum and total yield up to 18 h post-partum were greater for ewes offered the E diet than either of the other treatment groups ($P < 0.01$). While there was no difference in individual lamb birth weight ($P > 0.05$), lambs born to ewes offered the R diet had a lower ADG ($P < 0.01$) up to 21 d of age and remained lighter ($P < 0.05$) than those born to ewes offered the E diet up to weaning (d 98 post-partum). In conclusion, offering ewes a restricted level of ME for the final 6 wk of gestation negatively impacted ewe performance to parturition and compromised lamb growth to weaning.

Key Words: fetal programming, late pregnancy nutrition, lamb performance

1857 (W316) A sensory additive alters the eating behavior of dry dairy cows. C. Iglesias[1], F. Bargo[*2], A. Mereu[2], I. Ipharraguerre[2] and A. Bach[1,3], *[1]IRTA, Barcelona, Spain, [2]Lucta S.A., Barcelona, Spain, [3]ICREA, Barcelona, Spain*

Six Holstein dry cows were used to evaluate the effect of a sensory additive (ProEfficient, Lucta S.A.) on eating behavior in a complete randomized design. Cows divided into 2 pens were randomly assigned to 2 treatments: control TMR or the same TMR supplemented with ProEfficient (PE) at a dose of 15 g/cow/d. The TMR (73:27 concentrate: forage; 14.8% CP, 47.0% NDF, 1.32 Mcal NE_L/kg) was formulated to provide the nutrient requirements of dry cows following NRC (2001) recommendations. Cows were fed ad libitum through 4 automatic feeders mounted on scales within each pen. Feed consumption and feeding bouts were recorded automatically. Data were analyzed with a mixed-effects model with repeated measures using the PROC MIXED procedure of SAS (1999) with cow as a random effect and treatment, time, and their 2-way interaction as fixed effects. Although DM intake was not affected ($P > 0.05$) by treatments (11.4 kg/d ± 0.33 SE), cows receiving PE reduced ($P < 0.05$) the time dedicated to eat (119 vs. 149 min/d ± SE 7.60) whereas increased ($P < 0.05$) the eating rate (106.4 vs. 85.3 g/min ± 5.52 SE) compared with the control cows. Neither number of meals (4.3 ± 0.75 SE) nor meal size (2.66 kg/meal ± 0.19 SE) differed ($P > 0.05$) between treatments. Feeding a sensory additive increased eating rate without affecting total dry matter intake of dry cows.

Key Words: sensory additive, eating time, eating rate

1858 (W317) Effects of restricted versus conventional dietary adaptation over periods of 6, 9, and 14 d on blood lipopolysaccharide binding-protein concentration of feedlot cattle. D. V. Vicari[*1], A. Perdigao[2], L. L. Cursino[1], R. S. Barducci[2], M. D. Arrigoni[2] and D. D. Millen[3], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]São Paulo State Foundation (FAPESP), São Paulo, Brazil*

Two studies were conducted to determine the 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 six, nine and 14 d on blood lipopolysaccharide binding-protein (LBP) concentration of Nellore cattle. The first study was designed as a completely randomized block with a 2x2 factorial arrangement, replicated six times, in which 120 26-months 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 or 14-d and REST for 9-d or 14-d. The second study had the same design and characteristics just described, in which 120 22-months old yearling Nellore bulls

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(352.03 ± 19.61 kg) were fed according to the treatments: STEP for 6-d or 9-d and REST for 6-d or 9-d. In each study, 48 animals (two per pen) were randomly chosen for blood collection, which was performed at end of the adaptation period and on Day 21 of the studies. Blood samples were collected from the jugular vein, and blood LBP concentration, expressed as ng·mL^{-1}, was determined by using a commercial ELISA kit. For the first study, a significant ($P = 0.01$) period main effect was observed, in which animals on Day 21 presented greater concentrations of LBP than those at end of the adaptation period (128.1 vs. 56.7). A significant ($P = 0.01$) interaction was observed between protocols and duration of adaptation, where animals in REST protocol of 14-d had greater blood LBP concentration (157.2) than cattle in STEP protocol of 9-d (91.0), which had greater blood LBP concentrations than animals in REST protocol of 9-d (67.3) and STEP protocol of 14-d (54.2). In the second study, no significant ($P > 0.10$) protocols and duration of adaptation main effects were observed. However, a significant ($P = 0.01$) period main effect was observed, in which animals on Day 21 of the study present greater concentrations of blood LBP when compared to those at the end of the adaptation period (615.3 vs. 136.6). As the normal cattle blood LBP range varies from 50 to 500 ng·mL^{-1}, adapting feedlot Nellore cattle in 14-d, regardless of the protocol, seems to be the most feasible option.

Key Words: acidosis, endotoxin, Nellore

1859 (W318) The effects of OmniGen-AF on serum metabolites, calcium concentrations and hormones of the adrenal axis during heat stress in lactating Holstein cows. L. W. Hall[*1], F. A. Villar[1], J. D. Allen[2], J. D. Chapman[3], N. M. Long[4] and R. J. Collier[1], [1]*The University of Arizona, Tucson,* [2]*Northwest Missouri State, Maryville,* [3]*Prince Agri Products, Inc., Quincy, IL,* [4]*Clemson University, Clemson, SC*

The objective was to evaluate physiological, behavioral and hormonal changes in lactating cows supplemented with OmniGen-AF (Prince Agri Products, Inc.) subjected to heat stress. Thirty lactating Holstein cows from an Arizona were assigned to a control diet (CON, $n = 15$h) or control diet plus OmniGen-AF (OG, $n = 15$h). Cows within diet were balanced by DIM, milk production and parity (91 ± 5.9 DIM, 36.2 ± 2.5 kg/d, and 3.1 ± 1.4). The cows were fed OG at 56 g/h/d for 52 d on the dairy, added to the TMR. On d 52, six cows were randomly selected from each of the diet groups, transported to the Agricultural Research Center (ARC), University of Arizona and housed in environmentally controlled modules (EM). Original diet assignments were continued. The OG was top-dressed 2x/d (28 g/feeding) with molasses as the carrier and the CON cows received the molasses carrier 2x/d. Both were mixed into the top one-third of the TMR. In the EM, all cows were subjected to 7 d of thermal neutral (TN), 10 d of heat stress (HS), and 4 d of TN. Feed intake, milk production, and milk composition were measured daily. Rectal temperatures and respiration rates were recorded 3x/d (0600, 1400, and 1800 h). Blood samples were taken on Days 7 (TN), 8 (HS), 10 (HS), 17 (HS) and 18 (TN) during the ARC phase and analyzed for selected blood metabolites, hormones and immune biomarkers. Serum cortisol levels were highest on d 8 for both the CON and OG fed cows however OG cows had significantly lower cortisol ($P < 0.05$) on Day 8 (CON = 0.8372 ug/dL; OG = 0.4838 ug/dL). No differences were detected at the other time points. Serum insulin and plasma glucose levels were not different between CON and OG cows. The OG cows maintained lower SCC compared to CON ($P < 0.01$). Serum calcium were not different, however, serum NEFA ($P = 0.10$) tended to be greater in OG cows throughout the 21 d ARC phase. Although serum cortisol were lower in OG cows, serum ACTH levels at each sampling point were higher ($P < 0.0001$). Results suggest that feeding OG to lactating cows reduced many of the effects associated with HS by reducing cortisol. However, ACTH increased in OG cows suggesting that OG may alter adrenal response to ACTH. Additional research is needed to determine the cause of reduced serum cortisol and elevated serum ACTH in cows fed OG.

Key Words: heat stress, lactating cows, OmniGen-AF

1860 (W319) Assessment of the effect of plant tannins on rumen fermentation and gut microbial diversity in goats using 16S rDNA amplicon pyrosequencing. B. R. Min[*1], C. Wright[1], P. Ho[2], J. S. Eun[3], N. Gurung[1] and R. Shang[1], [1]*Tuskegee University, Tuskegee, AL,* [2]*Montgomery Blair High School, Silver Spring, MD,* [3]*Utah State University, Logan*

Two grazing experiments were performed to 1) investigate the effects of supplementing condensed tannins (CT)-containing pine bark (PB) powder on ADG, ruminal fermentation, and gut microbial diversity dynamics, and 2) to quantify the influence of different sources of tannins supplementations on ruminal fermentation and gut microbial diversity changes of goats grazing winter pea and ryegrass dominant forages. In Exp. 1, 20 Kiko cross male goats (*Capra hircus*; initial BW = 39.7 ± 2.55 kg) were randomly assigned to 2 experimental diets (alfalfa pellet vs. PB powder). Alfalfa pellet (no CT as a control) or PB (11% CT) was supplemented at 0.8% BW for targeted total DMI of 1.2% BW. The remainder DMI of each diet was obtained from grazing for 60 d. In Exp. 2, 12 Kiko cross goats were used to measure ADG, ruminal fermentation, and gut microbial population in the rumen of goats grazing bermudagrass. The animals were randomly assigned to 3 experimental diets: 1) no tannins (control), 2) chestnut extract at 100 g/d (CTE), and 3) quebracho CT extract at 100 g/d (QCTE). In Exp. 1, ADG was greater ($P < 0.05$) in PB (209 g/d) than the control (188 g/d). However, goats grazing winter pea and ryegrass forages with PB supplementation decreased ($P < 0.05$) concentrations of acetate (14.4 vs. 15.1 mM), propionate (3.34 vs. 3.83 mM),

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butyrate (1.82 vs. 2.00 mM), and total VFA (22.5 vs. 23.7 mM) compared to those in the control, respectively. Bacterial population in PB-supplemented group was greater for *Bacteroides* (20.5 vs. 33.2%), *Firmicutes* (67.2 vs. 57.3%), and Proteobacteria (1.15 vs. 1.44%) phylum compared with control group, respectively. In Exp. 2, ADG was greatest for CTE (275 g/d) than QCTE (148 g/d) and the control (79.4 g/d). Goats grazing bermudagrass pasture with CTE had greater ($P < 0.05$) concentrations of acetate, propionate, butyrate, and total VFA compared to those in QCTE and control. Bacterial population in CTE-supplemented group was greatest for *Bacteroides* (51.5, 52.9, and 35.3%), *Firmicutes* (40.2, 36.7, and 55.9%), and Proteobacteria (2.28, 2.18, and 1.49%) phylum compared with QCTE and control group, respectively. Rumen archaeal population, however, was greatest in control group (0.70%) compared with CTE (0.23%) and QCTE (0.22%) group. Supplementing tannins in goat diets such as CTE, QCTE, or PB powder has the potential to improve ADG and modify rumen bacterial and archael population.

Key Words: goats, gut microbial diversity, tannins

1861 (W320) Effect of supplemental chelated Cu, Zn, and Mn on antioxidant status and hoof health of lactating cows. X. J. Zhao[1], J. H. Wang[2], Y. M. Wang[*3] and L. Wang[1], [1]*College of Animal Science and Veterinary Medicine, Shandong Agriculture University, Taian, China, [2]College of Animal Science, Zhejiang University, Hangzhou, China, [3]Novus International Trading (Shanghai) Co., Ltd, Shanghai, China*

The objective of the study was to evaluate effect of supplemental Cu, Zn, and Mn as chelated trace mineral (CTM) on antioxidant status and hoof health of dairy cows. Forty eight Holstein cows in early lactation (DIM = 65) were randomly assigned into 1 of 2 treatments: 1) basal diet contains 17.2 mg Cu, 70.1 mg Zn, and 63.7 mg Mn/kg dry matter (CON); 2) basal diet supplemented with 150 mg Cu, 320 mg Zn and 130 mg Mn/head/d as CTM (Minitrex). Cows were gait scored using a 5-point Numerical Rating System where 1 and 2 are considered healthy, and ≥ 3 lame. Cows in each treatment were blocked as lame cows ($n = 12$) or healthy cows ($n = 12$) when data was analyzed. Over the 180 d experiment, DMI, milk yield and milk composition was tested every 10 d. Blood samples and hoof samples were taken at Day 0, 90, and 180 to test the blood antioxidant variables and hoof hardness, respectively. There was no difference in DMI, milk yield and milk composition between healthy and lame cows ($P > 0.05$). Cows receiving CTM had less milk fat concentrations ($P < 0.05$) than CON, but no difference was observed on milk fat yield or other milk components ($P > 0.05$). No differences were detected in blood superoxide dismutase (SOD), reduced glutathione (GSH), oxidized glutathione (GSSG), glutathione peroxidase (GSH-Px), catalase (CAT), and malondialdehyde (MDA) between healthy and lame cows ($P > 0.05$). Compared with CON, blood SOD, GSH, and GSH-Px in CTM cows were significantly increased while MDA and GSSG were significantly decreased ($P < 0.05$), and blood CAT was not affected by treatments ($P > 0.05$). Cows receiving CTM did not have hoof hardness that differed from the CON at Day 0 and 90, but had significant greater values than CON at Day 180 ($P < 0.05$). There was no interaction between CTM and cows health status. It was concluded that supplemental chelated Cu, Zn, and Mn could improve antioxidant status and hoof hardness regardless of lameness status.

Key Words: chelated trace mineral; antioxidant status; hoof health

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1862 (W321) Effects of supplemental bupleurum extract on serum hormone and immune globulin levels in heat-stressed dairy cows. X. Sun[1,2,3], J. Cheng[1,2,3], D. P. Bu[3], L. Pan[3], N. Zheng[1,3,4] and J. Wang[*1,3,4], [1]*Ministry of Agriculture- Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

This experiment was conducted to evaluate the effects of bupleurum extract (BE) on serum hormone and immune globulin levels in dairy cows under heat stress. Forty lactating Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to one of four treatments. Treatments consisted of 0 (control), 0.25, 0.5, or 1.0 g BE/kg DM. The experiment lasted 10 wk. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via tail vein before the morning feeding on Days 0, 21, 42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. Compared with controls, cows fed 1.0 g/kg BE had higher thyroxine (T3) (1.43 vs. 1.16 ng/mL; $P < 0.05$) and prolactin (PRL) (230.50 vs. 188.19 uIU/mL; $P < 0.05$) levels, and 0.5 g/kg BE had the tendence to increase the T3 (1.27 vs. 1.16 ng/mL; $P < 0.10$) level, but 0.25 and 0.5 g/kg BE had no effect ($P > 0.05$) on PRL level. Serum growth hormone (GH) level was increased (2.17 vs. 1.21 ng/mL; $P < 0.05$) in cows fed 0.25 g/kg BE compared with control cows, and tended to be higher (1.76, 1.69 vs. 1.21 ng/mL; $P < 0.10$) in cows fed 0.5 and 1.0 g/kg BE. Supplementation of BE had decreased the cortisol (COR) levels (48.35, 49.43, 49.86 vs. 64.49 ng/mL; $P < 0.05$), but had no effect ($P > 0.05$) on the levels of thyroxine, Insulin, glucagon, neuropeptide Y, leptin, insulin-like growth factor, and heat shock protein 70. Cows fed 0.5 g/kg BE increased the immunoglobulin (Ig) A content (279.25 vs. 179.78 ìg/mL;

$P < 0.05$), and IgG level was increased (36.54, 36.14 vs. 27.13 mg/mL; $P < 0.05$) in cows supplemented with 0.25 or 0.5 g/kg BE, while the IgM and tumor necrosis factor-á (TNF-á) levels showed no difference ($P > 0.05$) when compared with the control cows. These findings suggest that BE supplementation could relieve metabolic disorders and enhance immune function in heat-stressed cows.

Key Words: bupleurum extract;serum hormone; immune globulin

1863 (W322) Dry matter intake, milk yield, and composition of Holstein cows fed organic minerals.
T. A. Del Valle[*1], E. F. Jesus[2], A. G. B. V. B. Costa[1], G. F. Cabral[3], V. C. Galvão[1], P. G. D. Paiva[2], T. S. Acedo[4], L. F. M. Tamassia[4] and F. P. Rennó[1], [1]School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, Brazil, [2]School of Agricultural and Veterinary Sciences of UNESP, Jaboticabal, Brazil, [3]School of Animal Science and Food Engineering of University of São Paulo, Pirassunga, Brazil, [4]DSM Produtos Nutricionais, São Paulo, Brazil

The aim of this study was to evaluate the effects of organic sources of minerals diet of dairy cows in mid-lactation on dry matter intake, milk yield and composition. Twenty Holstein cows with an average body weight of 625.30 ± 80.37 kg and DIM averaging 146.83 ± 67.34 were allocated to receive one of two diets: INO (inorganic): diet with addition of inorganic mineral sources; ORG (organic) diet with addition of organic mineral sources (zinc, cooper, selenium, chromium, manganese, cobalt, iron and sulfur; DSM Produtos Nutricionais, Brazil). The design was crossover. Each experimental period had 14 d adaptation and 7 d for sampling. Samples of milk were collected on 16th, 17th and 18th days of each period to evaluate the composition. The cows were allocated in individualy barns type free-stall, fed ad libitum and intake were estimated by bromatological analyzes of feeds and orts. Increases in fat-corrected milk ($P < 0.05$), fat yield ($P < 0.05$) and protein ($P < 0.10$) were observed in the animals receiving the diets containing organic mineral sources compared to those fed inorganic sources. This increasing in fat corrected milk shows an increased efficiency of energy use, most likely due to higher preparation of enzyme apparatus for metabolizing energy. Milk yield has not influenced by the treatments, showed a mean of 32.43 kg.d^{-1} and difference of 0.63 kg.d^{-1} of milk, which, together with the average increase of 1.4 g.kg^{-1} fat led to increase in fat yield ($P < 0.05$). The protein content, although not statistically differ, was 0.8 g.kg^{-1} higher in diet with organic sources and result in increase 0.05 kg the protein yield ($P < 0.10$). The dry matter intake average 21.27 kg.d^{-1} and no effect of experimental diets was observed. Organic minerals increases energy efficiency in dairy cows, increasing the secretion of milk solids without change the intake.

Key Words: dairy cows, efficiency, milk fat

1864 (W323) Effects of sampling position on blood hormone concentration in dairy cattle.
M. Zhao, D. P. Bu, J. Q. Wang*, X. Q. Zhou, Y. Zhang, S. G. Zhao and P. Sun, State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China

To evaluate the effects of sampling position on blood hormone concentration in dairy cattle, ten dairy cows (Milk yield = 28.2 ± 2.1 kg/d, DIM = 121 ± 15 d) were selected. Blood samples from mammary vein, external pudic artery, coccygeal artery and vein were collected. Eight kinds of hormones were determined by radioimmunoassay method including insulin, growth hormone (GH), insulin-like growth factor-1 (IGF-1), leptin, adrenocorticotropic hormone (ACTH), estrogen, prolactin and progestin. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. The results showed that no differences were observed in these hormones. Concentrations of hormones in mammary vein, external pudic artery, coccygeal artery and vein were averaged as followed: insulin (5.56 vs. 6.39 vs. 5.35 vs. 5.38 µIU/ml, $P > 0.05$), GH (2.29 vs. 2.34 vs. 2.34 vs. 2.40 ng/ml, $P > 0.05$), IGF-1 (290.57 vs. 260.63 vs. 283.64 vs. 266.99 ng/ml, $P > 0.05$), Leptin (3.04 vs. 3.10 vs. 3.17 vs. 2.97 ng/ml, $P > 0.05$), ACTH (11.35 vs. 11.43 vs. 11.50 vs. 12.15 pg/ml, $P > 0.05$), Estrogen(12.67 vs. 12.70 vs. 14.45 vs. 11.47 pg/ml, $P > 0.05$), Prolactin (315.88 vs. 312.47 vs. 290.28 vs. 302.24 µIU/ml, $P > 0.05$), Progestin(0.21 vs. 0.24 vs. 0.23 vs. 0.33 ng/ml, $P > 0.05$). It was implied that either of the four sampling positions could be representative for hormones measurement when estimating mammary gland metabolism.

Key Words: blood, hormone, mammary gland

1865 (W324) Effects of dietary protein composition on blood hormone levels in dairy cattle.
M. Zhao[1], D. P. Bu[1], J. Q. Wang[*1], X. Q. Zhou[1,2], Y. Zhang[1] and P. Sun[1], [1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Northeast Agricultural University, Harbin, China

The objective of this experiment was to investigate the effects of different protein sources on blood hormones profile. Thirty two dairy cows were pen fed with total mixed ration (TMR), which were divided into group soybean (corn stover 36.1%, soybean meal 11.3%, extruded soybean 2.1%, whole cottonseed 10.4%, rapeseed meal 4.2%, cottonseed meal 2.1%, beet pulp 4.2%, grind corn 25.6% and other supplements 4.1%) and group non-soybean (corn stover 36.1%, whole cottonseed 10.4%, rapeseed meal 9.6%, cottonseed meal 6.7%, beet pulp 7.5%, grind corn 25.6%, wheat bran 4.5% and other supplements 1.7%). Crude protein (CP) and neutral detergent fiber

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(NDF) of TMR were 16.1% vs. 15.1% and 54.0% vs. 57.1% in group soybean and group non-soybean, respectively. The duration of this experiment was 15 wk (2-wk adaptation and 13-wk experimental period). Nine hormones were determined by radioimmunoassay method including insulin, growth hormone (GH), insulin-like growth factor-1 (IGF-1), Adrenocorticotropic hormone (ACTH), Leptin, Estrogen, Cortisol, Prolactin and Progestin. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. Dry matter intake (DMI) and milk yield were 17.4 vs. 19.1 kg/d ($P < 0.01$) and 23.2 vs. 22.9 kg/d ($P > 0.05$) in group soybean and group non-soybean. Concentrations of hormones were averaged insulin (13.44 vs. 12.55 µIU/ml, $P > 0.05$), IGF-1 (384.31 vs. 286.33 ng/ml, $P < 0.01$), ACTH (9.67 vs. 6.00 pg/ml, $P < 0.05$), Estrogen (10.69 vs. 10.44 pg/ml, $P > 0.05$), GH (2.37 vs. 2.26, $P > 0.05$), Leptin (3.67 vs. 3.32 ng/ml, $P > 0.05$), Progestin (0.38 vs. 0.36 ng/ml, $P > 0.05$), Prolactin (175.51 vs. 174.00 µIU/ml, $P > 0.05$) and Cortisol (10.92 vs. 7.38, $P > 0.05$) in group soybean and group non-soybean, respectively. It demonstrated that protein sources could significantly influence DMI and have no effect on milk yield, which can also influence the function of hypothalamus pituitary adrenal axis and stimulate the cell proliferate.

Key Words: protein source, blood hormone, dairy nutrition

1866 (W325) The small ruminant nutrition system: Considering the ruminal fiber stratification for goats. J. G. L. Regadas Filho[*1], L. O. Tedeschi[2], A. Cannas[3], M. T. Rodrigues[4] and R. A. Vieira[5], *[1]Universidade Federal de Vicosa, Vicosa, Brazil, [2]Texas A&M University, College Station, [3]Universita Di Sassari, Sassari, Italy, [4]Universidade Federal de Viçosa, Vicosa, Brazil, [5]Norte Fluminense State University, Campos dos Goytacazes, Brazil*

The objective of this research was to assess the ability of a mechanistic model named Small Ruminant Nutrition System (SRNS) to predict the metabolizable energy intake (MEI) and milk yield (MY) by using a heterogeneous ruminal fiber pool scenario (GnG1; Regadas Filho et al., 2014) in comparison to a traditional homogeneous scenario (G1), The GnG1 scenario considers that the first ruminal fiber pool (raft) follows an age-dependent fractional rate for particle transference from a raft to an escapable pool (λ_r) and that the second ruminal fiber pool (escapable) follows an age-independent fractional rate of particle escape from the escapable pool (k_e); for G1, a scenario with only a single fractional rate passage (k_p) is adopted. All parameters were estimated individually by using equations published in the literature; however, for the G1 scenario, two rate passage equations were used, with one from sheep data (G1-S; Cannas et al., 2004) and another from goat data (G1-G; Tedeschi et al., 2012). The MEI, MY and DMI estimated by using these scenarios were compared with the

results of an independent dataset ($n = 327$) that contained information regarding the DMI, MEI, MY, BW and milk and dietary compositions. The evaluation of the scenarios was performed using a coefficient of determination (r^2) between the observed and predicted values; mean bias (MB); bias correction factor (C_b) and concordance correlation coefficient (CCC). The MEI estimated by the GnG1 scenario yielded a precision and accuracy ($r^2 = 0.82$; MB = 0.21 Mcal.d^{-1}; C_b = 0.98) similar to that of the G1-S ($r^2 = 0.85$; MB = 0.10 Mcal.d^{-1}; C_b = 0.99) and G1-G ($r^2 = 0.84$; MB = 0.18 Mcal.d^{-1}; C_b = 0.98) scenarios. The results were also similar for the MY; however, a significant MB ($P < 0.01$) was found as follows: GnG1 ($r^2 = 0.74$; MB = 0.70 kg.d^{-1}; C_b = 0.79), G1-S (r^2 = 0.71; MB = 0.58 kg.d^{-1}; C_b = 0.85) and G1-G ($r^2 = 0.71$; MB = 0.65 kg.d^{-1}; C_b = 0.82). The GnG1 scenario can be assumed to maintain the theoretical basis of mechanistic models.

Key Words: fiber stratification, goat, heterogeneous fiber pool

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1867 (W326) Effect of "COGU" technology on glucose uptake and mineral utilization and deposition in growing lambs. A. M. Temple[*1], G. A. Ayangbile[1], D. R. Vandermyde[1] and C. R. Vandermyde[2], *[1]Agri-King Inc., Fulton, IL, [2]Morrison Veterinary Clinic, Morrison, IL*

"COGU" is a proprietary combination of GRAS microbial fermentation extracts meant to diminish the negative impact of mineral interactions that may be responsible for inefficient digestibility, absorption and utilization of nutrients in livestock. The objective of this study was to observe the effect of COGU technology additive (COGU) on blood glucose uptake, mineral utilization and deposition in the ruminant. Twenty-four Katahdin wethers (average BW 15.8 ± 1.5 kg) approximately 55 d of age were fed ad libitum either a silage based control diet (CON), or CON plus 3.4 g/head/d of a supplement containing COGU. Lambs were penned in groups of six with two pens per treatment. ADG was calculated for each animal and DMI was measured for each pen throughout d 100 of the experiment. Jugular blood samples were analyzed for each animal during wk 0, 4, 8, 10, and 12. Eight CON and 9 COGU sheep were housed in crates 5 d for total collection of orts, fecal and urinary samples for digestibility and nutrient utilization. All lambs were euthanized at the end of the experiment, and tissues collected for biological analysis. Data were analyzed by ANOVA CRD. No differences ($P > 0.05$) were observed between dietary treatments for DMI, ADG, or digestibility of nutrients. However, COGU-supplemented lambs had numerically greater digestibility of Na, P, S and Cu. Blood glucose in COGU lambs was higher (CON = 61.90 mg/dL, COGU = 72.98 mg/dL; $P = 0.0005$) throughout the trial. Previous unpublished research also showed higher blood glucose in COGU-supplemented lambs. Liver glycogen was numerically higher ($P > 0.05$) in COGU-supplemented lambs.

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No differences were observed in blood NH3, BHBA, BUN, cholesterol, or NEFA. Rumen fluid contents showed COGU tended to increase ($P = 0.054$) the molar proportion of acetate, propionate, and butyrate. Duodenum mucosal cell scrapings in COGU treatment had decreased ($P = 0.019$) Mg. Copper, Mn, and Zn were numerically higher ($P > 0.05$) and Fe lower ($P > 0.05$) in duodenum mucosal cell scrapings of COGU-supplemented lambs. In conclusion, supplemental COGU seems to increase blood glucose uptake in the growing lamb. It also may affect mineral passage and utilization through the duodenum mucosal cell membrane.

Key Words: glucose, mineral, lambs

1868 (W327) Effect on plasma metabolites of Nellore bulls fed ractopamine hydrochloride and protein level. N. R. B. Cônsolo[*1], F. Rodriguez[1], M. O. Frasseto[1], R. A. P. Maciel[2], V. Rizzi[3] and L. F. P. Silva[1], [1]University of Sao Paulo, Pirassununga, Brazil, [2]University of Sao Paulo, São Paulo, Brazil, [3]Ouro Fino, Cravinhos, Brazil

The aim of this study was to evaluate was to evaluate the effects of ractopamine hydrochloride (RH) and dietary crude protein (CP) on blood metabolites of Nellore young bulls. Forty eight Nellore bulls were grouped by BW, and randomly assigned to treatments in a 2x2 factorial arrangement of treatments. The factors were two levels of dietary CP (100 and 120% of MP requirement), and two levels of RH (0 and 300 mg/animal/d). Treated animal received RH for the final 35d before slaughter. Blood was collected at the beginning and at the end of RH supplementation by venipuncture and/or puncture of the coccygeal artery, before the morning feeding. Blood samples were collected into 10-mL BD Vacutainers, without anticoagulant, for the measurement of serum glucose, total protein, albumin, plasma urea nitrogen (PUN), aspartate aminotransferase (AST), γ-glutamyl transferase (GGT) and alkaline phosphatase (ALP). Blood parameters were analyzed using commercial kits (Laborlab, São Paulo, Brazil and CELM, São Paulo, Brazil) by endpoint or kinetic colorimetric methods in an ABS-200 Automatic Biochemistry Analyzer (CELM). The statistical analyses were conducted using SAS, version 9.1.2 for Windows (SAS Institute Inc., Cary, NC, USA). Data were analyzed as a randomized block design with a 2x2 factorial arrangement of treatments using the MIXED procedure of SAS. There was no effect of treatments, or of interaction, on plasma creatinine, AST or GGT ($P > 0.05$). Dietary CP level tended to increase blood urea (31.2 vs. 40.8 mg/dL, $P = 0.07$). RH supplementation altered glucose, ALP and total protein; however, the effect was dependent on the dietary CP level. RH supplementation decreased plasma glucose concentration at CP100 ($P = 0.05$), and had no effect at CP120 ($P = 0.87$). For ALP activity, RH supplementation increased its activity at CP120 ($P = 0.05$) and had no effect at CP100 ($P = 0.42$). RH supplementation increased plasma total protein at CP 120 ($P = 0.03$) and had no effect at CP100 ($P = 0.17$) In conclusion, RH supplementation and CP levels leads to slight changes on plasma metabolites.

Key Words: crude protein, β-agonist, plasma metabolites

1869 (W328) Impact of "COGU" technology on performance in lactating dairy cows. A. M. Temple*, G. A. Ayangbile, D. F. Jones and D. A. Spangler, *Agri-King Inc., Fulton, IL*

"COGU" is a proprietary combination of GRAS microbial fermentation extracts meant to diminish the negative impact of mineral interactions that may be responsible for inefficient digestibility, absorption and utilization of nutrients in livestock. Two studies were initiated to investigate the effect of COGU on blood profiles and lactation performance of dairy cows. The first study was conducted on a commercial dairy farm in the Pacific Northwest. Water and forages in this region are known to have certain minerals in excess causing depressed milk production, high somatic cell counts and other metabolic issues. In a Washington herd of 1500 cows, three groups of 130 cows each were selected. Each group contained fresh cows, heifers, or high cows. Cows were fed a supplement containing COGU at a rate of 15 g/head/d in a corn silage based TMR diet for 41 d. Twenty cows averaging 75 DIM (± 3 d) from the high group were randomly selected for blood sampling and milk data collection. Blood samples were obtained 2 wk before feeding COGU (BCOGU), followed by wk 1, 2, and 4 fed COGU (COGU), and subsequently by sampling at wk 1, 3, and 5 after removing COGU (ACOGU) from the diet. On-farm milk production data was collected daily 2 wk before feeding COGU through 4 wk after removing COGU. Data were analyzed by ANOVA CRD. Blood glucose, BUN, and hemoglobin were increased ($P < 0.0002$) for cows fed COGU, and BHBA and NEFA were decreased ($P < 0.0001$). The 150 DIM adjusted production was higher ($P < 0.0001$) for cows fed COGU. In a second study, 180 commercial dairy farms across the United States representing 29,346 cows were randomly selected. COGU was blended into a supplement and fed at a rate of 15 g/head/d. Data for milk yield and components was collected for a minimum of 10 d to maximum of 120 d on these farms. Statistical analysis was performed with Kruskal–Wallis One-Way Nonparametric AOV and Dunn's All-Pairwise Comparison test. There were no differences in DMI intake ($P = 0.98$); however, milk yield, milk butterfat, milk protein, ECM, and ECM feed efficiency were all significantly higher ($P < 0.03$) at the end of the experimental period compared to the start of the experiment. COGU increased glucose uptake and nitrogen utilization as well as improved milk yield and components in dairy cows.

Key Words: glucose, milk yield, dairy cows

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1870 (W329) A conceptual model of protein-precipitable polyphenols (condensed tannins) on protein binding and protein digestion in ruminants.
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There is a need to better understand the mechanisms by which biologically active protein-precipitable polyphenols (PPP) from forages bind to dietary protein in the rumen and how this impacts the ruminant animal's requirement for protein. The objective of this study was to model the effect of biologically active PPP on ruminal protein binding and the potential protection of rumen-bypass protein. Green live-leaf material from six species of warm-season perennial legumes was sampled during August of 2011 and 2012. The effect of biologically active PPP on protein-binding ability was evaluated by combining rhizoma peanut with experimental forages to create separate basal diets (by year) containing PPP ranging from 1–9%. Protein-binding ability was determined by an in vitro protein-precipitable phenolics assay and nitrogen analysis of the protein-phenolic precipitates. Data were analyzed in linear-segmented and quadratic-segmented regressions (PROC NLIN of SAS) to model the effects of biologically active PPP on protein-binding ability. The Model Evaluation System (MES; http://nutritionmodels.tamu.edu/mes.html) was used to compare the correctness of the linear- versus the quadratic-segmented regression. For the linear-segmented regression, β_0 is equal to α, β_1 is equal to β, and α, β, X_m and Y_m were equal to -3.2935, 6.3329, 6.4 and 37.24, respectively. For the quadratic-segmented regression, β_0 is equal to α, β_1 is equal to β, β_2 is equal to γ and α, β, γ, X_m and Y_m were equal to -10.7117, 11.4534, -0.6854, 8.32 and 37.14, respectively. The data pattern suggests that the relationship between PPP and protein bound is not linear in nature. Beyond a certain point, in this case a concentration of PPP occurring between 6.4 and 8.3%, the amount of protein bound does not increase as the concentration of PPP in the diet increases. While both segmented regressions were similar in terms of adequacy, the linear-segmented regression was slightly more precise than the quadratic-segmented regression (R^2 0.811 and 0.809, respectively) at accounting for variation that occurred in observed values. Overall, the regression comparison indicated that the linear-segmented regression is 1.2 times more likely to correctly predict observed values of protein binding by PPP than the quadratic-segmented regression. However, either model would be an acceptable tool for use in modeling the effect of forage PPP on rumen-protein binding and potential protection of rumen-bypass protein and in a decision support system.

Key Words: legume, protein, tannin

1871 (W330) Effect of sprouted barley grain supplementation of an herbage or haylage diet on ruminal fermentation and methane output in continuous culture.
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A 4-unit dual-flow continuous culture fermentor system was used to assess the effect of supplementing 7-d sprouted barley (SB) or barley grain (BG), with a pasture (orchardgrass) or haylage diet, on nutrient digestibility, VFA production, bacterial protein synthesis, and methane production. Treatments were randomly assigned to fermentors in a 4×4 Latin square design with a 2×2 factorial arrangement of treatments using 7 d for diet adaptation and 3 d for sample collection. Treatments were: 1) pasture+SB, 2) pasture+BG, 3) haylage+SB, and 4) haylage+BG. Feedings (60 g of DM) occurred 4 times daily (0730, 1030, 1400, 1900 h) throughout four 10-d periods. Gas samples for methane analysis were collected 6 times daily (0725, 0830, 1000, 1355, 1530, 1630 h). Samples for pH, ammonia-N, and VFA analysis were taken on d 8, 9, and 10 and analyzed for DM, OM, CP, NDF, and ADF for determination of nutrient digestibilities, and estimation of bacterial protein synthesis. Data were analyzed using the MIXED procedure of SAS with period and treatment as fixed effects and fermentor as random. Orthogonal contrasts were tested using haylage vs. pasture and BG vs. SB treatments. Apparent and true DM digestibility was not affected by forage type. True DM digestibility was greater ($P = 0.05$) for diets supplemented with SB. Apparent and true digestibilities of OM and apparent CP were not affected by treatment (68, 83, and 89%, respectively). Apparent NDF and ADF digestibilities of pasture diets were greater ($P < 0.05$) compared to haylage diets (79 vs. 72% and 76 vs. 73%, respectively); however, supplement did not affect fiber digestibility. Diets supplemented with SB had greater ($P < 0.05$) mean and minimum pH than BG. Haylage diets produced greater ($P < 0.01$) concentrations of total VFA compared with pasture diets (72 vs. 61 mmol/L). Supplementation with BG produced a greater ($P = 0.03$) concentration of total VFA compared to diets supplemented with SB (68 vs. 64 mmol/L). Haylage diets produced greater ($P < 0.05$) concentrations of daily methane compared with pasture diets (35 vs. 27 mmol) but supplementation did not affect methane production. Bacterial efficiency was greater ($P < 0.05$) for pasture diets compared with haylage diets with no effect of supplementation. Supplementation with SB increased true DM digestibility of pasture and haylage diets, but did not impact fiber and CP digestibility, methane production, or microbial efficiency, compared to BG.

Key Words: sprouted barley, pasture, methane

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1872 (W331) Effect of Lalsil bacterial inoculants on the pH of corn silage with low dry matter. M. Saberi[*], K. Rezayazdi and M. Dehghan Banadaky, *Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran.*

To study the effect of commercial lactic acid bacteria inoculants (Lalsil) on the pH during the ensiling of corn silage with low dry matter,this experiment was conducted according to completely randomized design with 3 treatments and 4 replicates in each treatment. Treatments were: 1- control (no additives) 2- treated with Lalsil Mso1 (*Lactobacillus plantarum* and *Propionibacterium acidipropionici* applied at 1×10^5 cfu/g of the corn silage) 3- treated with Lalsil Fresh (*Lactobacillus buchneri* applied at 1×10^5 cfu/g of the corn silage). pH of corn silage were measured at 1, 3, and 6 wk after ensiling. Statistical analysis of data was performed using PROC GLM and SAS statistical software. The results showed that DM (Dry matter), CP(Crude protein), NDF(Neutral Detergent Fiber) and ADF (Acid Detergent Fiber) composition of the corn silage were 18.87, 9.37, 61.75 and 25.50%, respectively. The difference between the first and sixth weeks of treatment was significant ($P < 0.05$). In the first and sixth weeks, treatment 1 had highest pH (3.92 and 3.80) and treatment contain Lalsil Fresh had lowest pH(3.83 and 3.70). There was no significant difference among treatments in the third week. It can be concluded that Lalsil bacterial inoculants could significantly reduced pH of corn silage, While Lalsil- Fresh was reduced pH of corn silage with low dry matter more effectively.

Key Words: corn silage, bacterial inoculants, pH

1873 (W332) The microbiome composition of the rumen is altered during the peripartal period in dairy cattle. H. Derakhshani[1], S. Alqarni[2], H. Khazanehei[*1], F. C. Cardoso[2], J. C. Plaizier[1], E. Khafipour[1,3] and J. J. Loor[2,3], *[1]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [2]University of Illinois, Urbana, [3]Department of Medical Microbiology and Infectious Diseases, Winnipeg, MB, Canada.*

Alterations in ruminal microbiota composition during the peripartal period were studied using eight multiparous fistulated Holstein dairy cows. Cows were fed a typical TMR to meet NRC (2001) requirements during the dry period and early lactation. Ruminal digesta samples were collected on days −14, −7, +10, +20 and +28 relative to calving. DNA was extracted after physical homogenization and utilized for PCR amplification of the V4 region of the 16S rRNA gene using barcoded universal primers to allow for multiplexing. Amplicons were purified, quantified and subjected to Illumina paired-end sequencing. The PANDAseq assembler was used to merge the paired-end sequences for further analyses using QIIME pipelines. After filtration and removing chimeric reads, assembled sequences were assigned to operational taxonomic units and aligned to Greengenes database. The Chao1 estimator of species richness and Unifrac distance matrices were used to calculate α-diversity and β-diversity of microbial communities, respectively. Differences in bacterial composition across time were tested using the PERMANOVA procedure in PRIMER v6 software. Partial least square discriminant analysis (PLS-DA) of SIMCA was performed to identify taxa that were most characteristic of each time point. A total of 1393,235 sequences were generated and an average of 35,990 high-quality sequences per sample were obtained after quality filtering steps, which resulted in identification of 16 phyla and 303 taxa of which 145 were classified at the genus level. The microbial profile of ruminal digesta differed across time points with highest differences observed when comparing day −14 to day +28 ($P = 0.03$), and day −7 to day +28 ($P = 0.05$). At the phylum level, the abundance of Actinobacteria increased while Armatimonadetes, Cloriflexi, Tenericutes, Verrucomicrobia, and WPS-2 decreased in the postpartum compared with prepartum. At the genus level, the abundance of *Atopobium, Clostridium, Coprococcus*, *Lactobacillus, Moryella*, *Olsenella, Pediococcus*, *Shuttleworthia Streptococcus,* and *Weissella* increased postpartum compared with prepartum. Variation in the ruminal microbiota among cows was smaller before calving but gradually increased after calving. This may have been associated with the normal decline in voluntary dry matter intake (DMI) before parturition. The greater dissimilarity postpartum in microbial communities among cows may be due to individual differences in physiological responses. Factors such as DMI, the degree of negative energy balance around parturition, and the occurrence of metabolic disorders during this period could affect the ruminal ecosystem and, thus, alter its microbial composition.

Key Words: dairy cows, rumen microbiota, transition period, illumina sequencing

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1874 (W333) Evaluating rations offered to a group of cattle as a component of ration formulation software. J. Ferguson[*], Z. Wu, D. T. Galligan, L. Baker and N. Thomsen, *University of Pennsylvania, Kennett Square.*

Rations are typically formulated for a target cow representing a group of cows. Lead factors may be used to select the target milk production for the group. Body weight, lactation number and milk composition are chosen based on mean values for the group of cows to be offered the ration. It is often not known how the offered ration impacts the ME and MP across all cows in the group. To provide an assessment of ME and MP balance for a ration fed to a group of cows, the UPenn Ration Analyzer incorporated a group model within its software program. Records from DHIA milk production (more than 1000,000) from 2000 farms and five breeds were used to construct production curves based on rolling herd averages

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(RHA) for parities 1, 2, and 3+. The user inputs breed, lactation number, the mean BW for parities 1, 2, 3, 4+, the range in DIM for the group, and the herd RHA. The group model constructs a production profile of cows based on the user inputs and assigns stochastic variation to production and DIM for the group. Intake of DM for each cow in the group is predicted using the NRC. The ME and MP balance for each cow in the group is calculated based on the formulated diet and plotted by DIM. The user can view graphs of the predicted range in milk production, ME and MP balance by DIM and a table with mean DMI, milk volume, and fat, protein content for the group. The user can adjust the scale of the variance in milk production, the mean milk production, DMI, and fat and protein content if the actual values in the herd differ from predicted. A second model allows imported DHIA milk production records for the group to be fed the formulated diet to compare with the model predicted values. A third model allows the user to least cost the diet for the group within constraints on ME and MP balance for the group of cows. The user can reformulate the ration to better meet the ME and MP needs of the group. Preliminary validation from farms suggests that the group evaluator model provides a useful tool for regrouping cows and evaluating rations for improved ME and MP balances, particularly avoiding excesses in MP.

Key Words: ration formulation, production, cattle groups

1875 (W334) Epidemiological study about the effects of chelated minerals on milk, reproductive performance, and locomotion scores of dairy cattle.

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The objective of this experiment was to evaluate the effects of a partial replacement of chelated trace minerals (CTM) (Mintrex, Zn, Cu, and Mn; with methionine hydroxy-analogue as a ligand; Novus International, MO) compared with a ration containing only inorganic trace minerals (ITM) on locomotion score, milk production, and reproductive performance of dairy cows in different herds. Twenty-seven herds that were feeding the same TMR were enrolled in a 6-mo study. Fifteen herds continued to receive the same TMR (containing ITM), and the remaining 12 herds fed the same TMR with a partial replacement of ITM for CTM. The ITM premix provided 57 ppm of inorganic Zn, 9 ppm of inorganic Cu, and 27 ppm of inorganic Mn; whereas the CTM premix contained 32 ppm of inorganic Zn and 25 ppm of chelated Zn, 3 ppm of inorganic Cu and 6 ppm of chelated Cu, and 17 ppm of inorganic Mn and 10 ppm of chelated Mn. The first month of study was used as a basal line, and then herds were exposed to dietary treatments for 5 mo. Feed composition, feed intake, milk production, lameness score, and reproductive performance were monitored for each herd. All data, except conception rates, were analyzed using a mixed-effects model and conception rates were analyzed with a three-level mixed-effects logistic regression model with herd as experimental unit. There were no differences in feed intake (24.1 ± 0.20 kg/d) and milk production (31.4 ± 0.23 kg/d) between treatments. The overall proportion of cows with a lameness score ≥ 3 (considered lame cows) was not different between ITM and CTM herds. However, there was an interaction ($P < 0.001$) between treatment and month of experiment due to a greater incidence of lameness in CTM than in ITM herds during the first 2 mo of study (32.70 vs. 29.47%, respectively), and a lesser incidence in the last 3 mo of study (31.30 vs. 34.73%, respectively). Conception rate was not affected by treatment, but when cows that were serviced with less than 30 d of exposure to treatments were removed from the dataset, cows in the CTM herds had 2.9 greater ($P < 0.05$) odds of becoming pregnant than cows in the ITM herds. It is concluded that a partial replacement of inorganic Zn, Cu, and Mn for organic sources decreases lameness scores over time and improves conception rate after a minimum exposure of 30 d.

Key Words: lameness, reproduction, trace minerals

1876 (W335) Apparent synthesis of thiamin and vitamin B$_{12}$ in rumen of lactating dairy cows fed alfalfa or orchardgrass silages at different maturity stages.

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Effects of maturity stage of forages on apparent ruminal synthesis and post-ruminal supply of thiamin and vitamin B$_{12}$ were evaluated in two experiments. Alfalfa and orchardgrass were harvested and ensiled as a) early-cut, less mature (EC) and b) late-cut, more mature (LC). Diets containing alfalfa or orchardgrass silages of each maturity stage as the sole forage were offered to ruminally and duodenally cannulated lactating Holstein cows in crossover design experiments. Experiment 1 compared diets containing EC and LC alfalfa silage (~22% forage NDF and ~27% total NDF) offered to 16 cows in two 17-d treatment periods. Experiment 2 compared diets containing EC and LC orchardgrass silage (~25% forage NDF and ~30% total NDF) offered to 13 cows in two 18-d treatment periods. Intakes of thiamin increased with maturity stage of forages in Experiment 1 ($P < 0.01$; 79.3 vs. 46.5 ± 2.08 mg/d) and in Experiment 2 ($P < 0.01$; 76.0 vs. 60.9 ± 1.84 mg/d for LC and EC, respectively). In contrast, intakes of vitamin B$_{12}$ were lower for LC than EC in Experiment 1 ($P < 0.01$; 191 vs. 329 ± 8.47 µg/d) and in Experiment 2 ($P < 0.01$; 53.1 vs.

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Table 1877. Effects of DCAD concentration on production parameters

| | DCAD, meq/kg | | | | | $P <$ | |
Item	250	375	500	625	SEM	Linear	Quadratic
DMI, kg/d	22.3	22.9	23.1	23.6	0.52	0.007	0.902
Milk, kg/d	38.9	39.5	39.5	38.8	1.52	0.937	0.228
Fat, %	3.28	3.50	3.50	3.62	0.146	0.001	0.418
Protein, %	2.95	2.99	2.95	2.92	0.056	0.167	0.152
3.5% FCM, kg/d	37.1	39.2	39.2	39.1	0.98	0.008	0.037
FE, 3.5%FCM/DMI	1.67	1.71	1.71	1.66	0.038	0.759	0.085

76.3 ± 1.71 µg/d). In Experiment 1, duodenal flows of thiamin were greater for LC than EC (P = 0.02; 156 vs. 130 ± 7.21 mg/d) but the duodenal flows of vitamin B_{12} were not affected by treatment (P = 0.21, 12182 ± 556.1 µg/d). In Experiment 2, duodenal flows of vitamins were not affected by treatment (thiamin, P = 0.20, 199 ± 8.47 mg/d; vitamin B_{12}, P = 0.28, 8518 ± 426.0 µg/d). The apparent ruminal synthesis of thiamin and vitamin B_{12} were not affected by treatment in either experiment (Experiment 1: thiamin, P = 0.45, 79.8 ± 6.56 mg/d; vitamin B_{12}, P = 0.28, 11924 ± 426.0 µg/d; Experiment 2: thiamin, P = 0.18, 130 ± 8.57 mg/d; vitamin B_{12}, P = 0.29, 8454 ± 426.0 µg/d). Delaying the harvest of alfalfa or grass resulted in a greater dietary supply of thiamin and a lower supply of vitamin B_{12}. Nevertheless, the stage of maturity did not affect apparent ruminal synthesis and had little or no effect on the post-ruminal supply of these vitamins.

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

1877 (W336) Potassium carbonate as a cation supplement to increase dietary cation anion difference and improve dairy feed efficiency in lactating dairy cows. A. E. Weidman, M. E. Iwaniuk* and R. A. Erdman, *University of Maryland, College Park*

Supplementation with potassium carbonate (K_2CO_3) increases dietary cation anion difference (DCAD) which results in increased dairy feed efficiency. Our previous study with early lactating Holstein cows showed that increasing DCAD from approximately 250 to 400 meq/kg (Na-K-Cl Equation, DM basis) resulted in a linear increase in 3.5% FCM/DMI [feed efficiency (FE)]. However, the optimal DCAD for maximal FE could not be determined as the maximal FE response was achieved at a DCAD of 400 meq/kg. The objective of this study was to determine the optimal DCAD required for maximal DMI, milk production and FE using a broader range in dietary DCAD concentrations. Twenty Holstein cows (8 primiparous and 12 multiparous) averaging 95 (± 25) DIM were individually fed a basal diet containing 64% corn silage, 6% alfalfa hay, and 30% concentrate (DM basis). Dietary treatments consisted of 250 (basal), 375, 500, and 625 meq/kg DCAD where K_2CO_3 was added to the basal diet to obtain the desired DCAD concentrations. The treatments were applied in a 4 × 4 Latin square design with 3-wk experimental periods. Dietary treatments had no effect on milk production or milk protein concentration. Increasing DCAD from 250 to 625 meq/kg linearly increased DMI (P = 0.007) and milk fat percentage (P < 0.001), while 3.5% FCM increased curvilinearly (linear, P = 0.008; quadratic, P = 0.037) with increasing DCAD. There was a quadratic trend (P = 0.085) for dairy FE where maximal FE occurred at DCAD concentrations of 375 and 500 meq/kg. The optimal DCAD for DMI and fat percent could not be determined since maximums occurred at a DCAD of 625 meq/k. FE and 3.5% FCM were optimized at a DCAD concentration of 442 meq/kg. Results of this and other studies in our laboratory show that DCAD can be used to increased feed efficiency to help dairy producers reduce feed costs and improve profitability.

Key Words: DCAD, feed efficiency, dairy cows

1878 (W337) Degradation ruminal kinetics of organic matter, neutral detergent fiber and crude protein of sorghum wet distiller grain without solubles in comparison to the original sorghum grain. A. I. Trujillo*[1], M. D. L. A. Bruni[2] and P. Chilibroste[3], *[1]Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay, [2]Facultad de Agronomia Universidad de la Republica, Paysandu, Uruguay, [3]Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay*

A study was conducted to characterize ruminal crude protein (CP) and energy supply of sorghum wet distillers grains (SWDG; 31.4 ± 0.7% CP and 70.2 ± 2.2% neutral detergent fiber–NDF, 11.0 ± 0.7% fat, dry basis) from an ethanol plant in Uruguay in comparison to the original sorghum grain (SG). In situ technique was conducted to determine ruminal organic matter (OM),NDF and CP degradation kinetics, their respective effective degradability (considering passage rate of 2% h^{-1}, ED) and the relationship between rumen available Nitrogen (N) and fermentable OM (N:OM ratio) from 3 batches of SWDG and SG. Duplicate samples (5 g of 2–mm ground) of each feed were incubated in the rumen of 2 lactating dairy cows for 0, 2, 4, 8, 12, 24, 48, and 72 h. Data were fitted to the nonlinear model D(t) = a+b(1-e$^{-kd(t-t0)}$) with PROC NLIN of SAS program to determine degradation parameters, where D is percentage disappearance of OM, NDF or CP at the time t, (a) soluble fraction, (b) slowly degradable fraction, (c) deg-

radation rate, and t0 is lag time. Parameters were analyzed with PROC GLM in a completely randomized design and compared by Tukey test. There were not differences for any degradation parameters between batches, neither in SWDG nor in SG. Comparing degradation parameters of SWDG with SG the results were: fractions (a) and (b) of OM were lower (8.1 vs. 22.7%, 54.5 vs. 73.9%; $P < 0.05$) but (c) was greater (4.8 vs. 3.5% h^{-1}; $P < 0.05$); (t0) was only present in SWDG (3.1 h); (c) of NDF was greater (6.3 vs. 3.5% h^{-1}, $P < 0.05$) but (c) of CP was lower (1.1 vs. 1.9% h^{-1}; $P < 0.05$); fraction (b) of NDF was lower (69.5 vs. 79.3%, $P < 0.05$) and fraction (b) of CP did not differ (71 vs. 71.7%); fraction (a) of NDF and (t0) were only present in SWDG (5.6% and 2.7 h), and fraction (a) of CP was lower (0.0 vs. 18.2%). The ED of OM and CP were lower in SWDG compared to SG (44.3 vs. 69.8; 25.5 vs. 52.8%, respectively; $P < 0.05$) but the ED of NDF was greater (58.3 vs. 50.6%; $P < 0.05$). The N:OM ratio for microbial growth was better in SWDG than in SG (29.4 vs. 8.4 g of N effectively degraded/kg OM effectively degraded). The SWDG seems to be a good supply of ruminal PC and energy in ruminants' diets.

Key Words: sorghum, ethanol by-product, in situ

1879 (W338) Relative bioavailability of phosphorylated ascorbic acid in lactating dairy cows. C. K. Reynolds[*1], D. J. Humphries[1], C. E. S. Barratt[1], P. C. Aikman[1] and W. Steinberg[2], [1]*University of Reading, Reading, United Kingdom, [2]DSM Nutritional Products, Basel, Switzerland*

Rumen degradation limits ascorbic acid (AA) absorption from the small intestine. The objective of the present study was to determine the relative bioavailability of AA and phosphorylated AA (PAA) introduced into the abomasum of dairy cows. Four rumen fistulated lactating (207 DIM; 33.3 ± 1.8 kg/d milk) Holstein cows were fed a TMR once daily for ad libitum DMI (17.3 ± 0.7 kg/d). Cows initially received one of 4 treatments in a balanced 4 × 4 Latin Square design experiment with 1 wk periods. Treatments were control, 10 g AA in 250 mL saline injected rapidly into a jugular vein (JV) catheter, 10 g AA in 2 gelatine capsules placed into the abomasum via the rumen, or 10 g of AA as PAA (Rovimix Stay-C 35) in 2 gelatine capsules placed into the abomasum. After period 2, abomasal AA and PAA dose was increased to 100 g AA in 750 mL water. Controls were JV saline injection and abomasal gelatine capsules or water. Blood (JV) was sampled at intervals from 1 h before to 8 h after dosing. Urine was collected and sampled at intervals before and for 10 h after AA doses. Blood and urine were sampled at 24, 48, and 72 h after dosing. Samples were treated to convert dehydroascorbic acid to AA, stored at −80°C, and analyzed for total AA within 10 d. The area under the curve (AUC) for plasma AA concentration was calculated and the decrease in plasma AA concentration following the JV dose used to calculate AA kinetics. Data were analysed using mixed models for effects of cow, period, and treatment ($n = 6$). Comparison of the AUC for abomasal versus JV doses suggests the relative bioavailability of AA (7%) and PAA (5%) were similar but very low. The half-life of the JV dose averaged 66 ± 23 min, with an estimated pool size of 178 ± 42 L and a clearance rate of 2.07 ± 0.34 L/min. Urinary excretion accounted for only 7% of the JV dose, and plasma AA concentration remained elevated for 48 h. Estimates of the relative bioavailability of AA and PAA in lactating dairy cows suggest absorption from the small intestine is low. This may in part be due to a lack of previous exposure of small intestinal enterocytes to AA or differences in metabolism of intravenously injected versus absorbed AA.

Key Words: ascorbic acid, dairy cows, absorption

1880 (W339) Changes in serum IgG and total protein concentrations in calves fed differing amounts of colostrum replacer. J. D. Quigley, L. L. Deikun*, T. M. Hill, H. G. Bateman, II, J. M. Aldrich and R. L. Schlotterbeck, *Provimi North America, Brookville, OH*

It is unclear whether differences in serum IgG concentration of calves at 24 h (acquired passive immunity) influence the onset of active IgG production or the age at which serum IgG concentrations normalize. Our objective was to monitor changes in serum IgG and total protein (TP) concentrations in calves fed to achieve high (H) or low (L) passive immunity. Newborn Holstein calves (initial BW = 42.2 ± 4.7 kg) were individually fed a colostrum supplement ($n = 23$; 50 g of IgG/feeding) or a colostrum replacer ($n = 22$; 150 g of IgG/feeding) at 0.5 ± 0.22, 6.6 ± 0.46, and 12.9 ± 1.94 h of age. Blood was collected and serum analyzed for IgG using radial immunodiffusion and total protein using optical refractometer every 7 d from wk 0 (2–3 d of age) to wk 8. Calves were vaccinated with Inforce 3 (Zoetis) on arrival, Bovi-shield Gold 5 (Zoetis) at 2 and 6 wk and Presponse HM (Boehringer Ingelheim Vetmedica) at 5 and 8 wk, as prescribed by a veterinarian. Data were analyzed as a completely randomized design using repeated measures ANOVA. Serum IgG (g/L) and total protein (TP; g/dl) concentrations at 24 h of age were 19.4 ± 0.63 and 4.07 ± 0.076, respectively, in calves fed H, and 8.52 ± 0.62 and 3.32 ± 0.074, respectively, in calves fed L. Serum IgG and TP were affected by a week ´ treatment interaction ($P < 0.001$). Serum IgG concentration in calves fed H declined to 13.7 g/L at wk 3, then increased to 20.7 g/L at wk 8. Serum IgG in calves fed L declined to 6.3 g/L at wk 1, then increased to 20.6 g/L at wk 8. By wk 7, serum IgG concentration were similar ($P > 0.05$). Serum IgG was < 10 g/L for 0.3 and 4.9 wk in calves fed H and L, respectively. Total protein concentrations were lower in calves fed L from wk 0 to 6 ($P < 0.01$); thereafter, differences were not significant. Temporal changes in serum TP and IgG concentrations were independent. Active IgG synthesis was dependent on age of calf and acquisition of passive immunity.

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Calves with lower serum IgG concentrations at wk 0 began producing IgG at an earlier age and produced more IgG, so that by wk 7, circulating IgG concentrations were similar to those in calves with successful passive immunity.

Key Words: colostrum, immunoglobulins, calves

1881 (W340) Apparent synthesis of thiamin, riboflavin, vitamin B_6 and vitamin B_{12} in rumen of lactating dairy cows fed 2 concentrations of nitrogen and 2 energy sources. V. Beaudet[*1,2], R. Gervais[1], P. Y. Chouinard[1], P. Noziere[3], B. Graulet[3], M. Doreau[3] and C. L. Girard[2], [1]*Université Laval, Québec, QC, Canada,* [2]*Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada,* [3]*INRA-URH, Saint Genès Champanelle, France*

Effects of nitrogen supply and energy sources on apparent ruminal synthesis (ARS) and post-ruminal supply of thiamin, riboflavin, vitamin B_6, and vitamin B_{12} were evaluated using 4 lactating Holstein cows distributed in a 4 × 4 Latin square design with treatments arranged according to a 2 × 2 factorial. The cows were fitted with cannulas in proximal duodenum. The treatments were 2 concentrations of nitrogen: HIGH: 14% CP, i.e., 110% of the protein requirements and an adequate supply in rumen-degradable protein (RDP), vs. LOW: 11% CP, i.e., 80% of the protein requirements with a shortage in RDP; energy sources were STARCH from barley, corn, and wheat vs. FIBER from soybean hulls and dehydrated beet pulp. Diets were corn silage based, had the same forage: concentrate ratio (60:40, dry matter basis) and were isoenergetic. STARCH resulted in greater ($P < 0.01$) intakes of thiamin (51 vs. 34 ± 2.4 mg/d), riboflavin (1172 vs. 1050 ± 25.8 mg/d) and vitamin B_6 (202 vs. 161 ± 3.9 mg/d) as compared with FIBER, whereas nitrogen concentrations had no effect ($P \geq 0.76$). Vitamin B_{12} intake was not affected by treatments ($P \geq 0.43$) and averaged 86 ± 2.0 μg/d. Duodenal flow ($P = 0.34$; 35 ± 7.0 mg/d) or ARS ($P = 0.46$; −6 ± 7.6 mg/d) of thiamin were not significantly affected by treatments. STARCH increased duodenal flow of riboflavin ($P < 0.01$; 1546 vs. 1091 ± 92.4 mg/d) and vitamin B_6 ($P < 0.01$; 68 vs. 45 ± 4.9 mg/d) but decreased vitamin B_{12} flow ($P < 0.01$; 3127 vs. 9319 ± 731.1 μg/d) as compared with FIBER. HIGH nitrogen increased riboflavin and vitamin B_6 duodenal flows ($P = 0.02$; 1481 vs. 1156 ± 85.5 mg/d and $P = 0.01$; 67 vs. 47 ± 4.6 mg/d, respectively) and ARS ($P = 0.04$; 372 vs. 43 ± 95.2 mg/d and $P = 0.04$; -114 vs. -135 ± 6.3 mg/d, respectively). Nitrogen supply had no effect on vitamin B_{12} duodenal flows ($P = 0.64$) or the ARS ($P = 0.63$). Energy sources had no effect on ARS of vitamin B_6 ($P = 0.11$) but STARCH tended to increase the apparent production of riboflavin ($P = 0.06$; 374 vs. 41 ± 102.3 mg/d). Inversely, FIBER enhanced ARS of vitamin B_{12} ($P < 0.01$; 9234 vs. 3040 ± 730.3 μg/d, respectively). There was no interaction between treatments ($P \geq 0.09$). The apparent ruminal balance was affected by the nitrogen concentration for

synthesis of riboflavin and degradation of vitamin B_6, and by the energy sources for synthesis of riboflavin and vitamin B_{12}.

Key Words: apparent ruminal synthesis, B vitamins, dairy cow

1882 (W341) Apparent synthesis of thiamin and vitamin B_{12} in rumen of lactating dairy cows fed alfalfa or orchardgrass silages of different particle lengths. D. S. Castagnino[*1], K. Kammes[2], M. S. Allen[2], R. Gervais[3], P. Y. Chouinard[3], D. E. Santschi[4] and C. L. Girard[1], [1]*Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada,* [2]*Michigan State University, East Lansing, MI,* [3]*Université Laval, Québec, QC, Canada,* [4]*Valacta, Ste-Anne-de-Bellevue, QC, Canada*

Effects of forage particle length on apparent ruminal synthesis and post-ruminal supply of thiamin and vitamin B_{12} were evaluated in two experiments. Alfalfa and orchardgrass were harvested and ensiled at two theoretical lengths of cut: 19-mm (long cut, LC) or 10-mm (short cut, SC). Within a forage type, rations containing silages of each length of cut as the sole forage were offered to ruminally and duodenally cannulated lactating Holstein cows in crossover design experiments. Experiment 1 compared diets containing LC and SC alfalfa silage (~47% forage, ~20% forage NDF and ~25% total NDF) offered to 13 cows in two 19-d treatment periods. Experiment 2 compared diets containing LC and SC orchardgrass silage (~50% forage, ~23% forage NDF and ~28% total NDF) offered to 15 cows in two 18-d treatment periods. In Experiment 1, intakes of thiamin and vitamin B_{12} were greater ($P < 0.01$) for LC than SC (thiamin: 89.4 vs. 77.5 ± 2.13 mg/d; vitamin B_{12}: 118.6 vs. 67.1 ± 2.55 μg/d). Neither duodenal flows of thiamin ($P = 0.94$, 174.2 ± 18.87 mg/d) and vitamin B_{12} ($P = 0.17$, 8223 ± 713.0 μg/d) nor apparent ruminal synthesis of these vitamins (thiamin, $P = 0.15$, 90.9 ± 17.82 mg/d; vitamin B_{12}, $P = 0.16$, 8131 ± 711.0 μg/d) were affected by treatment in Experiment 1. In Experiment 2, there was no effect of treatment on the intake of vitamins (thiamin, $P = 0.79$, 71.9 ± 2.55 mg/d; vitamin B_{12}, $P = 0.85$, 111 ± 3.9 μg/d), duodenal flows (thiamin, $P = 0.80$, 156 ± 9.5 mg/d; vitamin B_{12}, $P = 0.88$, 6887 ± 476.0 μg/d), or their apparent ruminal synthesis (thiamin, $P = 0.82$, 84.1 ± 8.14 mg/d; vitamin B_{12}, $P = 0.88$, 6725 ± 473.0 μg/d). The reduction of legume particle length decreased the dietary supply of thiamin and vitamin B_{12}. However, forage particle length, in the studied range, did not affect apparent synthesis of thiamin and vitamin B_{12} in rumen or the supply of these vitamins to the sites of absorption.

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

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1883 (W342) Concentration of vitamin B12 in colostrum and milk from dairy cows fed different energy levels during the dry period.

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Bovine colostrum and milk are an excellent source of vitamin B_{12} for calves and humans, respectively, who rely on exogenous sources to meet their vitamin B_{12} requirements. The aim of the experiment was to evaluate vitamin B_{12} concentration in colostrum and milk from dairy cows fed different levels of energy during the dry period. A total of 84 Holstein cows were assigned to one of the following dietary treatments 60d before the expected calving date: 1) High energy one-group dry cow diet (HE; 1.35 Mcal NE_m/kg DM; 56% corn silage, 12% wheat straw, and 32% concentrate mix on a daily DM basis); 2) Low energy one-group dry cow diet (LE; 1.14 Mcal NE_m/kg DM; 28% corn silage, 36% wheat straw, and 36% concentrate mix on a daily DM basis); or 3) Intermediate step-up diet (IE; low energy diet from dry off until 30d before the expected calving and then switching to a diet representing a 50:50 blend of the low and high energy diets until parturition). After calving, all cows were fed the same diet using a TMR (44% corn silage, 13% grass silage, and 43% concentrate mix on a daily DM basis) until 42 d in milk (DIM). Colostrum samples were taken at the first milking after the parturition and milk samples were taken during the morning milking at 11 and 39 ± 2 DIM. Data were analyzed using treatment, time as well as treatment x time interaction as fixed effects. A significant treatment × sample interaction was observed ($P = 0.02$; Table 1883). Vitamin B_{12} concentration in colostrum differed among treatments ($P = 0.0002$) whereas no diet effect was observed on milk samples ($P > 0.97$). Colostrum from LE cows had a vitamin B_{12} concentration higher than IE cows ($P = 0.001$; Table 1883). In summary, results suggest that energy levels in diets during the dry period could change vitamin B_{12} concentration in colostrum but had no effect later on milk concentration of vitamin B_{12}.

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

Table 1883. Vitamin B_{12} concentration in colostrum and milk according to treatments

Vitamin B_{12} (pg/mL)	HE	LE	IE
Colostrum	27,815[ab] ± 1353	31,677[b] ± 1353	23,502[a] ± 1378
Sample 1	3932[a] ± 1353	3701[a] ± 1378	3774[a] ± 1378
Sample 2	3339[a] ± 1353	3125[a] ± 1378	3000[a] ± 1378

[a,b] Means in the same row with different superscripts differ ($P < 0.05$)

1884 (W343) Ruminal bacterial community structure of dairy cows fed conventional and reduced-fat dried distillers grains with solubles.

H. A. Ramirez Ramirez, C. J. R. Jenkins*, S. C. Fernando, C. L. Anderson, N. D. Aluthge and P. J. Kononoff, University of Nebraska, Lincoln

Four lactating, ruminally cannulated Holstein cows with (mean ± SD) 98 ± 11 DIM and 603 ± 52 kg BW were used in a Latin square design to test the effects of feeding regular dried distillers grains with solubles (DDGS) or reduced-fat DDGS (RF-DDGS) combined with rumen inert fat (RIF, as Ca-salts of long chain fatty acids) on ruminal bacterial community structure using a DNA pyrosequencing approach. Cows were housed in a tie-stall barn, fed once daily, and milked twice daily. In each 21-d period, cows were randomly assigned to 1 of 4 dietary treatments (values expressed on a DM basis): control diet (CON) was a conventional dairy ration (no corn ethanol by-products); a second diet (DG) contained 30% DDGS; a third diet (RF) contained 30% LF-DDGS and; a fourth diet (COMBO) contained 30% LF-DDGS supplemented with 1.9% RIF. Ruminal digesta was collected at 0, 8, and 23 h post-feeding on d 21 of each period and was immediately frozen (-20°C) for later analysis of the bacterial community. The rumen bacterial community was evaluated from frozen samples using the Roche 454 pyrosequencing platform. The sequences generated were analyzed using established MOTHUR and QIIME (Quantitative Insights Into Microbial Ecology) pipelines. Diet did not affect bacterial community composition at phylum level. The most abundant phyla were Firmicutes (46 ± 4.78%) and Bacteroidetes (51 ± 4.87%). The phylum TM7 accounted for 2.25 ± 0.41%. The Tenericutes, SR1, and Spirochaetes phyla were grouped as "Others" and accounted for 0.58 ± 0.10%. Time post-feeding had an effect ($P = 0.02$) on phyla distribution; the proportion of Firmicutes decreased from 52 to 39 ± 4% by 9 h post-feeding and increased to 46 ± 4% by 23 h; conversely Bacteroidetes increased from 45 to 58 ± 4% at 9 h post-feeding and decreased to 51 ± 4% by 23 h post-feeding. The results from this experiment demonstrate that phyla distribution is relatively stable across diets; nonetheless diurnal patterns in ruminal bacterial phyla relative to time post-feeding were observed. To our knowledge, this is the first study in dairy cattle that utilizes high throughput sequencing to analyze bacterial community structure to evaluate diurnal variation of the rumen bacterial community.

Key Words: microbial community, bacteria, sequencing

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1885 (W344) Diet influences microbial community composition, and methane emission in growing and finishing beef cattle.

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Methane production in ruminants via enteric fermentation is dependent on the microbial community within the ruminant animal. The microscale processes of this microbial community are greatly influenced by diet. However, the interactions between diet, microbial community composition, and methane emission are poorly understood. To better understand how diet influences microbial community structure and methane emission, methane/CO_2 ratio and microbial community composition were evaluated in animals on a common diet and under different dietary conditions (high and low quality forage, with and without monensin supplementation, and different levels of modified distillers grain plus solubles (MDGS) supplementation) in a 84-d growing trial, followed by a 125-d finishing trial that evaluated four different fat sources (corn oil, tallow, MGDS, corn-no oil) and monensin supplementation. Methane and CO_2 measurements were made during feeding using an individual feeding facility that contained 120 individual bunks equipped with the Calan gate system and an automated gas collection system. Gases were analyzed using a mobile GC unit. CO_2 was used as an internal standard and the methane/CO_2 ratio was used to determine the effects of diet on methane emission. Samples were collected for microbial community analysis via stomach tubing, and the microbial community structure was analyzed by sequencing the 16S rRNA gene. In growing cattle and finishing cattle, microbial community structure (both archaea and bacteria) and methane levels were similar in all animals on the common diet. In growing cattle, diet quality (high vs. low quality forage) significantly influenced ($P < 0.05$) the methane/CO_2 ratio and the microbial community composition, where high quality forage produced higher levels of methane. However, the level of methane emitted did not change by level of supplementation, but the microbial community composition did change significantly. In finishing cattle, methane levels were highest in MDGS diets and significantly decreased ($P < 0.05$) in corn control diet and 3% tallow diets. The microbial community did not show significant changes in total microbial community structure during supplementation of different fat sources. These data suggest dietary intervention can be used in growing cattle to change microbial community structure, which in turn can affect methane emission levels. Identifying the members of the rumen microbial community from high and low methane emitting cattle and diets would help identify microbial community members that influence methane production in cattle, which may lead to dietary and other intervention strategies to change these microbial populations in the rumen.

Key Words: microbial community, methane, archaea

1886 (W345) Dietary fatty acid profile affects plasma metabolic profile of peripartum Holstein cows.

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Concentration of plasma NEFA usually increases around calving due to mobilization of adipose tissue as a result of the inability of high-producing cows to consume enough energy to meet requirements for milk production and maintenance. Elevated NEFA concentration in the periparturient period is the major factor influencing postpartum accumulation of lipid in hepatic tissue. Whereas postpartum fat supplementation is a common practice in the dairy industry, prepartum fat supplementation is less common. The objective of this study was to examine the effect of feeding diets containing fat supplements enriched in either saturated FA or PUFA on metabolic responses of periparturient Holstein cows. Twenty four multiparous Iranian Holstein cows were assigned to diets with different fatty acid profiles and supplemented through 30 d before expected calving date to 50 d in milk. Dietary treatments consisted of (1) Prilled Palm fatty acids (PO) [Energizer RP10 , 2 & 2.25% DM in pre- and postpartum, respectively]; (2) Ca-salts of sunflower oil (SO) [Persia Fat- SO]; (3) Ca-salts of fish oil (FO) [Persia Fat- FO] and (4) equal amounts of Persia Fat- FO & Persia Fat- SO. Calcium salts were supplemented as 2.2 and 2.5% of dietary DM in pre- and postpartum period, respectively. All rations contained identical forage and concentrate components. Metabolite analyses were performed on blood samples collected weekly pre and post-partum and daily from -10 to 10 d relative to expected calving from tail vein. Data were analyzed using PROC MIXED of SAS 9.1 according with repeated measures in time function. Prepartum plasma contents of glucose, triacyl glycerol, cholesterol, total protein, urea, NEFA, BHBA and glycerol were not affected by type of lipid supplement, but Insulin, LDL, HDL, albumin and TNF-α concentration significantly increased in PO supplemented group than those supplemented with Persia Fat. In postpartum period, plasma levels of triacyl glycerol, total protein and urea were not affected by dietary fatty acid profile. However, Feeding Persia Fat, greatly reduced plasma concentration of NEFA, BHBA and glycerol along with lowering effects for TNF-α, suggesting that feeding protected PUFA sources can manage mobilization of body reserves. Statistically significant lower glucose and higher Insulin concentration in PO fed cows, in line with higher TNF-α levels can be a hint to lower insulin sensitivity compared with Persia Fat fed animals. Different profiles of protected PUFA sources didn't have any significant difference.

Key Words: PUFA, palm oil, insulin resistance, NEFA

1887 (W346) Prediction of enteric methane emissions in Holstein dairy cows fed various forage sources.

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Milk fatty acid (FA) profile has been previously used as a predictor of enteric CH_4 output in dairy cows fed diets supplemented with plant oils. The objective of this study was to investigate the relationships between milk FA and enteric CH_4 emissions in lactating dairy cows fed different types of forage. A total of 81 observations from 3 separate 3×3 Latin square design (with 32-d periods) experiments using a total of 27 lactating cows (96 ± 27 DIM; Mean $\pm$ SD) were used. In all experiments, dietary forages were included at 60% of ration DM and were: 1) 100% corn silage 2) 100% alfalfa silage 3) 100% barley silage 4) 100% timothy silage 5) 50:50 mix of corn and alfalfa silages, 6) 50:50 mix of barley and corn silages, and 7) 50:50 mix of timothy and alfalfa silages. Enteric CH_4 was measured in individual air-flow controlled chambers during 3 consecutive days. Milk was sampled during the 6 d of each period and analyzed for components and FA profile. Test variables included DMI (kg/d), dietary NDF (%), dietary EE (%), milk yield (kg/d), milk components (%), and individual milk FA (% of total FA). Associations between test variables and CH_4 were analyzed using the CORR procedure of SAS. The GLMSELECT procedure was used to identify a set of candidate models using the LASSO and LARS methods. Data were then fitted into a random regression using the MIXED procedure including the random effects of cow and period. The VC and UN covariance structures provided best fit for the random and repeated statements, respectively. Denominator degrees of freedom were calculated by the Satterhwaite equation. A positive association was observed between CH_4 and DMI ($r = 0.59$, $P < 0.001$), whereas negative associations were observed between CH_4 and $c9$–17:1 ($r = -0.58$, $P < 0.001$), and $t8$, $c13$–18:2 ($r = -0.51$, $P < 0.001$). The selected model predicted observations with a coefficient of determination of 0.92 and was: CH_4 (g/d) = $357.1 + 15.2 \times$ DMI– 56.9×15:0– $81.7 \times c9$–17:1– $t10$–18:1×41.0– $c11$–18:1×53.3– $t8$, $c12$–18:2×243.0– $t8$, $c13$–18:$2 \times 563.7.0$– $t11$, $c15$–18:2×242.9. Milk FA profile and DMI can be used to predict CH_4 emissions in dairy cows across a range of dietary forage sources.

Key Words: dairy cows, methane emissions, milk fatty acids.

1888 (W347) RNA-Seq detection of differential gene expression in the rumen of beef steers associated with feed efficiency phenotypes.

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The efficient utilization of feedstuffs is an economically important trait in beef production. The rumen is important to the digestive process of steers interacting with feed, microbial populations, and volatile fatty acids indicating it may play a critical role in feed efficiency. To gain an understanding of the molecules and pathways involved in gain, intake and utilization and identify candidate genes associated with steer feed efficiency, RNA-Seq was performed on rumen papillae from steers with extreme feed efficiency phenotypes ($n = 16$). The study population was divided into four Cartesian quadrants for intake $\times$ gain and steers ($n = 4$) from each quadrant were sampled. Three statistical analyses were performed to identify differentially expressed genes among feed efficiency phenotype. Two analyses were performed on total gene expression, the Negative Binomial and the Kruskall-Wallis. A separate analysis was performed by Cofactor Genomics on exon cluster expression. The Negative Binomial analysis identified 27 genes differentially expressed among feed efficiency phenotypes based on false discovery rate (FDR < 0.05). The Kruskall-Wallis analysis identified 19 differentially expressed genes based on P-value ($P < 0.05$). Cofactor Genomics identified 187 differentially expressed genes based on P-value ($P < 0.05$) and fold change (FC > 2). All genes identified by the Negative Binomial and Kruskall-Wallis analyses were tested for validation using real-time PCR and a subset of genes ($n = 23$) identified by Cofactor Genomics were tested for validation. Several genes (*ACAT1, CYP1A2, KLK10, KLK12, MIF, PDEE1A,* and *MYL1)* were identified by at least one analysis in this study and are supported by other studies. Five genes were identified by more than one analysis in this study (*KLK7, KLK10, KLK12, ARHGAP27,* and *RGS5)*. Cell death and survival, immunological disease, and metabolic disease were the top gene networks identified in association with gain, intake, and efficiency, respectively. Genes expressed in rumen papillae of beef steers may play a role in the feed efficiency of the animal. USDA is an equal opportunity provider and employer.

Key Words: RNA-Seq, beef cattle, rumen papillae

1889 (W348) Bioassay activity of different tannin sources by gas production technique. N. Vahdani[1], M. Dehghan banadaky[*2], F. Khalighi-Sigaroudi[3] and K. Rezayazdi[4], [1]*University of Tehran, Karaj, Iran,* [2]*Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* [3]*Institute of Medicinal Plants, Academic Center for Education, Culture and Research (ACECR), Karaj, Iran,* [4]*Department of Animal Science, University of Tehran, Karaj, Tehran, Iran*

Use of agricultural by-products, (such as pistachio hull, Pomegranate hull, Grape pomace, etc.), is often a useful way of overcoming shortage of animal feeds in many countries. These by-products contain tannins, causing reduction of protein utilization in ruminants. Tannin activity is affected by its source so this study was conducted to evaluate the effect of different sources of tannins on tannin biological effect by gas production technique. Each assay was repeated three times (runs). In all assays, 1 g of each sample was incubated in 120 mL serum bottles with or without 1 gr polyethylene glycol, PEG (MW. 4000), in triplicate. Rate and extent of gas production was determined by reading gas volumes at 2, 4, 6, 8, 12, and 24h of incubation time. Results showed that tea green leaves (1.44 in 2h after incubation) and grape pomace (1.45 in 2h after incubation) had more active tannins than others in all of incubation times ($P < 0.05$). In spite of same TP (180.18 and 182.5 gr/kgDM) and TT (115.35 and 108.38 gr/kgDm) content, pistachio hull and oak fruit tannins had different biological effect. Because there is no significant correlation between TP, TT and biological activity of tannins in all of incubation times. These results prove that independent of tannin content, different sources of tannins have different activities.

Key Words: tannin, bioassay, PEG

1890 (W349) Differences in formulation and bioavailability of commercial injectable fat-soluble vitamin products. D. B. Snider[*1], R. A. Zinn[2] and R. L. Stuart[3], [1]*Iowa State University, Ames,* [2]*University of California-Davis, El Centro,* [3]*Stuart Products Inc, Bedford, TX*

Injectable fat-soluble vitamins are utilized more quickly and efficiently than oral products. The major concern with injectables is chemical form and bioavailability of vitamins. A commercial product (VITAL EAD (V); Stuart Products, Inc.) contains retinyl palmitate, the storage form of vitamin A, and another commercial product (Natural EAD (N); Neogen Corp.) contains retinyl propionate. Otherwise, vitamin D and vitamin E sources and concentrations were the same. Two experiments were conducted to compare bioavailability of vitamins E and A. Exp 1 compared bioavailability in serum collected at 0, 24, 48, and 72 h. post-injection, and Exp 2 compared bioavailability at 0, 4, 8, 12, and 24 h post-injection.

All serum samples were analyzed for α-tocopherol and total vitamin A. Exp 1 utilized ten animals (130 kg), and Exp 2 utilized eight animals (200 kg). In Exp 1, five animals were injected with 5 mL of either product to provide 500,000 I.U. A, 50,000 I.U. D and 1500 I.U.E per animal. In Exp 2, four animals were injected with 6 mL of either product to provide 600,000 I.U. A, 60,000 I.U. D and 1800 I.U. E per animal. In Exp one, serum α-tocopherol concentrations at 0, 24, 48, and 72 h for V-injected animals were 0.48, 20.02, 5.22, and 4.05 μg/mL, respectively. Total vitamin A concentrations were 0.13, 5.85, 3.39, and 4.18 μg/mL, respectively. For N, serum α-tocopherol concentrations were 0.57, 5.72, 3.74 and 4.00 μg/mL; and total serum vitamin A concentrations were 0.13, 0.17, 0.07, and 0.08 μg/mL for the four sampling times. At 24 and 48 h samplings, serum α-tocopherol concentrations were different between the two products ($P < 0.01$). For total vitamin A, all sampling periods were different ($P < 0.001$). In Exp 2, serum α-tocopherol concentrations at 0, 4, 8, 12, and 24 h were 1.13, 15.50, 28.30, 23.8 and 20.3 μg/mL, respectively and total vitamin A concentrations were 0.22, 3.05, 8.34. 8.49, and 11.87 μg/mL for the V-injected animals. For N, serum α-tocopherol concentrations were 1.15, 5.25, 7.18, 7.00, and 8.95 μg/mL; and serum total vitamin A concentrations were 0.25, 0.32, 0.31, 0.30 and 0.39 μg/mL for the five time periods. All post-injection times 24 h and below were significantly different ($P < 0.01$) in favor of V. The basis for differences in bioavailability of the injectable vitamin A forms, notwithstanding similar label concentrations is uncertain and warrants further consideration.

Key Words: vitamin E, vitamin A, injectable, bioavailability

1891 (W350) Individual and additive value of conventional and non-conventional technologies in beef steers housed and fed using a GrowSafe feeding system. A. R. Harding[*1], G. K. Jim[2], C. W. Booker[2], E. J. Behlke[2], S. L. Parr[2], S. J. Hannon[2], T. M. Greer[2], Z. D. Paddock[2], M. L. May[2], L. Burciaga-Robles[2] and C. R. Krehbiel[1], [1]*Oklahoma State University, Stillwater,* [2]*Feedlot Health Management Services, Ltd., Okotoks, AB, Canada*

This study evaluated the effects of conventional and non-conventional production technologies in cattle. Animals (384 steers, 1101 ± 63 lb.) were utilized in an RCBD. Non-conventional production (NCP) included non medicated supplement and; NCP1:DFM (Sage Biosciences Inc., Edmonton, Alberta); NCP2: enzyme (Sage Biosciences Inc., Edmonton, Alberta); NCP3: Oleobiotec Ruminant (Oleo; Laboratoires Phodé, Terssac, France); NCP4: DFM, enzyme and Oleo. Blended production (BP) systems included BP1: supplement with Rumensin and Tylan (Elanco Animal Health, Guelph, Ontario), DFM, enzyme, and Optaflexx (Elanco Animal

Health) for the last 28 d; BP2: supplement with Rumensin, Tylan, DFM, enzyme, Oleo, and Optaflexx (last 28 d). Controls included a negative control (NEG): non-medicated supplement; and conventional production (CP): supplement with Rumensin, Tylan, and Optaflexx for the last 28 d. Animals were randomized within each production system to receive an implant (Component TE-S with Tylan (Elanco Animal Health), parasiticide (Dectomax; Zoetis Canada, Kirkland, Québec), both, or neither. Cattle were fed an average of 91 d and individual DMI were measured using GrowSafe (GrowSafe Systems Ltd., Airdrie, Alberta). Data were analyzed using the GLIMMIX procedure (SAS Institute Inc, Cary, North Carolina). Carcass adjusted ADG was improved ($P < 0.05$) in the NCP3, BP1,BP2 and CP groups over the NEG cattle. Carcass adjusted G:F improved ($P < 0.05$) in the NCP3, NCP4, BP1, BP2, and CP treatments over the NEG cattle. No differences ($P < 0.05$) were detected in carcass characteristics or animal health variables. Live and carcass adjusted ADG and G:F were improved in implanted animals vs. non-implanted animals ($P < 0.001$). Carcasses of implanted animals were less likely ($P < 0.05$) to grade Canada AAA and more likely to grade Canada AA than non-implanted animals. No performance or carcass differences were noted ($P > 0.05$) for parisiticide treatments. No interactions ($P > 0.05$) were observed between dietary program,implant, or parisiticide and no differences ($P > 0.05$) in animal health were detected for any treatments. The results of this study indicate that Oleo has potential to improve the performance of beef steers but not to the same extent as conventional production practices.

Key Words: feedlot, cattle, technology

1892 (W351) Effects of supplemental bupleurum extract on serum hormone and immune globulin levels in heat-stressed dairy cows. X. Sun[1,2,3], J. Cheng[1,2,3], N. Zheng[1,3,4], D. P. Bu[3], L. Pan[3] and J. Wang[*1,3,4], [1]Ministry of Agriculture- Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China

This experiment was conducted to evaluate the effects of bupleurum extract (BE) on serum hormone and immune globulin levels in dairy cows under heat stress. Forty lactating Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to one of four treatments. Treatments consisted of 0 (control), 0.25, 0.5, or 1.0 g BE/kg DM. The experiment lasted 10 wk. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via

tail vein before the morning feeding on Days 0, 21, 42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. Compared with controls, cows fed 1.0 g/kg BE had higher thyroxine (T_3) (1.43 vs. 1.16 ng/mL; $P < 0.05$) and prolactin (PRL) (230.50 vs. 188.19 uIU/mL; $P < 0.05$) levels, and 0.5 g/kg BE had the tendence to increase the T_3 (1.27 vs. 1.16 ng/mL; $P < 0.10$) level, but 0.25 and 0.5 g/kg BE had no effect ($P > 0.05$) on PRL level. Serum growth hormone (GH) level was increased (2.17 vs. 1.21 ng/mL; $P < 0.05$) in cows fed 0.25 g/kg BE compared with control cows, and tended to be higher (1.76, 1.69 vs. 1.21 ng/mL; $P < 0.10$) in cows fed 0.5 and 1.0 g/kg BE. Supplementation of BE had decreased the cortisol (COR) levels (48.35, 49.43, 49.86 vs. 64.49 ng/mL; $P < 0.05$), but had no effect ($P > 0.05$) on the levels of thyroxine, Insulin, glucagon, neuropeptide Y, leptin, insulin-like growth factor, and heat shock protein 70. Cows fed 0.5 g/kg BE increased the immunoglobulin (Ig) A content (279.25 vs. 179.78 μg/mL; $P < 0.05$), and IgG level was increased (36.54, 36.14 vs. 27.13 mg/mL; $P < 0.05$) in cows supplemented with 0.25 or 0.5 g/kg BE, while the IgM and tumor necrosis factor-α (TNF-α) levels showed no difference ($P > 0.05$) when compared with the control cows. These findings suggest that BE supplementation could relieve metabolic disorders and enhance immune function in heat-stressed cows.

Key Words: bupleurum extract;serum hormone; immune globulin

1893 (W352) Influence of additional tannins extract level on feedlot performance of finishing hair lambs. R. Barajas*, E. B. Bonilla, L. R. Flores, J. J. Lomeli and J. A. Romo, *FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico*

Forty eight Pelibuey x Katahdin hair lambs weighing $21.3 \pm$ SD 3.23 kg were used in a 70 d experiment to determine the influence of tannins extract level supplementation on feedlot performance of finishing hair lambs. Animals were blocked by initial weight and in groups of three, lambs were placed in 16 plastic floor elevated pens (1.5×1.6 m). In a complete randomized block design, within a block, pens were randomly assigned to four treatments as follows: 1) A 92% concentrate diet (14% CP; 2.07 Mcal of NEm/kg) formulated with corn grain and soybean meal without addition of tannins extract (CTRL); 2) CTRL and supplementation with 0.15% (DM basis) of tannins extract (TE15); 3) CTRL plus 0.3% (DM basis) of tannins extract (TE30); and 4) CTRL added with 0.45% (DM) of tannins extract (TE45). Lambs were fed twice a day. Tannins extract was supplied as a condensed and hydrolyzable tannins-blend obtained from quebracho and chestnut trees (Silvafeed-Bypro; SilvaTeam-Inudor, S.A., Argentina). Results were analyzed by ANOVA for a complete randomized block design, and the influence of TE level on performance variables was explored using polynomial contrasts. Pen was used as the experimental unit. Quadratic responses to TE level

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supplementation on final weight and average daily gain were observed ($P = 0.05$), mean values of ADG were 0.214, 0.242, 0.236, and 0.220 kg/d for CTRL, TE15, TE30, and TE45 treatments, respectively. Dry matter intake was not affected by treatments ($P = 0.38$). Feed conversion (feed/gain ratio) responded in a quadratic form ($P < 0.01$) to tannin extract supplementation level, with mean values of 4.61, 4.06, 4.25, and 4.75 kg of DMI/kg of gain, for treatments containing 0, 0.15, 0.30, and 0.45% of tannin extract in dietary DM, respectively. It is concluded, that addition of tannin extract to the diet improves in a quadratic manner the feedlot performance of finishing hair lambs, and the better supplementation level could be between 0.15 and 0.3% of dietary dry matter.

Key Words: feedlot-performance, lambs, tannins

1894 (W353) Supplementation of dairy cows before calving with β-carotene. R. C. Oliveira[1], B. M. Guerreiro[2], N. N. Morais Junior[3], R. L. Araujo[1], R. A. N. Pereira[4,5] and M. N. Pereira*[1,5], *Universidade Federal de Lavras, Lavras, Brazil, [2]Universidade de São Paulo, São Paulo, Brazil, [3]Instituto Federal de Educação, Ciência e Tecnologia do Espírito Santo, Colatina, Brazil, [4]Empresa de Pesquisa Agropecuaria de Minas Gerais, Lavras, Brazil, [5]Better Nature Research Center, Ijaci, Brazil*

The pre-calving supplementation of β-carotene was evaluated. The data set contained 283 Holsteins that received a treatment for > 14 d (29.1 ± 6.9 d). Cows were paired blocked by parity and expected calving date and assigned to a treatment: Beta-carotene (1.2 g/cow/d. Rovimix, DSM) or Control. The same TMR batch was offered to all cows and β-carotene was top dressed per cow once a day. Milk yield was recorded daily and sampled at 30.1 ± 8.3 d post-calving. Frequency distributions were analyzed with GENMOD of SAS using logistic regression for binomial data. Continuous variables were analyzed with MIXED. Within parity, nonparametric estimates of the survivor function for reproductive variables were computed using the product-limit method of the Kaplan-Meier method with LIFETEST. Plasma β-carotene content at the start of the experiment was similar (2.99 μg/mL, $P = 0.59$) and peaked at 3.26 μg/mL on day -15 pre-calving for supplemented cows (2.62 μg/mL for Control, $P < 0.01$). Colostrum density, milk yield, and milk solids content were similar ($P > 0.32$). Milk yield from d 20 to 109 of lactation was 3105 kg for primiparous and 3595 kg for multiparous ($P < 0.01$). Beta-carotene tended to increase milk protein content from 2.90 to 2.96% ($P = 0.09$) and to decrease the proportion of primiparous with a milk fat to protein ratio > 1.4 from 25.8 to 9.7% ($P = 0.10$). The proportion of primiparous with difficult calving, SCC > 200,000 cells/mL, metritis, progesterone > 1 ng/mL at 21 and 42 d, % conception at first service, and % pregnant at 90 and 150 d were similar ($P > 0.46$). There was a trend for decreased incidence of SCC > 200,000 cells/mL in multiparous supple-

mented with β-carotene (38.9% vs. 28.1%, $P = 0.12$), other variables were similar ($P > 0.21$). Beta-carotene reduced the proportion of multiparous with retained placenta 12 h post-calving from 29.9% to 21.7%, time of placenta release was 392 min (340 to 440) for β-carotene and 490 min (395 to 540) for Control (Median and 95% confidence interval. LogRank $P = 0.05$ and Wilcoxon $P = 0.04$). For primiparous, β-carotene did not determine placenta release (incidence was 15.4%). Responses in the intervals from calving to first estrous, to first service, and to conception were not detected. The pre-calving supplementation of β-carotene increased the plasma content around calving. There was no detectable response in milk yield or reproductive performance. β-Carotene reduced the incidence of retained placenta in multiparous cows.

Key Words: β-carotene, retained placenta, transition period

1895 (W354) Relationship between residual feed intake and mitochondrial function. M. M. Masiero*, M. S. Kerley and W. J. Sexten, *University of Missouri, Columbia*

Crossbred steers were used to determine if mitochondria complex I (C1) differed among residual feed intake phenotypes (RFI) and if C1 subunits (B-RFI) could account for additional differences in DMI. All experiments were analyzed as a completely randomized design. In Exp. 1 ($n = 26$) and 2 ($n = 24$) steers were fed no-roughage corn-based diets. Steers ($n = 13$) were fed an alfalfa haylage (30% diet DM) based diet during growing phase of experiment three and finished using no-roughage corn-based diets. We hypothesized calf DMI was influenced by metabolic efficiency (RFI) and subsequently C1 subunits could describe additional animal to animal DMI variation. Individual DMI was collected using GrowSafe feed intake system and used to calculate RFI and B-RFI. Band RFI was calculated similar to RFI with DMI as dependent and ADG, metabolic mid weight (MMWT) and C1 subunit (Band3) as independent variables. Blood samples were collected during growing phase of all experiments with an additional sampling during experiment three finishing phase to isolate mitochondria from lymphocytes. Complex I quantities were measured using immunocapture. Complex I subunits were separated into bands using gel electrophoresis and three bands were measured by densitometry. Dry matter intake was less and G:F was greater for–RFI compared to +RFI ($P < 0.05$) steers in all experiments. Band-RFI improved coefficient of determination by 17.04, 1.66, 12.65, 7.12, 12.89, and 2.68% compared to regressing intake on ADG and MMWT for experiment one, two, growing phase of three, finishing phase of three, and total period of experiment three using mitochondria measurements of growing and finishing phase of three, respectively. In experiment three, RFI was calculated for growing (d 0 to 70) and finishing (d 71 to 140) phases independently and for the total 140 d period. Residual feed intake correlation was 0.14 be-

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tween growing and finishing phases ($P = 0.63$), 0.79 between growing phase and total period ($P = 0.001$) and 0.65 between finishing phase and total period ($P = 0.01$). Using band 3 in regression equations improved agreement of–RFI from 60 to 75% and +RFI from 57 to 83% between growing phase and total period of experiment three. Growing and finishing phases had 40 and 29% agreement of–RFI and +RFI steers, respectively. In conclusion, mitochondrial complexes accounted for additional variation in intake among steers. Adding band 3 to intake regression equations improved coefficient of determination of all experiments. Residual feed intake phenotype may be influenced by age or cattle growing phase.

Key Words: feed efficiency, mitochondria, residual feed intake

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1896 (W355) Bioavailability of rumen protected choline sources when supplemented at different concentrations. K. J. Herrick[*1], J. A. Davidson[2], F. R. Valdez[1], M. J. Christofferson[1] and S. E. Schuling[3], *[1]Kemin Industries, Inc., Des Moines, IA, [2]Land O'Lakes Purina Feed, Gray Summit, MO, [3]Hubbard Feeds, Inc., Des Moines, IA*

Plasma choline is not an accurate measure of choline supplementation because of extensive liver metabolism. Our objective was to evaluate a method to estimate the bioavailability of rumen protected choline (RPC) products by comparing the response of plasma metabolites involved with choline metabolism. Choline chloride (0, 3, 6, or 9 g/d) was mixed in 2 L of isotonic solution and infused daily into the duodenum of 4 duodenally and ileal cannulated steers (337 ± 23.7 kg BW) to determine a response curve. An additional 6 steers and 2 heifers (322 ± 23.7 kg BW) were used in a replicated 4×4 Latin square experiment with 7 d periods to evaluate the RPC products. Both experiments were run concurrently and plasma was collected from all animals for 1 wk before the start of the experiment. Choline chloride was provided using 2 rumen protection technologies (SF and BT; Kemin Industries, Inc.). Treatments provided the following daily amounts of choline chloride: 1) 13 g by SF (LSF), 2) 36.0 g by SF (HSF), 3) 14.5 g by BT (LBT), and 4) 39.0 g by BT (HBT). All treatments were mixed with 0.45 kg of a concentrate mix and individually fed. In both experiments, plasma was collected at 0, 4, and 8 h after feeding on the last day of the baseline and each period. Plasma was analyzed for choline and amino acids. Response curves were determined by regressing plasma choline, methionine, homocysteine, and cysteine against infused dose using the Fit Model procedure in JMP (SAS Institute, 2010). These curves were used to calculate choline chloride delivered by RPC treatments. Plasma and calculated delivered choline chloride were analyzed using the Fit Model procedure in JMP with hour of sampling and treatment as fixed effects and cow as random effect. Plasma amino acids and choline did not

differ ($P > 0.05$) between RPC treatments. Calculated delivered choline chloride (4.71, 3.81, 3.37, and 6.25 g/d) did not differ ($P > 0.05$) for the LSF, HSF, LBT, and HBT treatments, respectively. However, the calculated delivered choline chloride for the RPC products was greater ($P < 0.05$) than during the baseline period. This would suggest that the method was appropriate and both of the RPC products were effective in providing a source of choline chloride.

Key Words: rumen protection, choline chloride, bioavailability

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1897 (W356) Effect of method of flaxseed processing and tannins on the growth performance and carcass fatty acid profile of lambs. E. Castillo-Lopez*, M. Edrosolam, P. J. Shand, D. A. Christensen and G. B. Penner, *University of Saskatchewan, Saskatoon, SK, Canada*

The objective of this study was to evaluate the effect of flax, method of processing, and tannin inclusion on the growth performance of feedlot lambs and the carcass fatty acid composition. Forty Suffolk × Arcott lambs (22 females and 18 males) with an initial BW of 37.7 ± 5.87 kg were assigned to 1 of 2 blocks and within block to 1 of 5 dietary treatments in a randomized complete block design. Treatments (DM basis) were 1) CONT, a diet containing 15% barley silage, 53.6% ground barley, 11.9% canola meal, 6.4% alfalfa dehydrated, 4.0% oat hulls, 3.7% beet pulp, 3.3% fat and 2.1% mineral supplement; 2) FLAX, inclusion of 8.6% flaxseed; 3) FLAX+T, inclusion of 8.6% flaxseed and 4% tannins; 4) EF, inclusion of 20.5% extruded flaxseed; 5) EF+T, inclusion of 20.5% extruded flaxseed and 4% tannins. At the end of the 60 d study, ruminal fluid, blood, longissimus dorsi (LM), and subcutaneous back fat samples were collected and analyzed for fatty acid composition. Fatty acids were expressed as percentage of total fatty acid methyl esters. Data were analyzed as a randomized complete block design using the MIXED procedure of SAS. Treatment did not affect final BW ($P = 0.60$) or ADG ($P = 0.36$) with averages of 55.3 ± 3.10 kg and 324.0 ± 29.75 g/d, respectively. The proportion of saturated fatty acids in ruminal fluid ($P < 0.01$) and plasma ($P < 0.05$) was greatest in lambs fed CONT and CONT had the lowest ($P < 0.01$) proportion of polyunsaturated and omega-3 fatty acids in plasma. The proportions of saturated ($P = 0.93$) and polyunsaturated ($P = 0.15$) fatty acids in LM were unaffected. However, lambs fed FLAX+T, EF or EF+T had the greatest ($P < 0.01$) proportion of omega-3 fatty acids, with a minimum of a 2.3-fold greater concentration ($P < 0.01$) than CONT. The proportion of polyunsaturated fatty acids in subcutaneous fat was greatest ($P < 0.01$) in lambs fed FLAX+T or EF+T. Lambs fed FLAX+T had the greatest ($P < 0.01$) concentration of omega-3 fatty acids in subcutaneous fat with an estimate of $3.13 \pm 0.189\%$: a value 3.3-fold higher ($P < 0.01$) than CONT. Overall, the fatty acid profile of lamb was improved when flaxseed or extruded flaxseed was fed without

affecting growth performance. Tannins had minimal additional effects on carcass fatty acid profile.

Key Words: extrusion, flaxseed, omega-3 fatty acids

1898 (W357) Evaluating the energy and protein requirements for growing Nellore heifers and steers fed two levels of calcium and phosphorus.
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An experiment was conducted to evaluate the energy and protein requirements for growing Nellore heifers and steers fed with two levels of calcium and phosphorus. Thirty two Nellore heifers and eighteen Nellore steers were used. Heifers were divided in four groups. Four animals served as baseline reference animals, four were fed at maintenance (MAIN) and twenty four received ad libitum (ADLIB) access to feed. The ADLIB animals were further divided into four groups and assigned to treatments. Treatments were: 1) Ca and P fed at requirements (CaPR) with a 50:50 of roughage:concentrate (R:C) diet; 2) CaPR with at 70:30 R:C diet; 3) 43% of the Ca and 80% of the P requirement (CaPL) with a 50:50 R:C diet; and 4) CaPL with a 70:30 R:C diet. All steers in this experiment were fed CaPR. Half of the heifers and steers were slaughtered at d 50 and the other animals were slaughtered a d 100 of the feeding period while all MAIN animals were slaughtered at d 100. Total feces and urine were collected from all animals 72 h before slaughter. The net energy (NEm) and metabolizable energy (MEm) requirement for maintenance were obtained by exponentially relating the heat production and the metabolizable energy intake, while the net energy requirements for gain (NEg) were obtained using empty body weight (EBW) and EBW gain (EBG). The net protein requirements for gain (NPg) were estimated according to EBG and retained energy (RE). NEm and MEm were 70.1 and 118 kcal/kg $EBW^{0.75}$, respectively. Net protein for maintenance was 1.28 g/kg $BW^{0.75}$ and NEg and NPg were estimated using the following equations: $NEg = 0.053 \times EBW^{0.75} \times EBG^{0.6301}$ and $NPg = 137.85 \times EBG - 0.05 \times RE$, respectively. Under the conditions of this experiment, the energy and protein requirements for growth were: $NEg = 0.053 \times EBW^{0.75} \times EBG^{0.6301}$ and $NPg = 137.85 \times EBG - 0.05 \times RE$, respectively.

Key Words: energy, protein, sugarcane