(KNN), K-mean, support vector machines and genetic algorithm. Each technique will be briefly explained using an example. With PCA, we first find a direction that has maximum variance. A second direction is then found, which has maximum variance of all directions perpendicular to the first. The process is repeated until there are as many directions (vectors) as original variables. Advantages of PCA are the dimension reduction and the ability to handle more predictors than observations. Disadvantages are that they often lack interpretation, and are linear models. Issues when only summary statistics are available (i.e., meta-analysis) will be explained, including the importance of properly weighing observations and accounting for the inherent blocking in the meta-design.

Key Words: big data, principal component analysis, meta-analysis

1296 Evaluation of multilevel mixed effect models.

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Simple mixed effect models have been extensively used in animal science literature. However, in some instances biological relationships require that models account for deviations of individual animals from that of the population. Furthermore, some animals might share similar genetic background because they are closely related (e.g., pig littermates) thus specification of animal within litter relationship (i.e., nested random effects) is necessary to model the hierarchical data structure. In some cases measurements taken on the same individual may not be independent (e.g., weekly BW measurements). This will result in models with heteroskedastic and serial correlated errors, which need to be evaluated and the errors minimized. Recent developments in statistical theory and computational power allow for specification of multilevel mixed effect models, especially nonlinear models. To demonstrate implementation of such models, an example is provided using data collected from an experiment with 40 pigs of 3 sexes originating from 17 litters and their BW measured weekly or every 2 wk up to 1,007 d. A multilevel mixed effects model was used within a growth function because it allows for estimation of all growth profiles simultaneously, and different sources of variation. Furthermore, variance in-homogeneity and within-animal correlation were introduced to the growth function. In the basic model, the variance was assumed to equal to identity matrix, i.e., the within-animal errors are independent, identical and random vectors. The basic model fit suggested that the within-animal variability increased with increasing BW and auto-correlation was also present. The variance-covariance matrix was then relaxed and decomposed into variance structure component and a correlation structure component that allows specification of model variance heterogeneity and serial correlation. Variance of the within-animal errors was modeled using a variance function, which when implemented reduced Bayesian Information Criteria (BIC) values to 8,950 compared to 9,861 for the basic model but did not remove the strong auto-correlation in the residuals. A continuous time autoregressive process of first order was applied to the within-animal errors because it deals with unequally spaced observations. This further reduced BIC to 7,146 due to removal of the serial correlated errors and thus inclusion of a continuous auto regressive process of first order is recommended when modeling frequently sampled growth data.

Key Words: multilevel mixed effect model, variance structure, autocorrelation

RUMINANT NUTRITION

1297 Effect of lactose inclusion in calf starters on rumen fermentation of weaned calves.

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The objective of this study was to evaluate the effects of lactose inclusion in calf starters on ruminal pH and VFA profile. Sixty Holstein bull calves were raised on an intensified nursing program using milk replacer containing 28% CP and 15% fat, until 56 d of age. Calves were fed texturized calf starters containing lactose at 0% (Control), 5.0% (LAC5), or 10.0% (LAC10; $n = 20$ for each treatment) on a DM basis. All calf starters were formulated for 23.1% CP. All calves were fed treatment calf starters ad libitum from d 7 and their hay (Klein grass) intake was limited to 150 g/d (as fed). Ruminal pH was measured every 2 min using small ruminant rumen pH loggers (Dascor, CA) immediately after weaning (d 55 to 62) for 15 calves (5 calves per treatment), and 3 wk after weaning (d 77 to 80) for the other 45 calves (15 calves per treatment). Daily mean, minimum, maximum ruminal pH, and duration and area under rumen pH 5.8 were not affected by treatment for both periods (d 55 to 62 and d 77 to 80). However, Spearman's correlation coefficient (r_s) was 0.306 ($P < 0.05$) between lactose intake and minimum ruminal pH for d 77 to 80, indicating that actual lactose consumption may affect ruminal pH. In addition, hay intake was not affected by treatment, but it was positively correlated with daily mean ($r_s = 0.338$, $P < 0.05$) and maximum ruminal pH ($r_s = 0.408$, $P < 0.01$), and the variation in hay intake might have masked treatment effects on ruminal pH. Ruminal molar ratio of acetate (mean ± SE) was 40.6 ± 1.26 (Control), 42.8 ± 1.26 (LAC5), and 45.3 ± 1.26% (LAC10), molar ratio of propionate was 40.2 ± 0.98 (Control), 38.1 ± 0.98 (LAC5), 35.3 ± 0.98% (LAC10), and acetate/propionate ratio was 1.01 ± 0.06 (Control), 1.15 ± 0.06 (LAC5), 1.29 ± 0.06% (LAC10) on d 80, and the differences were significant

between Control and LAC10 ($P < 0.05$) for ruminal fluid samples collected on d 80. However, molar ratio of butyrate was not affected by treatment. These results indicate that inclusion of lactose in calf starter affects ruminal VFA profile, but its effects on rumen pH warrants further investigation.

Key Words: calf, lactose, rumen

1298 Methionine:lysine ratio for crossbred suckling calves fed milk replacer and an amino acid complex. J. C. Chagas[1], M. A. Ferreira[1], M. R. Entjes[2], F. S. Machado[3], L. F. Costa e Silva[4], and M. I. Marcondes[*5], *[1]Universidade Federal Rural de Pernambuco, Recife, Brazil, [2]VHL University of Applied Sciences, Leeuwarden, Netherlands, [3]EMBRAPA, Juiz de Fora, Brazil, [4]Universidade Federal de Vicosa, Vicosa, Brazil, [5]Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Brazil.*

Knowledge about the amino acid (AA) requirements of dairy cattle is rare, and information regarding limiting AAs for suckling calves does not exist. Due to the difficulties in studying the AA requirements for ruminants, research is necessary to evaluate and determine optimal levels when including these AAs in the diet. Based on studies demonstrating lysine (Lys) and methionine (Met) as limiting AAs for neonates, we hypothesized that it is possible to determine the Met:Lys ratio that maximizes the performance of suckling dairy calves. This study evaluated the effect of increasing dietary Met:Lys ratios (DMLR) on performance and body composition of crossbred suckling calves of two different ages. Thirty-six male calves (Holstein-Gyr) were introduced in the experiment on the eighth day of age and randomly distributed among two slaughter ages (16 animals slaughtered at 30 d of age, and 20 animals slaughtered at 60 d of age) and four DMLR (44, 48, 52, and 56%), which were provided in the form of an AA complex (18.93 g) added to 905 g of milk replacer. The experimental diets were provided without permission of refusals, so the intake of dry matter and nutrients were the same for all animals, regardless of DMLR. Average daily gain (ADG), gain composition and body composition were evaluated separately for the two age groups for the linear and quadratic effects of DMLR. When necessary, the linear-plateau model was adjusted. Calves from 0 to 30 d of age did not show an improved performance due to increased DMLR; it is possible that animals up to 30 d of age had other metabolic priorities over body growth and protein deposition. For calves from 30 to 60 d of age, a linear-plateau response was observed for ADG and crude protein gain (CP); the greatest ADG observed was 590 g/d for a DMLR of 52.56% ($P = 0.001$), and the greatest CP deposition observed was 89 g/d for a DMLR of 52.33% ($P = 0.027$). Total body CP presented a quadratic behavior, with a maximum of 11.72 kg of CP for a DMLR of 53.91% ($P = 0.040$). The increased DMLR did not influence performance of calves from 0 to 30 d, and the optimal DMLR that ensured the best performance of calves from 30 to 60 d of age was situated between 52 and 54%.

Key Words: bovine, body composition, crude protein

1299 Effects of organic or inorganic Co, Cu, Mn, and Zn supplementation to weaned calves during preconditioning on their productive and health responses. K. Lippolis[*1], R. F. Cooke[1], L. G. T. da Silva[2], K. M. Schubach[1], A. P. Brandao[1,2], R. Marques[1], C. K. Larson[3], T. DelCurto[4], and D. W. Bohnert[1], *[1]Oregon State University- EOARC Burns, Burns, [2]UNESP- FMVZ, Botucatu, Brazil, [3]Zinpro Corporation, Eden Prairie, MN, [4]Oregon State University- EOARC Union, Union.*

This experiment compared productive and health parameters of weaned calves receiving or not supplemental Co, Cu, Mn, and Zn from an organic or inorganic source during a 45-d preconditioning program. Ninety Angus × Hereford calves were weaned on d −1 and immediately allocated according to weaning BW and age (BW = 261 ± 2 kg, age = 224 ± 2) to a18-pen drylot with 5 calves per pen (steers, $n = 4$; heifers, $n = 1$). Pens were randomly assigned to receive: 1) supplementation with inorganic sulfate sources of Cu, Co, Mn, and Zn (INR), 2) supplementation with an organic source of Cu, Mn, Co, and Zn (ORG; Availa®4; Zinpro Corporation, Eden Prairie, MN), and 3) no supplementation of Cu, Co, Mn, and Zn (CON). During the preconditioning phase (d 0 to 45), calves received mineral treatments while offered free-choice hay and 2.7 kg/d of corn-soybean meal concentrate. The INR and ORG were included into the concentrate, and formulated to provide the same daily amount of Cu, Co, Mn, and Zn. Calf ADG during preconditioning was calculated based on average initial BW (d −1 and 0) and final BW (d 44 and 45). Liver samples were collected via needle biopsy on d 0, 22, and 45. Calves received vaccination on d 15 and 29. Blood samples were collected on d 15, 29, and 45, and analyzed for plasma concentrations of antibodies against *Mannheimia haemolytica*. No differences were detected ($P \geq 0.15$) among CON, INR, and ORG calves for initial (d 0) liver Co, Cu, Mn, and Zn concentrations. On d 22 and 45, liver Cu and Co concentrations were greater ($P < 0.01$) for INR and ORG calves compared with CON. Moreover, ORG calves had greater ($P = 0.05$) liver Co concentrations on d 45, but similar ($P = 0.35$) liver Co on d 22 and similar ($P \geq 0.63$) liver Cu on d 22 and 45 compared with INR calves. Liver Zn and Mn concentrations were similar ($P \geq 0.14$) among CON, INR, and ORG calves on d 22 and 45. No differences ($P \geq 0.17$) were detected among treatments for feed intake, BW gain, health variables, or antibodies against *M. haemolytica*. Therefore, supplementation with inorganic or organic Co, Cu, Mn, and Zn during a 45-d preconditioning period

did not impact performance and health response of weaned feeder calves.

Key Words: beef cattle, performance, preconditioning, trace minerals

1300 Dynamics of prepartum β-carotene supplementation among cow, colostrum, and calf. C. M. Prom*[1], M. A. Engstrom[2], and J. K. Drackley[1], [1]*University of Illinois, Urbana,* [2]*DSM Nutritional Products, LLC, Parsippany, NJ.*

Little is known about transfer of dietary β-carotene into colostrum, its absorption by the calf, and its effects on vitamins A and E in the cow when dietary vitamin A is adequate. Our objective was to assess the impact of β-carotene supplementation during the close-up dry period on the cow, colostrum, and calf. The study was conducted on a large commercial dairy farm in Indiana during early summer of 2015. Ninety-four multiparous Holstein cows were assigned to either control (CON) or β-carotene (BC) treatments. While locked in headgates each morning, each cow received a topdress of β-carotene (Rovimix, 8 g/d; provided 800 mg β-carotene) or carrier from 21 d before expected calving until calving. Blood samples were collected at 21 d before expected calving (before treatments began), 7 d before calving, immediately following parturition, and 7 d postpartum. Colostrum was collected immediately following parturition. Calf blood samples were obtained within 2 h of birth before receiving the dam's colostrum, at 24 h after birth, and at 7 d and 60 d of age. Blood serum was analyzed for vitamins A and E, cholesterol, and β-carotene. Colostrum was analyzed for β-carotene, vitamins A and E, and colorimetry profile. Data were assessed using the MIXED procedure in SAS. Calf serum β-carotene data were analyzed using the FREQ procedure. Compared with CON cows, BC cows had higher concentrations of β-carotene ($P < 0.01$), vitamin A ($P < 0.01$), and vitamin E ($P < 0.01$), and a greater vitamin E:cholesterol ($P < 0.01$) in serum at all times. Colostrum β-carotene was higher for BC cows ($P < 0.01$). Colostrum from BC cows had increased a* ($P < 0.01$) and b* ($P < 0.01$) colorimeter values, indicating that β-carotene altered colostrum color. Before receiving colostrum, the concentration of β-carotene in calf serum was below the detectable threshold of 0.05 ug/mL. At 24 h of age, the number of calves with detectable β-carotene concentrations increased, with more calves from BC cows (52.1%) having detectable concentrations than calves from CON cows (6.1%, $P < 0.01$). No differences in concentrations of vitamins A or E were observed in calves. In pregnant cows already receiving adequate vitamin A, supplementation of β-carotene increased concentrations of β-carotene, vitamin A, and vitamin E, increased concentration of β-carotene in colostrum, and increased serum β-carotene in calves.

Key Words: β-carotene, transition cows, colostrum

1301 Effect of supplementing increasing levels of RUP on growing performance in calves fed a silage-based diet. C. R. Oney*[1], R. G. Bondurant[1], F. H. Hilscher[1], A. K. Watson[1], G. E. Erickson[1], J. C. MacDonald[2], and T. J. Klopfenstein[1], [1]*University of Nebraska, Lincoln,* [2]*University of Nebraska-Lincoln, Lincoln.*

An 84-d growing study, utilizing 60 steers (initial BW = 290; SD = 18 kg), evaluated the effects of supplementing increasing levels of RUP on growing performance of calves fed a silage-based diet. All steers were individually fed using the Calan gate system. Five levels of supplementation were evaluated with 12 steers per level of supplement. Supplement levels consisted of 0, 3.25, 6.5, 9.75, and 13% RUP (as a % of diet DM). The RUP supplement consisted of 60% SoyPass and 40% Empyreal. The diet consisted of 85% corn silage with the remaining 15% of the diet being accounted for in the supplement (DM basis). Supplement included RUP, urea, minerals, and carrier replaced by RUP. Initial and ending BW were obtained by collecting BW across 3 consecutive days and averaging after cattle had been limit fed a 50% Sweet Bran and 50% alfalfa diet at 2% of BW for 5 d. Cattle were assigned to treatment based on d −1 and 0 BW. Interim BW were collected on d 36 and 37 and shrunk 4% to account for gut fill. There were no differences in DMI ($P = 0.33$) among treatments for period 1 (d 1 to 37). However, ADG ($P < 0.01$) and G:F ($P < 0.01$) both increased linearly as RUP inclusion increased during period 1. Using the NRC model, MP balance for period 1 increased from −200 to +65 g/d as RUP inclusion increased from 0 to 13%. At 9.75% RUP inclusion MP balance was reached at +2 g/d. There were no differences in DMI ($P = 0.16$), ADG ($P = 0.11$) or G:F ($P = 0.32$) for period 2 (d 38 to 84). For the overall growing period (d 1 to 84), as supplemental RUP inclusion increased from 0 to 13%, a linear increase was observed in ending BW ($P < 0.01$). With no difference in DMI ($P = 0.19$) between the five treatments, averaging 7.67 kg/d, and a linear increase in ADG ($P < 0.01$), G:F linearly increased ($P < 0.01$) from 0.148 to 0.174 as RUP inclusion increased. The MP balance increased from −186 to +98 g/d as RUP inclusion increased from 0 to 13%, at 9.75% RUP inclusion MP balance was reached at +26 g/d. Increasing the amount of RUP in silage growing diets increases ending BW, ADG and G:F by meeting MP requirements.

Key Words: corn silage, growing cattle, rumen undegradable protein

1302 The effects of a high- or low-plane of nutrition pre-weaning on growth and starter intake of group-housed calves. J. Haisan[*1], M. Oba[1], D. J. Ambrose[2], and M. Steele[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]Livestock Research Branch, Alberta Agriculture and Forestry, Edmonton, AB, Canada.*

The objective was to determine the effects of plane of nutrition, when fed through an automated calf feeder, on starter intake and growth of group-housed calves. Twenty-six female Holstein calves were fed 8L of colostrum in the first 36 h of life before being offered pasteurized whole milk and randomly assigned to either a HIGH (10L/d; n = 12) or LOW (5L/d; n = 14) plane of nutrition. All calves were allowed 2.5L of milk per meal until d 48 when a 10-d weaning transition began, where milk was reduced by 10% per day, resulting in all calves being weaned at d 58. Calf starter and water were provided ad libitum starting on d 3. Calves were housed in individual pens for the first 21 ± 3 d and fed using the Calf Rail system (Förster-Technik, Germany) before moving to a group pen where they were fed through an automated calf feeder. Individual starter intake was measured via an automated system on a daily basis from d 25 to 70, and body weights (BW) were measured weekly from birth to d 70. Blood samples were taken in the first week of life and with no differences observed in serum protein (5.3 ± 0.32 vs. 5.3 ± 0.32 mg/dL; P = 0.95) or immunoglobin concentration (17.67 ± 1.80 vs. 15.35 ± 1.80 g/L; P = 0.37). Birthweight of calves was not different between the treatment groups (40 ± 1.25 vs. 42 ± 1.25 kg; P = 0.27) however BW at d 70 was greater for HIGH than LOW calves (113.5 ± 2.03 vs. 100.11 ± 2.03 kg; P < 0.01). Pre-weaning average daily gain was greater for HIGH than LOW (0.90 ± 0.03 vs. 0.65 ± 0.03 kg/d; P < 0.01), however no difference was seen post-weaning (1.30 ± 0.06 vs. 1.29 ± 0.06 kg/d; P = 0.96). Before the weaning transition (d 42 to 48) starter intake (g/d) was greater in calves on the LOW than HIGH plane of nutrition (591 ± 89 vs. 1,273 ± 93, P < 0.01, respectively). Starter intake over the 10-d weaning transition tended to be greater for LOW than HIGH calves (1,490 ± 112 vs. 1,181 ± 116; P = 0.07), however post-weaning no difference was seen between treatments (2,723 ± 200 vs. 3,188 ± 200; P = 0.11). Results indicate that feeding more milk pre-weaning may suppress starter intake, however, the effect is not carried post-weaning and does not compromise growth.

Key Words: feeding system, group housing, starter intake

1303 Evaluation of stay strong for new born dairy calves. K. Froehlich[*1] and D. P. Casper[2], *[1]South Dakota State University, Brookings, [2]Dairy Science Department, South Dakota State University, Brookings.*

Stay Strong (SS) is a blend of essential oils designed to help diminish health challenges and stresses experienced by newborn calves. Current feeding inclusion rates are unknown to achieve optimal performance in the first 8 wk of life. Study objectives were to determine feeding inclusion rates of SS when added to milk replacer (MR) to achieve optimal performance, while comparing performance to a yeast cell wall (YCM) gut health technology. One hundred Holstein calves were used for the study blocked by birth date and randomly assigned to 1 of 5 treatments; 24:20 control MR (C), 24:20 MR with an inclusion rate of either 1.25 g (SS-0.5), 2.5 g (SS-1.0) or 3.75 g (SS-1.5) calf/feeding, or 24:20 MR with an inclusion of YCM at a rate of 2 g/calf/feeding. Calves were sourced from a commercial SD dairy farm where they were fed colostrum for the first 2d and then were transported to SDSU. 24:20 MR was fed at a rate of 0.28 kg/calf/d at 2x/d for 14d via bucket, and then increased to a feeding rate of 0.43 kg/calf/d at 2x/d until 35d. Feedings were reduced to 1x/d at 36d to facilitate weaning at 42d. Decoquinate was added to MR at 37.8 g/ton for coccidiosis control. Calves were housed in individual Calf-Tel hutches bedded with straw with ad libitum access to a 20% CP calf starter (CS) and water. SS-0.5 average daily gain (ADG) through 56d was greater (P < 0.05) compared to SS-1.0 and YCM, and tended (P < 0.10) to be greater for C and SS-1.5. ADG averaged 1.44, 1.57, 1.41, 1.40, and 1.39 kg/d for C, SS-0.5, SS-1.0, SS-1.5, and YCM, respectively. Total gain was increased for SS-0.5 vs. SS-1.0 and YCM, with body gains averaging 81.2, 87.89, 78.32, 78.9, and 78.04 kg for C, SS-0.5, SS-1.0, SS-1.5, and YCM, respectively. Body length gain was similar among treatments with an exception of SS-0.5 having a greater gain vs. SS-1.5 (P < 0.02). Hip width was similar among treatments. Wither height gain through 56d was greater for SS-0.5 vs. C, SS-1.0, SS-1.5, and YCM. Hip height gain was also increased for SS-0.5 vs. C, SS-1.0, SS-1.5 and was similar for SS-0.5 and YCM. This data demonstrates that feeding SS at 1.25 g/calf/d to a 24:20 MR will enhance growth rates compared to calves fed a modified accelerated 24:20 MR and a 24:20 MR containing YCW technology.

Key Words: calf, essential oils

1304 Effects of supplementing pasteurized waste milk with vitamins A, D and E on fat-soluble vitamin status, growth, and health of calves. L. Blakely*[1], M. Kweh[1], M. Poindexter[1], R. L. Stuart[2], and C. D. Nelson[3], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*Stuart Products Inc, Bedford, TX,* [3]*University of Florida, Gainesville.*

The objective of this study was to determine the effects of a milk supplement, MILKADE® (Stuart Products, Inc.), on growth, health and fat-soluble vitamin status of calves fed pasteurized whole milk. The MILKADE supplement contained 50,000 international units (IU) vitamin A as retinyl-palmitate, 50,000 IU vitamin D_3, and 500 IU vitamin E as *RRR-α-tocopherol* per milliliter of product. Forty Holstein calves (19 bulls, 21 heifers) were enrolled at birth and assigned to either control (n = 18, no supplement), 0.25 mL MILKADE (0.25ADE, n = 12), or 0.5 mL MILKADE (0.5ADE, n = 10) treatments. Calves were provided 2.85 L of pasteurized waste milk twice per day and the supplement was added individually to the calves' milk at the morning feeding. Feed intake and health scores were recorded daily. Bodyweight and height and serum samples were collected weekly from birth until 3 wk (bulls) or 6 wk (heifers) of age. Responses to treatments were analyzed as repeated measures. Serum retinol concentrations averaged near 400 ng/mL during the trial and were not different (P = 0.45) between treatment groups. In contrast, control calves were vitamin D deficient throughout the trial with average 25-hydroxyvitamin D (25(OH)D concentrations < 10 ng/mL of serum, whereas, 25(OH)D concentrations of 0.25ADE and 0.5ADE calves reached 90 and 150 ng/mL of serum, respectively, after 3 wk (P < 0.001). Similarly, serum α-tocopherol concentrations of control calves remained below 1.5 μg/mL throughout the trial but reached approximately 4.5 μg/mL of serum for both 0.25ADE and 0.5ADE groups after 5 wk (P < 0.05). There was a treatment effect on overall body weight (P = 0.004) such that 0.25ADE and 0.5ADE calves weighed less than control calves (49.3 kg and 46.4 kg vs. 52.1 kg, P = 0.013 and P < 0.001, respectively) at 3 wk of age. However, there was no difference in BW of heifers at week 6 of the trial (P = 0.171). There was no difference in feed intake or fecal and respiratory scores between groups (P > 0.05). In conclusion, calves fed pasteurized whole milk are deficient in vitamins D and E. Daily intakes for vitamins A and E were within ranges determined optimal for calves. Upper limits for supplemental vitamin D have not been established but the high serum 25(OH)D of the supplemented calves indicates vitamin D intakes above 10,000 IU/d are perhaps excessive for neonatal calves.

Key Words: dairy calves, nutrition, vitamins

1305 Effect of phytogenic compounds fed to preweaned calves. B. G. Miller*[1] and C. Scheider[2], [1]*Biomin USA, Warrenton, MO,* [2]*BIOMIN Holding GmbH, Herzogenburg, Austria.*

Maximizing early muscle growth is important in lifetime muscle development. Additionally, growth promoting antibiotics that have been typically used in the past may not be available in the future. Phytogenic (herbal) compounds may represent a potential to replace growth promoting antibiotics. A trial was conducted using Belgian Blue and Simmental bull calves in which mixed phytogenic products included in milk replacer and calf starter. Calves were separated into group based on breed and initial weight. (Control calves weighed 93 kg, Treatment calves weighed 94 kg) Calves were fed for 52 d. Control calves received a diet of calf milk replacer, for the first 3 wk. Cereal grains and a "calf starter feed" were offered from the first week on. Hay was made available throughout the trial and corn silage was offered from Day 21 to 52. Treatment calves received the same diet as control with the exception of Digestarom Milk (phytogenic product) added to the milk replacer at a rate of 500 gm/MT of calf milk replacer. The treatment calves also received Digestarom Calf in the calf starter at a rate of 300 gm/MT. Feed intake for calves was measured throughout the trial period. Calves were weighed on Days 21, 42, and 56. Data was analyzed via independent t test (SPSS). Control calves consumed numerically, but not statistically (P > 0.10) less average intake per day through out the total period, Days 1 to 56, than did treatment calves, 2.41 vs. 2.46 kg, respectively. Calves receiving Digestarom products improved in average daily gain throughout the trial at each weighing, and for the 56 d period demonstrated and increase of 0.10 kg in average daily gain (P < 0.05). Control calves gained 1.23 kg per day, while treatment calves gained at 1.33 kg per day (P < 0.05). Feed conversion improved numerically from 1.97 for control calves to 1.86 for treatment calves (P > 0.10). This work supports previous work with these and similar phytogenic products that have demonstrated a positive effect on the growth rate of neonatal and young ruminants. As such these and similar products represent a potential replacement of alternative growth promoting technologies.

Key Words: phytogenic calves

1306 Feeding steers extruded flaxseed and hay in a total mixed ration or sequentially can have substantial effects on beef fat polyunsaturated fatty acids and biohydrogenation intermediates.
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There has been growing interest in increasing the content of polyunsaturated fatty acid (PUFA; esp. α-linolenic acid, ALA) and their biohydrogenation intermediates (BHI) in beef, particularly *trans* 11–18:1 (VA, vaccenic acid) and *cis* 9, *trans* 11–18:2 (RA, rumenic acid) due to their potential positive health effects. However, high variability in PUFA and BHI have been found in beef between and within trials. The present trial was designed to determine if feeding steers extruded flaxseed (Linpro-R™; O&T Farms Ltd.,SK, Canada) and hay (25% and 75%; DM basis) together as a total mixed ration (TMR), or sequentially (non-TMR) would result in different enrichments of PUFA and BHI in different beef adipose tissues. Forty-eight Continental crossbred steers (325 ± 16 kg SD) were stratified by weight to 6 pens of 8 steers, pens were randomized to either TMR or non-TMR and steers were fed ad libitum for 240 d. At slaughter, subcutaneous fat (SCF) and perineal fat (PRF) samples were collected, freeze dried and directly methylated with 0.5 M sodium methoxide, and analyzed by GC using a 100 m CPSil 88 capillary column. Data were analyzed as a one-way ANOVA using the PROC MIXED procedure of SAS with diet as the main factor and pen as the experimental unit. Treatment means were generated and separated using the LSMEANS and PDIFF options, respectively. Compared to TMR steers, non-TMR steers had greater proportions of PUFA, *trans*-18:1, conjugated linoleic acids, and conjugated linolenic acids in both SC (+9.7%, +9.8%, +43.4%, +63.7%) and PR (+14.1%, +10.5%, +52.9%, +75.6%). In SCF, the percentages of ALA, VA and RA were increased ($P < 0.001$) from 0.91%, 4.92% and 1.91% in TMR steers to 1.10%, 6.82% and 2.69% in non-TMR steers. In PRF, the percentages of ALA,VA and RA were increased ($P < 0.001$) from 0.89%, 7.29% and 0.72% in TMR steers to 1.06%, 10.32% and 1.13% in non-TMR steers. Our results suggest that the method of feeding PUFA sources (e.g., flaxseed) can profoundly affect the enrichment of PUFA and their BHI in beef fat. In addition, the enrichment of these fatty acids also depends on fat depot, with PRF having greater proportions of VA, while SCF being higher in RA, which is likely due to the greater delta-9 desaturation of VA to RA in SCF.

Key Words: beef, flaxseed, feeding management, omega-3, rumenic acid, vaccenic acid

1307 Fatty acid composition of intramuscular lipids from Nellore and Brangus bulls fed diets supplemented with cottonseed.
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Finishing bulls were used in a factorial design with 2 breeds and 2 diets with contrasting fat levels to evaluate changes in marbling and fatty acid profile of intramuscular lipids. Nellore ($n = 20$) and Brangus ($n = 20$) bulls were randomly assigned to a low (LFD) or a high fat diet (HFD): 3.2% vs. 6.4% ether extract. The diets had similar energy and protein levels and were composed by sorghum silage (30% DM), soybean hulls, ground corn, soybean meal, urea and a mineral mixture. HFD additional fat derived from cottonseed (18% DM), in substitution to ground corn (31% vs. 52%, on HFD and LFD, respectively). The experiment lasted 71-d. All carcass were evaluated for marbling (1 to 18 scale) and back fat thickness (BFT). *Longissimus dorsi* (LD) samples were randomly selected from four animals of each treatment for fatty acid analysis by gas-chromatography. Fatty acid composition is expressed as g/100 g of total lipids. All data were analyzed using the GLM procedure of SAS (SAS, 2011) with animal as the experimental unit and genetic group, diets and the interaction between them as class variables. Back fat thickness was similar among treatments (5 mm, on average), but marbling was higher for Brangus. There was significant breed vs. diet interaction ($P < 0.01$), mainly because marbling with LFD was much more intense for Brangus than Nellore (8.0 vs. 3.3), while for HFD it was quite similar (Brangus = 5.8 vs. Nellore = 5.3). Fatty acid composition of intramuscular lipids showed that samples from Brangus bulls had more palmitic (C16; 17.7% vs. 15.3% $P < 0.05$), stearic (C18; 11.9% vs. 8.9% $P < 0.05$), oleic (C181c9; 28.1% and 23.3%), and elaidic (C181t9; 0.15% and 0.12%, $P < 0.05$) acids. They also had 20% and 18% greater saturated (SFA) and monounsaturated (MUFA) fatty acids ($P < 0.05$), respectively. HFD diet increased the amount of stearic acid (C18; 11.5% vs. 9.3% $P < 0.05$) and resulted in more than 20% higher ($P < 0.05$) elaidic acid and C18:2 non conjugated isomers, whereas the content of rumenic acid (C182c9t11, mean 0.19%) was unaffected by genetic group or diet. Differences in fatty acid content among Brangus and Nellore LD are in accordance with higher marbling from the former. Cottonseed fatty acid profile may have been extensively biohydrogenated, as suggested by the higher levels of stearic acid in HFD samples. Marbling differences among breeds had more impact in intramuscular fatty acid profile than supplementation with cottonseed.

Key Words: Meat, Lipid, Zebu

1308 Effects of dietary fat on fertility of dairy cattle: a meta analysis and meta-regression.

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There is increasing evidence of positive effects of feeding fats during transition on fertility and the adaptation to lactation. This study utilized meta-analytic methods to explore the effects of including fats in the transition diet on the risk of pregnancy to service ('proportion pregnant') and calving to pregnancy interval. Meta-analysis was used to integrate smaller studies, and increase the statistical power over that of any single study and explore new hypotheses. We explored the effect of fats and diet composition on fertility using meta-regression methods. There were relatively few highly controlled studies providing detailed descriptions of the diets used that examined interactions between fat nutrition and reproductive outcomes. Only 17 studies containing 26 comparisons were suitable for inclusion in statistical evaluations. Reproductive variables evaluated were risk of pregnancy 'proportion pregnant', primarily to first service, and calving to pregnancy interval. Production variables examined were milk yield, milk composition, and body weight. The sources of heterogeneity in these studies were also explored. A 27% overall increase in pregnancy to service was observed (RR = 1.27; 95% Confidence interval Knapp Hartung 1.09 to 1.45) and results were relatively consistent (I^2 = 19.9%). A strong indication of a reduction in calving to pregnancy interval was also identified, which was consistent across studies (I^2 = 0.0%) supporting a conclusion that overall, the inclusion of fats does improve fertility. Further exploration of the factors contributing to proportion pregnant using bivariate meta-regression identified variables that reflected changes in diet composition or animal response resulting from inclusion of the fat interventions in the experimental diets fed. Increased fermentable neutral detergent fiber and soluble fiber intakes increased the proportion pregnant while increased milk yield of the treatment group decreased this measure. Unexpectedly, the estimated energy costs of urea production also had a positive association with proportion pregnant. The limited number of suitable studies for the analysis highlights the need for more work to improve understanding of the critical nutritional factors affecting fertility. These factors include specific fatty acids in dietary interventions that contribute to increasing fertility of cows in dairy production systems.

Key Words: dietary fat, fertility, conjugated linoleic acid

1309 Altering the ratio of palmitic, stearic and oleic acids in diets with or without whole cottonseed impacts production responses and energy partitioning of dairy cows.

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We evaluated the effects of varying the ratio of dietary palmitic (C16:0), stearic (C18:0), and oleic (*cis*-9 C18:1) acids in diets with or without whole cottonseed on nutrient digestibility and production response of dairy cows. Twenty-four mid-lactation Holstein cows were used in split plot Latin square design. Cows were allocated to a main plot receiving either a basal diet without whole cottonseed (SH, n = 12) or a basal diet with whole cottonseed (CS, n = 12; 8% diet DM). Within each plot a 4 × 4 Latin square arrangement of treatments was used in four consecutive 21-d periods. Fatty acid (FA) treatments were: 1) Control (CON; no supplemental fat); 2) C16:0 supplement (PA; ~80% C16:0); 3) C16:0 and C18:0 supplement (PA+SA; ~40% C16:0 + ~40% C18:0); and 4) C16:0 and *cis*-9 C18:1 supplement (PA+OA; ~45% C16:0 + ~35% *cis*-9 C18:1). The final 5 d of each period were used for sample and data collection. The statistical model included the random effect of cow and the fixed effects of basal diet, FA treatment, period, and their interactions. Compared with SH diets, CS diets increased milk fat yield (1.71 vs. 1.51 kg/d; P = 0.05), yield of preformed milk FA (623 vs. 507 g/d; $P < 0.01$), and BW gain (1.0 vs. 0.71 kg/d; $P = 0.04$), tended to increase yield of de novo milk FA (396 vs. 383 g/d; $P = 0.06$), but reduced NDF digestibility (41.9 vs. 46.4%; $P < 0.01$) and total FA digestibility (74.2 vs. 76.3% $P = 0.05$). Compared with other treatments, PA increased yield of milk fat (1.60, 1.70, 1.64 and 1.64 kg/d; $P < 0.05$) and 3.5% FCM (45.2, 47.8, 46.8 and 46.5 kg/d; $P < 0.01$) for CON, PA, PA+SA and PA+OA, respectively. PA+OA increased BW gain compared with other treatments (0.82, 0.84, 0.70 and 1.05 kg/d; $P < 0.05$) for CON, PA, PA+SA and PA+OA, respectively. PA and PA+OA tended to increase NDF digestibility compared with PA+SA and CON (43.2, 44.9, 43.1 and 44.5%; $P < 0.10$) for CON, PA, PA+SA and PA+OA, respectively. Compared with the other treatments, PA+SA reduced 16-carbon (77.6, 73.0, 66.0 and 79.1%; $P < 0.01$), 18-carbon (79.2, 79.5, 72.0 and 79.7%%; $P < 0.01$), and total FA digestibility (78.6, 77.4, 68.2 and 79.4%; $P < 0.01$) for CON, PA, PA+SA and PA+OA, respectively. In conclusion, diet inclusion of C16:0 increased energy output in milk, while inclusion *cis*-9 C18:1 increased BW gain. The combination of C16:0 and C18:0 reduced NDF and FA digestibilities, which likely explains its reduced performance compared with other treatments.

Key Words: fat supplementation, animal performance, fatty acids

1310 Effect of high-oleic acid whole, heated soybeans or extruded soybean meal on production performance, milk fatty acid composition, and enteric methane emission in dairy cows.
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The objective of this study was to investigate the effect of 3 soybean sources differing in fatty acid profile and processing method on productivity, milk composition, and enteric CH_4 emission in lactating dairy cows. The soybean sources were: extruded conventional soybean meal (SBM; 48% CP and 8.7% ether extract; 22% oleic acid), extruded Plenish® (DuPont Pioneer, Johnston, IA), a high-oleic acid variety SBM (51.4% and 8.4%, respectively; 75% oleic acid), and whole, heated Plenish® soybeans (40.0% and 20.2%, respectively). The study involved 15 Holstein cows (54 ± 8.3 d in milk) in a replicated 3 × 3 Latin square design experiment with 3, 28-d periods. The inclusion rate of the 3 soybean sources in the diet was (all data are on DM basis): 17.1, 17.1, and 7.4%, diets CESBM, PESBM, and WHPSB, respectively, providing 1.4 to 1.5% soybean oil. The rest of the dietary ingredients were: corn silage, 41%; alfalfa haylage, 16%; grass hay/straw mix, 4%; ground corn grain, 10%; cottonseed hulls, 4%; molasses, 4.9%; and a mineral/vitamin premix, 3%. The WHPSB diet also contained 9.7% solvent-extracted SBM. The diets had similar content of CP (17.0 and 17.6%), NDF (31.0 and 32.0%), ether extract (3.8 and 4.0%), and NE_l (1.53 and 1.54 Mcal/kg). Compared with CESBM, the Plenish® diets tended to increase ($P = 0.09$) DMI (27.1, 27.8, and 27.8 kg/d, CESBM, PESBM, and WHPSB, respectively). Milk yield was not affected ($P \geq 0.10$) by treatment (average of 42.2 kg/d; SEM = 1.41). The Plenish® diets increased ($P < 0.01$) milk fat content (3.55, 3.74, and 3.76%, respectively). Feed efficiency was decreased ($P < 0.001$) by the Plenish® diets, compared with CESBM (1.50 and 1.51 vs. 1.57 kg/kg, respectively). Treatments had no effect ($P \geq 0.13$) on enteric CH_4 (average of 463 g/d, SEM = 29.7) or CO_2 (average of 12,113 g/d, SEM = 241.5) emissions and methane emission yield (16.6 to 17.2 g/kg DMI). Diets had a marked effect on milk fatty acid profile. Generally, the Plenish® diets increased ($P \leq 0.01$) mono-unsaturated and *cis*-9 18:1 and decreased ($P \leq 0.01$) poly-unsaturated, total trans-, and conjugated linoleic fatty acids concentrations in milk fat. In this study, compared with conventional extruded SBM, the Plenish® soybean treatments had no effect on milk yield, increased milk fat concentration, decreased feed efficiency, and modified milk fatty acid profile in a manner expected from the greater concentration of oleic acid in Plenish® soybean oil.

Key Words: high-oleic acid soybean, milk fatty acid, methane, dairy cow

1311 Biohydrogenation kinetics of oleic, linoleic and α-linolenic acids in vivo.
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Biohydrogenation (BH) of unsaturated fatty acids (FA) has been extensively studied in vitro; however, in vitro BH rates and extents may not parallel BH pathways in vivo. The objective was to assess rate and extend of oleic (OA), linoleic (LA) and α-linolenic acid (ALA) biohydrogenation in vivo. Each FA was characterized in a separate experiment (EXP.1– oleic, EXP.2– linoleic, and EXP.3– α-linolenic) using 4 ruminally cannulated lactating Holstein cows in each experiment. A single bolus consisting of 200 g of an oilseed (EXP.1 87% OA sunflower, EXP.2 70% LA safflower, and EXP.3 54% ALA flaxseed) and 12 g of heptadecanoic acid (17:0) was mixed with rumen contents. Rumen digesta was collected at −1, −0.25, 0.1, 0.25, 0.5, 0.75, 1, 1.5, 2, 3, 4, and 6 h relative to the bolus. Samples were immediately placed on dry ice, stored at −20°C, freeze-dried, methylated and analyzed by GC-FID. On the day of infusion, cows were fed at a rate of 4.2%/h of expected daily DMI. The geometric mean of the 4 cows was calculated and the disappearance of 17:0, OA, LA, and ALA was fit to a single exponential decay model using the nonlinear procedure of JMP Pro. Overall, the boluses increased total fat in the rumen from 4.1 to 7.4% and enriched 17:0 from 0.4 to 2.5% of FA. The bolus enriched OA from 9.0 to 30.1% of FA in EXP. 1, LA from 12.5 to 35.9% of FA in EXP.2, and ALA from 1.9 to 19.8% of FA in EXP.3. The fractional rate of 17:0 disappearance was 10.9, 8.5, and 6.7%/h in EXP.1, 2, and 3, respectively, and was used as a marker of FA passage. The fractional rate of disappearance of OA was 55%/h, LA was 61.2%/h, and ALA was 93.9%/h in EXP.1, 2, and 3, respectively, and all three unsaturated FA reached pre-bolus concentration within 4 h. Based on kd/(kd+kp), the extent of BH was 83.4% for OA, 87.8% for LA, and 93.3% for ALA in EXP.1, 2, and 3, respectively. Assuming that BH equals disappearance minus passage, the BH rates were 44.0, 52.7, and 87.1%/h for OA, LA, and ALA in EXP.1, 2, and 3, respectively. In conclusion, the extent of oleic, linoleic, and α-linolenic biohydrogenation was near expected values, but the rate of ruminal biohydrogenation was higher than that commonly observed in vitro for these three unsaturated FA.

Key Words: rumen, biohydrogenation

1312 Production response, nutrient digestibility, and energy partitioning of post-peak dairy cows when palmitic acid-enriched supplements are included in diets: a meta-analysis and meta-regression. J. de Souza*, R. J. Tempelman, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

This analysis was performed to evaluate the effects of palmitic acid-enriched supplements (PA; > 80% C16:0) on production response, nutrient digestibility, and energy partitioning of post-peak dairy cows. The database was formed with 1,056 individual observations from 215 dairy cows in 12 studies. Diet mean nutrient content (% DM) was 30% NDF (range 24 to 37%), 17% CP (range 16.7 to 17.8%), 27% starch (range 22 to 32%), and 3.95% fatty acids (FA; range 2.1 to 5.6%). PA was fed on average at 1.8% of diet DM (range from 0.75 to 2.25%) replacing either soyhulls or ground corn in diets. The effects of PA were compared to non-fat supplemented diets used as controls (CON). The meta-analysis was performed to calculate the mean difference in least square means between CON and PA treatments using a model considering the random effects of study and cow. The meta-regression evaluated the effect of C16:0 intake using a random regression model. PA compared with CON did not affect DMI ($P = 0.32$), milk yield ($P = 0.37$), BW ($P = 0.70$), or BCS ($P = 0.75$), but increased milk fat content (3.81 vs. 3.58%; $P < 0.01$), milk fat yield (1.59 vs. 1.49 kg/d; $P < 0.01$), 3.5% FCM (44.8 vs. 43.0 kg/d; $P < 0.01$), and feed efficiency (3.5% FCM/DMI; 1.60 vs. 1.53; $P < 0.01$). PA increased 16-carbon milk FA yield (590 vs. 475 g/d; $P < 0.01$) compared with CON but did not affect de novo ($P = 0.23$) or preformed ($P = 0.76$) milk FA yields. PA increased NDF digestibility (44.3 vs. 41.5%; $P = 0.02$), 18-carbon FA digestibility (80.3 vs. 78.4%; $P = 0.02$) and DM digestibility (68.2 vs. 66.7%; $P = 0.01$), but reduced 16-carbon FA digestibility (68.4 vs. 74.3%; $P < 0.01$), and total FA digestibility (71.5 vs. 75.8%; $P < 0.01$) compared with CON. PA increased net energy intake (47.4 vs. 46.0 Mcal/d; $P = 0.04$), milk energy output (31.1 vs. 29.9 Mcal/d; $P = 0.01$) and partitioned more dietary energy to milk (66.6 vs. 65.0%, $P = 0.03$) compared with CON. Using the random regression model we observed positive linear relationships between C16:0 intake and milk fat yield ($P < 0.01$; $R^2 = 0.57$), 3.5% FCM ($P < 0.01$; $R^2 = 0.53$), and 16-carbon milk FA ($P < 0.01$; $R^2 = 0.87$), as well as NDF digestibility ($P = 0.01$; $R^2 = 0.55$) and energy partitioned toward milk ($P = 0.01$; $R^2 = 0.47$), but a negative linear relationship for total FA digestibility ($P = 0.01$; $R^2 = 0.64$). In conclusion, supplementation of palmitic acid-enriched supplements increased yields of milk fat and 3.5% FCM, feed efficiency, and NDF digestibility with no reduction in DMI or loss of BW or BCS.

Key Words: fat supplementation, meta-analysis, production response

1313 Effect of potassium carbonate and soybean oil supplementation on rumen microbial population linked to lipid metabolism. A. R. Alfonso-Avila*[1], J. Chiquette[2], P. Y. Chouinard[3], E. Charbonneau[1], and R. Gervais[3], *[1]Département des sciences animales, Université Laval, Quebec, QC, Canada, [2]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada, [3]Département des sciences animales, Université Laval, Québec, QC, Canada.*

The rumen microbial ecosystem plays a crucial role in productivity through digestion of feeds and supply of nutrients to the host animal. It was suggested that milk fat synthesis in dairy cows is stimulated by a positive dietary cation-anion difference (DCAD). Despite that rumen bacteria are largely involved in hydrolysis and biohydrogenation of dietary lipids, the impact of DCAD on rumen microbiome is unknown. The objective of this study was to evaluate the effect of increasing DCAD, using K_2CO_3, in diets containing soybean oil (SBO) on rumen microbial population associated with lipid metabolism. Twenty four early lactation Holstein dairy cows (39 ± 22 DIM) were used in a randomized complete block design (6 blocks) based on DIM and number of calving with a 2 × 2 factorial arrangement of treatments. Within each block, cows were fed a basal diet formulated to achieve 40% forage (58% corn silage), 60% concentrate, and 47% non-fibrous carbohydrates, with 0 (DCAD: +95 mEq/kg) or 1.5% K_2CO_3 (DM basis; DCAD: +316 mEq/kg), and 0 or 2% SBO. Effects of K_2CO_3, SBO and the interaction K_2CO_3 × SBO were evaluated. Treatment period lasted 28 d; the last 5 d were used for data and sample collection. Equal volumes (?1.0 L) of rumen fluid and solid digesta were collected from different rumen sites 4-h postfeeding. Extracted DNA was amplified by quantitative real-time PCR. The absolute amount for each microbial group was expressed as logarithm (base 10) of DNA copies/g of fresh matter. A companion abstract showed an interaction between K_2CO_3 and SBO on milk fat yield and *t*10/*t*11 ratio (JDS 98-Suppl. 2:128). Supplementing diets with K_2CO_3 stimulated the growth of *Butyrivibrio hungatei* (5.79 vs. 5.62; $P = 0.03$), a bacteria recognized to produce *t*11 18:1 during biohydrogenation. Conversely, feeding SBO reduced the growth of i) *Butyrivibrio*/*Pseudobutyrivibrio* group (8.60 vs. 8.80; $P = 0.04$), also known to produce *t*11 18:1, ii) fibrolytic *Fibrobacter succinogenes* (9.34 vs. 9.63; $P = 0.04$), iii) *Butyrivibrio proteoclasticus,* a bacteria involved in 18:0 production (6.67 vs. 6.79; $P = 0.06$), and iv) amylolytic *Streptococcus bovis* (6.84 vs. 7.01; $P = 0.06$). Feeding K_2CO_3 had no effect on these four bacteria. Total eubacteria and total protozoa did not differ between treatments ($P > 0.13$). Feeding K_2CO_3 and SBO had distinct effects on rumen bacteria. However, the absence of interaction between treatments on microbial population does not allow to establish a clear link with

previously observed effects on milk fat yield and *t*10/*t*11 ratio.

Key Words: DCAD, rumen bacteria, biohydrogenation

1314 Abomasal infusions of linoleic and linolenic acid in lactating dairy cows differentially alter the fatty acid composition of plasma lipid fractions and immune cells.

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The balance of n-3 and n-6 fatty acids (FA) in immune system tissues can influence the degree of inflammatory responses in dairy cattle. Linoleic acid (C18:2 n-6) and linolenic acid (C18:3 n-3) are the most abundant n-6 and n-3 FA in lactating dairy cow rations, and are associated with pro-inflammatory and anti-inflammatory responses, respectively. Our objective was to evaluate the incorporation of these FA, and their downstream oxidized FA (oxylipids), into plasma and white blood cells (WBC) following supplementation. Six mid-lactation dairy cows were abomasally infused 4x/d for 7-d treatment periods with 7-d washout intervals in a replicated balanced Latin square design with 3 treatments: 1) CON = ethanol carrier, 2) LA = 45 g/d C18:2 n-6, and 3) LNA = 45 g/d C18:3 n-3. Blood was collected on d 7 of the treatment periods and analyzed for WBC and plasma lipid fraction FA and plasma oxylipid composition. Yields of milk and milk components were calculated for d 6 and d 7 of the treatment periods. Statistical analysis was performed using linear mixed models. Dry matter intake was not affected by treatment ($P = 0.68$). LA treatment increased the yield of milk and milk protein compared to CON and LNA ($P \leq 0.05$). LNA treatment increased milk fat concentration compared to CON and LA ($P \leq 0.05$). The concentration of C18:3 n-3 in WBC was increased by LNA (0.86 g/100 g FA; $P \leq 0.05$), compared to LA (0.39 g/100 g FA) and CON (0.34 g/100 g FA), but C18:2 n-6 was unaffected by treatment ($P = 0.15$). LNA increased C18:3 n-3 (3.17 g/100 g FA) and C20:5 n-3 (0.43 g/100 g FA) in the phospholipid fraction of plasma, compared to CON and LA ($P \leq 0.01$), while LA increased C18:2 n-6 (38.7 g/100 g FA), compared to the other treatments ($P < 0.01$). Plasma phospholipid C20:4 n-6 concentration was not altered by treatment ($P = 0.65$). LNA decreased C20:4 n-6-derived 8,9-DiHETrE ($P < 0.01$) and tended to decrease C18:2 n-6-derived 12,13 EpOME in plasma ($P = 0.09$). When C18:3 n-3 and C18:2 n-6 were abomasally infused at the same dose, C18:3 n-3 had a greater influence on the profile of plasma FA and oxylipids and the FA composition of WBC. These changes have the potential to mediate inflammatory responses in cattle at risk of infection.

Key Words: linoleic acid, linolenic acid, abomasal infusion

1315 Effect of increasing doses of abomasally infused linseed oil on animal performance and oxidative stability of milk in Holstein dairy cows.

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To evaluate the effect of increasing doses of post-ruminal supply of linseed oil (LO), as a source of polyunsaturated fatty acids (PUFA), on animal performance and oxidative stability of milk, five Holstein dairy cows (36 ± 2 DIM, 38.7 ± 4.7 kg milk/d; Mean ± SD) were randomly distributed in a 5 × 5 Latin square design (14-d periods; 11 d of adaptation). All cows were fed the same ration and LO was abomasally infused continuously at 0, 75, 150, 300, and 600 g/d using peristaltic pumps. Oxidation measurements were done on fresh non-homogenized milk and on homogenized milk stored at 4°C during 11 d under fluorescent light. Data were analyzed using a mixed model including the random effects of period and cow, and the fixed effects of treatment, time and their interaction in the repeated measures analyses. A peroxidability index (PI) was calculated as: 0.025×Monoenoates + 1×Dienoates + 2×Trienoates + 4×Tetraenoates + 6×Pentaenoates + 8×Hexaenoates, to account for individual oxidation sensitivity of FA. Dry matter intake and yield of energy corrected milk decreased linearly with increasing dose of LO ($P < 0.05$). Milk fat concentration decreased quadratically ($P < 0.05$) reaching a nadir at 300 g of LO/d, whereas the yields of fat and protein decreased linearly ($P < 0.05$). The concentration and yield of lactose were not different among treatments. The concentration of PUFA increased linearly with LO dose ($P < 0.001$). Accordingly, the PI of fresh milk increased linearly with dose from 2.0 mg/g milk in the control, to 10.8 mg/g milk at the highest dose ($P < 0.001$). Conjugated diene hydroperoxides in fresh milk increased linearly with dose ($P < 0.001$), whereas conjugated triene hydroperoxides and redox potential were not affected. Volatile lipid oxidation products such as propanal, hexanal, *trans*-2-hexenal/hex-*cis*-3-enal, and hept-*cis*-4-enal increased linearly with dose ($P < 0.001$), whereas 1-octen-3-one was not affected, and *trans*-2, *cis*-6-nonadienal and *trans*-2, *trans*-4-nonadienal were not detected in fresh milk. During storage, similar increasing trends were observed across treatments for propanal, hexanal, *trans*-2-hexenal/hex-*cis*-3-enal, hept-*cis*-4-enal, and *trans*-2, *cis*-6-nonadienal in homogenized milk (time $P < 0.001$). Treatment by time interactions were detected for 1-octen-3-one and *trans*-2, *trans*-4-nonadienal. In conclusion, increasing doses of abomasally infused LO negatively affected animal performance. Despite small differences among individual oxidation products, overall, a linear increase in milk PUFA led to a quadratic response in total identified volatile compounds

which tended to reach a plateau at 300 g of LO/d.

Key Words: dairy cows, n-3 fatty acids, oxidation

1316 Palmitic acid feeding increases ceramide availability in association with increased milk yield, NEFA availability, and adipose tissue responsiveness to a glucose challenge. J. E. Rico, A. T. Mathews, and J. W. McFadden*, *West Virginia University, Morgantown.*

Reduced insulin action facilitates glucose partitioning for milk synthesis and facilitates lipolysis during early lactation. Insulin sensitivity increases beyond peak milk yield, while circulating NEFA and milk production decline. Palmitic acid (C16:0) promotes insulin resistance in monogastrics through ceramide-dependent mechanisms, and ceramides are elevated in hyperlipidemic insulin resistant early lactation cows. We hypothesized that feeding C16:0 to mid-lactation cows would enhance circulating ceramide, and ceramide would be positively associated with milk yield. Twenty multiparous Holstein cows were enrolled in a study consisting of a 5 d covariate, 49 d treatment, and 14 d post-treatment evaluation. Cows were randomly assigned to a sorghum silage-based diet containing no supplemental fat (control; n = 10; 138 ± 45 DIM) or C16:0 at 4% of ration DM (PALM; 98% C16:0; n = 10; 136 ± 44 DIM). Blood was collected at routine intervals and milk yields were recorded. Intravenous glucose tolerance tests (GTT) were performed at d −1, 21, and 49 relative to start of treatment. Plasma sphingolipids were quantified using liquid chromatography tandem mass spectrometry. Data were analyzed as repeated measures using a mixed model (fixed effects of treatment and time). Pearson correlations were analyzed. The most abundant sphingolipids included C24:0-ceramide, C24:0-monohexosylceramide (GlcCer), and C16:0-lactosylceramide (LacCer). Relative to control, plasma concentrations of total ceramide, GlcCer, and LacCer decreased as lactation progressed (P < 0.01). Total ceramide and C24:0-ceramide were increased by d 8 of treatment in PALM, and remained elevated throughout the 7 wk treatment period (+80% average; P < 0.001). Similarly, C16:1-, C22:0-, C22:1-, C24:1-, and C26:0-ceramide levels were greater in PALM (P < 0.05). Post-treatment, total ceramide concentrations in PALM returned to control levels. PALM increased total GlcCer and C24:0-GlcCer levels in plasma by 32 and 33% at wk 3 and 7, respectively (P < 0.01). Also, PALM increased C16:0-, C22:0-, C22:1-, and C24:1-GlcCer in plasma (P < 0.01), but had no effect on LacCer levels. We observed a decline in GlcCer and LacCer concentrations as lactation progressed (e.g., C24:0-GlcCer; P < 0.01). Plasma C24:0-ceramide was positively correlated with plasma NEFA and milk yield, and inversely correlated with NEFA disappearance following GTT (r = 0.52, 0.44, and −0.57, respectively; P < 0.001), relationships shared by most detected ceramides. We conclude that increasing C16:0 intake to augment ceramide supply delayed the decline in ceramide supply observed with the progression of lactation. Future research should evaluate whether ceramide is intrinsically involved in the homeorhetic adaptation to lactation.

Key Words: ceramide, insulin resistance, lactation

1317 Effect of supplemental enriched palmitic acid in free fatty acid form vs. calcium salts of palm fatty acids on production performance in early postpartum cows. J. E. Nocek*[1], C. Wan[2], and T. M. Londergan[2], *[1]Overture Enterprises, LLC, Auburn, NY, [2]Centriq, Seattle, WA.*

Sixty multiparous cows were randomly assigned at calving to one of three treatment regimens to evaluate fat supplementation on production performance in postpartum dairy cattle. Cows entered the pens at calving and remained through 12 wk. postpartum. There were 4 cows/pen and 5 pens/trt. Pens were identical in layout. Treatments were Control (no supplemental fat), Control diet with supplemental calcium salts of fatty acids (MegaLac, Princeton, NJ,: ML) and Control diet with high palmitic acid (98%) fatty acids (PrimaFat 16, Centriq, Seattle, WA,: PF). Cows were fed a Fresh (1 to 21 d) and High (22 to 84 d) diet. Corn meal was removed from the Control diet to provide equal supplemental fat content in both Fresh and High diets among treatments (Fresh:1.95 and 1.55% of DM and High: 1.78 and 1.46% of DM for ML and PF, respectively). Daily pen intakes and milk weights (3X) were recorded and averaged by week. Milk samples were collected weekly for milk composition. Blood samples were collected for NEFA and BHBA analysis on wk. 1 and 3 postpartum. Pen was the experimental unit. Mean group DMI was similar among treatments. Milk yield was similar for both fat products and higher (P < 0.01) than Control (47.3, 47.8 and 46.4kg for ML. PF and Control respectively). Both FCM and ECM were higher (P < 0.01) for PF compared to Control and ML (54.9, 50.8 and 52.2, and 52.7, 48.8 and 50.2 kg for FCM and ECM respectively). Milk Fat (% and yield) were higher (P < 0.01) for PF compared to Control and ML (4.42, 4.11, and 4.17%, and 2.10, 1.89, and 1.95 kg, respectively). Milk protein yield was higher (P < .01) for PF compared to Control, with ML not being different from either (1.36, 1.27, and 1.31 kg, respectively). MUN was lower (P < 0.01) for PF compared to ML and Control (11.8, 12.6, and 13.1 mg/dL, respectively). There was no effect of trt on BHBA, however, wk 1 NEFA tended to be lower (P = 0.14) for PF compared to ML and Control (0.55, 0.83, and 0.81 mEq/L), whereas wk 3 NEFA were lower (P = 0.04) for PF and Control compared to ML (0.46, 0.42, and 0.85 mEq/L). These results demonstrate that early postpartum cows supplemented with fat produced more milk than non-supplemented cows and supplementing with an enriched C16 fat increased fat percentage and yield compared to Ca-salts of palm fatty acid and increased protein

yield compared to no fat supplementation.

Key Words: palmitic acid, milk fat, dairy cows

1318 Hepatic oxidation is responsive to prepartum energy and peripartum rumen protected choline supplementation. V. Caprarulo[*1,2], T. L. Chandler[1], M. G. Zenobi[3], B. A. Barton[4], C. R. Staples[3], and H. M. White[1], *[1]Department of Dairy Science University of Wisconsin, Madison, [2]Department of Health, Animal Science and Food Safety, University of Milan, Milan, Italy, [3]Dep. of Animal Sciences, University of Florida, Gainesville, [4]Balchem Corporation, New Hampton, NY.*

Controlling prepartum energy intake or supplementing rumen-protected choline (RPC) during the periparturient period, are 2 strategies to preserve hepatic metabolic function. The objective of this study was to examine the regulation of hepatic gluconeogesis and oxidation during the transition to lactation. At −48 d relative to calving (DRTC), multiparous Holstein cows were assigned to either a controlled (1.40 Mcal of NEL/kg DM; CE) or high (1.63 Mcal NEL/kg DM; HE) energy prepartum diet with or without RPC (top-dressed daily from −21 to +21 DRTC). Postpartum diets only differed by addition of RPC. Liver tissue biopsy samples were collected at −14, +7, +14, and +21 DRTC for RNA isolation and cDNA generation (n = 16/treatment). Quantitative PCR was performed and mRNA abundance was normalized to reference genes. Data were analyzed by Proc Mixed (SAS 9.4) with repeated measures in a model that accounted for the main effects of RPC, energy, DRTC, and corresponding 2-way and 3-way interactions, and the random effect of cow (energy × choline). When interactions were significant ($P < 0.05$), energy × choline means were separated by Tukey's and time interactions were separated within time point by slice. Data are presented as least squares means ± SE, arbitrary units (AU). *Pyruvate carboxylase* (*PC*) expression increased ($P < 0.05$) after calving. There was an energy×choline ($P < 0.05$) and choline×DRTC ($P < 0.05$) interaction where RPC increased PC expression at −14 and +7 DRTC. There was no interaction ($P > 0.1$) of prepartum energy and DRTC. Expression of *cytosolic phosphoenolpyruvate carboxykinase* (*PEPCKc*) was greatest ($P < 0.05$) at +14 and lowest at −14 and +7 DRTC (1.62a, 0.75b, and 0.62b ± 0.16 AU, respectively). Expression of *PEPCKc* was decreased ($P < 0.05$) in cows fed HE+RPC compared with other treatments (0.57b, 1.00ab, 1.26a, 1.21a ± 0.09 AU; HE+RPC, HE, CE+RPC, CE). Expression of *glucose-6-phosphatase* was increased ($P < 0.05$) at +14 and +21 DRTC, and decreased (energycholine; $P < 0.05$) in cows fed the CE+RPC (1.36 vs. 2.32, 2.33, 2.24 ± 0.17 AU; CE+RPC, CE, HE+RPC, HE). Expression of *carnitine palmitoyltransferase 1A* was greatest at +21 DRTC ($P < 0.05$) but was unaltered ($P > 0.1$) by energy or choline. The transcription factor *PPARalpha* was increased ($P < 0.05$) in CE+RPC (1.35 vs. 0.86, 0.68, 0.90 ± 0.08 AU; CE+RPC, CE, HE+RPC, HE). Increased *PC* peripartum with RPC, across energy treatments, may support increased oxidative capacity at calving. Decreased*PEPCKc*in HE+RPC may serve to increase oxidation of increased circulating NEFA by maintaining the oxaloacetate pool.

Key Words: gluconeogenesis, TCA cycle, transition cow

1319 Rumen-protected methyl donors during the transition period: hepatic short-chain acyl CoA concentration in response to supplemental methionine or choline. Z. Zhou[*1], C. L. Girard[2], B. Ouattara[2], M. Vailati Riboni[1], D. N. Luchini[3], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [3]Adisseo S.A.S., Alpharetta, GA.*

Hepatic short-chain acyl CoAs are key intermediary metabolites of liver metabolism. Elevated concentration of acetyl CoA was associated with lower dry matter intake (DMI) in lactating dairy cows. Objectives were to measure hepatic acyl-CoA profiles in response to rumen-protected methionine (MET) or rumen-protected choline (CHO) supplemented during the transition period. Forty multiparous Holstein cows were used in a randomized complete block design with 2 × 2 factorial arrangement of MET and CHO level (with or without). Treatments were control (CON), no MET or CHO; CON+MET (SMA); CON+CHO (REA); and CON+MET+CHO (MIX). Cows received the same diet (1.52 Mcal NE_L/kg DM) from −21 d (close-up) to calving. From calving to 30 d, cows were on the same diet (1.71 Mcal NE_L/kg DM) and continued to receive the same treatments through 30 d. MET supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow/d. Liver samples were harvested at −10, 7, 20, and 30 d relative to calving. Free CoA, acetyl-CoA, propionyl-CoA, succinyl-CoA, malonyl-CoA, and methylmalonyl-CoA were determined by HPLC. Data were analyzed using PROC MIXED in SAS. The CORR procedure of SAS was used to evaluate correlations between selected variables. Both pre- and post-partum DMI was greater with MET ($P = 0.01$) but did not change with CHO ($P > 0.05$). MET supplementation led to greater ($P = 0.03$) hepatic total CoA and had a strong tendency ($P = 0.07$) for increasing free CoA compared with other treatments. Positive correlations (168 observations, $P < 0.01$) were obtained for both total and free CoA with DMI ($r = 0.27$ and 0.30, respectively) and NE_L intake ($r = 0.29$ and 0.34, respectively). Hepatic acetyl-CoA concentration has been reported to be negatively correlated with DMI, but no correlation ($P > 0.05$) was detected between acetyl-CoA, DMI, or NE_L. In fact, acetyl-CoA was lower ($P < 0.01$) with CHO and did not change with MET ($P > 0.05$). Although MET cows had lower ($P < 0.01$) propionyl-CoA, succinyl-CoA concentration was greater ($P = 0.02$) and overall positively correlated (168 observations, $P <$

0.01) with DMI ($r = 0.23$) and NE_L ($r = 0.25$). Overall, results indicate that methyl donor supplementation altered hepatic short-chain acyl-CoA concentrations during the peripartal period. The greater DMI in response to MET supplementation might have been associated with higher hepatic succinyl-CoA concentration, potentially leading to greater gluconeogenesis.

Key Words: methionine, choline, CoA

1320 Development and validity of a lipid accessibility index that quantifies reaction exposure of internal fatty acids in animal feeds.

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Excessive lipid in the diet of dairy cattle can shift the pathways of biohydrogenation and the accumulation of conjugated linoleic acid isomers that cause milk fat depression. However, computer models that predict animal performance from unsaturated fatty acid load have been inconsistent in assessing the consequences of dietary lipid. One reason for their failure is the inability to determine the extent that lipid within the natural structure of plant matter will be released and exposed to the ruminal microorganisms. The purpose of this experiment was to develop and verify a lipid accessibility index (LAI) that could predict exposure of plant lipid to the microbial population. Based on the assumption that plant factors that limit microbial exposure would also limit chemical exposure of internal lipid, a LAI was developed by determining the proportion of fatty acids in samples quantified in a 10 min methylation relative to fatty acids quantified in the normal 2 h methylation. The 4 samples tested were alfalfa pellets, corn, cottonseed, and soybeans that were each tested in duplicate at four particle sizes; unground, finely ground through a 0.5-mm sieve in a centrifugal mill, and 2 intermediate sizes obtained by grinding for different lengths of time in a coffee grinder. Data were analyzed as a completely randomized design with a 4 × 4 factorial arrangement of treatments that included the effects of feed source, grind size, and the feed source × grind size interaction. The LAI for the main effect of grind size ($P < 0.05$) averaged 21.6, 35.2, 53.5, and 97.2% (SEM = 1.79%) going from unground to the most finely ground. For the main effect of feed source ($P < 0.05$), the LAI averaged 30.7, 45.4, 47.5, and 83.9% (SEM = 1.79%) for soybeans, corn, cottonseed, and alfalfa pellets, respectively. Relationships between grind size and LAI were linear for alfalfa, corn, and cottonseed with R^2 of 0.828, 0.937, and 0.957, respectively. A second order polynomial ($R^2 = 0.961$) best described the relationship between grind size and LAI for soybeans (0, 6.7, 17.1, and 99.1% LAI for whole to finely ground). The LAI proposed in this study was successful in reflecting differences in chemical reaction exposure of internal fatty acids across several feed sources and particle sizes suggesting it might also serve to quantify feed lipid exposure to microbial reaction in the rumen.

Key Words: lipid accessibility, feedstuffs, particle size

1321 Comparison of flax oil with varying lipid supplements in dairy ration: A meta-analysis.

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Feeding flax oil, a source of trienoic fatty acids (TRI-FA), to dairy cows contributes to improve fertility, reduce methane emissions and increase milk fat content of n-3 FA. However, studies on the effect of flax TRI-FA on milk production and composition have yielded contradictory results. The objective of this meta-analysis was to evaluate the effects of flax TRI-FA on lactation performance when compared with different sources of dietary lipids in which dienoic (DI), monoenoic (MONO), or saturated (SAT) FA were predominant. Three databases including 30, 20, and 15 studies, published between 1998 and 2015, were used for the comparisons of flax TRI-FA vs. DI-FA, vs. MONO-FA, and vs. SAT-FA supplements, respectively. For each database, dairy cow performance was adjusted with a linear mixed model where lipid source and supplemental lipid concentration were the independent variables, and study effect was included as a random variable. Concentrations of supplemental lipids, determined by ether extraction, varied from 0.7 to 6.0% (DM basis) for flax TRI-FA (3 databases combined), 0.5 to 6.6% for DI-FA, 0.9 to 5.9% for MONO-FA, and 1.0 to 4.1% for SAT-FA supplements. The interactions between lipid sources and their dietary concentrations were never significant and were removed from the models. Feeding flax TRI-FA tended to increase DMI (0.38 kg/d; $P = 0.07$) compared with SAT-FA, but no difference was observed with DI-FA or MONO-FA supplements. Actual, fat corrected, and energy corrected milk yields were not different between flax TRI-FA and the lipid categories evaluated. Feed efficiency of cows receiving flax TRI-FA was lower (−0.03 kg milk/kg DMI) compared with SAT-FA ($P = 0.03$), whereas no difference was observed with DI-FA and MONO-FA supplements. Milk fat and protein concentrations and yields were not different between flax TRI-FA and the other three lipid categories. Feeding flax TRI-FA increased lactose concentrations compared with DI-FA and SAT-FA supplements by 0.02 ($P = 0.03$) and 0.03 ($P = 0.03$) percentage unit, respectively. Despite minor effects on lactose, there was no difference between flax TRI-FA and other dietary unsaturated lipids on animal performance. Nevertheless, as a result of an increase in DMI, efficiency of milk production was reduced by feeding flax TRI-FA compared with SAT-FA supplements.

Key Words: dietary lipids, linseed, milk composition

1322 Milk bioactive fatty acids decrease in cows grazing pearl millet versus a cool-season pasture.

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Use of warm-season annuals, such as pearl millet (PM), has increased on northeast organic dairy farms because of their ability to grow in the mid-summer heat when cool-season perennial pastures experience less growth. The objective of this study was compare animal performance and milk bioactive fatty acids (FA) in milk of cattle grazed on PM versus cool-season pasture (CSP). Eight multiparous (parity: 2.9 ± 0.6 lactations) mid-lactation (114 ± 20 d in milk) Holstein cows were used in a repeated-measures design with three 4-wk periods. Cattle were grazed on CSP or PM in the following sequence: PM, CSP, and PM. Dry matter intake (DMI) was estimated using a calibrated rising plate meter. Individual milk weights and samples, representing a 24h period, were obtained during the last 2 wk (sampling days: 16 and 23) of each period. Milk samples were analyzed for components (fat, protein, organic solids) by mid-infrared spectrometry. Milk and forage FA proportions were determined using gas-liquid chromatography. Data were analyzed using a repeated measures ANOVA in the PROC MIXED procedure of SAS (vs. 9.4). CSP forages provided a higher content of n-3 FA when compared to PM (12.07 vs. 6.51 mg/g DM; $P < 0.05$), and higher content of polyunsaturated FA (17.17 vs. 8.33 mg/g DM; $P < 0.01$). Forage type had no effect ($P \geq 0.05$) on estimated DMI (17.2 and 17.4 kg/day for PM and CSP, respectively), milk production (13.8 and 13.1 kg/d for PM and CSP, respectively), fat yield (0.44 and 0.43 kg/d for PM and CSP, respectively), or protein yield (0.41 and 0.40 kg/d, for PM and CSP, respectively). Milk saturated FA were lower when cows grazed CSP compared to PM (59.5 vs. 63.0 g/100 g FA, respectively; $P < 0.001$). The content of CLA was higher during CSP treatment (2.11 g/100 g FA) than PM treatment (1.67 g/100 g FA; $P < 0.01$). Similarly, milk from cows grazing CSP had a twofold higher proportion of total n-3 FA when compared to PM (1.06 vs. 0.59 g/100 g FA; $P < 0.001$) and higher proportion of total n-6 FA in milk fat (1.29 and 1.04 g/100 g for CSP and PM, respectively; $P < 0.01$). Total branched-chain FA in milk fat were higher when cows grazed PM than CSP (3.12 vs. 2.86, respectively; $P = 0.01$). In conclusion, there was no difference in animal performance of cows grazing a CSP or PM, however, the contents of various bioactive FA were higher in milk fat of cows grazing a CSP compared to PM.

Key Words: milk production, n-3 fatty acids, branched-chain fatty acids

1323 Effect of early lactation feeding strategy on production, metabolic and endocrine responses of primiparous dairy cows.

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Primiparous Holstein cows ($n = 18$; 528 ± 40 kg BW, 3.2 ± 0.2 BCS) calved in fall were used in a randomized block design to study the effect of feeding strategy on production, metabolic, and endocrine responses in early lactation. At calving, cows were assigned within block to 1 of 2 feeding strategies during the first 65 d postpartum (DPP). Feeding strategies were either (G0) total mixed ration (TMR) ad libitum (17 kgDM/d offered; 70% forage, 30% concentrate) or (G1) grazing of alfalfa (*Medicago sativa*; 6-h am grazing in 3-d strips; pasture allowance = 20 kgDM/d) + TMR (70% of ad libitum TMR; 12 kgDM/d offered). Both groups consumed 2.2 kgDM/d of a commercial ration at each milking. Cows were milked twice a day, milk yield was recorded daily and samples were collected weekly for milk composition. Cow BW and BCS were recorded every 2 wk from −40 to +65 DPP. Blood samples were collected for metabolite and hormone analyses at −7 ± 2 and +42 ± 3 DPP. Data were analyzed as repeated measures with a mixed model that included: feeding strategy, DPP, and its interaction as fixed effects, block as random effect and calving date as a covariate. Milk yield (26.7 vs. 25.1 ± 0.58 kg/d), total solids (3.38 vs. 3.1 ± 0.09 kg/d) and NEL output (20.9 vs. 19.2 Mcal NEL/d) tended ($P < 0.07$) to be greater for G0 than G1 cows, being differences more marked from +30 to +60 DPP. Cow BW and BCS did not differ ($P > 0.30$) between feeding strategies. Concentrations of plasma NEFA decreased ($P < 0.01$) at +42 DPP when compared to −7 DPP and at +42 DPP tended ($P = 0.10$) to be greater for G0 than G1 cows (0.34 vs. 0.25 ± 0.03 mmol/L. Plasma BHB concentration at +42 DPP was greater ($P = 0.02$) for G0 than G1 cows (0.46 vs. 0.27 ± 0.05 mmol/L) as it decreased from −7 to +42 DPP only in the latter group. In contrast, plasma insulin was reduced ($P = 0.05$) in G0 than G1 cows at +42 DPP (11.7 vs. 7.2 ± 1.3 uU/mL) as it increased from −7 to +42 DPP only in the latter group. Concentrations of cortisol, leptin and adiponectin were not different ($P > 0.20$) at −7 than +42 DPP and neither differed between feeding strategies at +42 DPP. Metabolic and endocrine profile would indicate a greater lipolysis in early lactation in G0 than G1 cows which would be probably associated to their greater milk production.

Key Words: TMR, dairy cows and grazing

1324 Ratios of milk fatty acids accurately estimates plasma non-esterified fatty acid concentrations as an indicator of animal energy balance.

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Negative energy balance and elevated plasma NEFA in dairy cows can negatively affect animal health and milk production. Also, in short term feeding trials, failing to correct for negative energy balance can lead to overestimating the energy content of a given diet or the true feed efficiency for a given cow. The objective of this study was to evaluate the precision and accuracy of individual milk fatty acid proportions (IMFAP, g/100 g milk total fatty acids) or milk fatty acids ratios (MFAR) to predict plasma NEFA concentrations. Four models were developed using a dataset from three studies (n = 204 observations, individual animal). The developed models were: model 1 (IMFAP including the terms: C14:0, C15:0, C17:0, and C18:1), model 2 (MFAR C18:1 to C15:0), model 3 (MFAR C17:0 to C15:0) and model 4 (MFAR C18:1 to C14:0). Predicted model output for plasma NEFA was compared to 90 treatment means from an independent data set from 21 papers published in the literature. All models were developed based on an individual animal-level dataset, and validated with average values from groups of animals (literature dataset). Quality of the original prediction models was evaluated using the r^2 between the observed and predicted values, mean bias (MB), concordance correlation coefficient (CCC) and root mean square error of prediction (RMSEP). Results indicated that plasma NEFA predicted by model 2 (NEFA = 71.13 (± 68.04) + 8.87 (± 0.67) * C18:1/C15:0, r^2 = 0.55) and model 3 (NEFA = −47.50 (± 36.3) + 625.30 (± 40.63) * C17:0/C15:0, r^2 = 0.54) yielded more precise and accurate predictions (model 2: r^2 = 0.89, MB = −27.39 μEq/L, CCC = 0.92, RMSEP = 51.86 μEq/L, and model 3: r^2 = 0.89, MB = −77.79 μEq/L, CCC = 0.86, RMSEP = 102.32 μEq/L,) than the NEFA predicted by model 1 (r^2 = 0.74, MB = −186.08 μEq/L, CCC = 0.54, RMSEP = 233.17 μEq/L), and model 4 (r^2 = 0.81, MB = −69.75 μEq/L, CCC = 0.41, RMSEP = 110.65 μEq/L). Milk C18:1 to C15:0 and C17:0 to C15:0 ratios can be used as an indicator of herd energy balance and therefore the status of herd health.

Key Words: energy balance, fatty acids, transition cow

1325 Effect of linseed oil supplementation on milk fatty acid profile of dairy cows fed diets based on red clover silage or corn silage.

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The objective of this study was to examine the effect of linseed oil (LO) supplementation on milk fatty acid (FA) composition of dairy cows fed diets based on red clover (RCS) or corn silage (CS). Twelve lactating, multiparous Holstein cows (days in milk = 91 ± 25; milk yield = 45.2 ± 4.7 kg) were used in a replicated 4 × 4 Latin square design (35-d periods; 14-d adaptation) with a 2 × 2 factorial arrangement of treatments. Cows were fed (ad libitum; 5% orts on an as-fed basis) a TMR (60:40, forage:concentrate ratio) not supplemented or supplemented with 4% LO (DM basis) and with the forage portion of the TMR consisting of either RCS or CS. Milk FA profile was determined on samples collected over 6 consecutive days. Main effects of forage source, LO supplementation and their interaction were determined using the MIXED Procedure of SAS and significance was declared at $P \leq 0.05$. The *t*10/*t*11 18:1 ratio was unaffected by adding LO to the RCS-based diet, which is consistent with no change in milk fat yield reported in our previous study (JDS, 98:7993). In contrast, the *t*10/*t*11 18:1 ratio increased (2.04 vs. 0.77) and milk fat yield decreased (JDS, 98:7993) when LO was added to the CS-based diet. Milk fat concentration of *c*9*c*12*c*15–18:3 increased in cows fed LO-supplemented diets compared to cows fed non-supplemented diets (0.88 vs. 0.57) and in cows fed RCS compared to cows fed the CS-based diet (1.04 vs. 0.41). An increase in*c*9*t*11*c*15–18:3 concentration was observed when LO was supplemented to the RCS-based diet (0.12 vs. 0.04), but no effect was observed with LO supplementation to the CS-based diet (interaction, $P < 0.01$). Diets supplementation with LO increased the concentrations of *t*11–18:1, *c*9t11–18:2 and *t*11*c*15–18:2, but these increases were more pronounced when LO was added to the RCS-based diet than to the CS-based diet (interaction, $P < 0.01$). Regardless of the forage source, supplementation with LO decreased milk FA from de novo synthesis (< 16 carbon) and from rumen microbial origin (odd- and branched-chain FA) by 21% and 24%, respectively. It is concluded that the effect of LO supplementation (4% DM) on milk FA and more specifically on those originating from ruminal biohydrogenation of *c*9*c*12*c*15–18:3 is modulated by dietary forage source (CS vs. RCS).

Key Words: linseed oil, forages, milk fatty acid

1326 Characterization of rumen bacterial and protozoal fatty acid compositions from lactating Jersey cows offered alternative forage crops. L. M. Cersosimo[*1], R. Tacoma[1], S. Greenwood[1], K. Juntwait[2], A. F. Brito[2], and J. Kraft[1], *[1]University of Vermont, Burlington, [2]University of New Hampshire, Durham.*

Alternative forage crops (AFC) include cool and warm season grasses and legumes that could be used to overcome periods of limited pasture production. Rumen bacteria and protozoa cell membranes consist of varying proportions of fatty acids (FA) that contribute to milk FA. The objective of this study was to compare the rumen bacterial and protozoal membrane FA compositions from lactating Jersey cows fed pasture strip-tilled with AFC vs. a traditional grass-legume pasture mix. In spring (SPR) and summer (SUM), two separate, 21-d experiments were conducted using 16 lactating Jersey cows (SPR, 85 ± 46 DIM; SUM, 143 ± 58 DIM). Cows were divided into control (CON, $n = 8$) and treatment (TRT, $n = 8$) groups, matched by parity, DIM, and milk production, and offered (DM basis) 40% pasture as AFC or traditional and 60% TMR. On a DM basis, SPR TRT pasture consisted of AFC (barley, hairy vetch, triticale, rye, and wheat) representing 2.4% of total diet DM, while the SUM TRT pasture consisted of AFC (buckwheat, chickling vetch, and oats), representing 10% of total diet DM. Individual whole ruminal digesta samples (500 mL) were collected via esophageal intubation on d 20 and 21 of each experiment. Bacterial and protozoal fractions were isolated by differential centrifugation. Microbial FA were analyzed by GLC. Student's *t* tests (JMP Pro 12) were used to determine if least-squares means differed between groups. Total protozoal and bacterial branched-chain FA, PUFA, as well as *trans* 18:1 isomers and 18:0, the products of rumen bacterial biohydrogenation, did not differ by group in either experiment. In the SPR, bacterial *cis*-11 18:1 (CON, 0.57 g/100 g FA; TRT, 0.50 g/100 g FA), *cis*-13 18:1 (CON, 0.44 g/100 g FA; TRT, 0.37 g/100 g FA), and *cis*-15 18:1 (CON, 0.76 g/100 g FA; TRT = 0.68 g/100 g FA) were less abundant in the TRT than CON group ($P < 0.05$). Protozoal levels of CLA from SPR TRT (1.13 g/100 g FA) cows were higher than SPR CON (0.85 g/100 g FA). In the SUM, bacterial 17:0 was lower in cows grazing TRT pasture (0.67 g/100 g FA) than CON pasture (0.71 g/100 g FA; $P < 0.01$). In the SUM, no differences in the protozoal FA compositions were observed. In conclusion, few differences were identified in the microbial FA compositions in cows consuming pasture with or without AFC.

Key Words: branched-chain, microbial, pasture

1327 Effect of frequency of supplementation with Megalac-R on non-esterified fatty acids and blood urea nitrogen concentration in lactating beef cows. M. E. Garcia-Ascolani[*1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], D. D. Henry[1], F. M. Ciriaco[1], P. L. P. Fontes[1], G. C. Lamb[1], N. M. Long[2], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]Clemson University, Clemson, SC.*

An experiment was conducted to determine the effects of supplementing a ruminally-protected lipid (Megalac-R, Church & Dwight, Princeton, NJ) under 3 different frequencies, on the metabolic blood profile of suckled beef cows. Eighteen early lactating beef cows (first 90 d of lactation) were used in a completely randomized design. For 2 wk (d 0 to 14), all cows were individually supplemented an isocaloric, isonitrogenous amount of corn gluten feed (CGF) pellets (4.54 kg/wk, as is), at 3 frequencies (treatments): 3, 5, or 7 d/wk. For the duration of the study, cows and calves were grazing on a ryegrass pasture. From d 11 to 13, blood samples were collected before supplementation, and at 8 and 16 h later. Beginning on d 14, supplementation with Megalac-R was added to the CGF pellets at a rate of 1.59 kg/wk (as is). Supplementation frequency was maintained for the same 6 cows in each treatment for 3 wk. For the last 3 d of the study (d 32 to 34), blood samples were taken pre and post supplementation, similar to d 11 to 13. Blood samples were analyzed for concentrations of serum NEFA and blood urea nitrogen (BUN). Data were analyzed as a completely randomized design with double repeated measures, using cow as the experimental unit. The model included the fixed effects of treatment, day, hour (day), treatment × day, treatment × hour (day) interactions, and the random effect of cow. No effects of treatment ($P = 0.42$) or treatment × hour (day) ($P = 0.86$) were observed on serum NEFA concentrations. An effect of hour (day) ($P = 0.001$), and a treatment × day interaction ($P < 0.001$) were observed for NEFA concentrations; however, within each sampling day, no difference among treatments was observed ($P > 0.10$). No effects of treatment ($P = 0.74$), treatment × day ($P = 0.16$), or treatment × hour (day) ($P = 0.39$) were observed on BUN concentrations. There was an effect of day and hour (day) ($P < 0.001$), however, within each day, no difference among treatments was observed ($P > 0.10$). In conclusion, supplementing a mixture of CGF and Megalac-R either 3, 5, or 7 d/wk provided similar results with respect to concentrations of serum NEFA and BUN of lactating beef cows, thus implying that the frequency of supplementation could be reduced without compromising their health or metabolism.

Key Words: frequency of supplementation, lactating beef cows, Megalac-R

1328 Supplementation of palm oil to lactating dairy cows fed a high fat diet during summer.

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Dairy cows subjected to heat stress can benefit from fat supplementation. We evaluated the response of lactating cows to the supplementation of a basal diet containing fat from whole cottonseed and roasted soybeans [3.2% of DM as ether extract (EE) from oilseeds] with 2 palm oil sources (1.1% of DM as EE from supplements). Thirty cows were fed a standard diet for 14 d and were assigned to a treatment for 63 d, in a covariate adjusted randomized block design with repeated measures over time. Treatments were: Control (CTL), fractionated palm oil (F, 73.5% of fatty acids as C16:0 and 14.7% as C18:1), and calcium salt of palm oil (S, 41.5% of fatty acids as C16:0 and 38.4% as C18:1). Pre-planned contrasts were: CTL vs. (F + S) and F vs. S. The EE concentration of the diet was 7.3% of DM in CTL and 8.4% in F and S. The temperature humidity index was above 68 for 17.1 h/d during the experiment. Palm oil reduced rectal temperature ($P < 0.02$) and respiratory frequency ($P = 0.05$), but had no effect on sudoresis ($P = 0.97$) and jugular blood acid-base balance ($P > 0.31$). Rectal temperature at 2 PM was 38.9°C for S and 39.1°C for F ($P = 0.02$). Palm oil increased milk yield (31.0 vs. 30.1 kg/d, $P = 0.02$) and reduced DMI (19.2 vs. 19.9 kg/d, $P = 0.01$), increasing feed efficiency (1.65 vs. 1.54, $P = 0.01$), and S tended do reduce DMI ($P = 0.07$) and increase feed efficiency ($P = 0.01$) more than F. Secretions of milk fat and lactose were increased by 47 g/d ($P = 0.04$) and 37 g/d ($P = 0.08$) with palm oil, respectively. Plasma glucose concentration was similar among treatments ($P = 0.63$), as well as total tract apparent digestibility of EE ($P = 0.97$) and NDF ($P = 0.43$), the intake of TDN ($P = 0.17$), and BW ($P = 0.87$). The acetate to propionate ratio in ruminal fluid was 2.39 for F and 1.98 for S ($P = 0.05$), suggesting that palm oil sources differed in ruminal inertness. Ingestion time/DMI was 17.3 min for S and 14.9 min for F ($P = 0.01$). Lactating cows fed a diet rich in fat from oilseeds had increased feed efficiency and reduced signs of heat stress when fat from palm oil was supplemented.

Key Words: fat supplementation, heat stress, palm oil

Table 1328.

					P-value		
Item	CTL	F	S	SEM	Treat	CTL *vs.* F + S	F *vs.* S
Breaths/min	63.8	60.0	58.1	1.98	0.13	0.05	0.49
Rectal temperature, °C	39.15	39.07	38.91	0.050	<0.01	<0.01	0.02
DMI, kg/d	19.9	19.4	19.0	0.14	0.01	0.01	0.07
TDN[1], kg/d	15.3	15.1	13.8	0.65	0.17	0.22	0.16
Milk, kg/d	30.1	30.9	31.1	0.28	0.07	0.02	0.57
Fat, kg/d	0.922	0.962	0.975	0.0131	0.02	0.04	0.46
Lactose, kg/d	1.401	1.421	1.454	0.0172	0.08	0.08	0.18
Milk/DMI	1.54	1.62	1.68	0.012	0.01	0.01	0.01
BW, kg	616	617	618	3,1	0.87	0.64	0.81
Glucose, mg/dl	56.6	55.5	55.6	0.93	0.63	0.33	0.94
DNDF, % of intake	57.1	53.7	52.5	2.55	0.43	0.22	0.73
DEE, % of intake	71.0	70.7	70.4	1.87	0.97	0.85	0.90
Acetate/Propionate	1.89	2.39	1.98	0.150	0.06	0.12	0.05

[1] TDN = (Digestible OM intake – Digestible EE intake) + (Digestible EE intake x 2.25)

1329 Effects of dietary fat source on performance of lactating dairy cows fed a pre-mixed concentrate.

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Inclusion of a pre-blended concentrate (OneTrak; Cargill Corn Milling, Blair, NE) in the total mixed ration for dairy cows can benefit the producer by simplifying the daily mixing of dietary ingredients and providing a more uniform mix of dietary ingredients. Cow responses to fat supplementation can be affected by other dietary ingredients, but few studies have evaluated responses to dietary fat in diets reliant on non-forage fiber. OneTrak is a blend of feed ingredients from the wet corn milling industry supplemented with additional protein, minerals, and vitamins for high producing dairy cows. Our

objective was to evaluate productivity responses to dietary fat source when the ration contained 44.1% OneTrak, 35.8% corn silage, 10.8% corn grain, 7.8% alfalfa hay, and 1.5% soyhulls or fat source (DM basis). Seventy-two Holstein cows between 94 and 220 DIM (166 ± 25 DIM, parity 1.7 ± 0.9) were blocked by parity, stratified by DIM, and randomly assigned to pens (n = 6) within strata. Pens were randomly assigned to treatment sequence in a 3 × 3 Latin square design with 21-d periods ending with 4 d of data collection. Treatments consisted of a prilled saturated fat (SAT; Energy Booster 100, Milk Specialties Co., Dundee, IL), calcium salts of long-chain fatty acids (UNS; Megalac, Church and Dwight Co. Inc., Princeton, NJ), or no added dietary fat (CON), with fat sources included to provide 1.2% added fat (DM basis). Milk yield and composition, DMI, BW change, and BCS change were analyzed with mixed models using pen as the experimental unit. Contrasts were used to assess impact of added fat and the source of fat; significance was declared at $P < 0.05$. Milk yield tended to increase with added fat ($P = 0.06$; 33.5, 34.2, and 34.3 ± 1.3 kg/d for CON, SAT, and UNS, respectively). Protein content decreased with fat supplementation, to a greater degree for UNS (3.43, 3.37, and 3.31 ± 0.05% for CON, SAT, and UNS, respectively), but protein yield did not differ. Fat content, fat yield, and energy-corrected milk yield were not affected by treatment. Conversion of feed to milk tended to increase for UNS compared with SAT (1.41 vs. 1.38 ± 0.05; $P = 0.06$). No effects were observed for BW or BCS. Responses to dietary fat in diets containing OneTrak were similar to previous findings with more traditional diets.

Key Words: dietary fat, pre-mixed concentrate, non-forage fiber

1330 Effects of feeding different forms of polyunsaturated fatty acids on performance, plasma metabolites and milk fatty acid composition of dairy cows.

1331 Milk production responses to palmitic acid supplementation when fed as fatty acids or triglycerides. J. de Souza* and A. L. Lock, *Michigan State University, East Lansing.*

We evaluated the effects of feeding a palmitic acid-enriched supplement (PA; 85% C16:0) either as fatty acids (FA) or triglycerides (TG) on production responses of mid-lactation dairy cows. Fifteen Holstein cows (137 ± 49 DIM) were randomly assigned to treatment sequence in a 3 × 3 Latin square design. Treatments were a control diet (CON; no added PA), or 1.5% of FA added either as a FA supplement (PA-FA), or a TG supplement (PA-TG). PA replaced soyhulls and diets were balanced for glycerol content. Diets contained (% DM) 21% forage NDF, 17% CP, and 26% starch. Periods were 21 d in length with the final 5 d used for sample and data collection. The statistical model included the random effect of cow and the fixed effect of treatment, period and interaction between treatment and period. Two preplanned contrasts were used to evaluate: 1) the overall effect of PA treatments [CON vs. PA; 1/2 (PA-FA + PA-TG)]; and 2) the effect of PA as a FA or triglyceride supplement (PA-FA vs. PA-TG). PA treatments increased milk fat content (3.60 vs. 3.41%; $P < 0.01$), milk fat yield (1.69 vs. 1.60 kg/d; $P < 0.01$), yield of 16-carbon milk FA (570 vs. 471 g/d; $P < 0.01$), 3.5% FCM (47.6 vs. 46.5 kg/d; $P = 0.01$), and feed efficiency (3.5% FCM/DMI; 1.69 vs. 1.58; $P < 0.01$). PA did not affect DMI compared with CON (28.5 vs. 29.2 kg/d; $P = 0.13$), milk yield (47.0 vs. 47.4 kg/d; $P = 0.67$), milk protein yield (1.42 vs. 1.45 kg/d; $P = 0.15$), milk lactose yield (2.29 vs. 2.31 kg/d; $P = 0.46$), yield of de novo milk FA (360 vs. 370 g/d; $P = 0.23$), yield of preformed milk FA (642 vs. 630 g/d; $P = 0.56$), BW (720 vs. 723 kg; $P = 0.80$), or BCS (3.14 vs. 3.23; $P = 0.17$). PA-FA increased DMI compared to PA-TG (29.1 vs. 27.8 kg/d; $P = 0.05$), yield of 16-carbon milk FA (596 vs. 545 g/d; $P < 0.01$), and tended to increase milk yield (47.6 vs. 46.4 kg/d; $P = 0.06$), milk fat yield (1.71 vs. 1.66 kg/d; $P = 0.10$), and 3.5% FCM (48.1 vs. 47.2 kg/d; $P = 0.09$). In conclusion, the production response of dairy cows to PA tended to be greater for a FA than a TG supplement. Overall, PA increased milk fat yield, 3.5% FCM and feed efficiency in mid-lactation dairy cows.

Key Words: dairy cows performance, degree of esterification, palmitic acid

1332 Comparison of a palmitic acid-enriched triglyceride supplement and a calcium salts of palm fatty acids supplement on milk production responses of dairy cows. J. de Souza*and A. L. Lock, *Michigan State University, East Lansing.*

We evaluated the effects of feeding a palmitic acid-enriched triglyceride supplement (85% C16:0) and a calcium salts of palm fatty acids (45% C16:0 and 38% *cis*-9 C18:1) supplement on production responses of mid-lactation dairy cows. Fifteen Holstein cows (139 ± 39 DIM) were randomly assigned to treatment sequence in a 3 × 3 Latin square design. Treatments were a control diet (CON; no fat supplement), or 1.5% of fatty acids (FA) added either as a palmitic acid-enriched triglyceride supplement (PA-TG), or calcium salts of palm FA supplement (Ca-FA). The supplements replaced soyhulls and diets were balanced for glycerol and calcium content. Diets contained (% DM) 21% forage NDF, 17% CP, and 26% starch. Periods were 21 d in length with the final 5 d used for sample and data collection. The statistical model included the random effect of cow and the fixed effect of treatment, period and interaction between treatment and period. Ca-FA tended to decrease DMI compared with CON and PA-TG (29.5, 29.6 and 28.7 kg/d; $P = 0.10$; for CON, PA-TG and Ca-FA, respectively). PA-TG tended to increase milk yield compared

with CON, but did not differ from Ca-FA (48.3, 49.5 and 48.9 kg/d; $P = 0.10$; for CON, PA-TG and Ca-FA, respectively). Compared with CON and Ca-FA, PA-TG increased milk fat concentration (3.40, 3.57 and 3.50%; $P < 0.01$) and milk fat yield (1.64, 1.77 and 1.72 kg/d; $P < 0.01$; for CON, PA-TG and Ca-FA, respectively). Compared with CON, both PA-TG and Ca-FA increased 3.5% FCM (47.1, 49.7 and 48.9 kg/d; $P < 0.01$) and feed efficiency (3.5% FCM/DMI) (1.60, 1.68 and 1.71 for CON; $P < 0.01$ for CON, PA-TG and Ca-FA, respectively). Ca-FA tended to increase BW change compared with PA-TG and CON (0.61, 0.62 and 0.78 kg/d; $P = 0.08$) and BCS change (0.05, 0.06 and 0.12; $P = 0.10$; for CON, PA-TG and Ca-FA, respectively). Ca-FA decreased yield of de novo milk FA compared with CON and PA-TG (401, 393, and 371 g/d; $P = 0.01$), but increased yield of preformed milk FA (618, 640, and 700 g/d; $P = 0.01$), whereas PA-TG increased yield of 16-carbon milk FA compared with other treatments (500, 576, and 540 g/d; $P = 0.01$; for CON, PA-TG and Ca-FA, respectively). In conclusion, feeding a palmitic acid-enriched triglyceride supplement increased milk energy output due to increased yields of milk and milk fat, whereas feeding a calcium salts of palm FA supplement increased BW gain.

Key Words: calcium salts of fatty acids, dairy cow performance, palmitic acid

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1333 Changes in milk odd and branched-chain fatty acids during induction and recovery from biohydrogenation-induced milk fat depression.

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We have observed that the concentration of odd and branched-chain fatty acids (OBCFA) in milk fat markedly changes during biohydrogenation (BH) induced milk fat depression (MFD). The objective was to characterize the time course of changes in milk OBCFA during induction and recovery of BH-induced MFD. Nine Holstein cows were randomly assigned to a treatment sequence in a repeated design that allowed analysis of recovery from a MFD diet. A 36.9% NDF and 1.1% PUFA diet was fed during the control and recovery periods, and a 29.5% NDF and 3.7% PUFA diet was fed during the induction period. Treatment periods were 21 d long and milk was sampled every other day. Data were analyzed using the MIXED procedure of SAS with repeated measures, time was the repeated variable, and cow by treatment was the subject. Preplanned contrasts were control versus induction and control versus recovery at each time point. The production data has been previously published (Rico and Harvatine, 2013 JDS 96:6621). Briefly, milk fat percentage and yield decreased progressively during induction and were lower than control by d 3 and 5, respectively. Milk fat concentration and yield increased progressively when cows were fed the recovery diet and were not different from control on d 19 and 15, respectively. During induction of MFD milk fat content of *iso*-14:0, *iso*-15:0, *anteiso*-15:0, 15:0, *iso*-16:0,*anteiso*-17:0, 17:0, and total OBCFA decreased rapidly (3.8 to 3.0% of total FA; $P < 0.01$ for all) and generally the concentration of these fatty acids was lower than control by d 3 ($P < 0.05$ for all). Contrarily, during recovery milk fat content of *iso*-14:0, *iso*-15:0, *anteiso*-15:0, 15:0, *iso*-16:0,*anteiso*-17:0, 17:0, and total OBCFA increased rapidly and the concentration of these fatty acids was not different from control on d 3 ($P > 0.1$ for all). In conclusion, the changes in milk OBCFA during induction and recovery of MFD occur rapidly, suggesting that these milk fatty acids could be used as markers of altered rumen biohydrogenation during milk fat depression.

Key Words: fatty acids, milk, rumen

1334 Dynamics of enrichment of omega-3 fatty acids in plasma lipid fractions following a bolus dose in dairy cows.

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Transfer of dietary omega-3 fatty acids (n-3 FA) to milk is low. Understanding the trafficking of n-3 FA in plasma lipid fractions may allow improvements in this transfer. The objective of this experiment was to investigate the fate of n-3 FA in plasma lipids after an abomasal bolus infusion of n-3 FA. Ten ruminally cannulated, multiparous Holstein cows were used in a crossover design with 7 d periods. Treatments were abomasal infusion of 120 g (infused over 1 h) of a free FA mixture enriched in α-linolenic acid (EALA; 80 g of ALA) or in very long chain n-3 (EVLC; 45.5 g of Eicosapentaenoic acid [EPA] + 33 g of Docosahexaenoic acid [DHA]). Blood samples were collected at −6, 0, 6, 12, 30, 54, and 102 h relative to the bolus infusion. Data was analyzed as repeated measures and the model included random effects of cow nested in sequence, sequence and period and fixed effect of treatment, time and treatment by time (SAS). Plasma concentration of total n-3 FA peaked 6 h post infusion in both treatments and was higher in EVLC than in EALA ($P < 0.001$). At peak, plasma EPA and DHA were enriched 8.3 and 60 fold, respectively, in EVLC and plasma ALA was enriched by 1.3-fold in EALA. After peak, plasma ALA in EALA and EPA in EVLC gradually decreased over time, while plasma DHA in EVLC remained 40-fold enriched over baseline at 102 h. Treatments had no effect on plasma cholesterol esters (CE), phospholipids (PL) and NEFA concentration. In the plasma PL fraction, ALA in EALA and EPA in EVLC (mg/dL) peaked at 1.8 and 11 fold enrichment, respectively, 6 h post infusion and then gradually decreased over time while accumulating in CE, where they reached 1.2 and 2.8-fold enrichments at 102 h. Plasma DHA peaked at 6 h in CE and decreased rapidly back to pre bolus values, however it peaked later (30 h) and remained high in PL (0.03 to 1.28 mg/dL from −6 to 102 h). In conclusion, n-3

FA differ in their enrichment and depletion in specific plasma lipid fractions and their transfer to milk might be limited due to trafficking of very long chain n-3 FA into plasma lipid pools unavailable to the mammary gland.

Key Words: omega-3, fatty acids, plasma lipids

1335 Intravenous nicotinic acid suppresses adipose tissue lipolysis in Holstein dairy cows.

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The mobilization of adipose tissue is linked with insulin resistance in dairy cattle. Feeding rumen-protected nicotinic acid (NA) or abomasal infusion of free NA can suppress lipolysis; however, the efficacy of intravenous NA to lower circulating NEFA is uncertain. Therefore, our objective was to evaluate the effects of intravenous NA infusion on lipolysis and insulin tolerance. Nine non-pregnant, non-lactating Holstein cows (617 ± 51 kg BW) were utilized in a 3 × 3 balanced Latin square crossover design. Treatments consisted of ad libitum feeding, fasting, or fasting with intravenous NA infusion (5 mg of NA/h per kg BW in saline) for 32 h. Equal volumes of saline were infused in cows not administered NA. Post-treatment, all cows were provided ad libitum access to feed and monitored for 8 h. Two 14-d washouts were included. When provided access, cows were fed a mixed ration of grass hay and ground corn to meet or exceed requirements. Fasted cows were provided vitamins and minerals. Jugular catheters were inserted 16 h before use. An insulin tolerance test (0.1 IU/kg BW; ITT) was performed at h 32, relative to initiation of treatment. Blood was collected routinely. Serum was analyzed using colorimetry. Data were analyzed using a mixed model with repeated measures with fixed effects of treatment and time. Relative to feeding, fasting increased lipolysis by h 2 (114 vs. 65 μM; $P < 0.01$), a response that progressively increased to h 32 (749 vs. 76 μM; $P < 0.01$). NA caused a consistent elevation in NEFA compared to fed cows, beginning at h 10 (77 vs. 51 μM; $P < 0.05$). NA reduced fasting NEFA area under the curve (0 to 32 h) by 55% ($P < 0.01$). Characteristic of NA, serum NEFA surged to 2,936 μM following removal ($P < 0.01$), a response accompanied by a treatment-specific increase in serum triacylglycerol and glucose ($P < 0.01$). In contrast, serum glucose and triacylglycerol were not modified with treatment. Relative to feeding, fasting without NA elevated serum cholesterol by h 16 ($P < 0.01$), a response delayed for fasted cows infused NA (h 24; $P < 0.05$). Fasting without NA reduced insulin-stimulated glucose uptake 38% by min 30 of ITT ($P < 0.01$), relative to feeding; however, NA did not improve glucose uptake. We conclude that the intravenous infusion of NA can inhibit lipolysis in dairy cattle; however, complete suppression of NEFA mobilization is not sustained with prolonged infusion.

Key Words: dairy cow, lipolysis, nicotinic acid

1336 Ruminal metabolism of fatty acids from fish oil or algae in steers fed a finishing diet.

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Supplementing cattle with sources of unsaturated fatty acids in the diet could improve the fat profile of the meat, but unsaturated fats suffer biohydrogenation by rumen bacteria. The objective of this study was to evaluate heterotrophically grown microalgae as a source of omega-3 fatty acids in steers fed a high grain finishing diet. Eight steers were used in a replicated 4 × 4 Latin square (LS) design experiment with each period lasting 21 d. The diet was based on cracked corn (75%), corn silage (7.5%) and fescue hay (7.5%) offered at 1.75 × NEm. The treatments were control, tallow (60 g/d), fish oil (60 g/d) and intact algae (100 g/d). All treatments were dosed through a ruminal fistula mixed with 450 g of diet. Total urine and feces were collected d 15 to 21. Reticulum and omasal samples were obtained for each hour from 0700 to 1800 during d 16 to 18. Omasal contents were collected using a vacuum sampling pump and reticulum samples by placing a collection bottle in the reticulum. Rumen fluid was collected at 2 h intervals from 0700 to 1700 on d 19 for pH and VFA analysis. Blood plasma was collected on d 21 of sample collection for fatty acid profile. The experiment was analyzed as a LS design with a 2 × 2 factorial using mixed models in SAS. There was no difference among treatments for DMI, urine or fecal excretion, N balance, total VFA concentrations, omasal or reticular flow, and apparent digestibility. Reticulum samples indicated greater amounts of DM exiting the rumen and were not used for measures of rumen digestibility. Control animals had lower ruminal pH when compared to other treatments ($P = 0.0012$). Animals consuming algae had higher fecal crude fat digestibility ($P = 0.02$) when compared with fish oil. Algae and fish oil had highest percent of total long chain fatty acid digestibility in feces when compared to tallow ($P = 0.0830$). Fish oil, algae and tallow had lower blood plasma C18:0 than control ($P = 0.01$). Algae increased flow of C18:1 isomers compared with fish oil ($P = 0.04$) and increased DHA in plasma ($P = 0.02$) but this was not evident from omasal fatty acid flow. These data indicate that algae feeding may have potential to alter the fatty acid profile of finishing steers.

Key Words: algae, fat, omasum, polyunsaturated fatty acid, DHA

1337 Increases in milk fat yield are maintained with prolonged palmitic acid supplementation in mid-lactation dairy cows.

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Supplementing palmitic acid (C16:0) increases yields of milk and milk fat in mid-lactation dairy cows. Because previous research has characterized the effects of short-term C16:0

Table 1338.

Table 1. Feedlot performance of Nellore bullocks fed different sources of ruminally protected fats

Item	Treatment			SEM	*P*-Value	Contrast	
	CON	NUT	BRP			C1	C2
Initial BW, kg	315	315	315	1.52			
Final BW, kg	476	508	524	7.06	<0.01	<0.01	0.13
DMI, kg/d	7,27	8,15	8,08	0.24	0.03	<0.01	0.83
ADG, kg/d	1,137	1,366	1,475	0.05	<0.01	<0.01	0.11
G:F, kg gain/kg DM	0,156	0,168	0,183	0.003	<0.01	<0.01	<0.01
HCW, kg	268	284	297	4.16	<0.01	<0.01	0.03
Dressing Percentage, %	56.4	55.9	56.8	0.31	0.18	0.91	0.07
Carcass gain, kg	105	121	134	4.05	<0.01	<0.01	0.02
ADG Carcass, kg/d	0,740	0,853	0,946	0.03	<0.01	<0.01	0.03

CON= Control; NUT= Nutrigordura®, ruminally protected soil bean oil; BRP= Blend of ruminally protected vegetable oils.
Considered statistically significant differences at the 10% significance by f test.
DMI = dry matter intake; ADG= average daily gain; G:F = gain-to-feed ratio; FC = feed conversion; HCW= hot carcass weight; Dressing Percentage = ((HWC/BW)*100); Carcass gain = (HWC – Initial Carcass Weight (which was obtained by regression of carcass weight of six animals slaughtered at the beginning of the experiment).
C1= CON vs NUT+BRP; C2= NUT vs BRP.

feeding (~14 to 28 d) on production parameters, our objective was to determine whether prolonged C16:0 supplementation can maintain milk fat yield and FA incorporation into milk fat. Twenty multiparous Holstein cows were enrolled in a study consisting of a 5 d covariate, 49 d treatment, and 14 d post-treatment evaluation. Cows received a sorghum silage-based diet and were randomly assigned to treatments consisting of no added fat (control; soyhull pellets; n = 10; 138 ± 45 DIM) or C16:0 at 4% of ration DM (98% C16:0; PALM; n = 10; 136 ± 44 DIM). Milk yields were recorded and samples were composited at wk 0, 3, and 7 relative to the start of the treatment period, and 2 wk post-treatment. Data were analyzed as repeated measures using a mixed model with the fixed effects of treatment and time. Effects of PALM are presented as changes relative to control. We observed that PALM increased yields of milk and milk fat by wk 3 and 7 (P < 0.05), without changing milk fat concentration (P = 0.33). PALM increases in milk fat yield were preserved post-treatment (P < 0.05). PALM increased milk C16:0 yield by 52 and 46% by wk 3 and 7, respectively (P < 0.01). Similar observations were observed for yields of milk *cis*-9 C16:1. Although yields of de novo synthesized and preformed FA in milk remained unchanged, milk saturated FA yield increased in PALM by wk 3 and 7 (P < 0.01). Post-treatment, the yields of C16:0 (P = 0.19) and *cis*-9 C16:1 (P = 0.49) in PALM were comparable to control. Post-treatment, the sustained increase in milk fat yield with PALM was due to increased yields of de novo and preformed FA in milk (P < 0.01). Comparable to changes in milk FA yields, PALM increased milk C16:0 concentrations by 26 and 21% by wk 3 and 7, respectively (P < 0.01). Concentrations of milk de novo synthesized and unsaturated FA were lower in PALM-fed cows (P < 0.01). We did not observe any differences in the concentrations of milk FA post-treatment. We conclude that feeding mid-lactation dairy cows C16:0 for 7 wk maintained milk fat synthesis for the duration of supplementation because of sustained C16:0 and *cis*-9 C16:1 incorporation.

Key Words: fatty acid, milk fat, palmitic acid

1338 Feedlot performance of Nellore bullocks fed with two different types of ruminally protected fat.

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The objective of the study was to evaluate two different sources of ruminally protected fat on feedlot performance of Nellore bullocks. It was used 53 intact Nellore males with 315 ± 5,9 kg of initial body weight (IBW) and 20 mo old. Six animals were random selected and harvested at the first day of study for carcass gain calculation while 47 animals were allocated in individual pens for feedlot performance evaluation. Trial design was randomized blocks (based on IBW) divided in 3 treatments: Control– no addition of fat (CON, n = 16), Nutrigordura®- ruminally protected soybean oil (NUT, n = 16) and a blend of ruminally protected vegetable oils containing both saturated and unsaturated sources (BRP, n = 15). Animals were fed for 140 d with a 88% concentrate diet (14.2% of CP and 2.74 of Mcal/kg of DM, for NUT and BRP; 14.4% of CP and 2.63 Mcal/kg of DM for CON) composed of grounded corn, citrus pulp, peanut meal, trace minerals supplement and sugarcane bagasse. Diets of NUT and BRP treatments were isoproteic and isoenergetic with the same inclusion of protected fat (3.36% of DM). Animals were fed twice daily with total mixed ration management. Animals were considered as

experimental unit and variables were analyzed using ANOVA ($P \leq 0.10$; PROC MIXED of SAS), and means were compared by contrasts (C1 = CON vs. NUT+BRP; and C2 = NUT vs. BRP). No difference was observed for Dressing Percentage ($P = 0.18$; Table 1). However, differences ($P < 0.01$) were observed for final BW, DMI, and ADG, for animals fed NUT or BRP, compared to CON (C1). Additionally, it was observed differences in both contrasts (C1: $P < 0.01$, C2: $P < 0.10$) for feed efficiency (G:F), Hot Carcass Weight (HCW), Carcass Gain and ADG of carcass, whereas animals fed BRP presented better feedlot performance than CON and NUT (C2). Bullocks fed BRP presented carcasses 13 kg heavier ($P = 0.03$) than NUT. In conclusion, ruminally protected fat increases feedlot performance of Nellore bullocks and BRP provides better benefits (ADG, G:F, HCW and Carcass Gain) than a ruminally protected fat derived from soybean oil.

Key Words: nutrition, protected fat, saturated fatty acid

1339 Studies on different energy density of close-up diets on energy metabolism and lactation performance in montbeliarde-sired crossbred holstein cows.

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The objective of the experiment were to evaluate the effects of prepartum dietary energy density on dry matter intake (DMI), lactation performance, energy metabolism in montbeliarde-sired crossbred holstein cows. Eighteen dry cows (Half primiparous and half multiparous) were blocked and assigned randomly to three groups fed a low concentrate diet (Concentrate is 0.3% of body weight), middle concentrate diet (Concentrate is 0.6% of body weight), high concentrate diet (Concentrate is 0.9% of body weight) from 21 d before expected day of calving, and corn stover was free to access choice. After parturition, all cows were fed the same lactation diet to 28 d in milk. The DMI, net energy intake (NEI) and energy balance (EB) of prepartum were significantly decreased by the reduced amount of concentrate added. The 0.9% group consumed 43.52% more DMI, compared with 0.3% group in the last 1 wk before calving. The different amount of concentrate added had no effect on DMI and NEI, EB, milk yield in first 4 wk of lactation. Overall, energy metabolism and lactation performance of postpartum were not affected by energy density of the three treatments during the close-up period, and the 0.3% group is more economical compared with other groups.

Key Words: transition cow, dietary energy density, energy metabolism

1340 Prepartum body condition score and plane of nutrition affect the hepatic transcriptome during the transition period in grazing dairy cows.

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A transcriptomic approach was used to evaluate potential interactions between prepartum degree of body condition (BCS) and feeding management in the weeks before calving on hepatic metabolism during the transition period. Thirty-two mid-lactation grazing dairy cows of mixed age and breed were randomly allocated to one of four treatment groups in a 2 × 2 factorial arrangement: two prepartum BCS categories [4.0 (thin, BCS4) and 5.0 (optimal, BCS5); based on a 10-point scale], and two levels of energy intake during the 3 wk preceding calving (75 and 125% of estimated requirements). Liver samples were obtained at −7, 7, and 28 d relative to parturition and subsequent RNA was hybridized to the Agilent 44K Bovine (V2) Microarray chip. Data were adjusted for dye and array effect and a MIXED model with repeated measures was then fitted to the normalized $\log_2$–tranformed adjusted ratios using Proc MIXED. Differentially expressed genes (DEG) with fold change ≤ -1.5 and ≥ 1.5, and P-value ≤ 0.01 were considered for downstream analysis. The Dynamic Impact Approach was used for pathway analysis, and Ingenuity Pathway Analysis was used for gene network analysis. The greater number of differentially expressed genes in BCS4 cows in response to prepartum feed allowance underscored that these animals were more responsive to prepartum nutrition management than optimally-conditioned cows. Independent of prepartum BCS, however, pathway analysis revealed that prepartal feeding level had a marked impact on carbohydrate, amino acid, lipid, and glycan metabolism. Altered carbohydrate and amino acid metabolism indicated a greater and more prolonged negative energy balance post-calving in BCS5 cows overfed prepartum. This was surmised by the opposite effect of pre-calving feeding in BCS4 compared with BCS5 cows on pathways related to amino acid, vitamin, and co-factor metabolism. The prepartum feed restriction ameliorated the metabolic adaptation to the new lactation in BCS5 cows, while detrimentally affecting BCS4 cows, which seemed to better adapt when overfed. Alterations in the glycosaminoglycan synthesis pathway supported this idea, indicating better hepatic health status in feed-restricted BCS5 and overfed BCS4 cows. The IPA network analysis indicated liver damage in feed-restricted thin cows, likely due to metabolic overload. Overall, the data indicate that overfeeding in late-pregnancy should be limited to underconditioned cows, while cows with optimal degree of body condition should be maintained on an

Table 1339.

Table 1.Effect of close-up dietary amount of concentrate on DMI, NEI, Milk yield and EB intake

Item	Dietary treatments			SEM	*P*-value
	0.3%	0.6%	0.9%		Diet
DMI，kg/d					
Prepartum					
-3 ~ -1 W	7.04[a]	8.58[b]	9.94[c]	0.196	<0.001
-1 W	6.87[a]	8.37[b]	9.86[c]	0.255	<0.001
Postpartum					
1 W	10.48	10.5	11.00	0.381	0.57
2 ~ 4 W	16.77	18.15	18.97	0.922	0.27
NEI，MJ/d					
Prepartum					
-3 ~ -1W	48.69[a]	60.72[b]	71.23[c]	1.711	< 0.001
-1 W	47.59[a]	59.33[b]	70.67[c]	2.243	< 0.001
Postpartum					
1 W	78.01	78.19	81.75	2.921	0.60
2 ~ 4 W	119.76	129.58	135.43	6.583	0.27
Milk yield，kg/d					
1W	18.41	17.00	18.74	0.825	0.67
2 ~ 4 W	30.36	28.84	31.13	2.161	0.75
4% FCM yield，kg/d					
1W	20.42	19.27	20.27	2.077	0.91
2 ~ 4 W	30.29	29.02	31.49	2.769	0.82
EB，MJ/day					
Prepartum					
-3 ~ -1 W	-9.50[a]	2.04[b]	15.48[c]	1.228	< 0.001
-1 W	-11.88[a]	0.65[b]	14.91[c]	1.697	< 0.001
Postpartum					
1 W	-24.77	-21.23	-20.33	7.072	0.89
2 ~4W	-19.31	-18.38	-16.56	5.886	0.57

0.3%, 0.6%, 0.9% - concentrate is 0.3% ,0.6% and 0.9% of body weight, respectively.

a, b, c - different superscript letters with the same row represent a significant difference between treatments (P<0.05).

energy-restricted diet.

Key Words: BCS, prepartum nutrition, liver transcriptome

1341 Application of *Pediococcus pentosaceus* and chitinase to high moisture alfalfa hay at baling: effects on nutrient digestion and on growth performance of beef cattle.

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The objective of this study was to assess the effect of applying a *Pediococcus pentosaceus* and chitinase mixture (PED+CH) at baling on nutrient digestion and on growth performance of beef cattle. Pure alfalfa was harvested and sun-cured to either 23 to 30% (HMH) or 10 to 13% (NMH) moisture. The HMH (Treatment) was baled with application of PED (6.5×10^{11} cfu/tonne)+CH (1.5 g/tonne) and NMH was baled without additives (Control). A crossover experiment (Exp 1) used eight cannulated heifers that were divided into two groups and fed diets containing 77% of control or treated alfalfa hay and 33% concentrate (DM basis). Each period consisted of a 10-d adaption, 2-d for measuring rumen fermentation products and 7-d for measuring total tract digestibility using chromium oxide (Cr_2O_3) as an indigestible marker. In Exp 2, fifty Angus×Hereford crossed-bred steers (270 ± 1.12 kg) were stratified by BW and allocated randomly to two groups in 10 pens, and fed diets containing 57% (DM basis) of treated or control alfalfa hay for 112 d and DMI, ADG and feed efficiency (FE) were measured. Data were analyzed as a completely randomized design using PROC MIXED procedure of SAS with cattle (Exp 1) or pen (Exp 2) as the statistical unit. Differences among means were identified using LSMEANS with the PDIFF in SAS. Cattle fed both diets had similar ($P > 0.05$) DM, NDF and ADF digestibility. However, HMH alfalfa treated with PED+CH had lower ($P < 0.05$) CP digestibility as compared with NMH alfalfa hay. Both groups of cattle had similar rumen pH, VFA and ammonia concentrations and cellulolytic enzyme activity. The two groups of cattle also had similar ($P > 0.05$) DMI, ADG and FE over the 112-d backgrounding period. The similar rumen fermentation characteristics, nutrient total tract digestibility and growth performance between the 2 groups of cattle indicate that alfalfa HMH preserved with PED+CH exhibited similar ruminal and total tract digestibility and feed value to NMH alfalfa. The PED+CH additive has the potential to conserve high-moisture alfalfa hay so that its nutritive and feeding value is similar to that of sun-dried alfalfa hay.

Key Words: high moisture alfalfa hay, inoculant, digestibility beef cattle, growth performance

1342 The impact of *Saccharomyces cerevisiae* and *Lactobacillus acidophilus* on colon histomorphology and gene expression in rumen and ileum tissues of young dairy calves.

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Direct fed microbials (DFM) are increasingly used as a replacement for antibiotics growth promoters to maintain animal health, enhance performance and reduce environmental contamination. However, little information exists on the impact of DFM on the morphology of the gastro intestinal tract of calves and innate immune response during early life. The aim of this study was to evaluate the impact of *Lactobacillus acidophilus* and *Saccharomyces cerevisiae* on colon histomorphology and innate immune gene expression of rumen and ileum tissues of calves.

Forty eight Holstein calves (2 to 7 d-old) were grouped according to body weight and circulating IgG and randomly separated into 4 treatments: Control (CTRL)- fed milk replacer and starter diet introduced after the second week; CTRL supplemented with *Saccharomyces cerevisiae boulardii CNCM I-1079* (7.5×10^9 cfu/L milk replacer + 3×10^9 cfu/kg feed) (SCB); CTRL supplemented with *Lactobacillus acidophilus BT1386* (2.5×10^8 cfu/L milk replacer + 1×10^9cfu/kg feed) (LA); and CTRL supplemented with tetracycline (528 mg/L) and neomycin (357 mg/L) before weaning and chlortetracyclin (55 mg/kg) after weaning (ATB). Four calves per treatment were euthanized on Days 33 (d33; pre-weaning) and d96 (post-weaning) for RNA isolation and colon histomorphological studies. The expression levels of Muc1, Muc20, Claudin 3, TLR4, TLR6, TLR9 and TLR10 genes were analyzed by qPCR. Morphometric measurements of stained (hematoxylin & eosin and periodic acid Schiff) colon sections were used for the determination of crypt depth (NDPview 2 software) and goblet cell (imageJ software). The effects of treatments were analyzed following a complete randomized block design with repeated measures and Tukey adjustments for multiple comparisons. The levels of expression of genes were low in the ileum. In the rumen, Muc1 gene increased $P = 0.014$ whereas the expression of TLR 6 ($P = 0.07$) and TLR10 ($P = 0.081$) genes tended to increase with SCB when compared to CTRL. Crypt depth for both SCB and ATB decreased significantly ($P < 0.01$) on d33 and d96 as compared to LA and CTRL. Similarly, neutral mucins were increased ($P < 0.05$) with SCB (d33 and d96) and ATB (d33) as compared to LA and CTRL. Muc1 gene was up-regulated in the rumen but not in the ileum on d33 and d96. Data shows that feeding SCB altered the colon morphology and increased neutral mucin; an indication of early

maturation in the SCB treated group. Our results suggest that SCB could improve colon development in young dairy calves.

Key Words: Histomorphology, *Saccharomyces cerevisia, calf, Muc1 gene,* development

1343 Aflatoxin M1 levels reduction in milk after *Saccharomyces cerevisiae* or mannanoligosaccharides addition to aflatoxin B1 contaminated diet of dairy cows.

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The purpose of this study was to evaluate the ability of *Saccharomyces cerevisiae* (SC47) and a mananoligosaccharide (MOS) to bind aflatoxin B1 (AFB_1) in the diet of dairy cows fed with 200 ppb an AFB_1–contaminated diet daily and, consequently, to reduce the aflatoxin M_1 levels in milk. Toxigenic fungi that grow on crops can produce highly carcinogenic metabolites called aflatoxins (B_1, B_2, G_1, G_2). Aflatoxin M_1 is a hydroxylated AFB_1 metabolite secreted (0.3 to 6.2%) in milk of mammary glands of lactating animals. Thirty six early to mid-lactation dairy cows averaging 90 d were used in a 4 × 4 Latin square design with 3 replicates. Cows were blocked by parity, body weight and milk production. Ad libitum access to feed and water was provided. Within each replicate, cows were randomly assigned to 6 dietary treatments for 2 consecutive 7-d periods. Dietary treatments included: T1 Basic Diet (BD); T2 BD + AFB_1 [200 μg of AFB_1/kg of diet dry matter (DM)]; T3- BD + 10 g MOS/cow/day; T4- BD +AFB_1 [200 μg of AFB_1/kg of diet dry matter (DM)] + 10 g MOS/cow/day; T5- BD + 10 g SC47/cow/day and T6- BD + AFB_1 + 10 g SC47/cow/day. Milk samples were collected from first to fourth day, seventh and 10th to 14th day of the experimental period. The cows of treatments T2, T4 and T6 were feed with the AFB_1 contaminated diet until the 10th day of experiment. The AFM_1 analysis was performed using immunoaffinity clean-up and detection by HPLC with fluorescence detector. Adding SC47 or MOS to basal or AFB_1–contaminated diets at 10 g/day/animal had no effect on lactation performance. The maximum levels of AFM_1 averaged at 11th day were 2,04 +0,18 μg/L, 0,7+0,12 μg/L and 0,14+0.03 μg/L, respectively for cows fed BD + AFB_1 (T2), BD + AFB_1 + MOS (T4) and BD + AF + SC47. Transfer rates of AFB_1 from feed to milk (AFM_1) averaged 1.02, 0.35, 1.42, and 0.07% for cows fed BD + AFB_1 (T2), BD + AFB_1 + MOS (T4) and BD +AFB_1 + SC47, respectively. Results indicated that strain SC47 and MOS at 10 g/animal/day were effective in reducing milk AFM_1 concentrations in cows consuming a total mixed ration containing 200 μg of AFB_1/kg of DM.

Key Words: Yeast, mycotoxin, milk quality

1344 Effects of a plant extract-based feed additive on feed intake, milk production and composition, rumen fermentation, digestibility, and nitrogen utilization in lactating dairy cows.

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The objective of this study was to investigate the effect of a plant extract-based feed additive (PE, Laboratoires Phodé, France) on performance, rumen fermentation, nutrient digestibility, and nitrogen utilization in lactating dairy cows fed diets with 2 concentrations of CP. The study involved 21 Holstein cows (123 ± 58.4 d in milk) in a replicated 3 × 3 Latin square design experiment with 3, 28-d periods. Treatments were control (15.8% CP), a low CP diet (LCP, 14.0% CP), and LCP supplemented with 35 g/d PE (LCPPE). PE was mixed with one-third of the ration and top-dressed. The low CP diets decreased ($P < 0.01$) DMI compared with the control and there was no effect of PE on DMI (28.4, 27.4, and 26.9 kg/d for control, LCP, and LCPPE, respectively). Milk yield was similar (36.6 kg/d; SEM = 1.66, $P = 0.27$) among treatments. Treatment had no effect ($P = 0.14$) on feed efficiency (1.31, 1.33, and 1.36 kg/kg, respectively). Milk yield adjusted to 4% fat (FCM) was not affected by treatment; however, FCM feed efficiency as proportion of RUP intake (4% FCM ÷ RUP intake) was increased ($P = 0.05$) by LCPPE compared with the control and LCP (22.8, 20.7, and 20.2 g/g, respectively). Concentrations of milk fat, protein, and lactose and milk fat and protein yields were not affected ($P \geq 0.35$) by treatment. Milk N efficiency was higher ($P < 0.01$) for the low-protein diets compared with the control. Ruminal pH, lactate, ammonia, and VFA concentrations, except valerate, which was lowered ($P < 0.01$) by LCP, were also not affected ($P \geq 0.36$) by treatment. The low-protein diets had slightly higher ($P \leq 0.02$) total tract apparent digestibility of DM and organic matter, but lower CP digestibility than the control. PE did not affect ($P \geq 0.22$) nutrient digestibilities. The low-CP diets decreased ($P < 0.01$) urinary and fecal nitrogen excretions; nitrogen losses were not affected by PE. Excretion of purine derivatives in urine was not affected ($P = 0.17$) by treatment. Ruminal in situ degradability of dietary DM, CP, NDF, and ADF was also similar ($P \geq 0.31$) among treatments. In this study, dietary supplementation of PE had no effect on feed intake, production variables, feed efficiency, or nutrient digestibility, but increased FCM efficiency as proportion of RUP intake in lactating dairy cows.

Key Words: plant extract, dietary protein, milk production, feed efficiency, dairy cow

1345 Monensin and levels of narasin on rumen metabolism in lambs during adaptation to high-concentrate diets. D. M. Polizel*[1], S. S. Marques[2], M. F. Westphalen[3], M. H. Santos[1], M. V. C. Ferraz Junior[1], M. V. Biehl[3], R. G. Silva[1], I. Susin[3], and A. V. Pires[1,3], *[1]FMVZ/University of Sao Paulo, Pirassununga, Brazil, [2]Ponta Grossa State University, Ponta Grossa, Brazil, [3]ESALQ/University of Sao Paulo, Piracicaba, Brazil.*

The objective in this trial was to determine the effects of monensin and levels of narasin on short chain fatty acids (SCFA) profile and ruminal pH during adaptation of lambs fed high-concentrate diets. Fifteen White Dorper × Santa Inês and 15 Dorper × Santa Inês lambs, cannulated in the rumen, were assigned to a randomized complete block design, defined by breed and initial BW. Experimental diets were control (without ionophore), monensin (25 mg/kg DM) and 3 doses of narasin (5, 10, or 15 mg/kg DM), corresponding to the experimental diets C, M, N5, N10, and N15, respectively. The experimental period lasted 29 d. Rumen fluid was collected on Days 1, 7, 14, and 21, every 3 h, starting prior feeding, 3, 6, 9, and 12 after feeding. In every sampling time 20 mL of rumen fluid per animal were collected and these samples were stored in the same vial (1 vial per animal per day). Data were analyzed using the MIXED procedure (SAS Inst. Inc.). There were 2 contrasts previously defined (I: control vs. ionophores; II: monensin *vs*narasin). Orthogonal polynomials for the effects of levels of narasin (control, N5, N10, and N15) responses were determined by linear and quadratic effects. The effects were considered significant when $P < 0.10$, and tendency when $P < 0.15$. Experimental diets did not affect molar proportion of acetate (54.54 ± 1.05 mM/100mM), propionate (32.23 ± 2.00 mM/100mM), butyrate (9.07 ± 0.89 mM/100mM), isovalerate (1.61 ± 0.25 mM/100mM) and valerate (1.42 ± 0.12 mM/100mM). There was a tendency for quadratic effect of levels of narasin on isobutirate (C: 0.64; M: 0.72; N5: 0.85; N10: 0.70; N15: 0.70 mM/100mM; $P = 0.11$). Acetate:propionate ratio (2.04 ± 0.14) and ruminal pH (5.94 ± 0.07) were not affected by experimental diets. Animals fed the diet containing monensin tended to had lower total SCFA than animals fed narasin (C: 113.21; M: 102.24; N5: 110.22; N10: 111.32; N15: 109.25 mM/l; $P = 0.11$). There was no interaction between experimental diets and days for all variables. Monensin and narasin had a tendency to alter SCFA profile without affecting ruminal pH in lambs fed high concentrate diets during dietary adaptation.

Key Words: ionophores,lambs, rumen pH.

1346 Effect of narasin on rumen metabolism and dry matter intake in wethers fed high-forage diets. D. M. Polizel[1], M. F. Westphalen*[2], A. A. Miszura[1], M. H. Santos[1], R. G. Silva[1], A. V. Bertoloni[1], G. B. Oliveira[1], M. V. Biehl[2], M. V. C. Ferraz Junior[1], A. V. Pires[2], and I. Susin[2], *[1]FMVZ/University of Sao Paulo, Pirassununga, Brazil, [2]ESALQ/University of Sao Paulo, Piracicaba, Brazil.*

The objectives in this trial were to determine the effects of increasing levels of narasin on short chain fatty acid profile, pH and rumen protozoa concentration in whethers fed high-forage diets. Five White Dorper × Santa Inês wethers (BW 68.7 ± 2.1 kg), cannulated in the rumen, were used in 5 × 5 Latin Square design. Animals were fed daily and diet was composed of coastcross hay (91.0% DM; 67.2% NDF; 32.1% ADF; 6.8 CP; 5.5% ash). Narasin was offered twice a day and levels were 0 (control), 8, 16, 24 or 32 mg/kg DM, corresponding to 0, 80, 160, 240, and 320 mg of Zimprova 100®. The delivery vehicle of narasin was 20 g of ground corn containing the set dosage of narasin in 1 kg of DM. Every experimental period lasted 20 d and rumen fluid was collected in the last day, every 3 h, starting prior feeding, 3, 6, 9, and 12 h after feeding. Dry matter intake (DMI) was measured on d 20. Short-chain fatty acids (SCFA) and pH were analyzed as repeated measures over time. Protozoa concentration was analyzed at 3 h after feeding. Data were analyzed using MIXED procedure (SAS Inst. Inc.) and the LSMEANS option was used to generate individual means. Orthogonal polynomials for diet responses were determined by linear and quadratic effect. The effects were considered significant when $P < 0.10$. Increasing levels of narasin did not affect DMI (1.00 ± 0.12 kg/d; $P = 0.45$). There was an increased linear response for total SCFA (77.24, 81.30, 90.04, 83.65, 89.60 mM/L, $P = 0.02$). Acetate (78.40 ± 0.64 mM/100Mm, $P = 0.93$), propionate (15.03 ± 0.41 mM/100mM, $P = 0.79$), isobutyrate (0.62 ± 0.11 mM/100mM, $P = 0.97$), butyrate (4.34 ± 0.24 mM/100mM, $P = 0.62$), isovalerate (0.97 ± 0.19 mM/100mM, $P = 0.95$), valerate (0.64 ± 0.07 mM/100mM, $P = 0.30$) acetate-propionate ratio (5.28 ± 0.28, $P = 0.76$), pH (6.64 ± 0.13, $P = 0.46$) and rumen protozoa concentration ($2.44 \pm 0.22 \times 10^5$/ml, $P = 0.69$) were unaffected by the experimental diets. Increasing doses of narasin resulted in higher concentration of total SCFA.

Key Words: SCFA, ionophore, protozoa

1347 Monensin and levels of narasin on rumen metabolism in lambs fed high-concentrate diets.

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The objective in this trial was to determine the effects of monensin and narasin on rumen metabolism of lambs fed high-concentrate diets. Thirty Dorper × Santa Inês lambs, cannulated in the rumen, were assigned to a randomized complete block design, defined initial BW. Animals were fed daily and diets were composed of 90% concentrate and 10% hay. Diets were control, monensin (25 mg/kg DM) and doses of narasin (5, 10, or 15 mg/kg DM), corresponding to the experimental diets C, M, N5, N10, and N15, respectively. The experiment lasted 29 d. The first 24 d were used to adapt the lambs with experimental diets and the remaining 5 d were used for data collection. In the last day, rumen fluid was collected every 3 h, starting prior feeding, 3, 6, 9, and 12 h after feeding. Short chain fatty acids (SCFA) profile and pH were determined. Data were analyzed using the MIXED procedure (SAS). There were 2 contrasts previously defined (I: control vs. ionophores; II: monensin *vs*narasin). The effects of levels of narasin (control, N5, N10, and N15) were evaluated using linear and quadratic orthogonal contrasts. The effects were considered significant when $P < 0.10$. Animals fed diets containing ionophores had higher molar proportion of propionate than animals fed the control diet (C: 26.6; M: 33.3; N5: 31.0; N10: 33.7; N15: 30.2 mM/100mM; $P = 0.07$). There was an increased isobutyrate for animals fed narasin then animals fed monensin (C: 0.8; M: 0.7; N5: 0.8; N10: 0.8; N15: 0.8 mM/100 mM; $P = 0.06$). Diets containing monensin had lower butyrate than narasin ($P = 0.08$), however, the control diet had higher butyrate than the diets containing ionophore (C: 13.5; M: 9.4; N5: 11.5; N10: 11.1; N15: 11.4 mM/100 mM; $P = 0.02$). Experimental diets did not affect acetate (50.0 ± 2.4; $P = 0.41$), isovalerate (1.5 ± 0.2; $P = 0.70$) and valerate (1.3 ± 0.1; $P = 0.42$). Animals fed diets containing ionophore had lower acetate:propionate ratio than animals fed the control diet (C: 2.2; M: 1.7; N5: 1.9; N10: 1.6; N15: 2.0; $P = 0.06$). There was a decreased linear response of narasin levels on total SCFA (C: 133.4; M: 124.3; N5: 135.6; N10: 122.4; N15: 115.7; $P = 0.02$). Treatments did not affect ruminal pH (5.9 ± 0.1; $P = 0.90$). Monensin and narasin altered SCFA profile without effecting ruminal pH in lambs fed high-concentrate diets.

Key Words: acetate-propionate ratio, pH, propionate.

1348 Daily supplementation with an active dry yeast improved feed efficiency in lactating dairy cows.

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Research has demonstrated that supplementation with an active dry yeast (ADY) can have a positive effect on dairy cow performance. The aim of the current experiment was to test a new ADY which had been selected because it improved rumen fermentation in vitro and to measure its effects in vivo. The trial was split into a 3 wk pre-period followed by a 12 wk test period, which was further split into 3 wk periods. Forty-four cows (16 primiparous, 28 multiparous cows) with average DIM = 123 (ranging from 55 to 165) were allocated to 22 blocks on the basis of calving date, parity, weight, milk production and composition in the pre-period. Within block, cows were randomly assigned to either control (CTL) or treatment (LY). In the test period, CTL received 100 g of wheat pollards daily and the LY received 97 g wheat pollards + 3 g live yeast, delivering 60 billion cfu/cow/day, top-dressed on a partial TMR consisting of (on a DM basis) corn silage (65%), grass silage (29%) and protein supplement (6%). Concentrate requirement was delivered via an automated dispenser 3 times daily. Throughout the trial, individual milk yield, weight, and DMI (measured via Calan gates) was measured daily, averaged weekly. Milk composition was measured 4× a week, and BCS every 3 wk. Statistical analysis was performed by ANOVA using the pre-period as a covariate to assess LY effect on feed intake, milk production, milk composition and energy balance. Significance was declared at $P < 0.05$ and trends discussed at $0.05 < P < 0.1$. Results showed that over the total test period, LY tended to increase FPCM (32.25 vs. 31.53 kg/day, $P = 0.09$) and significantly increased feed efficiency kg FPCM yield/kg DMI (1.47 vs. 1.43, $P = 0.032$). Interestingly, in the last 3 wk, the effects on FPCM were higher, and the effects of LY reached significance (31.4 vs. 30.0, $P = 0.025$), driven by a significant increase in butterfat yield (1259 vs. 1193 g/day, $P = 0.009$). There were no significant effects of treatment on any of the other parameters measured. To conclude, daily supplementation of live yeast resulted in a significant increase in feed efficiency. There appeared to be a lag effect on performance and it was hypothesized this was due to time needed for the rumen microflora to adapt. Further trials will test this hypothesis.

Key Words: feed efficiency, lactation, yeast

1349 Effect of saponite (EcoMix) on toxin binding capacity, ruminal fermentation, diet digestibility and growth of steers fed high concentrate diets.

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Three experiments were conducted to determine the effect of increasing concentrations of the clay mineral, saponite (EcoMix, United Minerals Group), on toxin binding, ruminal fermentation, diet digestibility and growth of feedlot cattle. In experiment one, 150 mg of EcoMix was incubated in 10 mL of rumen fluid with 3 incremental concentrations of aflatoxin B_1 (AFB_1) or ergotamine tartate (ET) to determine binding capacity. In experiment two, 6 steers (initial BW = 596 ± 22.2 kg) were randomly allotted to 3 treatments in a replicated 3 × 3 Latin square design (21-d periods) to determine the effects of increasing amounts of EcoMix (0, 1, or 2%) on ruminal pH, VFA, and nutrient digestibility. EcoMix was top-dressed on an 80% concentrate diet at a rate of 0, 113, or 226 g/steer/d to achieve the 0, 1, and 2% treatments, respectively. In experiment three, 72 Angus × Simmental steers were blocked by BW (395 ± 9.9 kg) and allotted to the same 3 treatments (4 pens/treatment, 6 steers/pen) to determine the effects of EcoMix on performance. Steers were slaughtered at a target BW of 606 kg. EcoMix was able to effectively bind AFB_1 and ET at concentrations well above the normal physiological range (52 and 520 μg/mL), but % adsorption was decreased to 35.5 and 91.1% at 5200 μg/mL ($P < 0.0001$) for AFB_1 and ET, respectively. EcoMix linearly decreased ruminal lactate and propionate, and VFA production efficiency ($P \leq 0.04$), linearly increased formate and acetate:propionate ($P \leq 0.03$), and tended ($P = 0.07$) to linearly increase butyrate. EcoMix tended to linearly increase organic matter and crude protein apparent digestibility ($P = 0.06$). Ruminal pH, urine pH, and other digestibility measures did not differ among treatments ($P \geq 0.15$). During the first month there was a quadratic response of EcoMix on ADG ($P = 0.009$) and gain:feed ($P = 0.0003$), increasing from 0 to 1% EcoMix, and then decreasing from 1 to 2% EcoMix. However, during the second month, EcoMix decreased ADG and gain:feed linearly ($P \leq 0.03$) and overall ADG, DMI, or gain:feed were not impacted ($P \geq 0.46$). EcoMix linearly decreased marbling score ($P = 0.05$). Hepatic enzyme activity did not differ among treatments on d 0 or at slaughter ($P \geq 0.15$). In conclusion, EcoMix effectively binds ruminal toxins, decreases ruminal lactate, and improves performance during adaptation to a high concentrate feedlot diet.

Key Words: clay mineral, saponite, feedlot performance

1350 Use of *Aspergillus oryzae* extract containing α-amylase activity in finishing diets for Nellore cattle.

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The objective was to evaluate effects of supplementing *Aspergillus oryzae* extract containing α-amylase activity (Amaize®) in high concentrate diets fed finishing diets for Nellore cattle. The experiment was conducted at the Experimental Confinement Unit of Agência Paulista de Tecnologia dos Agronegócios-Colina/SP/Brasil. Fifty-four Nellore bulls (average age 24 mo.) with initial body weight 353 ± 13 kg were used in the study. Six animals were slaughtered initially (for subsequent calculation of carcass gain) and 48 individually-penned animals were used to evaluate performance. The experimental design was a randomized complete block with two treatments: 1) Control– no enzyme, and 2) Enzyme −5 g/Amaize® (Alltech Inc) per head daily. The experiment lasted 96 d, (24 d adaptation and three periods of 24 d each). The diet consisted

Table 1350.

Table 1. Means and mean standard error of Nellore performance variables in treatment with absence (control) and presence of *Aspergillus oryzae* extract containing α-amylase activity (Amaize®) with high concentrate in finishing diets for Nellore cattle

Variables	Tratament		SEM	*P-Value*
	Control	Enzyme		
DMI, kg/d	8.32	9.07	0.44	0.11
ADG, kg/d	1.187	1.330	0,055	0.08
G:F, kg ganho/kg MS	0.142	0.146	0.002	0.44
HCW, kg	267	276	4.74	0.09
Dressing Percentage, %	57.2	57.4	0.40	0.65
Carcass gain, kg	81.5	90.0	4.76	0.09
ADG Carcass, kg/d	0.87	0.96	0.05	0.09

Differences considered statistically significant at the 10% significance by t test.
ADG= average daily gain; DMI = dry matter intake; G:F = gain:feed; FC = feed conversion; HCW= hot carcass weight; Dressing Percentage = ((HWC/BW)*100); Carcass gain = (HWC – Initial estimated carcass weight (which was obtained by regression of carcass weight of six animals slaughtered at the beginning of the experiment).

of sugarcane bagasse (12.47% DM), ground corn (4 mm-hammer mill) (62.59% DM), citrus pulp (16.96% DM) and protein blend (52% soybean meal, 12% Optigen® (sustained release N), 36% mineral salt. Forage:concentrate was 12:88 and contained MS: 14.1% CP, 23.5% NDF and 2.62 Mcal/kg. The data were analyzed using the MIXED procedure with a fixed effect of treatment and weight block as a random effect, the differences between the means were compared by *t* test at 10% probability. No differences were observed for DMI, G:F and dressing percentage between animals receiving enzymes compared to controls (Table 1). However, there was an effect of Amaize on ADG ($P = 0.08$), which represented ~140 g over ADG when compared to controls. HCW, carcass gain and carcass ADG were numerically superior in cattle fed Amaize in carcass weight, and slaughter with an additional average weight of ~9 kg, which represents 3.37% more when compared to control weight values. Therefore the supplementation of *Aspergillus oryzae* extract containing α-amylase activity (Amaize®) with high concentrate finishing diets improves the performance of Nellore cattle.

Key Words: additives, enzymes, performance

1351 Inclusion of pelleted calcium hydroxide-treated corn stover in lactating Holstein cow diets: Effects on milk production and milk composition.

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Chemical treatment of corn stover with 6.6% $Ca(OH)_2$ (TCS) increases the availability of cellulose and hemicellulose, improving the feeding value of this abundant crop residue. The low bulk density limits transportation and the broader use of TCS. Manufacturing techniques were used to densify and fortify TCS to improve its nutritional value potentially making TCS an alternative to traditional forage sources. The objectives of this study were to evaluate the effects of feeding TCS as part of a pelleted feed supplement blended to have a nutrient profile that resembles corn gluten feed, a common byproduct feed used in US dairy and beef operations. Eight mid-lactation multiparous Holstein cows were used in a replicated 4 × 4 Latin square consisting of four 21-d periods to evaluate the effects of feeding pelleted TCS (PTCS) on milk production and composition. Diets were: 1) control (CON) containing corn silage and alfalfa haylage as the primary forages, or 2) the partial replacement of these forages with 21 (21PTCS) or 3) 40% (40PTCS) of the diet DM with PTCS, or 4) a combination of all ingredients used to manufacture PTCS that were not pelleted and fed at 40% (40NPTCS) of the diet DM. Milk production and 4% energy corrected milk did not differ ($P > 0.05$) among treatments. Compared to the CON, DMI was reduced ($P < 0.05$) with the inclusion of TCS regardless of physical form in the 40 PTCS and 40 NPTCS diets but was not different in the 21 PTCS diet (24.2, 23.0, 21.7, 21.3, and ± 0.97 kg/d, CON, 21PTCS, 40PTCS, and 40NPTCS, respectively). Milk fat percentage was reduced ($P < 0.05$) with the inclusion of TCS in the 21PTCS and 40PTCS diets and tended ($P = 0.09$) to be reduced in the 40NPTCS diet. However, milk fat yield was only reduced when cows were fed the 40PTCS diet. Percent milk protein and percent milk lactose were not affected by the inclusion of TCS in the diet ($P > 0.05$). Data indicate that partial replacement of corn silage and alfalfa haylage with a pelleted feed supplement containing TCS has no impact on 4% energy corrected milk yield although inclusion of PTCS at 40% of the diet DM reduces milkfat yield. These results suggest pelleted feed supplements containing TCS may serve as a valuable replacement for a portion of typical forages fed to lactating dairy cows.

Key Words: pelleted corn stover, milk fat, alternative forage

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1352 Influence of adding slow release urea and zeolite in growth performance and carcass traits of feedlot lambs.

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Twenty-four Pelibuey × Katahdin (45.4 ± 1.1 kg) crossbred male lambs were used in a 42-d feeding trial (6 pens per treatment in a randomized complete block design), to evaluate the influence of slow release urea and zeolite on growth performance and carcass characteristics. Lambs were fed a dry-rolled corn-based finishing diet (1.42 Mcal/kg of NEg; 14.6% of PC). Treatments consisted: 1) Control (C), 2) Slow release urea (SRU) (0.8%), 3) Zeolite (Z) (3%) and 4) combination of SRU and Z; DM intake averaged 1.282 ± 0.042 kg/d and was not affected ($P = 0.40$) by treatments. Compared with control lambs, SRU supplementation increased gain efficiency (13.14%, $P < 0.04$), average daily gain (17.8%, $P < 0.03$) and final body weight (3.60%, $P < 0.04$). Combination of slow release urea and zeolite supplementation affected ($P = 0.032$) hot carcass weight, longissimus muscle area (LM) and carcass dressing percentage (2.3%, $P = 0.04$), kidney-pelvic fat was not affected. Addition of slow release urea and zeolite combination improved growth performance and carcass traits of feedlot lambs.

Key Words: lambs, slow-release urea and zeolite

1353 Effect of different doses of a *Bacillus*-based probiotic on the in vitro digestibility of concentrates and forages. C. A. Oliveira[1], D. O. Sousa[1], J. F. Penso[1], P. F. Menegucci[2], and L. F. P. Silva[*1], [1]*University of Sao Paulo, Pirassununga, Brazil,* [2]*Chr. Hansen, Valinhos, Brazil.*

The objective was to evaluate the effect of different doses of probiotic containing $1.6x10^9$ CFU/g of *Bacillus licheniformis* and $1.6x10^9$ UFC/g of *Bacillus subtilis* (BioPlus® PS, Chr. Hansen) on in vitro digestibility of concentrates and forages. The feedstuffs analyzed included 2 types of concentrates: corn and sorghum, and 2 types of forages: sugarcane silage and *Megathirsus maximus* cv. Mombaça (mombaça-grass). The probiotic was added to the ruminal fluid simulating doses of 0, 1, 2, and 3 g head^{-1} d^{-1}. The doses of probiotic added to the rumen fluid was calculated supposing a volume of 37 L of rumen fluid per animal. Dry matter, NDF, and starch in vitro digestibility of feedstuffs were determined in 0.5 g of sample, in triplicate, after incubation for 6 and 12 h (concentrates); or for 24 and 48 h (forages), using the Daisy Incubator (ANKOM®Technology Corp., Fairpoint, NY, USA). The residues after fermentation were analyzed for NDF in the case of forages, and for starch in the case of concentrates. The experiment was repeated three times. Statistical model included the fixed effect of probiotic, feedstuff, and interaction between both factors, with the experiment repetitions as the random effect. Addition of probiotic improved 24-h NDF digestibility of both roughages (P = 0, 05), without a Dose × Feedstuff interaction (P = 0.36). There was a cubic effect of dose of probiotic on 24-h NDF digestibility, with the dose of 1 g head^{-1} d^{-1} promoting higher NDFD than the control (20.2 vs. 16.3%, P = 0.01). When analyzed after 48 h of incubation, there was a significant Dose × Feedstuff interaction (P < 0.01). Addition of 1 g head^{-1} d^{-1} of probiotic increased (P < 0.01) 48-h digestibility of mombaça-grass, but not of sugarcane silage (P = 0.73). Considering the effects on starch digestibility of concentrates, there was no effect of probiotic after 6 h of incubation (P > 0.05). However, after 12 h of incubation, there was a positive linear effect of addition of probiotic on starch digestibility of both concentrates (P < 0.01), with no Dose × Feedstuff interaction (P = 0.50). The addition of 3 g head^{-1} d^{-1} of probiotic increased by 10.9% starch digestibility after 12 h of incubation. In conclusion, addition of increasing doses of a bacillus based probiotic promoted a cubical increase in NDF digestibility of roughages, and a linear increased in starch digestibility of concentrates.

Key Words: fiber digestibility, starch digestibility, probiotic

1354 Net choline absorption of abomasally infused choline and rumen-protected choline in the lactating dairy cow. M. J. de Veth[*1], V. M. Artegoitia[2], S. R. Campagna[2], H. Lapierre[3], F. M. Harte[4], and C. L. Girard[3], [1]*BioNarus LLC, Cary, NC,* [2]*University of Tennessee, Knoxville,* [3]*Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada,* [4]*The Pennsylvania State University, University Park.*

Choline metabolites have a critical role in many biological processes and choline supplementation to the peripaturient dairy cow improves hepatic lipid metabolism. However, variability in responses to choline supplementation has highlighted a lack of understanding of choline absorption and metabolism in the lactating dairy cow. Our objective was to estimate net choline absorption by measuring net portal fluxes of choline and choline metabolites in cows receiving either dietary supplements of rumen-protected choline (RPC) or abomasal infusion of choline (AIC). Five lactating Holstein cows (237 ± 17 DIM) were used in a 5 × 5 Latin Square design, with 5-d treatment periods and a 2-d interval between periods. Treatments were 1) control (0 g/d choline), 2) 12.5 g/d choline fed as RPC, 3) 25 g/d choline fed as RPC, 4) 12.5 g/d choline provided as AIC, 5) 25 g/d choline provided as AIC. Choline chloride (CC) was the choline form for both sources; RPC (Reashure, Balchem Corporation) and AIC (CC70, Balchem Corporation) contained 21.6% and 52.3% choline ion, respectively. Cows were fed every 2 h to minimize post-prandial variation. On the last day of each period 9 blood samples were collected simultaneously from an artery and portal vein at 30-min intervals and analyzed for betaine, free choline (Cho), lysophosphatidylcholine, phosphocholine and sphingomyelin, using liquid chromatography-tandem mass spectrometry. The net portal flux of Cho (control- 1.7 mmol/h) increased linearly (P < 0.001) with AIC (4.0 and 7.1 mmol/h for 12.5 and 25 g/d AIC, respectively) indicating that the net absorption of Cho was 54% (95% confidence interval of 30 to 79%). No relationship was found between dose of RPC and net portal flux of Cho (P = 0.52). Net portal fluxes of the choline metabolites were not altered by choline treatment. However, the plasma arterial concentrations of betaine and phosphocholine increased (P < 0.001) in response to AIC: 30.6, 102.7 and 151.2 μ*M* and 3.47, 4.21 and 4.96 μ*M* for control, 12.5 and 25 g/d. In addition, plasma arterial concentration of phosphocholine increased (P < 0.01) with RPC, averaging 3.47, 3.81 and 4.08 μ*M* for control, 12.5 and 25 g/d, respectively). The results of this study suggests that AIC taken up by the gastrointestinal wall reached the portal circulation only as Cho and the incomplete recovery may indicate that a portion of AIC is metabolized by the portal-drained viscera of the lactating dairy cow.

Key Words: bioavailability, choline, cow

1355 Effects of Trigestamace on performance of lactating dairy cows. M. M. Masiero*[1], A. L. Kenny[1], R. L. Barnett[1], R. Morrison[2], and M. S. Kerley[1], [1]*University of Missouri, Columbia,* [2]*R&D LifeSciences, Menomonie, WI.*

Objective of this experiment was to determine if Trigestamace (mannan-oligosaccharide, β glucans and enzyme preparation), fed for 60 d to lactating dairy cows, altered milk production, efficiency and composition in early lactation (study initiated 14 to 45 d in milk). Sixty lactating Holstein cows were stratified by previous milk production and parity (2.2 ± 0.03 lactation number) and assigned randomly to control (CON) or CON with Trigestamace included (TRT) diets. Both diets (CON, 48.1% DM, 14.4% CP; TRT 48.1% DM, 15.0% CP) contained (DM basis) 32.5% alfalfa hay, 21.2% corn silage, 13.8% ground corn, 3.8% soybean hulls, 2.6% brewers grain, 26% protein and mineral. Treatment was added at a rate of 0.032% in the diet (as fed basis) providing about 17.7 g/d of Trigestamace based on feed intake. Cows were fed using Calan gates and individual intake measured. Milk yield was recorded twice daily and milk sampled once weekly and analyzed for protein (%), fat (%), lactose (%), somatic cell count (cells/mL) and milk urea nitrogen (%). Data were analyzed as a randomized complete design. Milk yield did not differ (P = 0.50; SEM = 0.22; CON 44.5, TRT 44.2 kg/d) between diets. Dry matter intake was greater (P = 0.01; SEM = 0.11) for cows fed CON (24.6 kg/d) compared to TRT (24.2 kg/d). Milk efficiency was greater (P = 0.02; SEM = 0.007) for cows fed TRT diet (1.86 kg milk/kg DMI) compared to CON (1.83 kg milk/kg DMI). Energy corrected milk (P = 0.97; SEM = 1.44; CON 43.52, TRT 43.44 kg/d) and 3.5% fat corrected milk (P = 0.93; SEM = 1.53; CON 45.1, TRT 44.9 kg/d) did not differ between diets. Milk fat (P = 0.92; SEM = 0.09; CON 3.80%, TRT 3.78%), milk protein (P = 0.42; SEM = 0.03; CON 2.79, TRT 2.82%), lactose (P = 0.59; SEM = 0.02; CON 4.89, TRT 4.91%), milk urea nitrogen (P = 0.96; SEM = 0.32; CON 13.3, TRT 13.4%) and somatic cell count (P = 0.89; SEM = 26.8; CON 79,779, TRT 71,837 cells/mL) did not differ between diets. In conclusion, adding Trigestamace to an early lactation dairy cattle diet reduced DMI without changing milk yield, resulting in a greater milk efficiency.

Key Words: milk performance, mannan-oligosaccharide, β glucans

1356 Effect of imprinted polymer based ergot-alkaloid adsorbent on in vitro ruminal fermentation. M. B. Kudupoje*, *Alltech-University of Kentucky Nutrition Research Alliance, Lexington.*

Previously, we have described the development and characterization of a synthetic polymer designed as an ergot-alkaloid adsorbent. Here, effects of ergotamine imprinted (MIP) and non-imprinted (NIP) methacrylate based polymer adsorbents on in vitro ruminal fermentation were evaluated in an experiment with a completely randomized design. Each adsorbent was evaluated at four different inclusion levels (0.3, 3, 30, 300 mg/0.5 g DM) and compared with a control which contained no adsorbent. Ruminal fluid for inoculum was pooled from 4 steers grazing endophyte-free fescue. Triplicate vessels were inoculated for each treatment in the 2 × 4 + 1 treatment structure. In each vessel, strained ruminal fluid (20 mL) was diluted with buffer (80 mL) under anaerobic conditions and incubated for 30 h at 39°C with 500mg (DM) alfalfa hay substrate. Gas pressure was monitored using an ANKOM RF gas production system at 1 min intervals. Fluid samples were collected following termination of fermentation at 30 h for ammonia-N, VFA and pH measurement. The cumulative gas production and production rate were determined using a Fitzhugh model [$y = (1 \pm e^{-rt})^n$] fit using nonlinear least squares methods. Statistical analysis was conducted using the GLM procedure of SAS, with model terms for polymer type, inclusion amount, and their interaction and orthogonal polynomial contrasts were used to evaluate effects of polymer inclusion level. There were no interactions ($P > 0.10$) between polymer type and inclusion level and no differences ($P > 0.10$) between polymer types. Although there was a quadratic effect ($P < 0.05$) on gas production rate with increasing polymer inclusion level, total gas production (plateau) was unaffected ($P > 0.10$) by inclusion level. Polymers did not affect ($P > 0.10$) total or individual VFAs or ammonia-N concentrations at any inclusion level. The pH declined linearly ($P < 0.01$) with increasing amount of polymer. However, given the logarithmic increase in polymer dose level, the influence on pH was minor (< 0.07 pH units) for all except the 300 mg inclusion level, which depressed pH an average of 0.24 units relative to control. Supplementation of methacrylate based polymer at inclusion rates from 0.3 to 300 mg/500 mg DM did not affect VFA profiles, total VFA concentrations, ammonia-N, or total gas production in rumen fluid containing alfalfa hay substrate. High inclusion levels of both imprinted and non-imprinted polymers lowered pH. However, the inclusion level at which this effect was observed far exceeds levels that would be used in practical supplementation strategies.

Key Words: Ergot alkaloid imprinted polymer rumen fermentation

1357 Effects of *Ascophyllum nodosum* meal and monensin on performance and iodine metabolism in lactating dairy cows. S. F. Reis[*1], A. F. Brito[1], C. P. Ghedini[1], D. C. Moura[2], and A. S. Oliveira[3], *[1]University of New Hampshire, Durham, [2]Universidade Federal de Mato Grosso, Cuiabá, Brazil, [3]Instituto de Ciências Agrárias e Ambientais, Universidade Federal de Mato Grosso– Campus Sinop, Sinop, Brazil.*

Ascoplyllum nodosum meal (ANOD) is a mineral-rich supplement with antimicrobial and antioxidant properties. The objective of the current study was to evaluate the impact of incremental amounts of ANOD on performance and iodine metabolism in lactating dairy cows. It was also of particular interest to compare the effects of ANOD against the ionophore monensin (MON) on animal performance. Five ruminally-cannulated lactating Jerseys cows were randomly assigned to 1 of 5 dietary treatments: 0 g (negative control), 57 g, 113 g, or 170 g of ANOD or 300 mg of MON (positive control) in a 5 × 5 Latin square design. Each experimental period lasted 28 d with 21 d for diet adaptation and 7 d for data and sample collection. Treatments were administered daily placed directly in the rumen. Cows were fed a TMR consisted (DM basis) of 40.5% mixed-mostly grass haylage, 25.5% corn silage, 21% corn meal, 3.5% roasted soybean, 7.5% soybean meal, and 2.0% minerals-vitamins premix. The TMR averaged (DM basis) 15.8% CP, 37.3% aNDFom, and 24.8% ADF. Milk samples were collected and analyzed for components using mid-infrared reflectance spectroscopy. Spot urinary and fecal grab samples were collected with internal markers used to estimate urinary volume (creatinine) and fecal output of DM (indigestible ADF). Blood was collected approximately 4 h after the morning feeding. Milk, feces, urine, and serum were analyzed for iodine using inductively coupled plasma mass spectrometry. The degrees of freedom for treatment were partitioned into 4 single-degree-of-freedom non-orthogonal contrasts: linear, quadratic, ANOD diets vs. MON diet, and 170 g ANOD diet vs. control diet. Results are shown in Table 1. Dry matter intake and serum concentrations of T_3 and T_4were not affected by treatments. Milk yield, concentrations and yields of milk fat and protein, and MUN responded quadratically in cows fed increasing amounts of ANOD. Iodine output in milk, urine, and feces, and serum iodine concentration increased linearly with feeding incremental amounts of ANOD. Concentrations of milk fat, protein, MUN, and yield of milk fat were greater when feeding MON vs. ANOD, and the difference was particularly larger when comparing MON vs. 170 g ANOD. Overall, ANOD supplementation linearly increased the concentration of iodine in serum, and the output of iodine in milk, feces, and urine. Feeding MON improved concentration and yields of milk components, but increased MUN when compared with ANOD.

Key Words: *Ascophyllum nodosum*, dairy cows, iodine

1358 Lactation performance and nutrient digestibility by dairy cows supplemented with calcium montmorillonite clay during an aflatoxin feeding challenge. A. D. Thomas[*1], C. Maki[2], E. M. Jimenez[3], S. E. Elmore[2], L. Kinman[3], A. Romoser[2], R. B. Harvey[2,4], T. Phillips[2], and H. A. Ramirez Ramirez[1], *[1]Iowa State University, Ames, [2]Texas A&M University, College Station, [3]Tarleton State University, Stephenville, TX, [4]United States Department of Agriculture, College Station, TX.*

Fifteen primiparous crossbred dairy cows (114 ± 14 DIM and 662 ± 52 kg BW) were used in replicated 5 × 5 Latin squares to evaluate the effects of feeding calcium montmorillonite clay (NovaSil Plus, NSP) on milk production and nutrient digestibility in rations contaminated with aflatoxin (AF). The

Table 1357.

Table 1. Effects of *Ascophillum nodosum* meal (ANOD) or monensin (MON) on performance and iodine metabolism in dairy cows

	ANOD (g/d)						Contrasts (*P*-values)			
Item	0	57	113	170	MON	SEM	Linear	Quad.	ANOD vs. MON	170 g ANOD vs. MOM
DMI, kg/d	20.1	19.8	19.7	19.8	19.2	0.60	0.48	0.61	0.10	0.17
Milk yield, kg/d	20.9	20.2	20.0	20.8	20.2	0.58	0.76	<0.01	0.65	0.10
Milk fat, %	4.70	4.70	4.80	4.60	5.00	0.06	0.85	0.001	<0.001	<0.001
Milk fat, kg/d	0.96	0.94	0.95	0.95	1.00	0.02	0.89	0.04	<0.01	0.02
Milk protein, %	3.59	3.62	3.62	3.55	3.64	0.11	0.07	<0.01	0.01	<0.001
Milk protein, kg/d	0.74	0.73	0.71	0.73	0.72	0.02	0.33	0.05	0.50	0.22
MUN, mg/dL	10.3	9.8	10.4	10.6	11.2	0.66	0.06	0.04	<0.001	0.01
Milk iodine, mg/d	7.3	14.4	19.5	24.6	6.1	1.7	<0.001	0.54	<0.001	<0.001
Urinary iodine, mg/d	4.3	13.0	15.3	22.3	6.3	1.9	<0.001	0.66	<0.001	<0.001
Fecal iodine, mg/d	20.5	48.1	60.6	86.6	20.1	8.0	<0.001	0.91	<0.001	<0.001
Serum iodine, ng/mL	106	208	303	362	109	20.1	<0.001	0.09	<0.001	<0.001
Serum T_3, ng/mL	1.08	1.03	1.01	0.97	1.02	0.71	0.27	0.97	0.79	0.57
Serum T_4, ng/mL	40.6	40.5	43.4	39.1	43.0	3.3	0.88	0.41	0.49	0.27

experiment consisted of five 14 d periods in which d 1 through 7 of each period were considered for data collection and d 8 through 14 were considered a wash-out phase. In each period, cows were randomly assigned to 1 of 5 dietary treatments: 1) control (CON), consisting of a basal total mix ration (TMR); 2) high dose NSP diet (NSP-1%), consisting of TMR plus 230 g of NSP; 3) aflatoxin diet (AFD), consisting of the TMR plus AF challenge; 4) low dose NSP with AF (NSP-0.5%+AFD), composed of TMR plus 115 g of NSP and AF challenge; 5) high dose NSP with AF (NSP-1%+AFD), consisting of TMR plus 230 g of NSP and AF challenge. Feed intake was recorded daily, TMR, milk and fecal samples were collected on d 6 and 7 of each period. Indigestible acid detergent fiber was used as an internal marker. Data were analyzed using the MIXED procedure of SAS where square, period within square and treatment were fixed effects and cow within square was random. Feed intake ($P = 0.34$) and fecal output ($P = 0.74$) were similar across treatments and averaged 19.7 ± 0.56 kg/d and 7.2 ± 0.56 kg/d, respectively. Digestibility of dry matter ($P = 0.75$), acid detergent fiber ($P = 0.74$), neutral detergent fiber ($P = 0.51$), and organic matter ($P = 0.75$) was similar across treatments averaging 64.0 ± 2.0%, 40.0 ± 3.2%, 41.6 ± 2.9%, and 68.0 ± 1.6%. Addition of NSP reduced milk AFM_1 from 1.10 ± 0.06 µg/L with the AF diet to 0.58 and 0.32 ± 0.06 µg/L with the NSP-0.5%+AF and NSP-1%+AF diets, respectively with no effect on milk yield. These results demonstrate that inclusion of calcium montmorillonite clay is an effective way to reduce aflatoxin excretion in milk with no deleterious effects digestibility of nutrients by dairy cows.

Key Words: food safety, mycotoxins

1359 Impact of a ferulic acid esterase producing lactobacilli on nutrient digestion of barley silage.

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Ferulic acid esterase (FAE) producing *Lactobacillus buchneri* inoculants have been shown to improve aerobic stability and ruminal fiber digestion. This study aimed to assess the effects of a FAE-producing inoculant applied at ensiling on rumen metabolism and nutrient total tract digestibility of whole crop barley silage. Approximately 100 tonnes of whole crop barley was cut at mid-dough and ensiled without (Control) or with a FAE producing-*L buchneri* mixed inoculant (Inoculated) in bunker silo. A crossover experiment was conducted using 8 cannulated heifers fed diets containing 73% (DM basis) of either control or inoculated silage that was ensiled for 104 d. Each period consisted of a 10-d adaption, 2-d sampling of rumen fluid and 7-d for measurement of digestibility using chromium oxide (Cr_2O_3) as an indigestible marker. Inoculated silage contained greater ($P < 0.01$) concentrations of acetic acid, propionic acid, NDF, and ADF concentration, but less ($P < 0.001$) water soluble carbohydrate than control silage after 104-d ensiling. Heifers fed diets containing inoculated silage had lower ($P < 0.05$) DMI than those fed the control diet, likely due to greater concentrations of acetic and propionic acid. Cattle consuming both diets had similar ($P > 0.05$) DM, NDF, ADF and CP digestibility, suggesting that the inoculant had no effects on total tract digestibility of these nutrients. Both groups of cattle had similar ($P > 0.05$) ruminal pH, protozoal numbers and fibrolytic enzyme activity. Ruminal concentration of total VFA tended ($P = 0.078$) to be lower whereas NH_3 tended ($P = 0.071$) to be greater in heifers fed inoculated as compared to control silage. Ruminal molar proportion of propionate was greater ($P < 0.001$) but molar proportion of butyrate was lower ($P < 0.001$), resulting in a lower ($P < 0.05$) acetate: propionate ratio in heifers fed inoculated as compared to control silage. These results indicate that FAE-producing inoculant applied at ensiling altered fermentation from a homolactic to heterolactic pattern during ensiling, had no effect on nutrient total tract digestibility but did have a positive impact on the acetate:propionate ratio.

Key Words: ferulic esterase-producing lactic acid bacteria, barley silage, total tract digestibility, rumen metabolism

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1360 Excretion of fumonisin B1 by dairy cows supplemented with calcium montmorillonite clay during a mycotoxin challenge.

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Six multiparous Holstein cows (662 ± 52 kg BW) in early lactation were used in a 2 × 2 crossover design to evaluate the effects of feeding calcium montmorillonite clay (Nova-Sil Plus, NSP) on excretion of fumonisin B1 (FB1) during a 3-d challenge consuming this mycotoxin. It was predicted that cows would consume 26 kg of dry matter, therefore NSP was fed at a dose equivalent to 0.5% of predicted dry matter intake equivalent to130 g/d. The FB1 challenge was performed by feeding 80 mg FB1/d via top dressed supplement. The experiment consisted of two 7-d periods in which d 1 through 3 of each period were considered for data collection and d 4 through 7 were considered a wash-out phase. In each period, cows were randomly assigned to 1 of 2 dietary treatments: 1) challenge diet (FBCH), consisting of a basal total mix ration (TMR) plus FB1 challenge; and 2) treatment diet with FB1 (NSP-0.5%+FBCH), consisting of basal TMR plus NSP supplement and FB1 challenge. Feed intake and

milk production were recorded daily, milk and urine samples were collected in the morning and evening from d 1 through 3 of each period. Data were analyzed using the MIXED procedure of SAS where period, treatment and period×treatment were fixed effects and cow within sequence was random. Milk yield was similar across treatments (P = 0.44) and averaged 40.5 ± 3.2 kg/d with no differences in milk composition for any treatment; presence of FB1 was not detected in milk samples. Concentration of FB1 in urine was not affected by treatment (P = 0.68) and averaged 0.51 and 0.47 ± 0.09 for FBCH and NSP-0.5%+FBCH, creatinine adjusted excretion was similar for both treatments (P = 0.86) averaging 0.89 ± 0.17 ng FB1/mg creatinine. These results demonstrate that dietary FB1 is not transferred to mammary secretions and that bovine urine is a suitable biomarker of fumonisin B1 exposure; further research is warranted to fully elucidate the effects of including calcium montmorillonite clay to reduce FB1 absorption by dairy cows.

Key Words: food safety, mycotoxins, milk quality

1361 Effect of rumen-protected *Capsicum* oleoresin on productivity and responses to a glucose tolerance test in lactating dairy cows.

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The objective of this experiment was to investigate the effects of rumen-protected *Capsicum* oleoresin (RPC) on productivity and responses to a glucose tolerance test in dairy cows. Nine multiparous Holstein cows (100 ± 9.1 d in milk; 665 ± 83.3 kg BW) were used in a replicated 3 × 3 Latin square design experiment balanced for residual effects with 3, 28-d periods. Treatments were 0 (control), 100, and 200 mg RPC/cow/d. RPC was mixed with a small portion of the total mixed ration and top-dressed. DMI (29.5 kg/d; SEM = 0.74) was not affected (P = 0.72) by RPC. Milk yield tended to increase (P = 0.06; SEM = 1.27) for RPC compared with the control: 42.8, 44.7, and 43.9 kg/d for the control, 100, and 200 mg RPC/cow/d, respectively. Feed efficiency was linearly increased (P < 0.01; SEM = 0.056) by RPC supplementation: 1.48, 1.52, and 1.57 kg/kg, respectively. Concentrations of fat, true protein, and lactose in milk were not affected ($P \geq 0.69$) by RPC. On the day of the glucose challenge, glucose was intravenously administered at 0.25 g/kg BW and blood samples were collected at 0, 5, 10, 15, 20, 30, 40, 50, 65, 80, and 110 min following administration. Serum glucose concentration peaked 5 min post-glucose administration. RPC did not affect serum glucose concentration during the glucose tolerance test. Insulin concentration at 5, 10, and 40 min and the area under the insulin concentration curve were lower ($P \leq 0.04$) for both RPC application rates compared with the control. Peak concentration of insulin tended to be decreased (P = 0.07) by RPC. Concentration of NEFA in serum was linearly increased (P = 0.03) by RPC at and after 65 min following glucose administration. Concentration of β-hydroxybutyrate in serum was not affected (P = 0.17) by RPC during the glucose tolerance test. In summary, milk yield and feed efficiency were increased by RPC in this experiment. RPC increased serum NEFA and decreased insulin concentration during the glucose tolerance test whereas glucose concentration was not affected by treatment. Data suggest that dietary supplementation of RPC increased insulin sensitivity and likely redirected glucose for lactose synthesis and milk production and also slightly enhanced fat mobilization in lactating dairy cows.

Key Words: capsicum, insulin sensitivity, milk production

1362 Supplementation of β-mannanase (CTCZYME) to lactating dairy cattle diets improves feed conversion efficiency and somatic cell count.

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Improving feed conversion efficiency (FCE) and health status of animals has economic and environmental benefit in dairy operations. Fibrolytic enzymes such as mannanases may improve nutrient digestion and utilization by releasing compounds contained within non-structural carbohydrates such as mannan and xylan, and may also help immune status. A trial was conducted to investigate the effects of β-mannanase supplementation on nutrient digestibility, FCE, and enteric methane emissions in lactating dairy cows. Twelve post peak-lactation multiparous Holstein cows producing 45.5 ± 6.6 kg/d milk at 116 ± 19.0 DIM were randomly allocated to one of 3 treatments in a 3 × 3 Latin square design with 3 18-d periods. Cows were fed the same basal diet with treatment 1 used as control and treatments 2 and 3 contained β-mannanase supplementation at 0.1% (low supplement [LS]), or 0.2% (high supplement [HS]) of DM. Effects of β-mannanase supplementation on nutrient intake and utilization, milk production efficiency, BW change, and methane emissions were determined using the MIXED procedure of SAS (version 9.4). Supplementation of β-mannanase enzyme did not affect DMI, milk yield, and milk composition. Somatic cell counts in milk was lower (P = 0.023) for cows fed the LS diet compared to cows fed control and HS diets. Methane yield (per unit of DMI) and intensity (per unit of milk yield or milk protein yield) were not affected by β-mannanase supplementation. Cows fed LS diet had lower DM, OM, and CP digestibility compared to cows fed control and HS diets. Starch, NDF, and ADF digestibility were not affected. Cows fed LS significantly improved (P < 0.05) FCE, BW gain, and efficiency of converting dietary N to milk protein compared to cows fed the control diet. β-mannanase supplementation had no effect on N excreted in

feces and urine. Dietary supplementation of β-mannanase can improve FCE, BW gain, and udder health of mid-lactating dairy cows without affecting methane emissions and manure N excretions. The role of β-mannanase supplementation may be more critical for early lactating cows, which are generally under significant metabolic and immune challenges and more likely to be in negative energy balance.

Key Words: dairy, feed efficiency, b-mannanase

1363 Effects of essential oils and exogenous enzyme in feedlot finishing cattle diets high in flint corn ground at different particle sizes.

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The objective of this study was to evaluate the interaction between 2 feed additives– MON (Sodium Monensin, Tortuga®) vs. CRINA-RUM (the combination of essential oils- Crina® Ruminants, DSM® and α-amylase- Ronozyme® RumiStar™) and 2 different groundflint corn particle sizes- ground corn (GC = 1.82 mm average particle size) vs. coarsely ground corn (CGC = 2.53 mm average particle size) on performance of finishing Nellore bulls. Two hundred fifty-six Nellore bulls (initial BW = 360 kg ± 38) were fed during 99 d with diets containing 82.5% ground corn (1.82 or 2.53 mm), 8.5% sugarcane bagasse, 5% soybean meal, 3% minerals-vitamins supplement and 1% urea. Animals were blocked based on initial BW and randomly allocated in 48 pens. Treatments were: GC + MON (1.82 mm ground corn and sodium monensin- 26 mg/kg DM), GC + CRINA-RUM (1.82 mm ground corn and the combination of essential oils- 90 mg/kg DM + α-amylase- 560 mg/kg DM), CGC + MON (2.53 mm ground corn and sodium monensin- 26 mg/kg DM) and CGC + CRINA-RUM (2.53 mm ground corn and the combination of essential oils- 90 mg/kg DM + α-amylase- 560 mg/kg DM). The data were analyzed using PROC MIXED of SAS in a 2 × 2 factorial arrangement (2 ground corn particle sizes and 2 feed additives). Pen was considered the experimental unit. No effect of treatment ($P > 0.05$) was observed for final BW. Animals fed CGC (2.53-mm) showed a tendency to greater average daily gain (ADG; $P = 0.08$) than animals fed GC (1.82 mm) – 1.60 and 1.50 kg, respectively. Effect of additive was also observed for DMI. Sodium Monensin (MON) decreased ($P = 0.013$) DMI compared to the combination of essential oils and α-amylase (CRINA-RUM) – 8.70 and 9.34 kg, respectively. No effects of treatment ($P > 0.05$) were observed on feed efficiency (G:F) and dressing percentage. There was an interaction effect ($P = 0.02$) between ground corn particle size and feed additives for hot carcass weight (HCW). Animals fed CGC diets and CRINA-RUM presented 11.5 kg greater HCW ($P < 0.05$) compared to animals fed CGC and MON- 295.2 and 283.7 kg, respectively. On the other hand, no effects ($P > 0.05$) of additives were observed for HWC on GC diets. The CRINA-RUM combination for finishing cattle fed flint CGC diets increases HCW and can be an effective substitute for sodium monensin.

Key Words: beef, carcass, starch

1364 The potential of a buffer (calcified marine algae) or plant extract (*Capsicum*) in combination with or to replace an ionophore (monensin) in lamb feedlot diets.

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Ionophore antibiotic supplementation is standard practice in almost all feedlots in South Africa and many other countries due to its positive effects on feed efficiency and feed intake. Public concern over the emergence of antibiotic resistant bacteria and the consumers' demand for safe, high quality nutritious food has stimulated the search for natural alternatives to ionophores in ruminant diets. The objective of this study was to evaluate the effect of a buffer (calcified marine algae [AB]) and/or plant extract (*Capsicum* [Caps]) in combination with or replacing an ionophore (monensin [Mon]) on the performance of lambs in a commercial feedlot. Two thousand three hundred and twenty-seven lambs were randomly allocated to 6 different treatments with 6 pens per treatment with pen being the experimental unit. Treatments were: 1) Mon; 2) AB; 3) Caps; 4) AB + Mon; 5) Caps + Mon and 6) AB + Caps. Mean starting live weight of lambs was 30.9 kg. The lambs were individually weighed on Day 0, 10, 21, 35, 50 and at slaughter. All lambs were slaughtered at a pre-determined end live weight of ± 48 kg. Average daily gain, dry matter intake, feed conversion ratio, cold carcass mass, rumen fluid pH and rumen score were among the parameters determined. The corn (23% to 37%), alfalfa hay (20% to 10%) based diets (starter, grower and finisher) were the same for all treatments with adjustments to the specific treatments. Days on feed were different between some treatments ($P < 0.05$). Difference in rumen pH (Day 30 minus Day 13) as well as rumen pH on day 1 and 3 were different between some treatments ($P < 0.05$). Other performance parameters such as average daily gain and feed conversion ratio did not differ between treatments ($P > 0.05$). Results suggest that monensin can be successfully replaced in lamb feedlot rations with natural alternatives (AB and/or Caps) with little impact on production performance. Further research, however, is needed on determining the dietary dependant responses and adaptation of rumen microbial populations. Furthermore, the cost: benefit

ratio should be determined under the prevailing conditions in different countries.

Key Words: ionophore, calcified marine algae, *Capsicum*

1365 Health, milk yield and milk quality records evaluated in 787 dairy herds before and during OmniGen-AF® supplementation to dry and lactating cows. J. D. Chapman[1], S. S. Bascom[1], L. O. Ely[2], G. A. Holub[1], J. P. Jarrett*[1], J. S. Lanier[1], D. Kirk[1], D. E. Nuzback[1], A. D. Rowson[1], and T. J. Wistuba[1], *[1]Phibro Animal Health Corporation, Quincy, IL, [2]University of Georgia, Athens.*

Health, milk yield and milk quality records representing 473,711 cows from 787 dairy herds from the U.S. and Canada were collected to evaluate herd effects of feeding *OmniGen-AF*® (Phibro Animal Health Corp., Quincy, IL) to the entire herd. *OmniGen-AF* (OG) was fed at 56 g/hd/d to all dry and lactating cows for a minimum of 90 d (Post-OG). Health and production metrics were compared to the previous 90 d period (Pre-OG). Herds were enrolled in all months of the year (Jan-Mar, $n = 239$; Apr-June, $n = 224$; Jul-Sep, $n = 176$; Oct-Dec, $n = 149$) and herd size ranged from 31 to 9,046 cows. Health and production records were collected from DC305, DRMS and PCDART systems and the data were analyzed using paired *t* test (SAS, Statistical Analysis System) comparing the Pre-OG to Post-OG health events and production. The data were analyzed for all herds ($n = 787$) by herd size ($\leq$ 100 hd, $n = 188$; 101 to 500 hd, $n = 340$; 501 to 1,000 hd, $n = 120$; $\geq$ 1,001 hd, $n = 141$). Monthly cases of mastitis, late term abortions, dead cows, and number of hospital cows/d, expressed as a % of total herd cows, differed ($P < 0.001$) between the Pre- and Post-OG 90 d periods (−24.6%, −28.6%, −23% and −17.4%, respectively). Health event responses to feeding OG were observed to vary by herd size and Pre-OG SCC; however significant reductions in cases/mo. of mastitis, abortions, deaths and metritis were common in all herds regardless of size and SCC during the Pre-OG period. Herds were also stratified by Pre-OG SCC cells/ml (< 200,000, $n = 309$; 200,001 to 300,000, $n = 237$; 300,001 to 400,000, $n = 146$; $\geq$ 400,001, $n = 95$).The average Pre-OG SCC across all herds was 275,753 cells/ml with 73% of herds reporting a reduction in SCC during the Post-OG period. Changes in SCC were proportional to the Pre-OG SCC level. Significant reductions ($P < 0.001$) in SCC were observed in herds with Pre-OG SCC of 200,001 to 300,000 (−23,087), 300,001 to 400,000 (−57,850) and > 400,001 (−128,465) cells/ml. Milk production was reported by 532 herds with an average milk yield change from Pre-OG to Post-OG of +0.35 kg/hd/d ($P <$ 0.001). Maintaining good health is a key component to cow productivity and these data suggest that feeding *OmniGen-AF* along with sound nutrition and management practices for dry and lactating cows can influence health, milk yield and milk quality in commercial dairies.

Key Words: Health, SCC, *OmniGen-AF*

1366 Comparison of the effects of laidlomycin propionate plus chlortetracycline vs. monensin plus tylosin and multiple β-agonist feeding strategies on feedlot performance and carcass characteristics. A. J. Thompson*[1], Z. K. F. Smith[1], M. Corbin[2], L. B. Harper[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Zoetis, Florham Park, NJ.*

One hundred ninety-two steers (initial BW = 354 ± 23.5 kg) were used in randomized complete block design to examine the effect of various ionophore and ractopamine hydrochloride (RH) supplementation strategies on performance and carcass characteristics. Twelve pens of 4steers were assigned to each of the following treatments: unsupplemented control (CON), laidlomycin propionate plus chlortetracycline (CTC) with or without RH (LP and LPRH, respectively), and monensin sodium plus tylosin with RH (MON). Steers were fed for a total of 151 d, of which RH supplemented treatments received the β-agonist for the final 32 d. Laidlomycin propionate and CTC were removed during this period for the LPRH treatment, as no combination clearance exists for the commercially applied β-agonist (Actogain; Zoetis LLC, Florham Park, NJ). When included in the diet, LP, CTC, monensin, tylosin, and RH were supplemented at 10.7 g/ton, 343 mg/(head · d), 32.0 g/ton, 10.7 g/ton, and 255 mg/(head · d) (DM basis), respectively. Upon harvest, carcass data was collected by trained personnel. Before RH supplementation (d 0 to 118), both LP and LPRH treatments had greater ADG ($P < 0.02$) and G:F ($P < 0.01$) than CON, while MON was intermediate. During the RH supplementation period (d 119 to 150), LP maintained greater DMI ($P < 0.01$) than both RH treatments; however, over the same period, MON treated cattle had improved G:F ($P < 0.02$) compared to LP supplemented cattle and CON. Feeding LP without RH increased final BW ($P = 0.02$) over CON, and all ionophore supplemented treatments had improved ADG ($P < 0.05$) and G:F ($P < 0.05$) over the entire 151 d feeding period. Hot carcass weight was significantly greater ($P =$ 0.04) in cattle fed LP with no β-agonist than CON, where LP cattle yielded an average of 12 kg more HCW, while both RH supplemented treatments were intermediate. Monensin plus tylosin with RH yielded significantly greater LM area ($P =$ 0.03) than unsupplemented controls; however LP and LPRH treatments were unaffected. All other carcass characteristics were not significantly different. The results of this study indicate that LP supplementation without the use of a β-agonist may yield similar live performance and carcass responses associated with the administration of RH. These results also suggest that performance and carcass characteristics for cattle fed LP plus CTC are similar to those of cattle fed monensin

plus tylosin throughout the feeding period.

Key Words: β-agonist, ionophore, laidlomycin propionate

1367 Effect of different inclusion rates of Fermenten on performance, carcass characteristics, and total tract digestibility of growing Angus crossbred steers. M. E. Garcia-Ascolani*[1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], D. D. Henry[1], F. M. Ciriaco[1], G. M. Silva[2], P. L. P. Fontes[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]UF/IFAS, Range Cattle Research and Education Center, Ona, FL.*

The objective of this study was to assess the effects of including increasing inclusion rates of the feed additive Fermenten (FER; Church & Dwight Co., Inc., Princeton, NJ) on performance, carcass characteristics, and total tract digestibility of growing steers. Eighty-one Angus crossbred steers (189 ± 22 kg) were used in a generalized randomized block design. Initial BW was used as the blocking factor. Steers were randomly assigned to one of 3 treatments: 0, 2, and 4% FER in the diet DM of a backgrounding diet comprised of peanut hulls, corn gluten feed, soybean hulls and soybean meal. Diets were formulated to contain equal amounts of RDP and energy (6.5% RDP, 70.6% TDN, DM basis). From d 0 to 56, steers were housed in 9 pens (9 steers/pen), with ad libitum access to diets. Individual intake was recorded using a GrowSafe feed intake monitoring system. From d 57 to d 112, steers were moved to a paddock with ad libitum access to a basal diet common to all animals, without FER, to assess potential residual effects of FER feeding. Every 14 d, unshrunk BW was recorded, and blood samples were collected to measure glucose, blood urea nitrogen (BUN) and NEFA in serum. Every 28 d carcass ultrasound was performed to assess fat thickness (FT) and longissimus dorsi area (LDA). Apparent total tract digestibility of nutrients was measured in a subsample of 27 steers (9/treatment) using indigestible NDF as a marker. Data were analyzed as a generalized randomized block design, using steer as the experimental unit. The model included the random effect of steer, and fixed effect of treatment, block and pen. Steers fed 4% FER had decreased ($P < 0.05$) DMI, BW (d 56), ADG (d 0 to 56), and G:F compared with 0 and 2% FER. No differences were observed ($P \geq 0.05$) in blood parameters, LDA, FT, DMI as a percentage of BW, final BW at d 112, and ADG from d 56 to 112. The inclusion of 4% FER increased the digestibility of DM, OM, NDF, and ADF compared with 2, and 0% FER ($P \leq 0.05$). Inclusion of Fermenten above 2% of the diet DM may reduce DMI, thus decreasing the performance and feed efficiency of growing Angus crossbred steers.

Key Words: fermenten, beef cattle, performance

1368 A meta-analysis of lasalocid effects on rumen measures, beef and dairy performance, and carcass traits in cattle. H. M. Golder*[1], T. Cowper[2], and I. J. Lean[1], *[1]Scibus, Camden, Australia, [2]Zoetis Australia, Sydney, Australia.*

The objective of this study was to evaluate the effects of feeding lasalocid on rumen measures, beef and dairy performance, and carcass traits in cattle, using meta-analytic methods. Meta-regression was used to investigate sources of heterogeneity. Rumen measures were assessed using 10 studies (20 comparisons). Lasalocid increased total VFA and ammonia concentrations by 6.46 and 1.44 m*M*, respectively. Lasalocid increased propionate and decreased acetate and butyrate molar percentage (M%) by 4.62, 3.18, and 0.83%, respectively. Valerate M% and pH were not affected. Meta-regression found butyrate M% increased linearly with duration of lasalocid feeding (DUR; $P = 0.017$). When > 200 mg/d was fed, propionate and valerate M% were higher and acetate M% was lower ($P = 0.042$, 0.017, and 0.005, respectively). Beef performance was assessed using 31 studies (67 comparisons). Lasalocid increased ADG by 40 g/d, improved feed-to-gain (F:G) by 410 g/kg, and improved feed efficiency (FE; combined measure of G:F and the inverse of F:G). Lasalocid did not affect DMI, but heterogeneity in DMI was influenced by DUR ($P = 0.004$) and linear effect of entry BW ($P = 0.011$). Heterogeneity of ADG was influenced by the linear effect of entry BW ($P = 0.028$) but not DUR. Combining entry BW $\leq$ 275 vs. > 275 kg and DUR showed cattle entering at > 275 kg fed $\leq$ 100 d had the highest ADG. The FE ($P = 0.025$) and F:G ($P = 0.015$) improved linearly with dose, and entry BW > 275 kg improved F:G ($P = 0.038$). Fourteen studies (25 comparisons) were used to assess carcass traits. Lasalocid increased HCW by 4.73 kg, but not dressing percentage, mean fat cover, or marbling score. Heterogeneity of carcass traits was low and not affected by DUR or dose. Seven studies (11 comparisons) were used to assess dairy performance but the study power was relatively low. Lasalocid decreased DMI in TMR-fed cows by 0.89 kg/d, but had no effect on milk yield, milk components, or component yields. Dose linearly decreased DMI ($P = 0.049$). The DUR did not affect heterogeneity of dairy measures. This work showed lasalocid improved ADG, HCW, FE, and F:G for beef production. These findings may reflect improved energy efficiency from increased propionate and decreased acetate and butyrate M%. Large dairy studies are required for further evaluation of effects of lasalocid on dairy performance.

Key Words: feedlot, ionophore, meta-regression

1369 Close-up diet DCAD, urine pH, and total plasma calcium at calving on a commercial Jersey herd. A. Valldecabres*, D. Rolle, V. J. Ramírez, S. Rodríguez, and N. Silva-del-Rio, *Veterinary Medicine Teaching and Research Center, University of California Davis, Tulare.*

The objectives of this study were to 1) evaluate the daily variability of close-up dietary cation-anion difference (DCAD) and the DCAD feedbunk distribution, 2) evaluate the daily variability of urine pH, 3) determine if acidification levels were maintained as parturition approached, 4) investigate if DCAD and urine pH were associated, and 5) evaluate if peri-partum urine pH and pospartum calcium levels were related on a commercial 3,500 Jersey herd. Before enrollment all cows had to be fed close-up diet > 10 d. Over a 40 d period feedbunk samples were collected daily for wet chemistry. Mixing uniformity was evaluated weekly by sampling 5 feedbunk locations. Midstream urine of 70 multiparous cows was collected via manual stimulation from enrollment to calving. Urinary pH was measured cow-side with a handheld meter (Horiba, Montpellier, FR). Coccygeal blood samples were collected after calving for total plasma calcium analysis (47 cows). Changes on urinary pH −10 to 0 d relative to calving (RC) was conducted with MIXED procedure of SAS with repeated measurements. The association between DCAD and urine pH was evaluated using CORR procedure of SAS. DCAD ranged from −136 to 151 mEq/kg of DM with a coefficient of variation (CV) of 216% and DCAD distribution throughout the feedbunk was highly variable (CV = 36 to 182%). The within-day variation on urine pH ranged from 3 to 19% of CV. There was a tendency for an effect of day of the week ($P = 0.07$) on urine pH, greatest on Monday (6.2) and lowest on Saturday (5.9). Urine pH was lower from −10 to −6 d RC (from 5.6 to 6.1) compared to −5 to 0 d RC (from 6.0 to 6.2; $P = 0.08$). There was a tendency for a weak association between the dietarian DCAD fed 24 h prior and the urine pH ($r = 0.31$; $P = 0.09$). Although urine pH was not associated with postpartum total plasma calcium from −10 to −4 d RC, it was from −3 to 0 d RC ($P = 0.02$); mostly because cows with acidic urine (pH < 5.8) had lower calcium levels. Our results indicate that in the study herd there was a wide within and across day variation in DCAD as well as urinary pH, and suggest that urine pH might not be a good indicator of postpartum plasma calcium levels.

Key Words: DCAD, urine pH, total plasma calcium

1370 Effects of bismuth subsalicylate and calcium-ammonium nitrate on in vitro fermentation of bahiagrass hay with supplemental molasses. D. D. Henry*[1], F. M. Ciriaco[1], R. C. Araujo[2], M. E. Garcia-Ascolani[1], P. L. P. Fontes[1], N. Oosthuizen[1], C. D. Sanford[1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]GRASP Ind. & Com. LTDA, Curitiba, Brazil.*

A randomized complete block design was used to determine the effects of increasing amounts of bismuth subsalicylate (BSS) and calcium-ammonium nitrate (CAN) on in vitro fermentation of bahiagrass hay (*Paspalum notatum*). Serum bottles (125-mL) containing 100 mL of a 4:1 buffer:ruminal fluid inoculum and 0.7 g of an 80:20 bahiagrass hay:molasses substrate (DM basis) were incubated for 48 h. Three d (block) of incubation were performed. Treatments were arranged as a 4 × 3 factorial with 4 concentrations of BSS (0.00, 0.33, 0.66, and 1.00% of diet DM) and 3 concentrations of CAN (0.0, 1.2, and 2.4% of diet DM). Treatments were made isonitrogenous with urea. Two ruminally cannulated crossbred steers (348 ± 29 kg BW) fed bahiagrass hay ad libitum and 2.27 kg/d (as is) of a 50:50 molasses:crude glycerol mixture, were used as ruminal fluid donors. In vitro OM digestibility (IVOMD) was determined in a separate set of tubes. Data were analyzed using PROC MIXED of SAS with fixed effects of BSS, CAN, BSS × CAN, and random effect of day. Gas production and IVOMD were linearly decreased ($P \leq 0.001$) as CAN and BSS increased. Ammonia-N was linearly decreased ($P = 0.001$) as CAN increased. Methane production (mmol/g substrate fermented) was linearly reduced ($P < 0.001$) as CAN and BSS increased. Both CAN ($P = 0.032$) and BSS ($P < 0.001$) reduced H_2S production, with 0.33% BSS reducing production by 61% compared with 0.00%. There was no effect ($P > 0.05$) of CAN on concentrations or molar proportions of any VFA analyzed. As BSS increased, concentration of acetate ($P = 0.002$), propionate ($P = 0.007$), and total VFA ($P = 0.003$) decreased linearly. When comparing treatment means, no difference ($P = 0.119$) in total VFA was observed between 0.33% and 0.00% BSS. The acetate:propionate (A:P; $P = 0.005$) and molar proportions of acetate ($P = 0.041$), and propionate ($P = 0.005$) were quadratically affected by BSS inclusion, where 0.33% BSS decreased A:P compared with 0.00% BSS ($P = 0.050$). Including BSS at 0.66% and 1.00% of the diet DM had negative effects on in vitro fermentation of bahiagrass hay. However, when BSS was included at 0.33%, A:P was decreased and total VFA concentrations were unaffected. Nitrate inclusion reduces methane production without negatively affecting fermentation. A combination of BSS and CAN may favorably affect ruminal fermentation while decreasing methane emissions.

Key Words: bismuth subsalicylate, nitrate, fermentation

1371 The effect of a monensin controlled release capsul at prepartum on betahydroxy butyrate, milk yield, fat, protein, postpartum diseases, rectal temperature, and body condition in Holstein cows. P. Melendez[*1], A. Arevalo[2], P. J. Pinedo[3], and M. Duchens[2], *[1]University of Missouri, Columbia, [2]University of Chile, Santiago, Chile, [3]Colorado State University, Fort Collins.*

The objective was to evaluate the effect of a monensin controlled release capsule given prepartum on blood BHB, milk yield, fat and protein, incidence of postpartum diseases, rectal temperature, and BCS in confined Holstein cows. The study was conducted in a 400-cow dairy operation (ME 305 12,500 kg). Cows were housed in a free-stall system, fed a TMR and milked 3X. Eighty cows of parity $\geq$ 2 were randomly assigned either a treatment (n = 40) or a control group (n = 40) at 30 d before expected parturition. Treatment group received a capsule of monensin orally (Rumensin®, ELANCO, Chile, releasing 300 mg of monensin daily for 95 d). Control cows were randomly matched by parity and expected due date. The outcome variables were blood BHB at 7, 14, 21, and 28 d postpartum, rectal temperature up to 3 d postpartum, incidence of retained fetal membranes, metritis, endometritis, monthly test day milk yield, fat (%) and protein (%) and changes in BCS from prepartum (~ 30 d before calving) to calving and from parturition to 30 DIM. Continuous variables over time were analyzed by repeated measure ANOVA. Postpartum disorders were analyzed by logistic regression. BCS changes were analyzed by ANOVA. Monensin group had lower rectal temperature at Day 1 postpartum (40.3 vs. 38.9°C; P = 0.08) and higher protein % on test Day 1 (3.51% vs. 3.20%) than controls (P = 0.0007). There were no differences for milk yield, blood BHB, fat % over time and incidences of postpartum disorders (P > 0.05). The change in BCS from prepartum to parturition was 0.01 and 0.17 for controls and treated cows, respectively (P = 0.01). The change in BCS from parturition to 30 DIM was –0.31 and –0.13 for controls and treated cows, respectively (P = 0.008). It is concluded that monensin improved milk protein on test Day 1, decreased rectal temperature on Day 1 postpartum and modulated positively the changes in BCS both prepartum and postpartum.

Key Words: monensin, milk yield, diseases

1372 Effects of essential oils and exogenous enzyme in low starch diets for finishing feedlot cattle. T. S. Acedo[1], L. F. M. Tamassia[1], C. S. Cortinhas[1], V. N. D. Gouvea[*1], V. R. M. Couto[2], and J. J. D. R. Fernandes[3], *[1]DSM Nutritional Products SA, Sao Paulo, Brazil, [2]Universidade Federal de Goiás, Goiânia, Brazil, [3]UFG, Goiania, Brazil.*

The objective of this study was to evaluate the effects of the combination of essential oils (Crina® Ruminants) and α-amylase (Ronozyme® RumiStar™) on performance of Nellore bulls finished in feedlot. One hundred twelve Nellore bulls (initial BW = 349 kg ± 33) were fed during 90 d with diets containing 54.5% ground corn, 8.5% sugarcane bagasse, 16% soybean hulls, 12% whole cottonseed, 5% soybean meal, 3% minerals and vitamin supplement and 1% urea. Animals were blocked based on initial BW and randomly allocated in 14 pens. Treatments were: MON (Sodium Monensin, Tortuga®– 26 mg/kg DM) or CRINA-RUM (Crina® Ruminants, DSM®, 90 mg/kg DM and Ronozyme® RumiStar™, DSM®, 560 mg/kg DM). Response variables included: final body weight (FBW); dry matter intake (DMI), average daily gain (ADG), feed efficiency (G:F), hot carcass weight (HCW) and dressing percentage (dressing, %). Pen was considered the experimental unit. The data were analyzed using PROC MIXED of SAS and means were compared by Tukey test considering the block as random effect and treatments as fixed effects. Animals fed with CRINA-RUM had 9.9% greater DMI (10.30 *vs*. 9.28 kg; P < 0.001) and a tendency for greater FBW (529 vs. 523 kg*; P* = 0.07) compared with animals fed MON, respectively. There was no effect of treatments on ADG (1.65 and 1.72 kg, for MON and CRINA-RUN respectively, P = 0.14). Animals fed MON had greater G:F compared with CRINA-RUN (0178 vs. 0166, P < 0.01). The combination of essential oils and α-amylase increased HCW and dressing percentage. Animals fed CRINA-RUM had 6.4 kg more carcass compared with MON (298.2 vs.291.8 kg respectively, P = 0.015) and dressing percentage were 56.3 *vs* 55.8% for CRINA-RUM and MON respectively (P < 0.01). In conclusion, the use of essential oil combined with α-amylase improved intake, carcass dressing and weight in animals fed low starch diets combined with coproducts and can be an alternative to monensin.

Key Words: beef, coproducts, starch

1373 Optimal blood sampling time points to determine bioavailability of rumen-protected Met products using the plasma free AA dose–response method.

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Determination of bioavailability of rumen-protected AA products using the plasma free AA dose–response method has relied on blood sampling 2, 4, 6, and 8 h after the morning feeding the last 3 d of each period in Latin square experiments with cows fed every 8 h. The objective of this study was to determine if this sampling protocol captured the diurnal variation in plasma Met concentrations that exists and adequately measures the bioavailability of Met in Smartamine M (SM; Adisseo Inc., Alpharetta, GA). Five multiparous lactating Holstein cows were used in a 5 × 5 Latin square design with 7-d periods. Treatments were: 1) control diet with no supplemental Met; 2) 12 g/d of abomasally-infused Met; 3) 24 g/d of abomasally-infused Met; 4) 15 g/d of fed Met from SM; and 5) 30 g/d of fed Met from SM. Blood samples were collected via jugular catheters every 2 h starting at 0700 h on d 5, 6, and 7 of each period. Plasma Met analysis was conducted using gas chromatography after chloroformate derivatization (EZ:-faast, Phenomenex). Data were analyzed using the MIXED procedure of SAS. Plasma Met concentrations (μ*M*) increased with infused Met or supplemental SM ($P < 0.001$). There was no diurnal variation in plasma Met concentrations ($P = 0.18$). Plasma Met concentrations were averaged across days for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h blood sampling periods. Plasma Met concentrations were regressed on 0, 12, and 24 g of infused Met and 0, 15, and 30 g of fed Met using the REG procedure of SAS. Slopes for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h sampling periods for infused Met were 1.356 (SE = 0.145), 1.369 (SE = 0.147), 1.329 (SE = 0.120), and 1.346 (SE = 0.123), respectively. Slopes for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h sampling periods for fed Met were 1.148 (SE = 0.038), 1.156 (SE = 0.059), 1.197 (SE = 0.038), and 1.140 (SE = 0.030), respectively. There was no effect of sampling period on the slopes for infused ($P \geq 0.91$) or fed Met ($P \geq 0.26$). The bioavailabilities of Met in SM averaged 84.7, 84.4, 90.0, and 84.6% for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h sampling periods, respectively. The similarity in estimates of bioavailability for SM for the 2 to 8 and 2 to 24 h sampling periods indicates our blood sampling protocol is adequate for determining the bioavailability of RP-Met products.

Key Words: bioavailability, methionine, sampling

1374 Effects of prophylactic supplementation with oral calcium boluses on peripartum calcium, urine pH and health in a commercial Jersey herd supplemented with anionic salts.

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The objectives of this study were to evaluate the effect of prophylactic supplementation with oral calcium boluses after calving on peripartum serum calcium and urine pH levels, as well as the prevalence of ketosis and endometritis. Multiparous Jersey cows from a 3,500 herd were randomly assigned to control (no calcium supplementation [$n = 67$]) or treatment (2 oral calcium boluses [$n = 64$], [QuadriCalMINI, Bio-Vet, Barneveld, WI]). The first calcium bolus was given at 2:30 h after calving (SD ± 1:54 h) and the second at 18:21 h after calving (SD ± 11:56 h). Coccygeal blood and midstream urine were collected immediately before the first and second bolus administration and 1 h after each bolus was administered. Serum samples were analyzed for total calcium. Urinary pH was measured cow-side with a handheld meter (LAQUAtwin B-712, Horiba, Montpellier, FR). Blood Beta-hydroxybutyrate (BHBA) concentrations were determined at 5, 8, and 11 d postpartum, using a handheld meter (Precision Xtra; Abbot, Alameda, CA). Ketosis was defined as ≥ 1.4 mmol/L of BHBA in blood at least once during the sampling period. Clinical endometritis was evaluated based on the observation of purulent or mucopurulent vaginal mucus retrieved with Metricheck (Simcro, NZ) from 28 to 40 d postpartum. Treatment effects on serum calcium and urine pH were evaluated with linear mixed models with repeated measures using the MIXED procedure of SAS (Cary, NC). The prevalence of ketosis and endometritis was evaluated with the chi-square option of the FREQ procedure (SAS). Subclinical hypocalcemia (≤ 8.5 mg/dL) before treatment administration was 58% for control and treatment ($P = 0.96$). One hour after bolus administration, serum calcium concentration was significantly greater in treated cows at first (8.65 vs. 8.01 mg/dL; $P < 0.0001$) and second (8.71 vs. 8.23 mg/dL; $P < 0.001$) bolus administration. However, no significant differences were observed before second bolus administration (8.23 vs. 8.01 mg/dL; $P = 0.12$). There was a treatment effect on urine pH (7.0 control vs. 6.1 treatment; $P < 0.0001$) and a significant treatment by time interaction ($P = 0.02$). No treatment effects were observed on ketosis (26.7%; $P = 0.97$) or endometritis (47%; $P = 0.93$). These results suggest that postpartum total serum calcium levels can be increased with oral bolus administration; however, serum calcium levels might not be maintained by the time the second bolus is administered.

Key Words: oral calcium supplementation, urine pH, serum calcium

1375 Effects of supplemental zinc sulfate concentrations on growth performance and carcass characteristics of feedlot heifers, and in vitro ruminal fermentative activity. C. L. Van Bibber-Krueger*, C. I. Vahl, and J. S. Drouillard, *Kansas State University, Manhattan.*

Effects of supplemental Zn as Zn sulfate on feedlot performance and carcass characteristics were evaluated using 480 crossbred heifers (BW = 385 kg ± 13.08) in a randomized complete block design. Heifers were blocked by BW and randomly assigned within block to receive 0, 30, 60, or 90 mg supplemental Zn/kg diet DM. Heifers were housed in dirt-surfaced pens (20 animals/pen; 6 pens/treatment) equipped with fence-line feed bunks and automatic water fountains. Heifers were fed once daily ad libitum. Plasma was collected Days 0, 63, and 115 from 4 or 5 heifers/pen to determine changes in plasma Zn concentrations. Heifers were transported on d 144 to a commercial abattoir where HCW and incidence of liver abscesses were recorded at harvest and carcass data were recorded after 36 h of refrigeration. Plasma Zn concentration increased linearly in response to increasing concentrations of dietary Zn ($P = 0.02$). Final BW and ADG were not affected by supplementation ($P \geq 0.29$). Increasing supplemental Zn concentrations tended to decrease DMI (linear effect, $P = 0.07$), resulting in a linear improvement in feed efficiency with increasing Zn concentration ($P = 0.03$). No differences were detected for HCW, dressing percentage, LM area, 12th rib fat, percentages of carcasses grading Select or Choice, or yield grade ($P > 0.53$). There was a tendency for a quadratic effect of Zn concentration on percentage of carcasses graded as USDA Prime, with percent Prime peaking at 60 mg/kg added Zn. Carcasses from heifers supplemented 60 mg Zn/kg diet DM yielded the greatest numerical increase ($25/carcass) in carcass value compared to other treatments ($P = 0.32$). In vitro fermentations were performed using ruminal fluid cultures containing 0, 30, 60, 90, 120, 150 mg Zn/kg substrate DM to determine impact of Zn on gas production, VFA concentrations, and IVDMD. There was no Zn × time interaction or effect of Zn on in vitro gas production ($P \geq 0.59$). Zinc supplementation tended to reduce acetate (quadratic effect; $P = 0.07$), and decreased isovalerate (linear effect; $P = 0.05$), but did not affect other VFA ($P \geq 0.17$) or IVDMD ($P \geq 0.20$). Overall, Zn supplementation up to 150 mg/kg substrate weight minimally affected in vitro fermentation. Supplementing up to 60 mg Zn/kg diet DM improves feed efficiency of feedlot cattle.

Key Words: feedlot cattle, feed efficiency, gas production, zinc

1376 Evaluating the effects of an injectable trace mineral product on steers raised in a natural beef feedlot program. E. K. Niedermayer*, O. N. Genther-Schroeder, and S. L. Hansen, *Iowa State University, Ames.*

To determine effects of an injectable trace mineral (TM) on growth and TM status of steers fed in a natural program 168 certified natural Angus steers (359 ± 36.6 kg), blocked by BW (6 steers per pen), received an injection of sterilized saline (SAL) or Multimin90 (MM) on d 0 at 1 mL/68 kg BW (n = 14 pens, 84 steers per treatment). Multimin90 contains 15 mg Cu, 60 mg Zn, 10 mg Mn, and 5 mg Se/mL. Steers received a growing diet for 56 d, followed by 3 wk of transition. On d 84 steers started a corn-based finishing diet and received a second injection of SAL or MM, creating 4 treatments (n = 7 pens, 42 steers per treatment): 1) d 0 Saline, d 84 Saline (SAL/SAL); 2) d 0 Saline, d 84 Multimin90 (SAL/MM); 3) d 0 Multimin90, d 84 Saline (MM/SAL); and 4) d 0 Multimin90 and d 84 Multimin90 (MM/MM). Blood and liver mineral concentrations were determined (n = 7 per treatment) on d −5, 14, 79, and 98. Steers were harvested on Day 162. Data were analyzed in SAS with the fixed effects of block and treatment (2 treatments for growing, 4 treatments for finishing), with mineral data as repeated measures. Steer was experimental unit except for DMI and G:F, where experimental unit was pen. Treatment did not affect growing or finishing ADG, DMI, or G:F ($P \geq 0.14$). There was a treatment × day interaction for finishing period ADG ($P = 0.01$), where ADG was similar across treatments from d 84 to 113, and greatest in SAL/SAL from d 113 to 144; however, MM/MM was greatest from d 140 to 161. There was a treatment × day interaction for liver Se ($P < 0.001$), where concentrations increased on d 14 in MM-treated steers, were similar across treatments on d 79, but increased on d 98 in SAL/MM and MM/MM. Liver TM concentrations tended ($P = 0.08$) to display treatment × day interactions where MM/MM had greater Mn and Cu on d 14, tended to have greater liver Mn and Cu than MM/SAL and SAL/SAL on d 79, and had greater liver Cu compared to SAL/SAL and MM/SAL on d 98. Adequate steer TM status at onset of this trial likely negated any potential benefits of injectable minerals and injectable TM can be utilized safely in natural finishing programs.

Key Words: beef, natural, mineral

1377 Interactive effects of supplemental Zn sulfate and ractopamine hydrochloride on growth performance, carcass traits, and plasma urea nitrogen in feedlot heifers. C. L. Van Bibber-Krueger[*1], J. M. Gonzalez[1], R. G. Amachawadi[2], H. M. Scott[3], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]Kansas State Univeristy, Manhattan, [3]Texas A&M University, College Station.*

Interactive effects of supplemental Zn and ractopamine hydrochloride (RH) were evaluated using 156 crossbred heifers (initial BW = 527 kg ± 6.61; gross BW × 0.96) to determine impact on feedlot performance, plasma urea nitrogen (PUN) and carcass characteristics. The study was conducted as a randomized complete block design with a 2 × 2 factorial arrangement. Factors consisted of: 1) 30 or 100 mg supplemental Zn/kg diet DM (30Zn or 100Zn) as Zn sulfate, and 2) 0 or 200 mg RH/animal daily. Heifers were blocked by BW and, assigned randomly within block to treatments. Heifers were housed in partially covered feeding pens (3 heifers/pen; 13 pens/treatment), fed once daily ad libitum, and RH was fed for 42 d and removed from the diet until cattle were harvested on d 43. Plasma samples were collected on d 0 and 36 to assess changes in plasma Zn and PUN. On d 43, heifers were transported to a commercial abattoir where HCW and incidence of liver abscesses were recorded. Carcass data were collected after 32 h of refrigeration. No Zn × RH interactions were observed for plasma Zn or PUN ($P \geq 0.58$); however, there was a tendency for RH × d interaction for PUN ($P = 0.08$). Supplementing 100Zn increased plasma Zn concentration ($P = 0.02$) compared to 30Zn. No interactions were observed for feedlot performance ($P \geq 0.24$). Final BW and ADG increased with RH supplementation ($P \leq 0.02$), but DMI was not affected ($P = 0.63$), thus feed efficiency improved ($P < 0.01$) when cattle were fed RH. Supplementing 100Zn tended to reduce ADG ($P = 0.07$), but did not affect other measures of feedlot performance or incidence of liver abscesses ($P \geq 0.12$). Zinc × RH interactions were observed for LM area and yield grade ($P \leq 0.01$); LM area decreased and yield grade increased when cattle were supplemented 100Zn with no RH compared to other treatments. A tendency for Zn × RH interaction was detected for dressing percentage ($P = 0.08$), but no other interactions or effects of Zn were observed for carcass traits ($P \geq 0.11$). Supplementing RH increased HCW ($P = 0.03$), but did not affect other carcass traits ($P \geq 0.13$). In conclusion, supplemental Zn had little impact on feedlot performance or PUN concentration, but may alter muscle and fat deposition when fed in conjunction with RH.

Key Words: feedlot cattle, urea nitrogen, ractopamine, zinc

1378 SafeGain™ (ruminally-protected lysine) for growing beef cattle. V. De Aguiar Veloso[*1], C. L. Van Bibber-Krueger[1], K. Karges[2], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]H.J. Baker, Animal Health and Nutrition Division, Little Rock, AR.*

Crossbred heifers ($n = 448$; 287 ± 14.1 kg initial BW) were used in a randomized complete block experiment to assess growth response to SafeGain, a lipid-encapsulated, ruminally-protected form of lysine sulfate. The basal diet consisted of (DM basis) of 45% brome hay, 25% steam-flaked corn, 25% wet corn gluten feed, and supplement. Based on Level 2 estimates from the Nutrient Requirements of Beef Cattle Update 2000, heifers were projected to consume 134% of their lysine requirement with the basal diet alone. Treatments consisted of dietary additions of 0, 15, 30, or 45 g/d of SafeGain. Heifers were blocked by initial BW; implanted with Component TE-IH; allocated within strata to 64 partially-shaded, concrete-surfaced (4.3 m × 8.6 m) pens with 7 heifers/pen and 16 pens/treatment; and fed once daily for 112 d. At the end of the 112-d growing trial, a subset of 12 blocks was consolidated, such that 2 pens from each growing treatment were combined to make one finishing pen. Cattle were weighed, re-implanted with Component TE-200, relocated to finishing pens, and fed a common finishing diet (no supplemental lysine) for 94 d until harvest to evaluate possible carryover effects of SafeGain. At the end of the finishing period pens of cattle were weighed, loaded onto trucks, and transported 450 km to a commercial abattoir for harvest. Liver abscess incidence and HCW were collected the day of harvest, and carcass traits were evaluated following 32 h of refrigeration. Growing phase performance and resulting HCW are summarized in the table, below. SafeGain was effective for improving performance of cattle fed roughage-based backgrounding diets.

Key Words: lysine, growing cattle, SafeGain™

1379 Effects of rotating antibiotic and ionophore feed additives on enteric methane and rumen microbial populations of steers consuming a high forage diet. W. L. Crossland[*1], L. O. Tedeschi[1], T. R. Callaway[2], M. D. Miller[1], and W. B. Smith[3], *[1]Texas A&M University, College Station, [2]USDA-ARS, College Station, [3]Texas A&M AgriLife Research, Overton.*

Ionophore and antibiotic feed additives have been shown to decrease ruminal methanogenesis, but evidence of long-term mitigation is lacking. We proposed a rotation of feed additives as an alternative to reduce methane (CH_4) production. Rumen-cannulated steers ($n = 12$) were fed a basal high forage diet at 2% of BW (DM) for 13 wk in a Calan gate facility receiving 1 of 6 treatments (trt): 1) control (Con) no additive, 2) bambermycin (B) = 20 mg B/hd/d, 3) monensin (M) = 200 mg M/hd/d, 4) B7M = rotating B and M treatments weekly, 5) B14M

= rotating B and M treatments every 14 d, and 6) B21M = rotating B and M treatments every 21 d. Steers were blocked by weight in a RCBD with repeated measures. Rumen fluid was collected weekly for analysis (n = 13) and results were normalized according to organic matter intake (kg OMI). Trt did not significantly affect CH_4 production (P = 0.60), but tended to affect CH_4 to Propionate ratio (CH_4:Pro) (P = 0.06) being highest for Con and lowest for M, B21M, and B14M (0.42 vs. 0.36, 0.36, and 0.33, respectively). Week affected both CH_4 and CH_4:Pro ($P < 0.05$) with significant reductions by wk 3 but this effect was not sustained beyond wk 6. Microbial analysis revealed rotationally treated steers had greater populations of gram positive (G^+) bacteria than continuously fed steers and Con ($P < 0.01$) and wk 0 populations were different from wk 5 and 6 but similar to wk 12 (51.1 vs. 37.5 and 35.1 vs. 44%, respectively; $P < 0.01$). A class of G^- bacteria (*Sphingobacteriia*), phylum *Bacteroidetes,* was not affected by trt or wk but was positively correlated with CH_4 production (r = 0.24, P = 0.04). Archaeal populations of *Methanobrevibacter spp.* and *Methanosphaera sp.*correlated with CH_4 production (r = 0.22 and r = 0.37, respectively) and were not affected by trt. Wk tended to affect *Methanobrevibacter spp*. populations being lowest during week 3 and highest during week 12 (53.64% vs. 68.89% of Archaea; P = 0.06). *Methanosphaera sp*. populations were lowest during week 5 and higher during week 0 and 12 (0.02% vs. 1.31 and 0.53% of Archaea respectively; $P < 0.05$). Our results suggest microbial adaptation to trt between 4 and 6 wk. Rotating monensin and bambermycin did not reduce CH_4 or delay microbial adaptation, more than continuously fed steers.

Key Words: CH_4, feed additives, microbes

1380 Effects of supplementing lactating dairy cow ration with sodium sesquicarbonate on reticulorumen pH, rumination, and dry matter intake. M. L. Jones*[1], J. D. Clark[1], N. A. Michael[2], and J. M. Bewley[1], [1]*University of Kentucky, Lexington,* [2]*Arm & Hammer Animal Nutrition, Princeton, NJ.*

The objective of this study was to assess the effects of sodium sesquicarbonate (SQ-810), a reticulorumen buffer, on rumen pH, rumination time, and dry matter intake (DMI). Sixteen early lactation multiparous, Holstein cows were housed in a tie-stall barn and milked twice daily at the University of Kentucky Coldstream Dairy from October 31, 2015 to January 1, 2016. Cows were balanced by parity and milk production then split into 2 treatment groups for a crossover study with a low buffer (LB, n = 8) group and a high buffer (HB, n = 8) group. The base TMR contained 16kg/d sodium bicarbonate. The LB group did not receive any SQ-810 while the HB group received 0.30 kg of SQ-810 as fed. Eight cows proceeded through sequence 1: three, 21 d periods receiving the LB diet in period 1, HB diet in period 2, and the LB diet in period 3. The remaining 8 cows proceeded through sequence 2: three, 21 d periods receiving the HB diet in period1, LB diet in period 2, and the HB diet in period 3. Each group was fed ad-libitum and dry matter intake (DMI) was collected. All cows were administered an iNovotec Animal Care (iNovotec Animal Care, Austria) reticulorumen pH and temperature bolus. Daily rumination time was recorded using HR tags (SCR Engineers Ltd., Netanya, Israel) and CowManager SensOor (SENRUM) tags (Agis Automatisering, Harmenlen, Netherlands). Low pH was calculated as the total time where pH was < 5.80. The MIXED procedure of SAS (SAS Institute, Inc., Cary, NC) was used to evaluate the effects of cow, sequence, treatment and period on each parameter measured. Rumen pH and low pH time (pH < 5.80) were significantly influenced by treatment ($P < 0.01$). Rumen pH was 5.82 ± 0.07 for LB cows and 5.85 ± 0.07 for HB cows. Low pH time (pH < 5.80) was greater ($P < 0.01$) for LB Days 10.70 ± 0.23 h/d than for HB days, 9.40 ± 0.23 h/d. Dry matter intake was 25.68 ± 0.61 kg/d with LB cows and 26.53 ± 0.61 kg/d for HB cows. Treatment affected SCR rumination times ($P < 0.01$) LB 457.84 ± 19.15 min/d and HB 435.02 ± 19.15 min/d. However, the rumination time measured using SENRUM was not significantly different between treatments. The addition of SQ-810 to the TMR increased reticulorumen pH and DMI significantly ($P <$ 0.01). This research demonstrates the positive effects of SQ-810 rumen buffer in a lactating cow diet.

Key Words: sodium sesquicarbonate, rumen pH

1381 Comparison of Titanium® 5 PH-M versus Titanium® 5 plus NUPLURA® PH with the presence or absence of monensin on health and performance of newly received feedlot calves fed RAMP®. R. M. Jones*[1], C. J. Bittner[1], F. H. Hilscher[1], R. A. Stock[2], and G. E. Erickson[1], [1]*University of Nebraska, Lincoln,* [2]*Cargill, Blair, NE.*

Crossbred steers (n = 704; initial BW = 269; SD = 22 kg) were utilized in a randomized block designed experiment with a 2 × 2 factorial arrangement of treatments. Factors included vaccine type and the presence or absence of monensin (Elanco Animal Health, Greenfield, IN) in the receiving diet. Vaccines were, Titanium® 5 PH-M (VacPH-M, Elanco Animal Health) or Titanium® 5 plus NUPLURA® PH (VacPH, Elanco Animal Health). VacPH-M is labeled to deliver effective immune response against bacteria (*Mannheimia haemolytica* and *Pasteurella multocida*) and viruses (BVD types 1 and 2, IBR, PI_3 and BRSV). VacPH is labeled similar to VacPH-M excluding protection against *Pasteurella multocida*. All steers were fed RAMP® product (Cargill Corn Milling, Blair, NE) with monensin included at 0 or 27.6 mg/kg. Steers were weighed on d 1 to establish initial BW. Steers were assigned to pen based on processing order, with every fourth steer being assigned to 1 of 4 treatments. Once a pen replicate was filled, new pen replicates were started until all steers were assigned to 40 pens (10 pens per simple effect treatment). The receiving trial lasted 28

d. Ending BW was an average of 2 consecutive day weights collected after limit feeding for 5 d. There were no significant monensin × vaccine interactions ($P > 0.27$) observed for growth performance or morbidity. Vaccine treatments (VacPH-M or VacPH) did not affect DMI ($P = 0.52$), ADG ($P = 0.95$), or G: F ($P = 0.79$). Monensin level (0 or 27.6 mg/kg) did not affect DMI ($P = 0.28$), ADG ($P = 0.94$), or G: F ($P = 0.65$). The number of steers pulled and treated for bovine respiratory disease one or more times was not different ($P = 0.17$) for VacPH-M compared to VacPH. Furthermore, no difference ($P = 0.34$) was observed when comparing second pull rates between vaccine types. There was a tendency ($P = 0.09$) for steers fed 27.6 mg/kg of monensin to have a lower percentage of first and second pulls as compared to steers receiving 0 mg/kg of monensin. We concluded that neither vaccine type nor monensin concentration affected steer growth performance or morbidity rate for the first 28 d of receiving.

Key Words: monensin, receiving, vaccine

1382 Effect of Bovamine® on performance of lactating dairy cows.

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The objective of this study was to determine if feeding Bovamine® has an effect on the production performance of dairy cows. Bovamine® (Nutritional Physiology Company, LLC, Overland Park, KS) is a direct-fed microbial consisting of *Lactobacillus acidophilus* and *Propionibacterium freudenreichii*. Thirty lactating Jersey cows (147 ± 49 d in milk) were used in a randomized complete block design for 12 wk with a 2-wk covariate period and 10-wk experimental period. The cows were blocked by parity, calving date, and milk yield. There were 2 treatments: a control group and cows that were fed Bovamine®. As a top dress, control cows received 454 g/d of ground corn and the cows fed Bovamine® were given 1 g/d of Bovamine® and 453 g/d of ground corn. All cows were milked and fed the same TMR twice daily. DMI and milk yield were recorded each day. DMI for the control cows (20.3 kg/d) was similar ($P > 0.10$) to that for the Bovamine®-fed cows (20.5 kg/d). There was a trend ($P = 0.07$) for greater milk yield in cows fed Bovamine® (25.3 kg/d) compared to control cows (24.4 kg/d). Percentage of fat and protein in the milk was similar ($P > 0.10$) between the 2 treatments, with control cows averaging 4.58% fat and 3.67% protein compared to 4.65% fat and 3.69% protein by the Bovamine®-fed cows. Milk urea nitrogen (MUN) was greater ($P < 0.05$) in the Bovamine®-fed cows (15.9 mg/dL) compared to the control cows (15.1 mg/dL). Fat corrected milk (FCM) and energy corrected milk (ECM) also tended to be greater ($P = 0.08$ and 0.07, respectively) in the Bovamine®-fed cows, averaging 29.8 kg/d for FCM and 30.5 kg/d for ECM compared to 28.6 and 29.3 kg/d for FCM and ECM by the control cows, respectively. BW was greater ($P = 0.02$) for the control cows with an average of 426.7 kg compared to 418.1 kg for the Bovamine®-fed cows. FCM/DMI and ECM/DMI were not different between the two treatments ($P > 0.10$) with the control cows averaging 1.42 and 1.45 and the Bovamine®-fed cows averaging 1.46 and 1.50, respectively. With a trend for increased milk yield, FCM, and ECM, results from this study indicate that Bovamine® may be a viable option to increase production in dairy cows without an increase in DMI.

Key Words: Bovamine®, direct-fed microbial, production

1383 Effects of rumen-protected choline (RPC) supplementation to periparturient dairy cows did not depend on prepartum energy intake.

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Objectives were to evaluate the effect of prepartum energy intake on performance of dairy cows supplemented without or with RPC (0 or 60 g/d ReaShure, Balchem Corp., New Hampton, NY). At 48 d before calculated calving date, 93 multiparous Holstein cows were assigned to 1 of 4 treatments. Cows were fed prepartum high energy (HE; 1.63 Mcal NEL/kg DM; 58% corn silage) or controlled energy (CE; 1.40 Mcal NEL/kg DM; 43% wheat straw) diets in ad libitum amounts with or without RPC. The RPC was top-dressed daily from 21 d prepartum to 21 d postpartum. After calving, cows were fed the same diet balanced for methionine, apart from RPC supplementation, through 15 wk. Liver tissue was collected for biopsy at −14, 7, 14, and 21 d relative to calving. Data were analyzed by ANOVA for repeated measures using the MIXED procedure of SAS. Cows fed the HE diet consumed energy at 24% above requirement whereas cows fed the CE-based diet consumed energy at 0.7% above requirement during the last 15 d prepartum. Cows fed RPC tended ($P < 0.10$) to produce more milk (43.5 vs. 41.3 kg/d) and energy-corrected milk (44.2 vs. 42.0 kg/d) without increasing DM intake (23.7 vs. 23.2 kg/d) and tended to have greater mean body condition (3.32 vs. 3.24) during the first 15 wk postpartum. Over the first 40 wk postpartum, feeding RPC in transition increased milk yield of cows ($n = 91$) fed HE (37.4 vs. 33.4 kg/d) or CE diets (36.5 vs. 36.1 kg/d) prepartum (RPC by prepartum energy diet interaction, $P = 0.16$). Cows fed the CE compared with the HE diet consumed more feed postpartum (24.0 vs. 22.9 kg/d, $P < 0.01$) but did not produce more milk (43.1 vs. 41.6 kg/d). Thus, postpartum cows fed the CE diet prepartum were in less mean negative energy balance ($P < 0.05$) and tended to have lower ($P = 0.10$) mean NEFA and had lower ($P < 0.01$) mean BHBA concentrations in plasma compared with cows fed HE diets prepartum. Mean postpartum concentration

of liver triacylglycerol was greater ($P < 0.05$) for cows fed the HE compared with the CE diet (10.7 vs. 8.3% DM) whereas RPC had no effect on hepatic triacylglycerol (Control = 9.0 vs. RPC = 9.9%DM). Compared with an HE diet, feeding a CE diet prepartum improved energy balance and DM intake postpartum. Feeding RPC during the transition period increased yield of milk for 40 wk regardless of prepartum energy intake.

Key Words: choline, transition, wheat straw

1384 Effects of Peptein supplementation on ruminal microbiota and feed digestibility in dairy cows.

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The aim of this study was to evaluate the performance of Peptein (APC Europe, Spain), a protein hydrolysate derived from red blood cells with 2 degrees of hydrolysis, either high (HDH) or low (LDH) as a N source for rumen microbial growth in comparison with other N supplements including urea, pork peptone, fish peptone, soy peptone, and spray dried red blood cells (SDRBC), and to determine the potential consequences on feed degradation. In experiment 1, four replications of Tilley Terry incubations with all N sources providing an isonitrogenous supply of 0.3% N were performed from rumen aliquots obtained from 3 cows. Growth of Gram positive and Gram negative bacteria was estimated by quantitative RT-PCR. In experiment 2, 4 cows (2 dry and 2 lactating) received 320 g/d of Peptein HDH via a rumen cannula split in 2 doses of 160 g for 12 d, and 4 other cows (2 dry and 2 lactating) received an equivalent amount of N in the form of 100 g/d of urea per day via a rumen cannula, split in 2 daily doses. On Day 10, in situ bags containing 0.8 ± 0.06 g of corn, soybean hulls, alfalfa, or beet pulp were placed in the rumen for 2, 4, 8, 12, 16, 24, and 48 h. Each sample was run in duplicate bags at each time point on two consecutive days. Data were analyzed using a mixed-effects model. In Experiment 1, Peptein HDH and LDH and pork peptone increased ($P < 0.05$) the growth of Gram negative bacteria in comparison with the other peptones and SDRBC, but contrarily, fostered ($P < 0.05$) a slight decrease in the growth of Gram positive bacteria. In Experiment 2, the effective rumen degradation of DM from beet pulp in dry cows supplemented with Peptein HDH (68.1 ± 1.11%) tended ($P = 0.07$) to be greater than when incubated in unsupplemented dry cows (64.6 ± 1.11%). The effective rumen degradation of CP and NDF from corn was greater ($P < 0.05$) in lactating cows supplemented with Peptein HDH (52.7 ± 0.96 and 44.8 ± 0.23%, respectively) than in unsupplemented lactating cows (44.6 ± 0.96 and 37.5 ± 0.23%, respectively). It is concluded that Peptein fosters the growth of Gram negative and decreases that of Gram positive bacteria in the rumen and improves degradation of CP and NDF from corn.

Key Words: bacteria, nitrogen, rumen

1385 Effects of different doses of sodium monensin on nutrient digestibility on feedlot Nellore cattle.

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The objective of this research was to examine the effects of different doses of sodium monensin (MON) on digestibilities of DM, NDF and starch of feedlot Nellore cattle. This study, conducted at the São Paulo State University feedlot, Dracena campus, Brazil, was designed as a completely randomized block, replicated 12 times, in which 60 20-mo-old yearling Nellore bulls (402.52 ± 33.0 kg) were fed in individual pens for 84 d according to the different doses of MON (DM basis): 1) 0 ppm (D0); 2) 9 ppm (D9); 3) 18 ppm (D18); 4) 27 ppm (D27), and 5) 36 ppm (D36). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 68% to 84% of diet DM. The finishing diet contained: 71.5% cracked corn grain, 16.0% sugarcane bagasse, 7.7% soybean meal, 3.0% supplement, 1.2% urea, and 0.6% limestone (DM basis). Diet samples were collected just after morning delivery (0830) on Days 7, 8, 19, and 20 of experimental period, and composite samples were made per pen for Days 7 and 8, and 19 and 20. Samples of orts and feces were collected just before morning (0800) meals on Days 8, 9, 20, and 21 of experimental period, and composite samples were made per pen for Days 8 and 9, and 20 and 21. The digestibility of DM, NDF and starch was determined by using chromium dioxide as an external marker. Orthogonal contrasts were used to evaluate linear, quadratic, and cubic relationship between doses of MON and the dependent variable. The use of different doses of sodium monensin did not affect ($P > 0.10$) DM and starch digestibility in the adaptation period; however, NDF digestibility increased ($P = 0.01$) linearly (D0: 56.77%; D9: 59.39%; D18: 65.75%; D27: 63.22%; D36: 70.74%) as doses of MON increased. In the finishing period (d-21), as doses of MON increased, NDF digestibility decreased ($P = 0.01$) linearly (D0: 74.00%; D9: 65.35%; D18: 69.83%; D27: 64.50%; D36: 52.30%) and starch digestibility was affected ($P = 0.03$) cubically (D0: 91.38%; D9: 95.05%; D18: 90.32%; D27: 94.63%; D36: 96.03%). Thus, based on the results of this study, increasing doses of MON affected nutrient digestibility of feedlot Nellore cattle. Also, the dose of 36 ppm per kilogram of DM seemed to be the best option.

Key Words: ionophore, NDF, starch

1386 Effects of carbohydrases on the digestibility of fibrous feed ingredients using a rumen simulation model. V. R. Vasconcelos[1], K. G. Arriola[2], A. F. Campos[3], F. Amaro[4], M. C. Walsh[5], and A. T. Adesogan[*2], *[1]Universidade Federal do Piaui, Piaui, Brazil, [2]Dep. of Animal Sciences, IFAS, University of Florida, Gainesville, [3]IFC (Instituto Federal Catarinense), Videira, Brazil, [4]Federal University of Vicosa, Vicosa, Brazil, [5]Danisco Animal Nutrition, DuPont Industrial Biosciences, Marlborough, UK, United Kingdom.*

The objective of this experiment was to determine the effect of an enzyme mixture on the digestibility of fibrous feed ingredients under simulated rumen conditions. Feed ingredients evaluated included 1) ground corn, 2) corn distillers dried grains (cDDGs), 3) Corn stover (CS), 4) dilute ammonia pretreated CS (DACS), 5) caustic delignified CS (DCS), 6) caustic delignified switchgrass (DSG), and 7) enzyme-treated CS (ECS), 8) DACS (EDACS), 9) DCS (EDCS), and 10) DSG (EDSG). Each substrate was incubated in duplicate in Ankom bags (0.5 g) within 250-mL gas-tight culture bottles. The enzyme was a mixture of a cellulase/hemicellulose enzyme preparation and β1–4, endoxylanase (Danisco, UK) at respective rates of 15 and 1 g/kg on as fed basis. Enzymes were diluted in 2 mL of 0.1 M citrate-phosphate buffer (pH = 6.0) and added with 52 mL of buffered-rumen fluid to the substrate in culture bottles sealed with screw-on caps on which a pressure sensor-syringe assembly was fitted. Bottles were incubated for 24 h at 39°C in a forced-air incubator. Rumen fluid was collected from 2 non-lactating, non-pregnant ruminally-cannulated Holstein cows 3 h after feeding. The experiment had a completely randomized design with ten treatments, two replicates/treatment and five runs. Data were analyzed with the GLIMMIX procedure of SAS and the model included treatment, run and treatment × run. Ground corn was more digestible than all other feed ingredients. The DM digestibility (DMD) of cDDGs was greater than those of CS and DSG (42.2 vs. 19.8 and 25%). Ammonia pretreatment (35.7 vs. 44.9%) and caustic delignification (35.7 vs. 46.2%) increased the DMD of CS ($P < 0.0001$). Enzyme treatment also increased the DMD of DSG (25.0 vs. 33.8%). Enzyme treatment increased total gas production during fermentation of DCS and DSG but did not affect those of other substrates. Pretreatment of CS by either delignification or dilute ammonia increased the NDF and ADF digestibility compared to untreated CS but addition of enzymes did not further enhance the digestibility of the pretreated CS. Dilute ammonia pretreatment of CS had no effect on ammonia-N concentration compared to CS, however caustic delignification resulted in a reduction in ammonia-N concentration ($P < 0.01$). Enzyme treatment had no effect on total VFA concentration but decreased acetate proportion of DCS and increased the propionate proportion from both DCS and ACS. Enzyme treatment decreased the acetate to propionate ratio of all substrates except untreated CS.

Key Words: corn stover, enzyme, in-vitro

1387 Microbial and chemical additives inhibit the growth of *Escherichia coli* O157:H7 in corn silage. I. M. Ogunade*, D. Kim, Y. Jiang, A. A. P. Cervantes, K. G. Arriola, D. Vyas, and A. T. Adesogan, *Dep. of Animal Sciences, IFAS, University of Florida, Gainesville.*

This study examined if adding bacterial inoculants or propionic acid to corn silage contaminated with *Escherichia coli* O157:H7 at ensiling, at silo opening, or after aerobic exposure would inhibit the growth of the pathogen. Corn forage was harvested at approximately 35% dry matter, chopped to 10-mm lengths, and ensiled after treatment with one of the following: 1, distilled water (Control); 2, 1×10^5 cfu/g of *E. coli* O157:H7 (EC); 3, EC and 1×10^6 cfu/g of *Lactobacillus plantarum* (ECLP); 4, EC and 1×10^6 cfu/g of *Lactobacillus buchneri* (ECLB); and 5, EC and 2.2 g/kg of propionic acid (ECA). Each treatment was ensiled in quadruplicate in laboratory silos for 0, 3, 7, and 120 d and analyzed for EC counts, pH, and organic acids. Samples from d 120 were also analyzed for chemical composition, ammonia-N, yeasts and molds, and aerobic stability. Data were analyzed with the GLIMMIX procedure of SAS. The pH of silages from all treatments decreased below 4 within 3 d of ensiling and remained low until d 120. Consequently, the pathogen was eliminated within 3 to 7 d of ensiling. The ECLB and ECA silages resulted in fewer ($P < 0.05$) yeast counts, and greater ($P < 0.05$) acetate and propionate concentrations, respectively, and hence increased ($P < 0.05$) aerobic stability compared to the control, EC and ECLP silages. Subsamples of d 120 silages were reinoculated with 5×10^5 cfu/g of *E. coli* O157:H7 either immediately after silo opening on d 120 or after 168 h of aerobic exposure (d 127), and the pathogen was enumerated after 6 and 24 h, respectively. All silages had similar low pH values and no EC was detected after 6 h of aerobic exposure. Twenty-four h later, the EC and ECLP silages reinoculated with the pathogen after 168 h of aerobic exposure had relatively higher ($P < 0.05$) pH values (5.50 and 6.13) and EC counts (5.39 and 5.3 log cfu/g), respectively. Whereas those treated with *L. buchneri* or propionic acid had low pH values (4.24 or 3.96, respectively), and lower (1.32 log cfu/g) or no EC count, respectively. *Escherichia coli* O157:H7 was eliminated during ensiling of corn within 7 d of ensiling across treatments. Application of propionic acid or *L. buchneri* at ensiling suppressed the growth of the pathogen in aerobically exposed silage

Key Words: corn silage, *Escherichia coli* O157:H7, propionic acid

Table 1388.

		pH	DM	DM loss	Prolamin	Deg 3 h	Deg 7 h	Deg 18 h
			% of as fed	% of ensiled	% DM	% of incubated		
Glucoamylase	Control	4.45	69.9	2.3	3.97	14.0	26.4	55.4
	GAM	4.09	68.1	4.4	4.04	16.6	30.6	56.3
Particle size	584 µm	4.09	69.6	2.7	4.00	16.4	28.5	57.1
	844 µm	4.46	68.4	3.9	3.99	17.1	28.5	54.6
Duration	30 d	4.37	68.2	3.2	4.28	16.3	26.9	50.5
	250 d	4.18	69.8	3.4	3.73	17.3	30.1	61.1
SEM		0.02	0.13	0.19	0.13	0.02	0.02	0.02
					P-value			
G		<0.01	<0.01	<0.01	0.69	0.01	0.13	0.76
PS		<0.01	<0.01	<0.01	0.95	0.74	0.99	0.36
D		<0.01	<0.01	0.44	<0.01	0.65	0.25	<0.01
G*PS		<0.01	0.42	<0.01	0.09	0.27	0.36	0.48
G*D		<0.01	0.83	0.68	0.82	0.56	0.66	0.50
PS*D		0.12	0.31	0.08	0.38	0.70	0.92	0.69
G*PS*D		0.32	0.29	0.30	0.62	0.64	0.56	0.74

1388 Effect of glucoamylase, particle size, and duration of silage storage on dry matter loss and digestibility of ground corn rehydrated and ensiled. N. M. Lopes[1], P. C. Cardoso[2], and M. N. Pereira[*1,3], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]University of Illinois, Urbana, [3]Better Nature Research Center, Ijaci, Brazil.*

Storing mature corn grain by rehydration and ensiling can improve digestibility by prolamin degradation in the silo. Particle size (PS) can determine the rate of grinding during ensiling and the duration of silage storage (D) determines farm cash flow. We evaluated the digestibility and DM loss of rehydrated and ensiled corn (REH) in response to PS, D, and glucoamylase addition at ensiling (G). Treatments were formed by a 2 × 2 x 2 factorial combination of PS (584 vs. 844 µm geometrical mean PS), D (30 vs. 250 d), and G (CTL vs. GAM. Sanferm Yield, 120 AGU/g, Novozymes. 0.35 mL/kg of corn). Particle distribution of fine and coarse corn were (% above screen): 2360 µm: 0.2 and 9.9. 2000 µm: 0.5 and 10.6. 1180 µm: 2.2 and 14.4. 850 µm: 21.3 and 21.8. 425 µm: 57.9 and 24.8. 300 µm: 4.7 and 3.9. Bottom pan: 13.1 and 14.5. Mature corn (86.8% DM, 49.2% vitreous endosperm, 4.3% prolamin/starch) was hydrated to a targeted DM concentration of 65%. Approximately 1 kg of corn DM was ensiled in heat sealed, nylon-polyethylene vacuum pouches, 5 silos per treatment combination. At opening, silages were frozen, dried at 55°C for 72 h, and ground through a 1 mm mesh diameter screen for determination of ruminal in vitro DM degradation in 3, 7, and 18 h. Coarse corn had higher pH and DM loss and lower DM concentration than fine corn. There was no effect of PS on digestibility and prolamine concentration. Longer D reduced pH and prolamine concentration, increased DM concentration and degradation in 18 h, and had no effect on DM loss. Glucoamylase reduced pH and DM concentration and increased DM loss and degradation in 3 h, and also induced greater decrease in silage pH and greater increase in DM loss when added to coarse (4.20 vs. 4.71 and 5.65 vs. 2.25% of ensiled) than to fine corn (3.98 vs. 4.19 and 3.09 vs.2.34% of incubated). The increase in DM loss induced by GAM was smaller when D was 30 d (4.21 vs. 2.25% of ensiled) than 250 d (4.52 vs. 2.35% of ensiled). Glucoamylase increased the proportion of rapidly degradable fraction in corn grain, but at the expense of increased DM loss, especially with coarse grinding. Longer storage increased prolamin degradation and the potentially degradable grain fraction.

Key Words: amylase, corn ruminal degradation, corn grain silage.

1389 Effect on a crude fermentation extract derived from *Trichoderma* on the performance of early lactation primiparous cows. N. D. Walker[*1] and G. Povey[2], *[1]AB Vista Feed Ingredients, Marlborough, United Kingdom, [2]ADAS, Stratford on Avon, United Kingdom.*

Research has demonstrated that pre-treating rations with fermentation extracts (FE) derived from Trichoderma sp., may improve the digestibility of the ration. The aim of the current study was to evaluate the effect of pre-treating a ration with FE on the performance of early lactation primiparous cows. Fifty early lactation primiparous cows (DIM 55 ± 15) were fed a diet containing (on a DM basis), grass silage (26%), corn silage (24%), and concentrate (50%). The trial was split into a 3 wk co-variate pre-period, followed by a 12 wk test period. Individual milk yield was measured daily, averaged weekly; BW and BCS were measured every 3 wk and fertility and health records were maintained throughout. Animals were placed into 25 blocks on the basis of DIM, milk production during the pre-period. Within each block, cows were randomly assigned to either Control (CTL) or treated (TRT) groups. Either water (750 mL/T DM, CTL) or FE (750

mL/T DM, TRT) were sprayed onto each group's TMR. Every week, CTL and TRT TMR samples were analyzed by NIR to determine whether there was any effect of pre-treatment on TMR composition (%DM, %CP, %Starch, %NDF, %ADF, theoretical D-value and theoretical ME value). The statistical model included effects of FE, week, their interactions, as well as covariate milk production and analyzed by ANOVA. Significance was declared at $P < 0.05$, while numerical trends were discussed at $0.05 < P < 0.1$. NIR analysis of the CTL and TRT TMR samples indicated that digestibility was affected by FE, with an average increase in the predicted D-value from 63% to 67% and in predicted ME value from 10.5 to 11.1 MJ/kg DM. Over the entire test period, milk yield tended ($P = 0.09$) to be increased in the TRT versus CTL group, 28.2 vs. 27.6 kg/day. In the last 3 wk of the trial, the effect of FE on milk yield reached significance ($P < 0.05$), 27.7 vs. 26.3 kg/day. Fertility was also significantly ($P < 0.05$) improved in the TRT group, with higher confirmed pregnancy rates (84% vs. 64%), and less inseminations required (2.3 vs. 3.2). Body weight change was also higher in the FE group. To conclude, pre-treating the ration with FE led to an increase in the predicted digestibility and ME of the ration as determined by NIR. Milk yield tended to be increased and fertility improved.

Key Words: pre-treatment, digestibility, Trichoderma

1390 Whey protein-based composite gels fed to Jersey cows to protect β-carotene from rumen degradation. K. P. Ortega*, M. Rosenberg, J. G. Fadel, and E. J. DePeters, *University of California, Davis, Davis.*

Cow's milk has a low concentration of β-carotene (BC) due in part to low BC concentrations in feedstuffs, limited absorption of BC in the small intestine, and metabolism by and storage in tissues. There is also a phenomenon not well understood where dietary BC appears to be degraded in the rumen. Previously, a whey protein-based composite gel was demonstrated to increase the omega-3 concentrations in cow's milk by protecting the unsaturated fatty acids from biohydrogenation in the rumen. Our hypothesis was that the same technology if applied to BC would increase the BC concentration in the milk of Jersey cows. Jersey cows were used because this breed tends to have a higher concentration of BC in their milk than Holstein cows. The objective was to test the efficacy of a whey protein-based composite gel to protect BC from rumen degradation and increase the BC concentration of Jersey milk. Four primiparous and four multiparous Jersey cows were fed a basal total mixed-ration with 500 mg BC fed in 2 physical forms, either in a whey protein-based composite gel (GEL) or as free, rumen available BC (CTL) in a crossover design. The BC was fed once daily at the morning feeding. Periods were 21 d with a 2-wk interval between periods to minimize carryover effects. Concentrations of BC were measured in blood plasma and milk. Feeding the GEL significantly increased BC concentration in plasma by 0.6619 μg/ml in primiparous cows 0.6620 μg/ml in multiparous cows ($P < 0.0001$), but no significant increase in BC concentration occurred in milk. The WPI gel was effective in increasing the BC concentration of plasma; however, further research should address the transfer of BC from blood into milk.

Key Words: β-carotene, whey protein, Jersey, plasma, milk

1391 Rumen morphometrics of Nellore cattle fed different combinations of sodium monensin and virginiamycin. M. C. Pereira*[1,2], A. L. Rigueiro[3], A. C. J. Pinto[3], A. M. Silvestre[2], A. Perdigao[2], L. V. Toledo[2], L. D. Miranda[2], F. P. Luiz[2], M. D. Arrigoni[2], C. L. Martins[2], and D. D. Millen[3], *[1]Grant provided by São Paulo State Foundation (FAPESP), São Paulo, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu campus, Brazil, was designed to evaluate the effect of the combined use of monensin (MON) and virginiamycin (VM) in high-concentrate diets during adaptation and finishing periods on rumen morphometrics and rumenitis of Nellore cattle. The experiment was designed as a completely randomized block, replicated 6 times (3 animals/pen), in which 72 26-mo-old yearling Nellore bulls (388.0 ± 31.1 kg) were fed in 24 pens for 90-d according to the treatments: MON (30 mg per kg of diet DM) during both adaptation and finishing periods (MON-MON); MON (30 mg/kg of DM) plus VM (25 mg/kg of DM) during the adaptation period, and only VM (25 mg/kg of DM) during the finishing period (MONVM-VM); MON (30 mg/kg of DM) plus VM (25 mg/kg of DM) during both adaptation and finishing periods (MONVM-MONVM); and only VM (mg/kg of DM) during the adaptation period, and MON (30 mg/kg of DM) plus VM (mg/kg of DM) during the finishing period (VM-MONVM). The adaptation program consisted of ad libitum feeding of three diets over adaptation period of 19 d with concentrate level increasing from 69% to 84% of diet DM. The finishing diet contained: 72.2% high-moisture corn grain, 14.0% sugarcane bagasse, 8.0% peanut meal, 2.0% coast cross hay, 3.0% supplement, and 0.8% urea (DM basis). Also, cattle were fed ad libitum twice daily throughout the study. At harvest, rumenitis incidence was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative RUM). Likewise, a 1-cm^2 fragment of each rumen was collect from cranial sac. The number of papillae per cm^2 of rumen wall (NOP) was determined, as well as the mean papillae area (MPA). The rumen wall absorptive surface area (ASA) in cm^2 was calculated as follows: 1 + (NOP*MPA)–(NOP*0.002). No significant ($P > 0.10$) treatment effects were observed for any of the variables evaluated in this study:

Table 1392.

	G		A			D		*P*-value		
	Sorghum	Corn	CTL	AMG	GAM	30	180	G	A	D
DM, % of as fed	65.0	65.2	66.1	64.7	64.5	66.7	63.6	0.34	<0.01	<0.01
DM loss, % of ensiled	5.3	6.8	3.8	7.7	6.5	3.1	8.9	<0.01	<0.02	<0.01
Prolamin, % of starch	9.2	9.8	9.3	9.8	9.4	11.6	7.4	0.13	0.44	<0.01
Starch, % of DM	64.7	70.9	67.8	70.7	64.8	80.4	55.2	<0.01	0.06	<0.01
pH	3.99	3.92	3.92	3.94	4.01	4.17	3.74	0.02	0.03	<0.01
kd of Fraction B, %/h	3.14	3.33	3.30	3.20	3.21	3.17	3.30	0.01	0.42	0.05
Degradation 0 h, % of DM	39.8	32.5	33.7	38.2	36.6	32.9	39.4	<0.01	0.02	<0.01
Degradation 3 h, % of DM	47.7	41.2	43.7	44.7	44.9	39.9	49.0	<0.01	0.80	<0.01
Degradation 6 h, % of DM	51.5	47.1	50.3	48.5	49.2	43.8	54.8	0.03	0.76	<0.01
Degradation 12 h, % of DM	56.8	55.4	55.2	55.9	57.2	52.3	59.9	0.42	0.66	<0.01
Degradation 18 h, % of DM	62.1	60.6	61.3	61.2	61.5	57.6	65.0	0.28	0.98	<0.01
Degradation 48 h, % of DM	86.8	86.3	86.8	86.5	86.3	85.1	88.0	0.51	0.89	<0.01
ERD6, % of DM	60.3	56.5	57.1	59.6	58.5	56.0	60.8	<0.01	0.17	<0.01

rumenitis incidence (MONVM-VM = 1.00, MON-MON = 1.11, MONVM-MONVM = 1.00, VM-MONVM = 1.22; P = 0.92), NOP (P = 0.34), MPA (P = 0.46), and ASA (MON-VM-VM = 38.9 cm^2, MON-MON = 38.3 cm^2, MONVM-MONVM = 41.8 cm^2, VM-MONVM = 36.5 cm^2; P = 0.57). Thus, based on the results of this study, the combined use of monensin and virginiamycin in high-concentrate diets during adaptation and finishing periods did not negatively impact rumen morphometrics and rumenitis incidence of Nellore cattle.

Key Words: adaptation, additive, papillae

1392 Effect of glucoamylase and duration of silage storage on ruminal degradation and dry matter loss of corn and sorghum grain rehydrated and ensiled. T. Fernandes[1], K. T. Silva[1,2], D. R. Gomide[2], R. A. N. Pereira[2,3], C. L. S. Avila[1], and M. N. Pereira[*1,3], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]Empresa de Pesquisa Agropecuaria de Minas Gerais, Lavras, Brazil, [3]Better Nature Research Center, Ijaci, Brazil.*

Flint corn and sorghum grain are slow rumen degradable starch sources. Storing grain by rehydration and ensiling can improve ruminal degradability, by prolamin degradation in the silo. We evaluated the ruminal degradation and DM loss of rehydrated and ensiled grains of sorghum and flint corn (G) and the interaction of G with glucoamylase addition at ensiling (A) and duration of silage storage (D). Treatments were a 2 × 3 × 2 factorial combination of G (Sorghum, 129 µm geometrical mean particle size vs. Corn, 211 µm geometrical mean particle size), A (CTLvs. AMG vs. GAM), and D (30 d vs. 180 d). Dosage of glucoamylases AMG (AMG, Novozymes) and GAM (Sanferm Yield, Novozymes) was 0.35 mL/kg of grain. Mature grain was rehydrated to a targeted DM concentration of 65%. Approximately 4 kg of rehydrated grain was ensiled in 10 cm diameter × 60 cm length PVC silos with Bunsen valves (6 silos/treatment combination). At opening, silages were frozen and dried at 55°C for 72 h for determination of ruminal in situ DM degradation in 0 (bag wash), 3, 6, 12, 18, and 48 h of incubation (3 rumen cannulated cows). Time 0 DM disappearance was the fast degrading Fraction A. The slowly degradable Fraction B was 100– Fraction A (a 2 pool model). The fractional rate of Fraction B degradation (kd) was calculated as the slope of the linear regression over time of the Ln of bag residue/incubated. Effective ruminal degradation (ERD6) was calculated as: A + B [kd/(kd + kp)], kp at 6%/h. Glucoamylases increased Fraction A, but had no effect on DM degradation at other incubation times and ERD6, and increased DM loss, especially in longer storage (P < 0.01 for the interaction of A and D). Corn had greater DM loss and kd than sorghum, but lower DM degradation up to 6 h of ruminal incubation and ERD6, the smaller particle size of ground sorghum may explain such response. Longer storage increased DM loss, kd, ruminal degradation at all incubation times, and ERD6. Glucoamylase increased the rapidly degradable grain fraction at the expense of increased DM loss. Longer storage increased ruminal degradation and DM loss. Rehydrated and ensiled sorghum was as degradable in the rumen as corn and had lower DM loss, but had lower starch concentration than corn.

Key Words: amylase in silage, corn grain silage, sorghum grain silage

Table 1393.

Variable	Optifeed® (n=76)	Control (n=78)	P-value
Feed intake (FI) days 1-21, g	2,798 ± 190.8	2,755 ± 186.6	0.87
FI,days 22-42, g	21,082 ± 690.2	19,544 ± 675.9	0.11
FI, days 35-42, g	11,200 ± 365.8	10,155 ± 358.2	0.04
FI, days 1-42, g	32,282 ± 1,045.4	29,700 ± 1,023.7	0.08
Live weight (LW) Day 1, kg	36.3 ± 0.19	36.1 ± 0.18	0.43
LW Day 14, kg	39.3 ± 0.33	38.6 ± 0.32	0.13
LW Day 28, kg	50.3 ± 0.44	49.8 ± 0.44	0.37
LW Day 42, kg	60.4 ± 0.61	58.8 ± 0.60	0.05
LW Day 56, kg	79.6 ± 1.08	77.3 ± 1.07	0.13

1393 Effect of Optifeed on feed intake and live weight of Holstein calves. D. A. Vermeire*, *Nouriche Nutrition, Ltd., Lake Saint Louis, MO.*

Effect of a plant extract-based additive (Optifeed®, OF, Phode Laboratoires, Albi, France) on feed intake and live weight was tested in 154 Holstein calves raised for dairy beef in a naturally ventilated barn for a 42 d trial. Calves were individually housed and fed, and were fed 1 of 2 treatment feeds. Calves in pens 1, 2, 5, 6, 9, 10, etc. (Optifeed®) were assigned to the pre-starter feed (Smart Starter, BABY DOLL Nutrition Ltd, Lake St. Louis, MO) containing OF which was incorporated into the supplement pellet to provide 1 kg OF/1,000 kg of complete feed. Calves in pens 3, 4, 7, 8, 11, 12, etc. (Control) were assigned to receive the same pre-starter feed without OF. On d 43, calves were moved into group pens and fed a common starter feed. Calves were weighed on arrival (d 1), and d 14, 28, and 42. Daily feed provision was monitored with plastic cups which held an average 165 g (blue cup, d 1 to 21) or 316 g (white cup, d 22 to 42) of textured pre-starter feed. Data were analyzed using Statistix 10.0 using ANOVA for completely randomized experiment with calf as the experimental unit. Estimated (using cups) differed from actual (by weight) feed consumption by < 3% demonstrating that the cup delivery model was a good method for measuring daily intake of pre-starter feed by young Holstein calves. Calves fed OF consumed more feed from Day 35 to 42 (11,200 ± 365.8 vs. 10,155 ± 358.2 g, $P = 0.04$), tended to consume more feed over the entire 42 d trial (32,282 ± 1045.4 vs. 29,700 ± 1023.7 g, $P = .08$), and had heavier LW (60.4 ± 0.61 vs. 58.8 ± 0.60, $P = 0.05$) than calves fed control. Optifeed® appears to be an efficient plant extract-based additive to enhance early pre-starter intake and growth of calves.

Key Words: calves, feed intake

1394 Dose-dependent effects of a sensory additive on the eating behavior of TMR-fed dairy cows. F. Bargo*[1,2], I. Guasch[3], G. Tedo[1], A. Bach[4,5], and I. R. Ipharraguerre[1,6], *[1]Lucta S.A., Barcelona, Spain, [2]FAUBA, Buenos Aires, Argentina, [3]Blanca, Lleida, Spain, [4]ICREA, Barcelona, Spain, [5]IRTA, Caldes de Montbui, Spain, [6]University of Kiel, Kiel, Germany.*

Forty four Holstein dairy cows (156 DIM, 28.9 kg/d of milk, 648 kg of BW) were assigned to a 4 × 4 Latin Square design with 25-d periods replicated 11 times to evaluate the dose response to a sensory additive (ProEfficient, PE; Lucta S.A.) on eating behavior of dairy cows fed a TMR. Cows were grouped in 11 blocks and, within blocks, randomly assigned to 4 doses of PE: 0, 15, 30, and 45 g/d. The TMR averaged 16.4% CP, 31.4% NDF, and 1.63 Mcal NE_L/kg. Cows were fed ad libitum on electronic scales and eating behavior and feed consumption were recorded automatically. Data were analyzed using a model with fixed effects of dose (treatment), period, block, and the random effect of cow within block using PROC MIXED of SAS. Treatments effects were evaluated using linear, quadratic, and cubic orthogonal contrasts. Dose of PE affected ($P < 0.05$) eating time, intake rate, dry matter (DM) intake, and energy corrected milk (ECM) of dairy cows. Eating time responded cubically ($P < 0.05$) to PE dose because cows fed 30 g/d dedicated more time to eat than cows fed the other doses. There was a quadratic effect ($P < 0.05$) of PE dose on intake rate given that cows fed 15 and 30 g/d had lower rates than cows fed 0 and 45 g/d. Lying time was not affected ($P > 0.05$) by PE dose. DM intake and ECM responded cubically ($P < 0.05$) to PE dose because cows fed 30 g/d consumed the most DM and produced the largest amount of ECM. In summary, cows fed a TMR supplemented with 30 g/d of PE spent more time eating but at a lower rate than cows receiving other PE doses. These results confirm the positive impact of the sensory additive PE on the eating behavior of dairy cows and indicate that such an effect is most pronounced at 30 g/d.

Key Words: dose response, eating behavior and sensory additive

Table 1394.

	Sensory additive dose, g/d					Contrast, $P <$		
	0	15	30	45	SEM	Linear	Quadratic	Cubic
Eating time, min/d	198	209	229	211	5.4	<0.01	<0.01	<0.01
Intake rate, g DM/min	204	190	194	227	5.4	<0.01	<0.01	0.45
Lying time, min/d	728	723	727	721	14.4	0.69	0.97	0.62
DMI, kg/d	22.2	21.7	23.1	23.1	0.35	<0.01	0.51	<0.01
ECM (3.5%F 3.2%P)	30.7	30.4	31.3	30.7	0.66	0.46	0.64	0.03
Milk fat, %	4.02	3.99	4.00	4.07	0.03	0.13	0.06	0.77
Milk protein, %	3.42	3.45	3.48	3.48	0.02	<0.01	0.38	0.54

1395 Effect of rumen-protected capsicum on milk production in early lactating cows in a pasture-based system.

K. Stelwagen*[1], E. H. Wall[2], and D. M. Bravo[2], [1]*SciLactis, Hamilton, New Zealand,* [2]*Pancosma, Geneva, Switzerland.*

In monogastric animals capsicum affects insulin homeostasis, glucose metabolism and nutrient partitioning. Recent research has shown a beneficial response on milk production and glucose utilization in dairy cows fed rumen-protected *Capsicum* oleoresin. During early lactation, when cows are in negative energy balance, they are in a state of insulin resistance (IR), promoting increased lipolysis, decreased peripheral tissue sensitivity and making more glucose available for mammary milk synthesis (i.e., "glucose-sparing"). The hypothesis of the current study is that rumen-protected capsicum extract enhances milk production during early lactation. Multiparous New Zealand Holstein Friesian cows on a commercial farm were randomly assigned to a Control group (CON; $n = 25$) or a group receiving 100 mg/d per cow of rumen-protected capsicum oleoresin (Nexulin, Pancosma, NEX; $n = 25$) during the first 100d in milk to determine the effect of Nexulin on milk production and body weight during early lactation under pasture-grazing conditions. All cows were managed exactly the same, as a single group, and were milked using 3 automated milking systems, allowing daily measurements of milk yield and composition and body weight. Nexulin was provided in 0.22 kg/d concentrate to NEX cows. All cows received < 3kg concentrate, 0.5 kg molasses and ad libitum access to grass pasture. Data were analyzed by (multivariate) analysis of variance (M)ANOVA, using initial body weight as a covariate for production parameters. Average milk yield was increased in NEX cows (27.9 vs. 26.1 kg/d, ± 0.9, $P < 0.06$) during the first 100 d of lactation. However, the effect occurred after peak production (wk > 5; 27.7 vs. 25.7 kg/d, ± 0.9, $P < 0.04$). Milk composition did not differ, but yield of fat, protein and lactose were increased in NEX cows (respectively, g/d: 1,397 vs. 1,313, ± 60, $P < 0.17$; 1,118 vs. 1,014 ± 39, $P < 0.02$; 1,409 vs. 1,321 ± 48, $P < 0.07$). All cows maintained their body weights (no differences) and prevalence of subclinical ketosis, based on milk fat: protein > 1.5, was lower in the NEX group (1.7 vs. 10.2%, ± 1.0, $P < 0.02$; nonparametric analysis). Rumen-protected capsicum increased milk production during early lactation in cows on pasture, but not until after peak lactation (wk > 5). This delayed response is consistent with delayed glucose sparing and may be due to the previous observation that in the New Zealand pasture-adapted strain of Holstein Friesian cows, IR is lower and insulin levels are higher immediately post-partum compared to American Holstein cows.

Key Words: *Capsicum* oleoresin, early lactation, milkproduction

1396 Effects of Valkalor on feed intake and digestibility, rumen functions, milk yield and composition in mid lactating dairy cows.

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The inclusion of feeds with nutraceutical properties in the livestock diets has been proposed to modulate rumen fermentations, improve post rumen-digestive processes and physiological status. This approach is considered a new tool to improve animal health and to increase feed efficiency. The aim of this research was to assess the effects of Valkalor (Idena, Sautron, France), a dietary supplement which contains yeast cell wall, an extract from *Hibiscus sabdariffa*, and minerals, on the health status, feed intake and digestibility, rumen functions, milk yield and composition of mid-late lactating cows. 36 Italian Friesians were used in a change-over design with 2 treatments in two 35-d periods, with a 1 wk washout period in between. Each period started with 14 d of adaptation. Cows were divided into 2 homogeneous groups, each one further divided in 3 boxes of 6 subjects. The control group (CTR) received a standard total mixed ration (TMR) diet for lactating dairy cows whereas the treated group (TRT) received the same diet supplemented with Valkalor (TRT) at 50 g/cow/day, included in the TMR. Daily feed intake of each box, individual milk yield, health status, BW and rumination time were recorded daily. In each period, BCS was evaluated at Day 14 and 35. Individual samples of milk and blood were taken at Day 14 and 34 to assess milk composition and metabolic profile. Samples of feces and TMR were collected at Day 33 and 34 to estimate the feed digestibility, using AIA as indigestible marker. At Day 35, rumen samples were taken 6h after the morning feeding, to assess the VFA profile. Treated

cows showed higher feed intake ($P < 0.05$), feed digestibility ($P < 0.05$ for DM, OM, CP and starch), rumination time (interaction treatment × day: $P < 0.05$) and total VFA concentration (CTR 121 vs. TRT 129 mmol/L; $P < 0.01$); BW showed a slight increase ($P < 0.05$) in TRT compared to CTR. Milk yield was higher in TRT (31.7 vs. 30.5 kg/d in TRT and CTR, respectively; $P < 0.01$), whereas milk composition was only slightly affected and the lactose and total protein yield were higher in TRT ($P < 0.01$ and NS respectively). At metabolic level, treated cows showed a better liver functionality (higher albumin, paraoxonase and lower ceruloplasmin; $P < 0.05$). Positive effects of the supplementation became progressively more evident during the treatment. Results suggest the effectiveness of Valkalor on the improvement of the production and the health status of dairy cows.

Key Words: nutraceutic, rumen fermentation, milk yield

1397 Screening for effects of live yeast or yeast derivative on dry matter disappearance in batch culture. P. X. Jiao[*1,2], F. Liu[2], Z. X. He[1,3], S. Ding[1], N. D. Walker[4], K. A. Beauchemin[1], T. W. Alexander[1], and W. Z. Yang[1], *[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Northwest Agriculture and Forestry University, Yangling, China, [3]Key Laboratory for Agro-Ecological Processes in Subtropical Region, Hunan Research Center, The Chinese Academy of Sciences, Changsha, China, [4]AB Vista Feed Ingredients, Marlborough, United Kingdom.*

The objective of this study was to screen for the effects of live yeast (LY) or yeast derivative (YD) on DM disappearance (DMD) in batch culture varying yeast products, media pH and dosage of yeast. The study was arranged in a 5 yeasts × 2 pH × 4 dosages + monensin (positive control) factorial design. Substrate was a high-grain diet containing 10% barley silage and 90% concentrate (DM basis). Five yeast products were 3 LY (LY1, LY2, LY3) and 2 YD (YD4, YD5). The buffer pH was low (5.8) and high (6.5). Doses of LY (cfu/ml) were control (no LY), 4×10^6, $8 \times 10^6$and 1.6×10^7, and doses of YD (mg/bottle) were control (no YD), 15, 30, and 60. The dose of monensin was 0.17 mg/bottle. Inoculum was obtained from 2 ruminally fistulated beef heifers fed the same diets to the substrate. Substrate (0.75 g) ground through a 1-mm sieve was weighed into a filter bag and incubated for 24 h in a gas-tight culture bottle in 3 replications by each combination of treatments. The culture was repeated at different day. Data were analyzed using mixed procedure of SAS with a model that includes fixed effects of yeast, pH, dosages, and 2 way interactions, and the random effects of day. There was interaction ($P < 0.05$) of LY2, LY3, YD4 and YD5 with media pH or yeast with its dosage. Supplementation of LY1 had higher ($P < 0.01$) DMD (61%) at pH 6.5, whereas the DMD was lowest ($P < 0.05$) for YD5 (54%) and medium for other yeasts (averaged 57%). Increased media pH from 5.8 to 6.5 improved ($P < 0.01$) DMD (low vs. high pH; averaged 47 vs. 59%). Increasing the dose of LY3 and YD5 linearly ($P < 0.05$) increased the DMD at pH 6.5 with no dose effect of other yeasts. Adding monensin overall improved ($P < 0.05$) the DMD (62 vs. 57%) compared with yeasts at pH 6.5; whereas, at pH 5.8, the DMD was lower with monensin (44%) vs. LY2 (47%; $P < 0.05$), LY3 (47%; $P < 0.05$) or YD5 (49%; $P < 0.01$). These results suggest that in vitro DMD of high-grain diet varied with source and dosage of yeast and media pH. The improved DMD at pH 5.8 with LY2, LY3 and YD5 over monensin would be beneficial to high-grain fed cattle.

Key Words: dry live yeast, yeast derivative, batch culture, fermentation pH

1398 Supplementation of β-mannanese (CTCZYME) tends to improve immune traits in early lactating dairy cows. M. L. C. B. Azevedo[1], T. Tewoldebrhan[2], R. Appuhamy[2], G. C. Reyes[2], K. J. Bolek[2], S. Seo[3], J. J. Lee[4], and E. Kebreab[*2], *[1]Wageningen University, Wageningen, Netherlands, [2]University of California, Davis, Davis, CA, [3]Chungnam National University, Daejeon, The Republic of Korea, [4]CTC Bio Inc, Seoul, The Republic of Korea.*

Early lactating dairy cows typically face metabolic and immune challenges. Therefore, improving health status, besides feed conversion efficiency, can affect their productivity and welfare positively. β-mannanase is a fibrolytic enzyme that breaks down the non-structural carbohydrate mannan. It is currently used in pig and poultry production to increase nutrient digestion and may also improve their immune status. However, information about the effects of β-mannanase on ruminants is scarce. In a previous experiment, β-mannanese supplementation improved feed conversion efficiency and reduced somatic cell count of mid-lactating dairy cows. The objective of this study was to examine immune responses to β-mannanese supplementation in early-lactating cows. Fourteen early-lactating Holstein cows, paired by parity and milk production, were allocated to 2 treatments; control (50:50 forage:concentrate) and β-mannanese supplemented (0.1% of concentrate DM) diet. Acute phase protein, haptoglobin, and Immunoglobulin G (IgG) levels in blood were measured weekly from 14 to 50 d in milk. The CD4 and CD8 lymphocytes percentages in blood drawn at one time point were also evaluated by flow cytometry. Absolute numbers of CD4 and CD8 lymphocytes, total white blood count and the differential count of the 5 major white blood counts (neutrophils, lymphocytes, monocytes, eosinophils and basophils) were measured. Significance of β-mannanese supplementation on the blood immune traits were analyzed using linear mixed effects model including fixed effects of treatment, parity and days in

milk, and random effect of cow. Blood haptoglobin concentration tended to decrease ($P = 0.088$) in cows fed β-mannanese supplemented diet (0.373 ± 0.042 mg/ml) compared to those receiving control diet (0.498 ± 0.048 mg/ml). Higher concentrations of plasma haptoglobin may indicate a response to inflammation. Blood IgG concentrations and CD4:CD8 ratio were numerically higher in cows fed β-mannanese, but not significantly different ($P = 0.376$ and $P = 0.181$, respectively). Results for total white blood count and the five major white blood counts were also not significantly different. Dietary supplementation of β-mannanase has a potential to improve immunity of early-lactating cows.

Key Words: β-mannanase, immune traits, lactating cows

1399 To guarantee its threshold concentration in the rumen, live yeast *Saccharomyces cerevisiae* (CNCM I-4407) needs to be supplemented daily to dairy cows. C. Julien[1], M. Rey[*1], J. P. Marden[1], E. Auclair[1], and C. Bayourthe[2], *[1]Phileo Lesaffre Animal Care, Marcq-en-Baroeul, France, [2]Université de Toulouse, INRA, INPT UMR1388 GenPhySE, Castanet-Tolosan, France.*

It has already been stated that live yeast (LYSc47, 10^{10} CFU/g DM, *Saccharomyces cerevisiae* CNCM I-4407, Phileo Lesaffre Animal Care, France) is unable to colonize the digestive tract of cows. But, is the LY ruminal concentration stable after few days of distribution and how does it change within the day? Four early-lactating Holstein cows fitted with permanent ruminal cannulas were assigned to 4 treatments in a 4 × 4 Latin square design: 2 control diets consisting of a corn-silage-based TMR with ground corn (CD) or ground wheat (WD) top dressed at 0 to 5.10^{10}CFU/cow/day of LYSc47 in the morning meal (YCD and YWD, respectively). Each 14-d experimental period consisted of 9 d of adaptation to the diet, 3 d of measurement (d 1 to d 3) and a 2-d transition phase. During d 1 to d 3, ruminal fluid of cows was individually sampled −1 h, +0.5 h and +7 h around the morning meal. The concentration of live LYSc47 was determined by the method for counting the CFU (CFU/mL of ruminal fluid) on YM agar containing 1% chloramphenicol. Data were analyzed using general mixed model procedure of SPSS (IBM SPSS Statistics V22) including fixed effect of day, diet and hour nested in day and cow as random effect. No LySc47 was detected in ruminal fluid of cows receiving WD or CD. For cows receiving LYSc47, ruminal concentration of LYSc47 was affected ($P < 0.001$) by time of sampling during the day: 3.91, 4.94 and 4.16 log CFU/mL at −1 h, +0.5 h and 7 h around morning meal, respectively. LYSc47 content significantly increased 30 min after ingestion of the daily dose: +1.03 log CFU/mL and then decreased significantly toward lower level (−0.78 log/mL over 7 h whatever is the diet). LYSc47 content at +7 h remained significantly higher than at −1 h, but after 9 d of daily supplementation, LYSc47 ruminal concentration remained similar ($P = 0.432$) over the 3 d of sampling whatever was the diet. It clearly showed that LYSc47 had a quick revival capacity in ruminal content and that its daily supplementation is essential to maintain a threshold concentration in ruminal ecosystem.

Key Words: live yeast, rumen, dairy cow

1400 Feedlot performance and carcass traits of Nellore cattle fed different combinations of sodium monensin and virginiamycin. A. L. Rigueiro[*1], F. P. Luiz[2], M. M. Squizatti[1], A. H. Assumpção[1], M. M. Ferreira[1], C. P. Garcia[2], L. R. Muller[2], A. P. D. Bueno[2], C. L. Martins[2], M. D. Arrigoni[2], and D. D. Millen[1,3], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]SÃ£o Paulo State University (UNESP), Dracena campus, Dracena, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu campus, Brazil, was designed to evaluate the effect of the combined use of monensin (MON) and virginiamycin (VM) in high-concentrate diets during adaptation and finishing periods on feedlot performance and carcass characteristics of Nellore cattle. The experiment was designed as a completely randomized block, replicated 6 times (3 animals/pen), in which seventy-two 26-mo-old yearling Nellore bulls (388.0 ± 31.1 kg) were fed in 24 pens for 90-d according to the treatments: MON (30 mg per kg of diet DM) during both adaptation and finishing periods (MON-MON); MON (30 mg per kg of diet DM) plus VM (25 mg per kg of diet DM) during the adaptation period, and only VM (25 mg per kg of diet DM) during the finishing period (MONVM-VM); MON (30 mg per kg of diet DM) plus VM (25 mg per kg of diet DM) during both adaptation and finishing periods (MONVM-MONVM); and only VM (25 mg per kg of diet DM) during the adaptation period, and MON (30 mg per kg of diet DM) plus VM (25 mg per kg of diet DM) during the finishing period (VM-MONVM). The adaptation program consisted of ad libitum feeding of three diets over adaptation period of 19 d with concentrate level increasing from 69% to 84% of diet DM. The finishing diet contained: 72.2% high-moisture corn grain, 14.0% sugarcane bagasse, 8.0% peanut meal, 2.0% coast cross hay, 3.0% supplement, and 0.8% urea (DM basis). Also, cattle were fed ad libitum twice daily throughout the study. Cattle fed the combination of MON and VM during the adaptation period and only VM during the finishing period had greater ($P < 0.05$) final BW in kg (MONVM-VM = 536.1^{a}, MON-MON = 516.0^{b}, MONVM-MONVM = 512.7^{b}, VM-MONVM = 518.2^{b}), DMI in kg (MONVM-VM = 9.62^{a}, MON-MON = 8.73^{bc}, MONVM-MONVM = 8.47^{c}, VM-MONVM = 9.09^{b}), ADG in kg (MONVM-VM = 1.65^{a}, MON-MON = 1.42^{b}, MONVM-MONVM = 1.38^{b}, VM-MONVM = 1.44^{b}), as well as heavier HCW in kg (MONVM-VM = 284.2^{a}, MON-MON

= 266.4[b], MONVM-MONVM = 264.1[b], VM-MONVM = 270.8[b]) and increased dressing percentage (MONVM-VM = 53.0[a], MON-MON = 51.7[b], MONVM-MONVM = 51.5[b], VM-MONVM = 52.2[b]). No treatment effect on G:F ratio was observed ($P = 0.32$). Thus, Nellore yearling bulls should be fed high concentrate diets containing MON and VM during the adaptation period and only VM during the finishing period.

Key Words: adaptation, additive, ionophore

1401 Effects of supplementation of isoquinoline alkaloids and monensin on microbial protein synthesis, ruminal fermentation and nutrient digestibility in steers fed a finishing diet.

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Four Holstein steers with ruminal and duodenal cannulas were used in a 4 × 4 Latin square design to examine the effect of different treatments on ruminal fermentation and digestive function. Treatments consisted of a steam-flaked corn-based finishing diet supplemented with Sangrovit® RS (IQs) and monensin sodium (MS) as follows: 1) no additives (Control), 2) 1.35 mg IQs/kg diet, 3) 30 mg MS/kg diet, and 4) 1.35 mg IQs/kg diet plus 30 mg MS/kg diet. Experimental periods consisted of a 10-d adjustment period followed by a 4-d collection period. Between each experimental period, steers were allowed a 7-d recovery period during which all steers were fed the control diet. There were no differences ($P > 0.05$) between controls and IQs on ruminal digestion of OM, starch and NDF, but ruminal microbial efficiency and protein efficiency increased ($P < 0.05$) 7.6 and 9.1%, respectively with IQs supplementation. IQs increased (6.1%, $P = 0.02$) postruminal digestion of N and tended (3.7%, $P = 0.06$) to increase total tract digestion of N. Compared to the control, duodenal flow of feed N was greater (14.7%, $P = 0.04$) for steers which were supplemented with MS and tended to be greater in the IQs group (11.9%, $P = 0.09$). There was no difference ($P = 0.17$) between IQs and the MS group. Duodenal flow of microbial N was lower ($P \leq 0.01$) in the MS group compared to control and IQs. Microbial efficiency and protein efficiency were greater in the IQs group (13.8 and 10%, respectively, $P < 0.01$) compared to the MS group. IQs supplementation increased ruminal molar proportion of acetate 11.9% ($P = 0.05$) with no differences ($P > 0.12$) in molar proportions of propionate or acetate:propionate molar ratio. Compared to the control diet, MS did not affect ($P > 0.80$) ruminal pH, molar concentrations of total VFA, ruminal VFA molar proportions or estimated methane production. Combining IQs + MS did not improve the responses on digestion nor ruminal fermentation compared to the IQs or the MS group. IQs represent a tool to improve N utilization in ruminants.

Key Words: isoquinoline alkaloids, steers

1402 Effect of pelleted feed products and bambermycins on performance when fed to cattle grazing corn residue.

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Two corn residue grazing trials (84 and 85-d) were conducted from November to January in successive years to evaluate the effects of a corn byproduct pellet and bambermycins (Gainpro) on growing cattle performance. Both trials were arranged as a 2 × 3 factorial, inclusion of bambermycins (0 or 10 mg/d and 0 or 20 mg/d for years 1 and 2, respectively) was the first factor. The second factor was level of supplemental pellet (year 1) and amount of RUP supplied in the supplemental pellet (year 2). Supplement was delivered daily via Calan gates. In year 1, 60 steers (initial BW = 254 kg; SD = 26) were supplemented a pellet consisting of 54% corn stover treated with calcium oxide, 32% dried distillers grains, and 14% solubles at 0.3, 0.7, or 1.1% of BW. In year 2, 60 steers (initial BW = 222kg; SD = 14) were supplemented a pellet consisting of 44.5% corn stover treated with calcium oxide, 40% Soypass, soybean meal (SBM), or processed SBM, and 15.5% solubles at 1.82 kg/d. In year 1, steers were dosed with 10 g of titanium dioxide daily to measure residue intake. Steers were limit fed 5-d and weighed on 2 consecutive days for beginning and ending BW. There was no interaction between bambermycin inclusion and level of supplement on ending BW, ADG, or DMI in year 1 ($P \geq 0.82$). Bambermycin inclusion did not affect ending BW, ADG, or DMI ($P \geq 0.78$). There was a linear increase ($P < 0.01$) for ending BW and ADG as pellet supplementation increased. For steers supplemented at 0.3, 0.7 and 1.1% of BW, ADG was 0.01, 0.28 and 0.56 kg/d, respectively. There was a quadratic decrease in DMI as the trial progressed and supplement increased ($P < 0.01$). In year 2, there was no interaction between inclusion of bambermycins and RUP supplied in the pellet for ending BW or ADG ($P \geq 0.61$). Bambermycin inclusion at 20 mg/steer daily did not affect ending BW or ADG ($P \geq 0.79$). Likewise, there was no main effect of pellet type on ending BW or ADG ($P \geq 0.57$). For steers receiving pellet with supplemental protein provided by SBM, Soypass, or processed SBM, ADG was 0.35, 0.35, and 0.33 kg/d, respectively. Neither bambermycins nor increased amounts of RUP in the supplemental pellet affected performance of steers grazing corn residue.

Key Words: growing, pellet, corn residue

1403 Mineral-glycinate supplementation improves the systemic immune response to lipopolysaccharide challenge in lactating dairy cows. E. H. Wall*[1], K. Tran[2], C. Wallinger[2], J. S. Hogan[2], and W. P. Weiss[2], *[1]Pancosma, Geneva, Switzerland, [2]Department of Animal Sciences, OARDC, The Ohio State University, Wooster.*

Previously, it was observed that supplementation of growing steers with a Zn-glycinate complex improved immunity compared to an inorganic Zn source. The objective of this experiment was to test the hypothesis that supplementation of dairy cows with minerals in glycinate form would improve immune responses. Twelve mid-lactation Holstein cows were fed either a diet (UNSUP) void of supplemental Cu, Zn, and Mn (containing approximately 8, 30, and 30 ppm of each mineral, respectively in inorganic form) or a diet (GLY) containing Cu, Zn, and Mn in the glycinate form (B-TRAXIM® 2C, Pancosma; 16, 60, and 60 ppm, respectively) for 30 d. After 30 d, blood samples were collected for measurement of Cu in the serum as well as isolation of neutrophils to assess function. Cows were then exposed to intramammary infusion with lipopolysaccharide (LPS) of*Escherchia coli* O111:B4 (10 mL of a 10 μg/mL solution infused into the teat canal) to compare host defense responses, which were monitored for 7 d. Milk samples were collected for analysis of SCC and visual characterization. Clinical scoring (1 = normal; 5 = severe) was conducted and rectal temperature was monitored to estimate the systemic response to the LPS challenge. As expected, concentrations of Cu in the serum were increased with GLY (0.77 vs. 0.91 μg/g; $P < 0.05$). Percentage of intracellular kill and phagocytic neutrophils were not affected by treatment ($P > 0.05$); however, the phagocytic index (number of bacteria ingested per phagocyte) was decreased in GLY cows (2.47 vs. 1.85; $P < 0.05$). Before, during, and after the LPS challenge there was a trend for decreased SCC in GLY cows ($P < 0.15$). By design, the LPS challenge elicited a marked increase in clinical score (peak score = 4) and this was not affected by supplementation ($P > 0.70$). Rectal temperature during the first 24h post-LPS challenge was lower in the GLY cows, characterized by a lower area under the curve (933.8 vs. 927.7; $P < 0.05$) and a lower peak temperature (40.5 vs. 40.0°C; $P < 0.05$). The decreased body temperature combined with the lower SCC in GLY cows indicates that mineral-glycinate supplementation influences immune responses in dairy cows and may improve the ability to fight off infection. This has implications for mammary health; however, additional research is needed to distinguish the role of each metal, and their form, in this response.

Key Words: glycinates, immunity, mastitis

1404 Effects of replacing soybean meal with canola meal or treated canola meal on ruminal digestion, and omasal nutrient flow in lactating dairy cows. E. Marostegan de Paula*[1], M. A Camargo Danes[2], N. E Lobos[3], F. L. Drago[4], G. I. Zanton[5], G. A. Broderick[6], and A. Faciola[1], *[1]University of Nevada, Reno, [2]Federal University of Lavras, Lavras, Brazil, [3]Kemin Industries, Des Moines, IA, [4]University of Sao Paulo, Piracicaba, Brazil, [5]USDA-Agricultural Research Service, U.S. Dairy Forage Research Center, Madison, WI, [6]Broderick Nutrition & Research, LLC, Madison, WI.*

Treated canola meal (TCM) was produced as an attempt to increase the RUP fraction of canola meal (CM) with the goal of increasing AA availability for absorption in the small intestine. The objective of this study was to measure nutrient and microbial omasal flow when CM and TCM replaced soybean meal (SBM) in the diet of dairy cows. Six rumen-cannulated

Table 1404.

Table 1. Intake, DM flow, and flow of N fractions at the omasal canal in dairy cows

	Diet				Contrasts *P* -value	
Item	SBM	CM	TCM	SEM	SBM vs. CM+TCM	CM vs. TCM
DM intake, kg/d	25.4	26.0	26.7	1.62	0.28	0.48
DM Flow, kg/d	18.9	19.3	19.8	1.33	0.34	0.52
OM truly digested in the rumen, kg/d	15.1	15.5	15.1	0.91	0.81	0.72
Dietary N intake, g/d	625	668	679	39	0.04	0.64
Total NAN[1], g/d	669	688	671	50	0.82	0.76
N truly digested in the rumen, g/d	413	472	471	29	0.10	0.97
RDP supply, kg/d	2.58	2.96	2.95	0.18	0.10	0.81
RUP flow, kg/d	1.33	1.28	1.30	0.18	0.78	0.92
NMNAN flow[1], g/d	187	200	183	21	0.72	0.31
FAB-NAN flow[1], g/d	185	176	190	7.89	0.82	0.20
PAB-NAN flow[1], g/d	298	306	298	35	0.89	0.84
Total microbial NAN flow, g/d	482	482	488	41	0.94	0.90
Microbial efficiency, g of NAN/kg of OMTDR[1]	32.2	30.5	32.8	1.95	0.81	0.38

[1]NAN = non-ammonia-N, NMNAN = nonmicrobial NAN; FAB - and PAB-NAN = fluid- and particle-associated bacterial NAN; OMTDR = OM truly digested in the rumen.

cows were blocked into 2 blocks of 3 cows and randomly assigned within blocks to 3 dietary sequences in a replicated, 3 × 3 Latin square design with 21 d of adaptation and 7 d of sampling. Treatments differed only in CP source, which were: SBM, CM, or TCM. The TCM was treated by extrusion, with added molasses to promote the browning reaction. All diets contained (DM basis) 30% alfalfa silage, 30% corn silage, 4% soy hulls, 2.4% mineral-vitamin premix and 16% CP. The SBM diet contained 25% high moisture corn (HMC) and 8.6% SBM; the canola diets contained 22% HMC and 11.4% CM or TCM. Omasal sampling was performed during the last week of each period. Data were analyzed using the MIXED procedure of SAS. Orthogonal contrasts were used to compare effects of different protein sources (SBM vs. CM + TCM) and (CM vs. TCM). Partial data are presented in Table 1. Compared to SBM, CM and TCM increased N intake ($P = 0.04$) and there was a trend ($P = 0.10$) to increase RDP supply (kg/d), and N truly digested in the rumen (kg/d). There were no differences in DMI, ruminal digestibility, efficiency of ruminal microbial synthesis, and flows of: RUP, non-microbial-non-ammonia-N, and total microbial-non-ammonia-N among diets. Results indicate that both canola diets may increase N intake and RDP supply. Treating CM by extrusion did not affect microbial N flow at the omasal canal. Under the conditions of the present study, treating CM by extrusion was not effective in increasing RUP flow in dairy cows.

Key Words: nitrogen metabolism, rumen undegraded protein, omasal flow

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1405 Growth performance of dairy heifers limit-fed distillers dried grains with ad libitum forage.

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Most previous research on feeding distillers dried grains with solubles (DDGS) to dairy heifers has been conducted using a set forage to concentrate ratio in total mixed rations. Our objective was to determine the growth performance and DMI of heifers when fed DDGS or a corn and soy products concentrate mix with ad libitum grass hay. Our hypothesis was that heifers fed DDGS would have improved G:F because of slightly greater dietary fat, but growth performance would be maintained. A 16-wk randomized complete block design study was conducted using 24 heifers (18 Holstein and 6 Brown Swiss; 219 ± 2 d of age; 230 ± 4 kg BW). Heifers were blocked based on age and breed. Treatments were: 1) a control corn and soy products concentrate mix (CON) and 2) DDGS based concentrate mix (DG). Both concentrate mixes were fed at 0.8% of BW (DM basis) and grass hay was fed ad libitum. Heifers were individually fed respective concentrate mixes at 0800 h and hay was offered at 0900 h using a Calan gate feeding system. Orts were recorded daily before feeding. Frame sizes, BW, and BCS were measured at 4 h post feeding on 2 consecutive d during wk 0 and then every 2 wk thereafter throughout the feeding period. Data were analyzed using the MIXED procedures of SAS 9.4 with means compared using Tukey's test. Significance was declared at $P < 0.05$ and tendencies were declared at $0.05 \leq P < 0.10$. There were no significant interactions of treatment by wk. Heifer DMI (6.18 and 6.31 kg/d; SEM = 0.276 for the CON and DG, respectively), BW (269.8 and 266.9 kg; SEM = 9.86), and ADG (0.99 and 0.96 kg/d; SEM = 0.050) were similar ($P > 0.05$) between treatments. The G:F (0.168 and 0.156 kg/kg; SEM = 0.0099) was also similar ($P = 0.38$) between treatments. There were no differences ($P > 0.05$) in hip height (123.3 and 122.8 cm; SEM = 0.38), heart girth (140.6 and 139.9 cm; SEM = 0.40), or hip width (36.6 and 36.2 cm; SEM = 0.71) between treatments. Body condition scores (3.10 and 3.11; SEM = 0.026) were similar ($P = 0.68$) between treatments. Feeding heifers DDGS at 0.8% of BW with ad libitum forage maintained frame growth, ADG, DMI, and G:F compared to the CON concentrate mix.

Key Words: distillers grains, dairy heifer, growth performance

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1406 Effects of roughage inclusion and particle size on performance and rumination behavior of finishing beef steers.

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This experiment was conducted to determine the effects of feeding 5 or 10% corn stalks at various grind sizes with 30 or 25% wet corn gluten feed (WCGF), respectively, on rumination behavior, animal performance, and carcass characteristics of finishing beef steers. Fifty-one crossbred beef steers (BW = 881 ± 8 lbs), outfitted with rumination monitoring collars, were used in a randomized complete block design. Corn stalks were either passed through a commercial tub grinder once (large grind; LG) or twice (short grind; SG). Steam-flaked corn-based finishing treatment diets included: 10% SG with 25% WCGF (10%SG), 5% SG with 30% WCGF (5%SG), and 5% LG with 30% WCGF (5%LG). Animals were fed once daily at 0900 h using Calan head gates for an average of 155 d (heavy block = 148 d, light block = 162 d). Particle size of individual ingredients and treatment diets were quantified using the Penn State Particle Separator. Data were analyzed using the MIXED procedure of SAS with animal as the experimental unit. Means were separated using LSMEANS with the PDIFF option. There were no differences ($P = 0.52$) in final shrunk body weight between 5%SG, 5%LG, and 10%SG (1401, 1393, and 1373 ± 25.46 lbs, respectively), ADG (3.8, 3.8, and 3.7 ± 0.08 lbs, respectively; $P = 0.14$), or G:F (0.180, 0.175, and 0.176 ± 0.003, respectively; $P = 0.27$). However, DMI was greater ($P = 0.03$) for steers consuming the 5%LG

diet compared to the 10%SG (21.9 and 21.0 ± 0.31 lbs, respectively). Dressing percent also was greater ($P = 0.05$) for steers consuming 5%LG compared to 5%SG and 10%SG (64.3, 63.1, and 62.5 ± 0.007%, respectively). Hot carcass weight tended ($P = 0.10$) to be greatest for steers fed 5%LG. Steers consuming 10%SG had the greatest daily minutes of rumination ($P < 0.001$) followed by 5%LG, and 5%SG being the least (310, 288, and 244 ± 2.98 min/d, respectively). Steers consuming a longer particle size had increased dry matter intake and dressing percent, and tended to have greater carcass weights. With similar roughage inclusion rate, steers consuming a longer particle size also had increased daily rumination minutes. Therefore, increasing roughage particle size has the potential to allow a decrease in roughage inclusion without sacrificing feedlot performance and rumen function.

Key Words: rumination, corn stalks, corn gluten feed

1407 Automation of statistical procedures to screen raw data and construct feed composition databases.

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Millions of feed composition records have been generated from feed testing laboratories annually, providing high-valued assets that could be leveraged to benefit the animal nutrition community. Unfortunately, managing, handling, and processing feed composition data that originate from multiple resources are challenging, due in part to inconsistencies of how data are reported and the time needed to develop databases. Methods that consolidate and utilize these data are needed to develop accurate and precise feed composition databases. The objectives of this project were to: 1) develop automated statistical procedures to screen for outliers of feed composition data obtained from multiple resources; and 2) evaluate the efficiency of these procedures on classifying feedstuffs. A published statistical procedure (Yoder et al., 2014) was employed, modified, and programmed to operate using Python (Python Programming Language, v. 2.7) and SAS. A total of 2.761×10^6 records received from four commercial feed testing laboratories were used to develop the procedures and to construct tables summarizing feed composition. Briefly, feed names and variables across laboratories were standardized before the erroneous datapoints and duplicated samples were removed. Histogram, univariate, and principal component analyses were used to identify and remove outliers having key nutrients outside of the mean ± 3.5×SD. Clustering analyses were conducted to identify groups of feeds within a named feedstuff. Aside from the clustering step that was programmed in Python to automatically execute SAS, all steps were programmed and automatically conducted using Python followed by a manual evaluation of the resulting Pearson correlation matrixes and clusters. The input data contained 94, 162, 270, and 42 feeds, respectively, for laboratories 1 through 4 and were composed of 28 to 37 nutrients. The resulting database included 173 feeds (1.489×10^6records) with 111 feeds having more than 1 cluster. The developed procedures effectively classified byproducts (bakery byproducts, brewers grains, distillers grains and solubles, rice bran), forage (legume vs. grass, mature vs. immature and mid-maturity), and oilseeds vs. meal (cottonseed, canola seed, linseed/flaxseed, soybeans, sunflower) into distinct sub-populations. Results from these analyses provide a robust tool for the National Animal Nutrition Program (A National Research Support Project supported by USDA-NIFA and the State Agricultural Experiment Stations) to efficiently and consistently construct and update large feed datasets in an accurate, precise, and timely manner. This approach may also be used by commercial laboratories, feed manufacturers, animal producers, and other professionals to process feed composition datasets.

Key Words: automation, feed composition database, statistics

1408 Effect of pelleting at different temperatures and times on nutrient supply of co-products form canola oil processing.

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The objective of this study was to evaluate effects of conditioning temperatures (70, 80, and 90°C) and conditioning time (50s and 75s) and their possible interaction during pelleting on predicted truly absorbed protein supply of canola meal. Truly absorbed protein supply were measured for dairy cows according to DVE/OEB system and NRC-2001 model. The treatments were designed in 3 × 2 factorial arrangement and experiment design was RCBD. Statistical analysis was performed using the PROC MIXED of SAS 9.3. The results showed that conditioning time had a quadratic effect ($P < 0.05$) on total protein supplied to the small intestine (TPSI), microbial protein synthesized in the rumen based on available nitrogen (N_MCP), truly absorbed microbial protein in the small intestine (AMCP),rumen bypass feed crude protein (BCP) and truly absorbed bypass protein(ABCP). Samples conditioned at 80°C were highest in AMCP and N_MCP while lowest in TPSI and ABCP between pellets. Pelleting decreased ($P < 0.01$) TPSI, BCP and ABCP (261.39 vs. 241.66 g/kg DM, 195.68 vs. 174.20 g/kg DM and 55.49 vs. 41.61 g/kg DM, respectively) but increased AMCP of canola meal (55.86 vs. 57.34 g/kg DM). Pelleting induced decreased truly digested protein in the small intestine (DVE; 99.26 vs. 86.77

g/kg DM) and increased degradable protein balance (OEB; 115.26 vs. 135.27 g/kg DM) were observed ($P < 0.01$). In NRC-2001 model, affected by quadratic effect of conditioning temperature ($P < 0.05$), samples conditioned at 80°C between pellets were lowest in rumen undegradable feed crude protein (RUP), truly absorbed rumen undegradable protein in the small intestine (ARUP) and metabolizable protein (MP). Rumen endogenous protein (ECP) and truly absorbed rumen endogenous protein in the small intestine (AECP) were decreased by increasing conditioning time (10.58 vs.10.21 g/kg DM and 4.23 vs. 4.08 g/kg DM, respectively; $P < 0.01$). Pelleting decreased ($P < 0.01$) MP, AECP and ECP of canola meal (107.09 vs. 94.65 g/kg DM, 4.43 vs. 4.16 g/kg DM and 11.08 vs. 10.39 g/kg DM, respectively). RUP and ARUP of canola meal were decreased by pelleting as well (176.29 vs. 156.94 g/kg DM and 49.99 vs. 37.49 g/kg DM, respectively; $P < 0.01$). Summarily, pelleting changed potential protein supply of canola meal; alteration of pelleting conditions caused differences between pellets in predicted protein supply profiles.

Key Words: co-products from oil processing, nutrient supply and pelleting conditions

Table 1409.

1409 Okara meal can completely replace soybean meal in diets of early to mid-lactation dairy cows.

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Okara meal is a byproduct from the production of soy milk and tofu that can potentially replace soybean meal due to its high CP concentration. We aimed to evaluate the effects of okara meal as a replacement for soybean meal on performance and plasma concentration of metabolites in lactating dairy cows. Twelve multiparous (65 ± 33 DIM; 451 ± 45 kg of BW) and 8 primiparous (100 ± 35 DIM; 370 ± 51 kg of BW) Jersey cows were used in a crossover design with 21-d periods (14 d for diet adaptation and 7 d for data and sample collection). Diets were fed as TMR and formulated to be isonitrogenous and isofibrous and contained (DM basis) 50% grass-legume baleage, 2% liquid molasses, 2% minerals-vitamins premix, and: 1) 8.1% soybean meal, 10% soyhulls, and 27.9% corn meal (SBM treatment); 2) 15% okara meal, 8% soyhulls, and 23% corn meal (OKM treatment). The dietary nutrient composition averaged 15.4 vs. 15.9% CP, 35.3 vs. 36.3% NDF, and 24.1 vs. 24.1% ADF for SBM and OKM, respectively.

Table 1. Effects of a soybean meal (SBM)- or a okara meal (OKM)-based diet on performance and plasma metabolites in dairy cows

	Treatments			
Item	SBM	OKM	SEM	*P*-value
DMI, kg/d	18.1	17.9	0.58	0.30
Milk yield, kg/d	20.5	20.8	1.08	0.44
4% FCM, kg/d	24.1	24.2	1.05	0.73
ECM, kg/d	25.9	26.1	1.15	0.63
Milk fat, %	5.24	5.16	0.12	0.37
Milk fat, kg/d	1.05	1.06	0.04	0.59
Milk true protein, %	3.81	3.76	0.09	0.02
Milk true protein, kg/d	0.77	0.78	0.04	0.71
MUN, mg/dL	9.47	8.51	0.40	<0.01
PUN, mg/dL	22.2	21.1	0.41	0.03
Plasma Met, μ*M*	21.6	23.0	0.91	0.27
Plasma Lys, μ*M*	99.5	95.5	4.24	0.44
Plasma His, μ*M*	37.7	35.8	2.81	0.52
Plasma Leu, μ*M*	152	140	4.18	0.02
Plasma total EAA, μ*M*	109	103	3.03	0.09

Cows were fed and milked twice daily, and milk (d 15 to 16) and blood (d 16 to 17) samples were collected and analyzed for components and plasma metabolites [AA, urea-N (PUN)], respectively. Results are shown in Table 1. No significant differences were observed for DMI (mean = 18.0 kg/d), milk yield (mean = 20.7 kg/d), 4% FCM (mean = 24.2 kg/d), and ECM (mean = 26.0 kg/d) in cows fed SBM or OKM. Whereas milk fat concentration was not affected by treatments, milk true protein concentration was greater ($P = 0.02$) in cows fed SBM than OKM. Yields of milk fat and true protein did not differ significantly between treatments and averaged 1.06 and 0.78 kg/d, respectively. However, MUN ($P < 0.01$) and PUN ($P = 0.03$) were greater in cows fed SBM compared with those fed OKM suggesting an improvement in N use efficiency. Plasma concentrations of Met, Lys, and His did not differ significantly in cows fed SBM or OKM. Conversely, the plasma concentration of Leu was greater ($P = 0.02$), and that of total EAA tended ($P = 0.09$) to be greater in cows offered SBM vs. OKM, which may explain the observed increase in milk true protein concentration when feeding SBM. Overall, replacing soybean meal with okara meal maintained animal performance and appeared to improve N use efficiency.

Key Words: dairy cows, okara meal, soybean meal

1410 Effect of flax meal supplementation on oxidative stress and metabolic status of early lactation dairy cows infused with flax oil in the abomasum.

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The addition of flax oil (FO) to the diet of high-yielding dairy cows is a good strategy to improve the energy balance during early lactation. Although polyunsaturated fatty acids have numerous healthy attributes, they are easily oxidized and promote oxidative stress. In this project, we tested if the inclusion of natural antioxidants, flax meal (FM) rich in plant lignans, in cow's diet could decrease oxidative stress and optimize the potential of FO as a source of energy. This experiment was conducted using twenty (20) multiparous high-yielding Holstein cows fitted with ruminal cannulas. Cows were assigned to two dietary treatments: (1) 250 g flax oil/d infused in the abomasum ($n = 10$, FO) and (2) FO + 15% flax meal (FM) in the dry matter ($n = 10$, FMFO). Treatments were administered over a 21 d (d) period from d 7 to d 28 post calving. Plasma and urine samples were collected on d 7 (before treatment initiation), 14, 21, 28 (end of treatment) and 49 (for carryover effect) to evaluate systemic oxidative damage to proteins (carbonyls) and DNA (8-hydroxy-2'-deoxyguanosine), and to determine the enzymatic activity of the antioxidants glutathione peroxidase (GPx) and superoxide dismutase (SOD), and diet had no effect ($P > 0.05$). Biopsies were taken from the liver and mammary gland tissue on d 7, 28, and 49 to measure the activity and mRNA expression of antioxidants and evaluate energy production in the form of adenosine triphosphate (ATP), and diet had no effect ($P > 0.05$) on activity of GPx and SOD. The mRNA expression of *SOD1* in mammary tissue was lowered by the addition of FM to the diet ($P < 0.01$). In the liver, *SOD1* mRNA levels remained stable throughout the experimental period in the FMFO group while it was higher on d 49 in cows infused with FO (interaction treatment × day, $P < 0.05$). Analysis of hepatic levels of ATP revealed that the addition of FM suppressed the increase in energy production observed on d 49 in the FO group (interaction treatment × day, $P < 0.05$). Infusion of FO in the abomasum decreased the level of proteins carbonyls in mammary gland tissue from d 7 to d 49, and this effect was counteracted by the addition of FM (interaction treatment × day, $P < 0.05$). Taken altogether, these results suggest that the oxidative status of early lactating cows infused with FO is not significantly affected by the addition of FM to the diet.

Key Words: dairy cows, oxidative stress, antioxidant

1411 The effect of by-product inclusion and concentrate feeding level on milk production and composition, pasture dry matter intake, body weight and body condition score of mid-late lactation spring calving grazing dairy cows.

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There is growing interest in the use of by-products (or co-products) as economical sources of nutrients that complement grazed grass when grass supply is not sufficient to meet the nutritional demands of lactation. The objective of this research was to investigate the effect of by-product inclusion and concentrate feeding rate on milk production and composition, pasture dry matter intake (DMI), body weight (BW) and body condition score (BCS) of mid-late lactation spring calving grazing dairy cows. Forty eight (41 multiparous, 7 primiparous) Holstein Friesian dairy cows were blocked according to parity, balanced for days in milk, predicted 305 d milk yield, BCS and pre-experimental milk yield and randomly assigned to one of four dietary treatments in a 2 × 2 factorial design. All cows were grazed in one group on a perennial ryegrass based sward. The dietary treatments (T) were: concentrate containing 35% by-products offered at either 3 kg (T1) or 6 kg (T2)/d or a concentrate containing 95% by-products offered at 3 kg (T3) or 6 kg (T4)/d. The by-products used were maize dried distillers grains (DDG), palm kernel expeller (PKE) and soybean hulls (SH), included in equal proportions on a DM

basis. The experimental diets were offered for 63 d. Pasture DMI (14.5 kg/d) was not affected by feeding rate ($P = 0.37$) or by-product inclusion level ($P = 0.27$). Similarly, there were no effects of treatment on BW change (−9.3 kg, $P = 0.20$) or BCS change (+0.07, $P = 0.94$). By-product inclusion level had no effect on milk yield (27.33 kg/d, $P = 0.65$) or fat and protein yield (2.00 kg/d, $P = 0.54$). However, cows offered 6kg of concentrate produced more milk (+1.94 kg/d, $P = 0.08$) and milk fat (+0.10 kg/d, $P = 0.02$) than cows offered 3kg of concentrate. In conclusion, the results of this research show that by-products (DDG, PKE and SH) can be included at up to 95% of the concentrate fed to pasture based cows without impacting on milk production or composition, pasture DMI, BW or BCS. Cows offered 6kg of concentrates produced more milk and milk fat yield than cows offered 3kg, however, this response is unlikely to yield an economic return.

Key Words: by-products, dairy cow, milk production.

1412 Evaluating the feeding value of field peas for growing and finishing cattle. H. L. Greenwell*[1], K. H. Jenkins[2], and J. C. MacDonald[1], [1]*University of Nebraska-Lincoln, Lincoln,* [2]*University of Nebraska, Scottsbluff.*

A two year experiment was conducted to determine the effects of field pea (FP) supplementation during grazing and finishing phases on animal performance and carcass characteristics. In year one, 110 steers (initial BW = 348 kg; SD = 22 kg) and in year 2, 113 heifers (initial BW = 249 kg; SD = 11 kg) were arranged in a 3 × 2 factorial. The first factor was supplementation during grazing, consisting of three treatments: 1) FP; 2) mixture of dry rolled corn (70.8%), solubles (24%), and urea (5.2%); (DRC); (mixture was used to ensure RDP was not limiting); 3) control group receiving no supplement (CON). The second factor was finishing treatment, cattle were fed a DRC-based finishing diet with or without 20% FP (DM basis). Cattle grazed crested wheatgrass pastures and were supplemented at a rate of 0.5% BW (DM basis). During the growing phase ending BW and ADG ($P < 0.01$) were greatest for calves supplemented DRC (413 ± 11 kg, 0.89 ± 0.05 kg, respectively) followed by FP (399 ± 11 kg, 0.78 ± 0.05 kg, respectively) and the CON treatment (379 ± 11 kg, 0.62 ± 0.05 kg, respectively). In the finishing phase there was an interaction between growing and finishing treatments for G:F ($P = 0.03$), a result of cattle supplemented with FP during the growing phase and with no FP in the finisher performing better than cattle supplemented with FP during growing and with FP also included in their finishing diet (0.142 ± 0.004 kg vs. 0.132 ± 0.004 kg, respectively). There were no other interactions of finishing and growing treatments on other variables ($P \geq 0.10$). Feedlot ADG was affected by growing treatment ($P < 0.01$), where cattle in the CON treatment had greater ADG (1.95 ± 0.04 kg) than cattle that were supplemented DRC (1.80 ± 0.04 kg) and FP (1.78 ± 0.04 kg), which were not different. Final BW and HCW tended ($P = 0.07$) to be affected by growing treatment in a similar manner to feedlot ADG. Inclusion of FP in the finishing diet had no impact on carcass characteristics. In conclusion, cattle supplemented DRC during grazing had greater ADG than cattle supplemented FP or CON. However, in the finishing phase CON cattle compensated in feedlot ADG. Inclusion of FP in grower supplement or finishing diets may be advantageous if appropriately priced.

Key Words: cattle, field peas, finishing, grazing

1413 Cotton burrs as alternative roughage to adapt beef steers to steam-flaked corn-based finisher diet. L. A. Ovinge*[1], J. O. Sarturi[1], P. R. B. Campanili[1], B. J. M. Lemos[2], B. C. Bernhard[1], and D. Pettit[1], [1]*Texas Tech University, Lubbock,* [2]*Universidade Federal de Goiás, Goiânia, Brazil.*

Effect of cotton burrs as a roughage source during the transition of beef cattle (hay to finisher diet) was evaluated on intake, ruminal characteristics, nutrient digestibility, and feeding behavior. Ruminally cannulated steers ($n = 6$; BW = 235 ± 81 kg) were assigned using a complete randomized design to 1 of 2 adaptation strategies: Alfalfa hay-based or cotton burrs-based. In both strategies, roughage sources decreased as steam-flaked corn gradually increased. Steers were fed ad libitum once daily, a series of six diets (7-d period each): wheat hay; 4 step-ups; and a finisher. In situtechnique was used to assess ruminal fiber degradability (substrate = wheat hay). Wireless rumen pH probes were used. A 3-d spot fecal collection (twice daily, last 3 d of each period) and AIA were used to estimate total tract apparent nutrient digestibility. Rumen fluid samples (0, 4, 8, and 16 h post-feeding) were taken (d-6 of each period) for VFA and NH_3. Data were analyzed using Glimmix procedure of SAS (wheat hay period used as a covariate). Intake was not affected by adaptation strategies ($P \geq 0.16$), except for a tendency ($P = 0.10$) for steers adapted with alfalfa-strategy to ruminate more per kg of NDF consumed during finisher diet, than those adapted with cotton burrs-strategy. Steers fed cotton burrs-strategy showed lower ruminal pH average on step-3 and finisher periods (5.62 and 5.51 vs. 6.04 and 5.83; $P < 0.01$ and $P = 0.05$, respectively) compared with alfalfa-strategy. A greater area of pH below 5.6 (200 vs. 15 min*pH; $P < 0.01$); lower ruminal NH_3 concentration (5.1 vs. 8.8 mg/L; $P < 0.01$); and lower digestibility (OM, ADF, and hemicellulose; $P \leq 0.02$) during step-3 were also observed for steers fed cotton burrs-strategy compared to alfalfa-strategy, respectively. However, cotton burrs-strategy steers showed greater ($P = 0.01$) NDF digestibility during step-4; greater ($P < 0.01$) OM digestibility during finisher diet; and lower acetate/propionate ratio ($P = 0.04$) with a tendency ($P = 0.08$) to have greater propionate molar proportion during step-2, compared to alfalfa-strategy steers. Ruminal fiber degradability was not affected by adaptation strategies ($P \geq 0.36$), neither was dietary starch digestibility during common

finisher ($P = 0.73$). Cotton burrs adaptation strategy induced an improved ruminal fermentation environment during finisher diet, although with riskier ruminal pH and rumination than alfalfa-strategy. Further evaluation must consider cattle growth performance and economic aspects.

Key Words: adaptation, cotton burrs, alfalfa

1414 Temporal effects of ruminal propionate infusion on feeding behavior of Holstein cows In the postpartum period.

1415 Evaluation of five cool season grasses and alfalfa-grass mixtures. J. Paulson*[1], D. Holen[2], D. Nicolai[3], and B. J. Heins[4], *[1]University of Minnesota Extension, Rochester, [2]University of Minnesota, Morris, [3]University of Minnesota, Farmington, [4]University of Minnesota West Central Research and Outreach Center, Morris.*

Our increased knowledge of NDF digestibility has shown a benefit to feeding grasses in ruminant diets. However, data on the yield and nutrient analysis of alfalfa/grass mixtures with modern grass varieties and harvest management are lacking. The objective of this study was to determine the yield and nutritional value of selected alfalfa-grass mixtures and grass monocultures. At 2 MN locations, plots of grasses alone, alfalfa alone, and alfalfa-grass mixtures were planted using a forage plot seeder. Four randomized replications were planted of all plot variables. Each location was seeded with 1 alfalfa (A) variety and each of 5 grass species. Grass species included smooth brome (SB), meadow brome (MB), orchard (OG), tall fescue (TF), and meadow fescue (MF). Forage samples were sent to Dairyland Laboratories, St. Cloud, MN and analyzed by NIRS for DM, CP, NDF, and TDN. Data were analyzed using the MIXED procedure of SAS. Independent variables for analyses were the fixed effects forage, and replicate was a random effect. Nutrient analysis for Otter Tail forage showed no significant differences for CP, NDF or $NDFD_{30}$ for any of the forage species or mixtures evaluated. However, at Lanesboro, the mixture of A × MF × MB was significantly higher ($P < 0.05$) in CP than the mixture of A x MF and A or MF in pure stands. NDF tended to be higher in pure grass but was significantly lower ($P < 0.05$) in the A × MF × MB mixed stand. In conclusion, high quality alfalfa/grass forage can compare favorably with alfalfa for both yield and nutrient analysis.

Key Words: alfalfa, grasses, meadow fescue, forage

Table 1415.

Table 1. LANESBORO	Nutrient analysis, % of DM					
species	CP	NDF	NDFD30	RFV	RFQ	Yield t/a
A	18.68^{a}	44.63^{ab}	43.32	130	125	4.03^{c}
MF	18.24^{a}	47.67^{b}	45.01	121	120	4.06^{c}
TF	19.76^{ab}	44.25^{ab}	43.52	133	121	5.62^{d}
SB	19.99^{ab}	43.59^{ab}	39.15	131	120	4.51^{cd}
OG	20.03^{ab}	42.82^{ab}	41.05	136	128	4.48^{cd}
MB	18.92^{ab}	47.81^{b}	46.36	121	110	4.39^{c}
A MF	18.64^{a}	45.75^{ab}	43.98	128	123	3.89^{c}
A MF TF	19.24^{ab}	45.51^{ab}	44.61	128	125	3.85^{c}
A MF SB	19.98^{ab}	42.71^{ab}	42.27	138	131	4.07^{c}
A MF OG	20.17^{ab}	42.63^{a}	41.22	138	127	4.01^{c}
A MF MB	20.62^{b}	43.18^{ab}	44.79	138	136	4.04^{c}

Uncommon superscripts (a,b)differ P<.01. Uncommon superscripts (c,d) differ P<.1

1416 A novel bm3 corn silage hybrid with floury kernel genetics improves lactational performance and feed efficiency in Holstein cows. E. M. Remick*[1], S. M. Fredin[1], K. W. Cotanch[1], H. M. Dann[1], C. S. Ballard[1], J. P. Brouillette[2], and R. J. Grant[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Dow AgroSciences, Mycogen Seeds, Indianapolis, IN.*

Dry matter intake, lactation performance, feed efficiency and chewing behavior of multiparous Holstein cows ($n = 15$) fed diets containing a novel *bm3* corn silage (CS) hybrid with floury kernel genetics were compared to diets containing commercially available conventional and *bm3* hybrids using a replicated 3 × 3 Latin square design with 28-d periods. Cows were housed in tie-stalls, milked 3×/d, and fed a diet containing (DM basis) 49.0% of 1 of 3 CS hybrids (Mycogen Seeds, Dow AgroSciences, LLC): 1) a conventional CS hybrid (CON); 2) a brown midrib hybrid (BMR); and 3) a *bm3* hybrid with floury kernel genetics (BMRFL). All diets contained 6.3% hay crop silage and 44.7% concentrate. Diet nutrient composition averaged 14.8 ± 0.3% CP, 2.7 ± 0.5% NDF, and 26.3 ± 0.5% starch. Dry matter intake and milk yield were measured on d 22 to 28. Milk composition was measured on d 25 to 26. Cow behavior was monitored for 48 h over d 24 to 26. Data were analyzed by ANOVA using the MIXED procedure in SAS. Dry matter intake was increased ($P = 0.01$; SE = 0.5)

for cows fed BMR (28.0 kg/d) compared to CON (26.8 kg/d); DMI for cows fed BMRFL was intermediate (27.6 kg/d). Energy-corrected milk yield was increased ($P < 0.01$; SE = 1.5) for cows fed BMR (50.3 kg/d) and BMRFL (51.8 kg/d) compared to CON (47.2 kg/d). Milk fat yield was increased ($P \leq 0.05$; SE = 0.06) for cows fed BMRFL (1.87 kg/d) compared to CON (1.74 kg/d) and BMR (1.80 kg/d). Milk protein yield was increased ($P < 0.01$; SE = 0.06) for cows fed BMR (1.49 kg/d) and BMRFL (1.54 kg/d) compared to CON (1.36 kg/d). Milk urea-N was reduced ($P < 0.01$; SE = 0.3) for cows fed BMR (11.61 mg/dL) and BMRFL (11.16 mg/dL) compared to CON (13.60 mg/dL). Feed efficiency (Energy Corrected Milk/DMI) was increased ($P \leq 0.03$; SE = 0.04) for cows fed BMRFL (1.87) compared to CON (1.76) and BMR (1.79). Milk N efficiency ($P = 0.001$; SE = 1.2) was greatest for cows fed BMRFL (40.4%) followed by BMR (38.1%) and CON (35.3%). Cows fed CON chewed 5 min more per kg NDF consumed than cows consuming either *bm3* hybrid ($P < 0.01$). Lactational performance was increased for cows fed diets containing both *bm3* CS. Greater feed efficiency indicates that a *bm3* CS hybrid containing floury kernel genetics improves lactational performance and energy utilization compared to *bm3* and conventional CS. Additionally, improved milk N efficiency indicates greater ruminal carbohydrate fermentability can be achieved when feeding a BMRFL diet.

Key Words: brown midrib, floury corn, feed efficiency

1417 Alternative forage crops modify the composition and content of bovine milk fatty acids.

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Bioactive fatty acids (FA) found in milk have been linked to human health benefits. Alternative forage crops (AFC) include small grains, warm-season grasses and legumes that can potentially enhance forage production. The objective of this study was to determine if traditional pasture strip-tilled with AFC (treatment, TRT) would alter the composition (g/100 g FA) and content (g/kg milk) of milk FA compared with traditional grass-legume pasture (control, CON). Two 21-d experiments, spring (SPR) and summer (SUM), were conducted using 16 lactating Jersey cows (SPR, 85 ± 46 DIM; SUM, 143 ± 58 DIM). Cows were divided into 2 groups and offered 60% TMR (DM basis) and 40% pasture as AFC or traditional. SPR AFC included barley, wheat, rye, triticale, and hairy vetch (2.4% diet DM), while SUM AFC included buckwheat, chickling vetch, and oat (10.0% diet DM). From d 19 to 21 of each experiment, milk samples were collected during four consecutive milkings. Forage and milk FA were analyzed via gas-liquid chromatography. Differences between least-squares means were evaluated using the student's *t* test (JMP Pro 12). SPR forage FA (% total) included CON (total n-3 FA: 30.1%; total n-6 FA: 35.2%) and TRT (total n-3 FA: 46.2%; total n-6 FA: 21.5%), whereas the SUM forage FA included CON (total n-3 FA: 44.4%; total n-6 FA: 22.6%) and TRT (total n-3 FA, 45.7%; total n-6 FA, 22.0%). No differences in the milk content of total PUFA, branched-chain FA, or biohydrogenation intermediates (e.g., *trans*-11 18:1) were observed in either experiment. Milk proportions of total odd-chain FA were higher ($P < 0.01$) in SPR TRT (2.07 g/100 g) than in SPR CON (1.96 g/100 g). Milk proportions of n-3 FA and *trans*-18:1 were respectively lower ($P < 0.01$) in SPR TRT (0.64 g/100 g; 20.5 g/100 g) than in SPR CON (0.71 g/100 g; 22.8 g/100 g), but the contents of these FA were not different between groups. Milk content of 12:0 was higher ($P < 0.05$) in SPR TRT (1.86 g/kg milk) than in SPR CON (1.56 g/kg milk) ($P < 0.05$). Total milk SFA content was higher ($P < 0.05$) in SUM TRT (33.7 g/kg) than in SUM CON (29.1 g/kg). Milk content of de novo FA (CON: 11.6 g/kg milk; TRT: 13.2 g/kg milk) and mixed FA (CON: 13.0 g/kg milk; TRT: 16.2 g/kg milk) were higher ($P < 0.01$) in SUM AFC-fed cows. In conclusion, AFC altered the composition and content of milk FA.

Key Words: dairy, organic, pasture

1418 Effects of post-ethanol extraction sorghum silage as an alternative forage in growing and finishing diets on steer performance, carcass characteristic and nutrient digestibility.

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Two experiments evaluated use of post-ethanol extraction sorghum silage as an alternative forage to hay in feedlot diets. In experiment one (Exp1), 72 crossbred steers (397 ± 23, SD) were used to evaluate growth and carcass characteristics. Steers were blocked by BW into pens of 6 steers and randomly assigned to growing diets containing 40% (DM basis) of sorghum silage (SS; 57.6% NDF) or grass hay (CON; 63.3% NDF) for 56d ($n = 6$ pens per treatment). Within each treatment steers transitioned to dry-rolled corn-based finishing diets (fed for 56d) containing 6% effective NDF contributed by the forage source, resulting in forage inclusions of 16% for SS and 13.1% for CON. Experiment two (Exp2), utilized a subsample of steers ($n = 12$ per treatment) housed in pens equipped with Growsafe bunks for determination of growing phase diet total tract digestibility. From d28- 42, steers received titanium dioxide at approximately 10 $g^{-1} \cdot steer^{-1} \cdot d^{-1}$. Fecal samples were collected on d 41 and 42. Fecal and total mixed ration samples were dried, and ground for analysis of DM, OM, NDF, ADF, CP, ether extract (EE), and starch. Data were analyzed using PROC MIXED of SAS with the fixed effects of treatment and block (Exp1) or treatment (Exp2); significance was determined at $P \leq 0.05$ and tendencies at $P \leq 0.10$. Growing phase DMI and ADG did not differ due to treatment ($P \geq 0.19$); however, SS-fed steers had improved

G:F compared to CON ($P = 0.04$). Finishing period ADG or G:F did not differ ($P \geq 0.15$), despite SS-fed steers having lesser ($P = 0.008$) DMI than CON-fed steers. No differences in DMI, ADG, or G:F over the whole trial were noted between treatments ($P \geq 0.12$), nor were any carcass traits affected ($P \geq 0.23$). Growing phase total tract apparent digestibility of DM and starch did not differ ($P \geq 0.19$), due to treatment; however, OM digestibility tended to be greater ($P = 0.09$) in SS-fed steers. During the digestibility assessment period DMI was lesser ($P = 0.003$) in SS-fed steers. Steers fed the SS diet had greater ($P \leq 0.03$) digestibility of EE, CP, NDF, hemicellulose, and cellulose than CON-fed steers. Interestingly, CON-fed steers had greater ($P < 0.0001$) ADF digestibility than SS-fed steers. These data suggest that post-extraction sorghum silage can be effectively utilized in feedlot diets as an alternative forage.

Key Words: sorghum silage, cattle performance, digestibility

1419 Effect of lactic acid bacterial inoculants on the fermentation parameters and aerobic stability of sorghum-sudangrass silage. X. Li[*1,2], Y. Zhu[2], D. Vyas[1], and A. T. Adesogan[1], [1]*Dep. of Animal Sciences, IFAS, University of Florida, Gainesville,* [2]*Institute of Grassland Science, China Agricultural University, Beijing, China.*

Sorghum-sudangrass (*Sorghum vulgare* × *Sorghum sudanense*) has great potential to be widely used for silage making because of its rapid growth, high yields and nutritional value, and acceptability to cattle. However, it is prone to aerobic spoilage, which reduces its nutritional value. The aim of this study was to examine the effect of lactic acid bacterial inoculants on fermentation quality and aerobic stability of sorghum-sudangrass silage. Sorghum-sudangrass was harvested at 20% DM, chopped to approximately 20-mm lengths and treated in triplicate with 10^6 cfu/g of fresh weight of *Lactobacillus buchneri* (LB), *L. plantarum* (LP), and *Enterococcus fecalis* (EF) or distilled water (Control). Samples were stored at room temperature (about 25°C) for 264 d in polyethylene bags. Silage chemical composition was analyzed, and aerobic stability was determined by measuring the number of hours the temperature in the silages remained stable before rising more than 2°C above room temperature. Data were analyzed using the General Linear Model procedure of SAS and means were separated using Duncan's test. Silage treated with LB had greater pH compared to Control, LP, and EF silages (3.78 vs. 3.75, 3.73, 3.75, respectively; $P \leq 0.05$). Similarly, acetic acid concentration was greater for the silage treated with LB compared to Control, LP and EF silages (2.59 vs. 2.05, 1.59, 2.20, % DM, respectively, $P \leq 0.05$); however, no effects were observed on butyric or propionic acid concentration. The NH_3–N/TN concentration was greater in EF silage and lower in LB silage compared to that of the Control silage (6.92, 5.13 vs. 5.90%, $P \leq 0.05$). The lactic acid concentrations were 15 and 13% greater in LP and EF silages, respectively compared to the Control silage (12.30, 12.04 vs. 10.70, % DM, $P \leq 0.05$). Silages treated with LB and EF took longer to heat than untreated silage when exposed to air (169, 166.5 vs. 133.5, h, $P \leq 0.05$). In contrast, silages inoculated with LP had lower aerobic stability compared to the Control silage (99.5 vs. 133.5, h, $P \leq 0.05$). Inoculating sorghum-sudangrass silage with LB and EF improved aerobic stability, whereas inoculating the silage with LP improved fermentation parameters.

Key Words: aerobic stability, fermentation, inoculants

1420 Effects of feeding triticale and wheat silages on feed intake, milk production and composition, and enteric methane production in lactating dairy cows. M. T. Harper*, J. Oh, F. Giallongo, G. Roth, and A. N. Hristov, *The Pennsylvania State University, University Park.*

The objective of this experiment was to evaluate the production effects of replacing corn silage (serving as the control) with either triticale or wheat silage in a total mixed ration fed to lactating dairy cows. Twelve Holstein cows (days in milk 38 ± 5.6, BW 632 ± 101.6kg) were used in a replicated 3 × 3 Latin square design experiment with 3, 28 d periods. Feeding was ad libitum for 5 to 10% refusals. The control diet consisted of (DM basis): 44% corn silage, 8% alfalfa haylage, 5% hay/straw mixture, 9% ground corn, 8% canola meal, 7.5% whole roasted soybeans, 7% SoyPLUS, 4.5% molasses, 4% cottonseed hulls, and 3% mineral premix. For the triticale diet, 22.7% (DM basis) of the corn silage was replaced with triticale silage. Similarly, 22.7% of the corn silage in the wheat diet was replaced with wheat silage. Diets met or exceeded the MP and NE_lrequirements of the cows. The triticale (Hyoctane) and wheat (Malabar) were harvested May 13 and 20, 2015, respectively, at the boot stage. The silages had DM of 30.7 and 40.7%, pH 4.48 and 4.46 and (DM basis): lactic acid, 7.03 and 6.43%; NDF, 51.1 and 51.0%; and CP, 17.3 and 14.6%, respectively. Diet did not affect DMI (27.5 kg/d; SEM = 1.8, $P = 0.37$), enteric methane emission (470 g/d; SEM = 23.4, $P = 0.16$), or milk fat yield (1.55 kg/d; SEM = 0.11, $P = 0.35$). Milk yield was higher in control versus triticale or wheat diets (42.7, 41.2, and 41.4 kg/d, respectively; SEM = 5.2, $P = 0.01$). Energy corrected milk yield was also higher ($P = 0.05$) in control (40.9 kg/d) versus triticale (38.6 kg/d) or wheat (38.5 kg/d) diets. Triticale and wheat diets increased ($P < 0.001$) milk urea nitrogen concentration compared with the control (12.7 and 13.1 vs. 10.8 mg/dL, respectively). Milk true protein and lactose yields were lower for both triticale and wheat diets compared with the control: 1.20, 1.20, and 1.27 kg/d (SEM = 0.096, $P = 0.02$) and 2.00, 1.98, and 2.14 kg/d (SEM = 0.173, $P = 0.01$), respectively. The results indicate that a 22.7% replacement of corn silage DM with either triticale or wheat silage in the diet of lactating dairy cows did not affect enteric methane emission

or DMI, but decreased milk yield.

Key Words: triticale, wheat, silage

1421 Effects of feeding sorghum and oat silages on feed intake, milk production and composition, and enteric methane production in lactating dairy cows. M. T. Harper*, J. Oh, F. Giallongo, J. C. Lopes, G. Roth, and A. N. Hristov, *The Pennsylvania State University, University Park.*

The objective of this experiment was to evaluate the production effects of replacing corn silage (serving as the control) with either sorghum or oat silage in the total mixed ration fed to lactating dairy cows. Twelve Holstein cows (days in milk 81 d ± 24; BW 615 kg ± 49.6) were used in a replicated 3 × 3 Latin square design experiment with 3, 28 d periods. Feeding was ad libitum for 5 to 10% refusals. The control diet consisted of (DM basis): 44% corn silage, 7.5% alfalfa haylage, 4% hay/straw mixture, 11% ground corn, 7.5% SoyPLUS (West Central Cooperative, Ralston, IA), 7.5% whole roasted soybeans, 7% canola meal, 4.5% molasses, 4% cottonseed hulls, and 3% mineral premix. For the sorghum diet, 22.7% (DM basis) of the corn silage in the diet was replaced with sorghum silage. Similarly, 22.7% of the corn silage in the oat diet was replaced with oat silage. The MP balance of the control, sorghum, and oat diets was 199, 238, and 290 g/d, respectively, whereas the balance of NE_l was 2.8, 2.4, and 2.8 Mcal/d. The forage sorghum (Alta AF 7202) was harvested on November 11, 2014 with the harvester set to 1 inch total chop length. The oats (Forage Plus) were mowed in a vegetative state and harvested on November 14, 2014. Sorghum and oat silages had DM of 30.5 and 30.8% and (DM basis): lactic acid, 2.89 and 7.27%; NDF, 62.7 and 54.7%; and CP, 9.5 and 11.7%, respectively. Enteric methane emission measurements were collected with the GreenFeed system. Control and oat diets resulted in higher DMI and milk yield than sorghum: 26.7, 27.1, vs. 26.0 kg/d (SEM = 1.68, $P = 0.02$) and 39.6, 40.2, vs. 38.7 kg/d (SEM = 3.57, $P < 0.01$), respectively. Methane emission (502 g/d; SEM = 26.7, $P = 0.59$) and milk fat yield (1.41 kg/d; SEM = 0.07, $P = 0.78$) were not affected by diet. The sorghum silage diet decreased milk true protein concentration ($P = 0.03$) compared with the control or oat silage (2.78 vs. 2.85 and 2.83%, respectively). Similarly, milk protein yield was decreased ($P = 0.05$) by the sorghum diet (1.04 vs. 1.13, and 1.13 kg/d, respectively). The results indicate that a 22.7% replacement of corn silage DM with oat silage is a viable alternative for dairy producers in the Northeast U.S.

Key Words: sorghum, oats, silage

1422 Effect of harvest method on digestibility of corn residue. T. M. King*[1], M. L. Jolly-Breithaupt[1], J. L. Gramkow[2], J. C. MacDonald[1], and T. J. Klopfenstein[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]University of Nebraska, Lincoln.*

Advanced techniques of harvesting corn residue has led to improved residue quality by reducing proportion of stem in the bale. The objectives of this study were to determine 1) the effect of harvest method on the digestibility and quality of corn residue and 2) the effect of drying method used to process feces on digestibility estimates. An 85 d digestion study was conducted utilizing 9 crossbred wethers (initial BW = 42.4 kg; SD = 7 kg) blocked into 3 blocks based on initial BW. Residue based diets contained corn residue harvested with 1 of 3 methods (low-stem, high-stem, and conventional) at 70:27:3 residue: Sweet Bran®: bromegrass hay (DM basis). Five periods of 17 d provided 10 d for adaption and 7 d for total fecal collection. Sweet Bran® and bromegrass hay were fed at a 9:1 ratio in the fourth period for determination of residue digestibility by difference. Feces were collected twice daily, composited at the end of the period, and dried using 1 of 3 methods (60°C forced air oven, 100°C forced air oven, and freeze dry technique). No differences in DM intake, OM intake, or NDF intake were observed among residue type ($P > 0.05$). Low-stem had greater DM digestibility (DMD) than conventional ($P = 0.02$) and had a tendency to be greater than high-stem ($P = 0.06$). There were no differences in DMD ($P = 0.63$) or OM digestibility (OMD; $P = 0.86$) between high-stem and conventional. Low-stem had greatest OMD and NDF digestibility (NDFD, $P < 0.05$). High-stem had a NDFD which was greater than conventional ($P < 0.01$). Drying method had no effect on digestibility determination by lab assays for both OMD and NDFD ($P = 0.99$). Overall low-stem had the greatest digestibility with high-stem being intermediate and conventional having the lowest digestibility. Reducing the proportion of stem in the bale through changes in the harvest method can lead to an increased quality of corn residue.

Key Words: corn residue, digestibility, harvest method

Table 1422.

Table 1. Digestibilities of Residues from 3 Harvest Methods

	Conventional	High-stem	Low-stem	SEM	P-value
DMD, %	46.05^{c}	47.22^{bc}	51.74^{ab}	2.3	0.05
OMD, %	51.41^{b}	51.05^{b}	55.56^{a}	2.0	0.06
NDFD, %	44.46^{c}	52.37^{b}	58.53^{a}	2.1	< 0.01

^{abc}Means with differing superscripts are different

1423 Supplementing Corn on Alfalfa Pasture to Alter Growth Performance, Carcass, and Quality Traits. Chloe Gresel, Cheryl Campbell, Lisa Duizer, Brian McBride, and Ira Mandell. *University of Guelph, Guelph, ON, Canada.*

Pasture finishing of beef cattle can be used to improve the fatty acid composition of beef (omega 3s and CLA) but at the possible expense of deleteriously affecting palatability traits. While pasture finished beef can command a premium in the marketplace, increased time on feed relative to finishing on a high grain diet can lead to production challenges due to much slower rates of gain for grass-fed beef. Supplementing corn on pasture may increase cattle gains and beef palatability attributes without necessarily deleteriously affecting beef fatty acid composition. The objective of this study was to examine how corn grain supplementation on alfalfa pasture alters carcass, meat quality, and fatty acid traits in an attempt to increase cattle performance and beef palatability. Fifty black Angus and Angus cross steers were randomly assigned to one of four management regimens: 1) 85.4% corn-based concentrate/14.6% forage diet fed in a drylot as a TMR (n = 12); 2) pastured cattle supplemented with corn at 1% BW (n = 13); 3) pastured cattle supplemented with corn at 0.5% BW (n = 12); 4) pastured cattle with no corn supplementation (n = 13). Pastured steers were rotationally grazed through 20 acres of predominantly alfalfa pasture while high concentrate-fed steers were housed in 2 drylot pens equipped with Calan gates to measure individual feed intakes. Cattle were fed for 111 d with BW taken every 14 d to track performance. Steers were harvested at a commercial packing plant where a rib section from each animal was shipped back to the University of Guelph Meat Lab for evaluation. Management regimen effects on performance, carcass, meat quality, trained taste panel and fatty acid data were evaluated using a Proc Mixed procedure in SAS. Average daily gain differed ($P < 0.0001$) across most management regimens. While grain feeding decreased ($P < 0.01$) dissectible lean, backfat and marbling were generally similar ($P > 0.14$) across management regimens. Grain feeding decreased ($P < 0.0001$) n-3 fatty acids without affecting ($P > 0.27$) CLA concentrations. Taste panel assessment of tenderness, juiciness, and beef flavor attributes were similar ($P > 0.30$) between beef from grain-fed cattle and beef from cattle that only consumed alfalfa pasture.

Key Words: beef cattle, grass-fed, fatty acids

1424 Effect of harvest method and ammoniation on apparent digestibility and intake of baled corn residue in lambs. A. C. Conway*, T. M. King, M. L. Jolly-Breithaupt, J. C. MacDonald, T. J. Klopfenstein, and M. E. Drewnoski, *University of Nebraska-Lincoln, Lincoln.*

The objective of this study was to assess the effect of three different harvest methods and ammonia treatment on the in vivo digestibility of baled corn residue. Nine wether lambs (49.2 ± 0.5 kg BW) were used in a 9 × 6 Latin Square design with a 3 × 2 factorial treatment structure; 3 harvest methods [conventional rake and bale (COV), New Holland Cornrower with 8 rows (high-stem; HS) or 2 rows (low-stem; LS) of corn stalks chopped into the windrow containing leaf, husk and upper stem] and ammoniation at 3% of DM of the resulting baled residue. Diets consisted of 64.2% corn residue, 29.8% Sweet Bran, 3.3% smooth-bromegrass hay, and 2.8% mineral mix (DM basis). Periods were 21 d (14 d adaptation and 7 d total fecal collection). Lambs were fed ad-libitum (110% of the previous day's DMI) during d 1 to 12 and reduced to 95% of ad-libitum intake for d 13 to 21. Treatment diets were fed over 6 periods, with the non-residue proportion of the diet (Sweet Bran, smooth-bromegrass hay, and mineral mix) fed alone in an additional period to determine the digestibility of the residue by difference. There was a harvest method by ammoniation interaction for ad-libitum DMI (d 7 to 12). Intake of non-ammoniated residue diets did not differ ($P \geq 0.92$) among harvest methods, however, ammoniation increased ($P \leq 0.05$) intake with LS having the greatest increase, COV

Table 1424.

Table 1. Effect of harvest method and ammoniation on *ad-libitum* DMI (% BW) and the DM and OM digestibility of the corn residue component of the diet.

	Non-ammoniated			Ammoniated			*P-value*			
	COV	LS	HS	COV	LS	HS	SEM	Harvest	Ammonia	Interaction
Diet DMI	2.6	2.6	2.6	3.6	4.1	3.1	0.15	<0.01	<0.01	<0.01
DMD,%	40.3	46.4	41.6	49.1	56.9	52.9	2.65	0.04	<0.01	0.89
OMD,%	45.9	50.6	45.6	55.1	60.1	57.4	2.43	0.12	<0.01	0.85

being intermediate and HS having the least increase. There was no harvest method by ammoniation interaction for DM or OM digestibility. Digestibility of DM (DMD) differed between harvest methods, with LS being greater than COV ($P = 0.01$) and tending ($P = 0.10$) to be greater than HS. Ammoniation increased DMD of the residues by 25% (10.2% units). Digestibility of OM (OMD) tended to be affected by harvest method with LS tending ($P = 0.06$) to be greater than COV. Ammoniation improved OMD of all harvest methods, resulting in a 22% (10.1% units) increase. Utilizing alternative harvesting technologies and ammoniation can improve the feeding value of baled corn residue.

Key Words: corn residue, digestibility, harvest method, ammoniation

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1425 Effects of growing system and silage type on feedlot growth performance, carcass characteristics, and nutrient digestibility of beef steers. P. R. B. Campanili*[1], J. O. Sarturi[1], S. J. Trojan[1], M. A. Ballou[1], B. J. M. Lemos[2], L. A. Ovinge[1], and J. B. G. Mayorquin[3], *[1]Texas Tech University, Lubbock, [2]Universidade Federal de Goiás, Goiânia, Brazil, [3]Zamorano, Tegucigalpa, Honduras.*

The effects of beef cattle growing systems (grazing vs. bunk) and silage type (corn vs. sorghum) on finishing phase growth performance, carcass characteristics, and nutrient digestibilities were evaluated. Steers ($n = 128$; BW = 394 ± 21 kg) were backgrounded by either grazing (forage sorghum AF7401, 104 d) or bunk fed (65% concentrate diet, 85 d). Following the backgrouding period, animals were blocked by BW, and randomly allocated to one of the two dietary treatments, corn (BH8895) or sorghum (AF7401) silage at 20%, DM basis, in a randomized complete block design. During the finishing phase, steers were fed once daily at approximately 0800 h. A 5-d spot fecal collection (twice daily) and acid insoluble ash were used to estimate total tract apparent digestibility. Slaughter was performed on 132, 146, or 174 d on feed. Data were analyzed using the Glimmix procedure of SAS, using pen as the experimental unit. No interaction (growing system × silage type) was observed ($P > 0.16$), except for a tendency ($P = 0.06$) of bunk backgrounded steers to consume more sorghum than corn silage diet, compared with grazing backgrounded steers. Steers that grazed forage sorghum had greater ADG (25%), DMI (23%), and greater gain:feed (5%) during the finishing phase, compared with bunk backgrounded steers ($P < 0.01$). A greater HCW (7.8%), lower dressing percent (0.8% unit), and lower fat thickness (18%) were observed for steers grown under sorghum grazing conditions compared to backgrounded bunk fed steers ($P < 0.01$). Steers fed the corn silage diet had lower DMI (7%), greater ADG (5%), and consequently greater gain:feed (10%) compared with steers fed sorghum silage diet ($P < 0.01$). A 0.5% unit greater ($P = 0.03$) dressing percent and 0.1% unit greater ($P = 0.04$) KPH were observed for steers fed corn silage compared to those fed sorghum silage. Steers fed the corn silage diet also had greater ($P < 0.01$) DM (11%), CP (9%), EE (1.9%), and starch (8%) digestibilities compared to steers fed sorghum silage diet. Digestibility of fiber components were not affected ($P \geq 0.12$) by silage type or growing system. Sorghum grazing backgrounded steers positively affected finishing phase, but such strategies must be further be evaluated considering economical aspects and water use. Replacing corn silage with sorghum silage in beef finishing diets even at low roughage inclusion requires adjustments to balance dietary energy.

Key Words: grazing, silage, sorghum

1426 Effects of feeding green chopped winter forages on digestibility, ruminal fermentation and blood parameters in beef steers. T. M. Schulmeister*, M. Ruiz-Moreno, M. E. Garcia-Ascolani, F. M. Ciriaco, D. D. Henry, J. Benitez, J. C. B. Dubeux Jr., G. C. Lamb, and N. DiLorenzo, *University of Florida, North Florida Research and Education Center, Marianna.*

An experiment was conducted in the winter over 2 consecutive yr to evaluate the effects of feeding green chopped winter forages on digestibility and ruminal fermentation parameters in beef steers. Each yr, 9 ruminally cannulated Angus crossbred steers (yr 1: 359 ± 79 kg; yr 2: 481 ± 105 kg) received fresh chopped forage ad libitum, from pastures planted with one of the following mixtures: 1) FL401 cereal rye (*Secale cereale* L.)/Prine annual ryegrass (*Lolium multiflorum* Lam.) (RYE); 2) Horizon 201 oats (*Avena sativa* L.)/Prine annual ryegrass (OAT); 3) Trical 342 triticale (*X Triticosecale* spp.)/Prine annual ryegrass (TRIT). Intake was measured throughout the study using GrowSafe, and any unconsumed forage was discarded before the next d feeding. After a 14 d adaptation period, feed and fecal samples were collected twice daily for 4 d, to determine apparent total tract nutrient digestibility using indigestible NDF as a marker. On d 19, blood and ruminal fluid samples were collected every 3 h during a 24 h period, to analyze blood urea nitrogen (BUN) and glucose in the plasma, as well as NH_3–N, pH, and VFA concentrations in ruminal fluid. Data were analyzed as a generalized randomized block design with repeated measures, using the Mixed Procedure of SAS, with treatment as a fixed effect and animal and yr as random effects. Treatments did not affect ($P > 0.05$) intake of DM, OM, CP, NDF, or ADF; however, apparent total tract digestibility of DM, OM, CP, NDF, and ADF was greater ($P < 0.05$) for OAT and TRIT, when compared with RYE. Steers fed OAT had greater concentrations of plasma glucose ($P < 0.05$) compared with TRIT and RYE. An effect of sampling time ($P < 0.01$) was observed for ruminal pH; however no treatment or treatment × sampling time interactions were observed ($P > 0.05$). Steers fed RYE had greater ($P < 0.05$) concentrations of NH_3–N,

BUN, and the least concentrations of total VFA ($P < 0.05$). Molar proportion of acetate, branched-chain VFA and acetate:-propionate were greater ($P < 0.05$) for RYE when compared with OAT and TRIT. In conclusion, OAT and TRIT resulted in greater digestibility of nutrients, and ruminal fermentation and blood parameters that are conducive to enhanced growth performance when compared with RYE.

Key Words: fermentation, ruminants, winter forage

1427 Effects of feeding steers extruded flaxseed and hay together (total mixed ration) or sequentially (non-total mixed ration) on animal performance and erythrocyte vaccenic, rumenic, and α-linolenic acid content.

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Considerable research has been conducted to try and increase PUFA and their biohydrogenation intermediates (BHI) in beef, mainly vaccenic acid (VA; *trans*-11 18:1) and rumenic acid (RA; *cis*-9, *trans*-11 18:2), due to their purported health benefits. There is often large between-trial variation, and the objective of the present trial was to determine if feeding steers extruded flaxseed (Linpro-R; O&T Farms Ltd., SK, Canada) and hay (25 and 75%, respectively, DM basis) together as a total mixed ration (TMR) or sequentially (non-TMR) could help explain differences in PUFA BHI. Forty-eight Continental crossbred steers (325 kg [SD 16]) were stratified by weight to 6 pens of 8 steers and pens were randomized to either TMR or non-TMR. Steers were fed ad libitum for 240 d, feed intake was recorded daily, and steers were weighed every 28 d. Blood was collected on 0, 112, and 228 d, and erythrocyte fatty acid compositions were analyzed (i.e., erythrocyte composition correlates well with other tissues). Blood was centrifuged, and erythrocytes were direct methylated with methanolic HCl and analyzed by GC using a 100-m CPSil 88 capillary column. Data were analyzed using PROC MIXED of SAS. For animal performance, diet was the main effect and pen was the experimental unit. For erythrocyte fatty acids, the experimental model included diet as a main effect, days on test as a repeated measure and the diet × day interaction, with individual animal as the experimental unit. Dry matter intake was lower for non-TMR vs. TMR steers (10.56 vs. 11.42 kg/d; $P = 0.019$), but final weight (286 kg), ADG (1.18 kg/d), and feed efficiency (7.95) did not differ ($P > 0.05$). At 0 d, percentages of VA, RA, and α-linolenic acid (ALA) in erythrocytes (0.93, 0.29, and 0.07%, respectively) did not differ between TMR and non-TMR steers ($P > 0.05$). At 112 d, percentages of VA, RA, and ALA increased and non-TMR (2.82, 0.53, and 7.87%, respectively) were greater than TMR (1.71, 0.36, and 6.36%, respectively). At 228 d, the VA, RA, and ALA percentages were still greater than 0 d but were less than 112 d. The non-TMR (1.24, 0.20, and 5.90%) were still, however, greater than TMR (2.01, 0.25, and 6.78%). Our results suggest that the method of feeding management of supplementary sources of PUFA has minimal effects on animal performance but can profoundly affect the content of PUFA and their BHI in erythrocytes during the feeding period.

Key Words: α-linolenic acid, flaxseed, rumenic acid, total mixed ration, vaccenic acid

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1428 Transcriptome responses to different forage allowance in the hypothalamus of grazing beef cows.

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The hypothalamus plays a major role in the response to changes in dietary nutrients supply. The aim of this study was to evaluate the effect of long-term nutrition at two different forage allowances (FA) of native pastures on the hypothalamic transcriptome of beef cows. Thirty-two multiparous cows (Angus, Hereford, and F_1 crossbreeds) were used, from May 2007 to May 2010, in a complete randomized block design with two FA throughout the year (4 vs. 2.5 kgDM/100 kg BW; HI vs. LO, respectively). At the end of the third experimental year and at 190 ± 10 d postpartum (45 d after calf weaning), cows were slaughtered and the hypothalami were collected. A subsample of 10 hypothalami ($n = 5$/treatment) from F_1 crossbreed cows was used. Total RNA extraction, amplification, library preparation, and sequencing were performed following the Illumina mRNA-Seq. Reads were mapped to the bovine reference genome using Tophat, and the resulting alignments were used to reconstruct transcript models using Cufflinks. Differential gene expression was evaluated using Cuffdiff. Additionally, gene set enrichment analysis was performed using goseq and meshr R packages. Overall, 217 genes were found to be differentially expressed at FDR < 0.05 and fold change ≥ 2 between HI vs. LO. Most differentially expressed genes were related to defense response and immune system, brain and neuronal development, neuronal regeneration and synaptic plasticity, neuronal communication, receptor and intracellular signaling, and metabolic hormone activity. The enrichment analysis using Gene Ontology (GO) and Medical Subject Headings (MeSH) databases revealed that GO biological process and MeSH terms related to defense response and immune system, negative regulation of proteolysis, chemotaxis, and regulation of JAK-STAT cascade were upregulated

in HI cows compared with LO cows. Meanwhile, GO biological processes and MeSH terms related to brain and neuronal development, synaptic plasticity, and neuronal communication were upregulated in LO cows compared with HI cows. These transcriptional changes in the hypothalamus would indicate a differential adaptation of grazing crossbreed cows to different nutritional environments. (This study was supported by CSIC Research Funds, UdelaR, Uruguay.)

Key Words: RNA-seq transcriptomic grazing

1429 Effects of feeding alfalfa stemlage or wheat straw for dietary energy dilution on growth performance and sorting behaviors of Holstein dairy heifers. H. Su*[1], N. M. Esser[2], W. K. Coblentz[3], K. F. Kalscheur[4], R. D. Hatfield[5], and M. Akins[1], *[1]University of Wisconsin, Madison, [2]University of Wisconsin, Marshfield, [3]U.S. Dairy Forage Research Center, Marshfield, WI, [4]USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI, [5]U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI*.

Feeding high-quality forage diets may lead to excessive weight gains and overconditioning for pregnant Holstein heifers. Restriction of energy density and DMI by heifers by using low-energy forages, such as straw, is a good approach for controlling this problem. Alfalfa stems containing high fiber and moderate protein content have the potential to be used to replace straw to reduce dietary energy. The objective of this study was to compare the growth performance and sorting behavior of dairy heifers offered an alfalfa silage/corn silage diet (CON; 13.1% CP, 67.4% TDN, and 39.7% NDF) with two energy-diluted diets replacing the corn silage and alfalfa silage with either alfalfa stemlage (STM; 12.6% CP, 60.1% TDN, and 46.4% NDF) or wheat straw (STW; 12.6% CP, 62.7% TDN, and 43.7% NDF) to get a similar diet composition. Seventy-two pregnant Holstein heifers (16.8 ± 1.3 mo) were stratified (24 heifers/block) by initial BW (light, 440 ± 18.0 kg; medium, 486 ± 18.6 kg; and heavy, 534 ± 25.1 kg) and then assigned to 1 of 9 identical pens (3 pens/block and 8 heifers/pen), where each of the 3 diets was randomly assigned to 1 pen within each block. Diets were offered in a 56-d feeding trial. Statistical analyses were performed using a MIXED procedure in SAS 9.3 with pen as the experimental unit. Daily DMI was greater for CON than for diluted diets (11.3 vs. 10.3 kg/d; $P = 0.01$), with no differences observed between STM and STW ($P = 0.61$). Average daily gains were greater for heifers offered the CON compared with heifers offered diluted diets (1.32 vs. 1.00 kg/d; $P = 0.02$). The feed:gain ratio tended to be less for heifers offered the CON relative to heifers offered diluted diets (8.6 vs. 10.7; $P = 0.08$). There were no differences detected across all growth measures within the diluted diets ($P > 0.05$). Physically effective fiber (pef) particle content was relatively static across sampling times for CON (overall sorting factor mean = 1.02), which indicates minimal sorting. Sorting against pef particles was observed for diluted diets and much more severely for the STM diet (overall sorting factor mean = 1.14 vs. 1.06; $P < 0.05$). These results indicate that diets diluted with low-energy forages (both STM and STW) were effective in reducing intakes of DM and energy and maintaining appropriate weight gains and body condition for pregnant Holstein heifers.

Key Words: alfalfa stemlage, dairy heifer, wheat straw

1430 Effect of partially replacing barley grain with liquid whey permeate in diets for finishing lambs on dry matter intake, average daily gain, and total tract digestibility. F. Joy* and G. B. Penner, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada*.

The objective of this study was to evaluate the effect of partially replacing barley grain with liquid whey permeate in diets for finishing lambs on DMI, ADG, and apparent total tract digestibility. Eighteen wether lambs were individually housed and randomly allocated to 1 of 3 dietary treatments in a completely randomized design. The control diet (CON) consisted of 67.7% barley grain, 20% barley silage, and 12.3% mineral and vitamin supplement on a DM basis. For the moderate-sugar (MOD) and high-sugar (HIGH) treatments, whey permeate was included in the diet at 5 and 10% on a DM basis, respectively, by replacing an equal proportion of barley grain. Water was added to equalize dietary DM content among diets with a targeted DM content of 53.5%. Lambs were provided with a 12-d dietary transition protocol (2 dietary steps) to gradually adapt them to the finishing diet. Subsequently, a 28-d treatment period was imposed with the final 4 d used for measurement of DMI and total fecal collection. Data were analyzed using the mixed model of SAS with the fixed effect of treatment. Addition of whey permeate did not affect DMI ($P = 0.96$) or ADG ($P = 0.43$) with average values of 1.22 ± 0.148 and 0.19 ± 0.026 kg/d, respectively. Total tract digestibility of sugar in the MOD treatment was greater (95.1 vs. 69.5 ± 6.32%; $P = 0.04$) than for CON whereas the HIGH treatment did not differ from CON or the MOD treatment. The apparent digestibility coefficients for DM (74.7 ± 2.74%), OM (76.8 ± 2.55%), starch (98.7 ± 1.32%), CP (65.5 ± 3.47%), NDF (36.43 ± 7.07%), and ether extract (74.34 ± 3.57%) did not differ among treatments ($P > 0.10$). The results of this study indicate that liquid whey permeate can partially replace barley grain without negative effects on DMI, ADG, or digestibility. In addition, our results show that a low inclusion rate (5% DM) may improve sugar digestibility.

Key Words: lamb, sugar, whey permeate

Table 1431.

	Treatment				*P*- values		
Item, % DM	CS	CS:CPR	CS:SLV	SEM	Trt	d	Trt x d
Sinigrin, mg/g	0.00[c]	0.14[b]	1.72[a]	0.04	< 0.01	< 0.01	< 0.01
pH	4.25[b]	4.42[a]	4.40[a]	0.02	< 0.01	< 0.01	0.04
Acetic acid	0.63[c]	0.86[a]	0.76[b]	0.02	< 0.01	< 0.01	0.01
Lactic acid	3.66[a]	3.22[b]	3.47[b]	0.11	0.03	< 0.01	0.36
CP	7.3[b]	16.3[a]	16.4[a]	0.21	< 0.01	0.14	0.04
NDF	31.2[a]	25.9[b]	30.1[a]	0.59	< 0.01	< 0.01	0.34
EE	2.55[b]	7.59[a]	2.48[b]	0.09	< 0.01	< 0.01	0.02

[a-c]Means in the same row with unlike letters differ ($P < 0.05$).

1431 Evaluation of the fermentation characteristics and glucosinolate content of cold-pressed or solvent-extracted carinata meal ensiled with corn forage. K. Rodriguez-Hernandez*[1,2], J. L. Anderson[1], M. A. Berhow[3], and A. Garcia[1], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]CIRNOC-INIFAP, Matamoros, Mexico, [3]USDA, ARS, NCAUR, Peoria, IL.*

Carinata meal (CRM) is a quality protein source but contains high concentrations of sinigrin, a glucosinolate, which limits its use as a feedstuff. Previous research shows that CRM ensiled with forages reduces sinigrin content. Solvent extraction (SLV) or cold pressing (CPR) are methods used to extract oil from carinata seeds, leaving different residual oil content in the meals. We hypothesized that the oil content in CRM affects the fermentation when it is blended with forage for ensiling. The objectives were to determine the effects of CRM fat content when blended with corn forage on silage fermentation and sinigrin content. A micro-silo experiment was conducted with three treatments: 1) corn forage (CS), 2) CS and solvent-extracted CRM blend (CS:SLV), and 3) CS and cold-pressed CRM blend (CS:CPR). Both blends of CRM to forage were 25:75 on a DM basis. Micro-silos were packed at 86 kg of DM/m^3 in triplicate for 0, 7, 21, and 60 d of ensiling. Data were analyzed using MIXED procedures of SAS 9.4. The model included treatment, day, and treatment × day interaction, with significance declared at $P < 0.05$. The sinigrin content of CRM before blending was 15.3 vs. 16.2 mg/g for CPR and SLV meals, respectively. On d 0, within hours after mixing, the sinigrin content was reduced 94.8% in the CS:CPR blend but not in the CS:SLV blend. Compared with the original meal, by d 60, sinigrin content decreased 99.7% in CS:CPR and 99.4% in CS:SLV. Sinigrin was greater ($P < 0.01$) in CS:SLV compared with CS:CPR over time. Fat content as determined by ether extract was greater ($P < 0.01$) in the CS:CPR than in CS:SLV and CS. The pH decreased in all treatments over time but was greater in the blends. Acetic and lactic acids increased over time in all treatments. Acetic acid was less in the CS compared with the blends. Acetic acid was greater ($P < 0.01$) in CS:CPR than in CS:SLV. Lactic acid was less in CS:CPR. The CP was greater in both blends with CRM. Despite different fat contents, ensiling cold-pressed or solvent-extracted CRM with corn forage decreased sinigrin concentration without major detriment to silage fermentation.

Key Words: carinata meal, ensiling, glucosinolates

1432 Magnitude of difference in chemical and nutrient profiles, ruminal degradation kinetics, and intestinal digestion of three barley silages varieties in comparison with corn silage for dairy cattle. B. Refat*[1,2], W. Yang[3], J. J. McKinnon[4], J. Nair[1], A. D. Beattie[5], T. A. McAllister[6], D. A. Christensen[7], and P. Yu[1], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [2]Animal Production Department, Faculty of Agriculture, Zagazig University, Zagazig, Egypt, [3]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [4]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [5]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [6]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [7]University of Saskatchewan, Saskatoon, SK, Canada.*

Whole-crop barley (*Hordeum vulgare* L.) silage is the main forage source for dairy producers in western Canada. There are many varieties that are constantly being developed. However, there is limited knowledge on their nutritional quality. The main objective of this study was to assess the magnitude of difference among barley silage varieties in comparison with corn silage in terms of their 1) chemical composition and energy values, 2) protein and carbohydrates fractions, 3) rumen degradation kinetics, and 4) intestinal absorbed true protein supply to dairy cattle. The experiment was a complete randomized design with four treatments: corn silage (P7213R), CDC Cowboy barley silage, CDC Copeland barley silage, and Xena barley silage. Five cannulated lactating dairy cows were used for measuring the in situ rumen degradation kinetics. Intestinal digestibility of rumen undegraded feed protein was estimated

using a 3-step in vitro procedure. This study showed no significance difference in total carbohydrates (CHO; % DM) among the three varieties of barley silage. Corn silage showed a higher CHO when compared with barley silage varieties (82.6 vs. 78% DM; $P < 0.05$). Corn silage had the highest total digestible nutrient TDN_{1x} (71% DM) and energy content NEL_{p3x} (1.5 Mcal/kg DM), whereas Cowboy barley silage had the lowest NEL_{p3x} (1.3 Mcal/kg DM; $P < 0.05$). Studying the CNCPS system, predicted values showed no significant difference among the three barely silage varieties on rumen degradable of NDF RDCB3 (averaged 14% DM; $P > 0.10$) but Cowboy barley silage was lower in total rumen degradable of carbohydrates (TRDC) when compared with other barley silages varieties (32 vs. 38% DM; $P < 0.05$). Corn silage had the highest TRDC compared with all barley silage varieties (42.5% DM; $P < 0.05$). In terms of the in situ rumen degradation kinetics, Cowboy barley silage showed a significant high degradation rate Kd (%/h; $P < 0.05$). Cowboy and Copeland barley silages had higher effective degradability of CP, whereas Xena had an intermediate level and corn silage showed the significant lowest values ($P < 0.05$). The corn silage had the highest intestinal digestible protein (IDP), whereas Xena barley silage had the lowest values of IDP. In conclusion, among the three barley silages, Cowboy barley silage had the highest degradation rate of fiber and more effective degradability of protein when compared with the other barley silage varieties. Corn silage has a potential to be used as a good forage source in western Canada compared with barley silage.

Key Words: energy, ruminal degradation kinetics, silage

1433 Production of high-quality and digestible forages to increase milk production and nutrient supply for lactating dairy cows. J. P. Pretz*[1], C. Ramsier[2], and D. P. Casper[1], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Ag Spectrum, Inc., De Witt, IA*.

Two forage production programs based on soil amendments and foliar nutrition were used to produce corn silage and alfalfa haylage followed by a feeding study to evaluate the lactational performance of Holstein dairy cows. Thirty peak-lactation (58 DIM ± 2.9 and 38.9 kg/d milk ± 7.6) Holstein dairy cows (8 primiparous and 22 multiparous) were blocked by milk yield, DIM, and parity and randomly assigned to 1 of 2 treatments using a randomized complete block design. Treatments were 1) CONTROL, which is a normal forage (65%) ration formulated using alfalfa haylage and corn silage produced via standard soil and agronomy programs, and 2) TEST, which is the same forage inclusion rates (65%) using alfalfa haylage and corn silage produced on an enhanced soil (base saturations) and agronomy program (foliar applications). Cows were fed the CONTROL ration during the covariate period of 7 d followed by 12 wk of data collection when CONTROL and TEST diets were fed. Milk production was increased ($P < 0.04$) for cows fed TEST compared with cows fed CONTROL forage (32.6 and 36.9 kg/d for CONTROL and TEST, respectively, throughout results). Dry matter intakes (23.9 and 22.8 kg/d) were similar ($P = 0.46$). Milk protein (0.98 and 1.09 kg/d; $P < 0.04$), lactose (1.62 and 1.88 kg/d; $P < 0.04$), and total solids (3.77 and 4.25 kg/d; $P < 0.05$) yields were increased for cows fed TEST forages compared with cows fed CONTROL forages. Fat-corrected milk (4%) tended ($P < 0.09$) to be higher (33.6 and 39.0 kg/d) for cows fed the TEST forages compared with cows fed CONTROL forages. Energy-corrected milk was increased ($P < 0.05$) for the TEST-fed cows (33.0 and 36.8 kg/d). A decrease ($P < 0.01$) in ruminal butyrate percentage was found for cows fed the TEST diet. Ruminal propionate concentration ($P < 0.10$) and percentage ($P < 0.10$) tended to increase when cows were fed TEST forages. There was a trend ($P < 0.06$) for an increase in total tract starch digestibility for cows fed TEST forage compared with CONTROL-fed cows (97.9 and 98.4% digestible). Digestibility of NDF (48.5 and 54.7%; $P < 0.03$) and ADF (48.3 and 54.4%; $P < 0.03$) were increased for the TEST-fed cows compared with cows fed CONTROL forages. Feeding higher-quality forages obtained from enhanced agronomy procedures increased milk production, milk composition, and fiber digestibility when lactating dairy cows are fed a high-forage ration.

Key Words: dairy cattle, forage quality, high-forage diet

1434 Increased forage neutral detergent fiber digestibility (in vitro or in situ) is positively related to dry matter intake and milk yield both across and within forage type. D. Sousa*, M. J. VandeHaar, and M. S. Allen, *Michigan State University, East Lansing*.

Effects of laboratory measures of forage NDF digestibility (fNDFD) on DMI and milk yield (MY) were determined by meta-analysis using a database of 135 treatment means from 52 trials reported in 47 peer-reviewed articles published from 1979 through 2015. Trials must have been conducted comparing divergent fNDFD (measured in vitro or in situ) within the same forage type in experimental diets with cows past peak lactation (>60 d postpartum). Meta-analyses were performed with all forages together and also separated by forage type: alfalfa ($n = 29$), grass ($n = 22$), corn silage without BMR ($n = 26$), brown midrib corn silage (BMR; $n = 47$), and sorghum silage ($n = 11$). Data were analyzed by ANOVA including the random effect of trial, fixed effect of fNDFD, diet forage NDF, and their interaction as continuous variables. Treatment means were weighted by the inverse of their variance. Statistical significance was declared at $P \leq 0.05$ and a trend at $P > 0.05$ to $P \leq 0.10$, and the interaction of fNDFD with fNDF was kept in the model if $P \leq 0.30$. Enhanced fNDFD increased DMI and MY; a one-unit increase in fNDFD in vitro or in situ was associated with a 0.07 kg/d increase in DMI ($P < 0.01$) and a 0.08 kg/d increase in MY ($P < 0.01$) for all forages, a

0.07 kg/d increase in DMI ($P = 0.02$) and no effect on MY for alfalfa, a tendency of 0.08 kg/d increase in DMI ($P = 0.06$) and a 0.23 kg/d increase in MY ($P < 0.01$) for grass, 0.09 kg/d increase in DMI ($P = 0.04$) and a 0.20 kg/d increase in MY ($P < 0.01$) for all corn silage, a tendency of 0.13 kg/d increase in DMI ($P = 0.06$) and a 0.27 kg/d increase in MY ($P < 0.01$) for BMR corn silage, and a tendency of 0.06 kg/d increase in DMI ($P = 0.09$) and a 0.19 kg/d increase in MY ($P < 0.01$) for corn silage excluding BMR corn. The sorghum data included only 11 treatment means from 5 trials that showed a tendency of 0.12 kg/d increase in DMI ($P = 0.09$) and no effect on MY but, when combined with corn silages, resulted in a 0.12 kg/d increase in DMI ($P < 0.01$) and a 0.21 kg/d increase in MY ($P < 0.01$). Forage NDF digestibility is an important parameter of forage quality that is positively related to DMI and MY within or across forage families.

Key Words: fiber digestibility, forage quality, intake

1435 Lactation performance, in situ degradability, and rumen fermentation of Holstein cows fed BMR-6 sorghum silage versus corn silage based diets.

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The objectives of the study were to determine 1) the lactation performance, in situ degradability, and rumen fermentation of Holstein cows fed a bmr-6 sorghum silage (SS) vs. a leading non-bmr corn silage (CS) variety and 2) degradation kinetics of DM and starch from sorghum grain isolated from SS. In Experiment 1, four second lactation Holstein cows (578 ± 41 kg BW) in mid lactation, 101 to 113 DIM, were randomly assigned to diets containing SS or CS in a 2 × 2 crossover design with 14-d adaptation periods followed by 7-d collection periods. Cows were individually housed in open corrals (3.3 by 10 m) and fed once daily at 1000 h. Diets were formulated to supply 28% of the DM as each silage. Additionally, the diets were formulated to supply similar concentrations of NDF and total tract digestible starch, assuming 50% starch digestibility for SS. This was accomplished by replacing a portion of the steam-flaked corn (8% of diet DM) in the SS diet with 4% each of soy hull pellets and cottonseed hulls in the CS diet. All other dietary ingredients were similar between treatments. Milk production (32.6 vs. 31.4 ± 5.7 kg/d; $P > 0.725$) and percentages and yields of milk components did not differ ($P \geq 0.246$). In situ degradability of CS and SS were determined at 0, 6, 12, 18, 24, 36, 48, and 72 h. Cows fed CS had greater ($P \leq 0.001$) DM, OM, and NDF disappearances compared with cows fed SS at all incubation times. There was a treatment × time interaction ($P = 0.004$) for rumen pH recorded with greater pH at 1, 2, 3, 11, 12, 17, 23, and 24 h relative to feeding for SS. Total gas and methane produced from samples taken 3 h after feeding were greater ($P \leq 0.002$) for SS than for CS. The grain portion of SS was manually separated and ruminally incubated for 0, 3, 6, 12, 18, 24, 36, 48, and 72 h during Experiment 2. There were no differences ($P > 0.315$) between DM and starch disappearances of the sorghum grain until 18 h ($P \leq 0.001$). The DM disappearance continued to increase up to 72 h, but maximum starch disappearance, 55.7%, was reached at 18 h. Sorghum silage is an energy forage that may be used in lactating cow rations in areas where water availability may limit corn silage production; however, NDF and starch degradation should be improved.

Key Words: rumen, silage, sorghum

1436 Factors affecting methane production from ruminal fermentation of fiber isolated from dried distillers' grains and solubles.

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Ruminants produce more methane (CH_4) than any other livestock animal. Consequently, focus has been placed on developing mitigation strategies for ruminants in both the dairy and the beef industries. The objective of this study was to determine the effect of addition of fat or cellulose to fiber from dried distillers' grains and solubles (DDGS) on ruminal CH_4 production. Three representative samples of DDGS were obtained from different commercial biorefineries and NDF residue was isolated. The purified NDF residue was fermented 1) alone (control), 2) with feed-grade corn oil, or 3) with microcrystalline cellulose powder using the in vitro gas production technique. Both cellulose and corn oil were added along with NDF residue at a 4:1 ratio (DM basis). Inoculum was obtained by collecting a mixture of rumen fluid from two steers (BW = 543.3 ± 20.6 kg) consuming a diet containing 30% concentrate and 70% roughage. For each treatment within each run, gas production was measured in real time over a 48-h period. Using a paired but separate bottle, the concentration of CH_4 gas produced was measured using a gas chromatograph at 0, 4, 8, 18, 24, and 48 h. The volume of methane produced at each time point was calculated by multiplying total gas produced by the concentration of CH_4. Three separate runs ($n = 3$) were conducted and data were analyzed as a randomized complete block in which run and source of DDGS were considered random effects and treatment was considered a fixed effect. Compared with the control (74.0 ± 6.06 mL/g), addition of corn oil tended ($P = 0.11$) to reduce total gas production (58.0 ± 6.04 mL/g) whereas addition of cellulose increased ($P = 0.02$) gas production (85.7 ± 6.06 mL/g). Similarly, compared with the control (0.075 ± 0.0125 mL/g), the addition of corn oil tended ($P = 0.12$) to reduce CH_4 production (0.043 ± 0.0125 mL/g) whereas the addition of cellulose increased ($P = 0.02$) CH_4 production (0.099 ± 0.0125 mL/g). In an in vitro setting, the addition of oil or cellulose to NDF resulted in the decrease or increase of methane production, which suggests that dietary components can be used to mitigate methane in

ruminant livestock.

Key Words: gas production, in vitro, methane

1437 Effect of native and hybrid varieties of whole-plant corn silage on digestion in diets for cattle. L. Corona-Gochi*, *Universidad Nacional Autonoma de Mexico, Mexico City, Mexico*.

Whole-plant corn silage (WPCS) in many production systems is the main component of forage in the diets of cattle, due to its yield, cost, and nutritional quality. The objective of this study was to evaluate two native varieties (red and white) and two commercial hybrids ("A" and "B") commonly planted in the valley of Mexico on DM yield and nutrient digestibility in cattle through a metabolism trial. The corn was planted at a density of 80,000 plants/ha and row spacing of 0.8 m, harvested 135 d after sowing with chop length 2.17 inches, and stored in plastic bag silos (70 kg). Four bulls (489 kg average BW) were used in a 4 × 4 Latin square design on a diet containing 55.4% (DM) WPCS, with the following treatments: T1-red native (RN), T2- white native (WN), T3-A hybrid (AH), and T4-B hybrid (BH). Data were analyzed with the MIXED procedure in SAS and comparison of means by the following contrasts: RN vs. WN, AH vs. BH, and natives vs. hybrids. Dry matter yield was higher ($P = 0.04$; 18.6%) for native varieties than for hybrids (25.5 vs. 2,145 ton DM/ha, respectively), and total tract digestion (%) of DM (76–84 ± 8), OM (78–85 ± 7), NDF (73 to 79 ± 6), FDA (73 to 84 ± 11), starch (91 to 86 ± 6), nitrogen (61 to 75 ± 14), and DE (57 to 71) was higher ($P < 0.01$) for native varieties than for commercial hybrids. No differences ($P > 0.05$) between natives and between hybrids were observed. Digestibility was higher for native varieties than for hybrids for DM (7.4%; $P = 0.002$), OM (6%; $P = 0.003$), NDF (8.3%; $P = 0.003$), FDA (12.9%; $P < 0.001$), starch (5.9%; $P = 0.031$), N (15.6%; $P = 0.002$), and DE (16.5%; $P = 0.005$). Because the native varieties of corn plant showed higher DM yield and nutrient digestibility compared with the hybrids, they are advisable for planting and use in cattle diets.

Key Words: cattle, corn varieties, digestibility

1438 Evaluation of brown midrib sudangrass silage in the diets of lactating dairy cows. K. F. Kalscheur* and B. Geoff, *USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI*.

Forages that use less water but are high in digestibility are sought as alternatives to traditional forages such as corn silage. Brown midrib (BMR) sudangrass is a possible alternative that can provide high-quality forage as a replacement for corn silage. The objective of this study was to evaluate the replacement of corn silage and alfalfa silage with increasing concentrations of sudangrass silage in the diets of lactating dairy cows. Forty-eight Holstein cows in mid lactation were assigned to treatments in a randomized complete block design. Cows were fed a common covariate diet for 2 wk followed by 8 wk of experimental diets. Diets were formulated to contain 40% corn silage, 20% alfalfa silage, and 40% concentrate on a DM basis. Sudangrass silage was included in experimental diets at 0, 10, 20, and 30% of the diet DM. Proportionally, sudangrass silage replaced 2 parts corn silage and 1 part alfalfa silage. All other ingredients (high-moisture corn, canola meal, roasted soybeans, soyhulls, and minerals and vitamins) were included equally for all diets. Data were analyzed using MIXED procedures of SAS. Polynomial orthogonal contrasts were used to determine the effect of increasing BMR sudangrass silage in the diets of lactating dairy cows. Dry matter intake linearly decreased as sudangrass silage replaced corn silage and alfalfa silage ($P < 0.01$). Similarly, milk production decreased from 43.1 kg/d for cows fed 0% sudangrass silage to 39.2 kg/d for cows fed 30% sudangrass silage. Milk fat and lactose percentage were not affected by changes in forages; however, milk protein percentage was quadratically affected ($P = 0.02$). Yields of milk fat, protein, and lactose linearly decreased ($P < 0.05$) with increasing sudangrass silage. Similarly, energy-corrected milk (ECM) linearly decreased with increasing concentrations of sudangrass silage. Feed efficiency, defined as ECM/DMI, was not affected by changes in forage because milk production changes and DMI changes were the same. Although it was expected that increased digestibility of the BMR sudangrass silage would benefit the dairy cow, it is possible that the increased fiber in the sudangrass diets limited intake, resulting in a linear decrease in milk production.

Key Words: brown midrib sudangrass silage, dairy cows, forages

1439 Chemical composition and fermentation profile of corn silage ensiled for zero, thirty, ninety, or one hundred fifty days from corn treated with a foliar fungicide at different growing stages.

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Foliar fungicide application to the corn plant may reduce disease and provide developmental benefits to the crop. The objective of this study was to evaluate the effect of various applications of foliar fungicide on the nutrient composition and the energy and fermentation profile of corn silage ensiled for 0, 30, 90, or 150 d after harvest. Eight one-acre plots of corn were planted in April 2015. Treatments were replicated once and randomly assigned to one of the plots. Treatments were no foliar fungicide application (CON), one application of pyraclostrobin (Priaxor; BASF Corp.) foliar fungicide at corn vegetative growth stage V5 (V5), one application of pyraclostrobin and metconazole (Headline AMP; BASF Corp.) foliar fungicide at corn reproductive growth stage R1 (R1), and one application of pyraclostrobin foliar fungicide at V5 and one application of pyraclostrobin and metconazole foliar fungicide at R1 (V5/R1). At harvest, samples of the chopped corn silage were collected from each plot and immediately vacuum sealed. Corn silage ensiled for 0 d was frozen on the day of harvest, whereas corn silage ensiled for 30, 90, and 150 d was left in the vacuum-sealed bags for each respective time frame and frozen for later analysis. Statistical analysis was performed using the MIXED procedure of SAS. A treatment × time point interaction was observed for lignin ($P = 0.03$), water-soluble carbohydrate (WSC; $P = 0.02$) concentrations, and a tendency ($P = 0.07$) for VFA score. At 90 d of ensiling, R1 had lower lignin concentration (1.15 ± 0.21) than CON (2.55 ± 0.21), V5 (2.15 ± 0.21), and V5/R1 (2.55 ± 0.21) and higher concentrations of WSC (3.20 ± 0.49) than CON (2.45 ± 0.49), V5 (2.50 ± 0.49), and V5/R1 (2.60 ± 0.21). At 30 d of ensiling, CON tended to have a lower VFA score (8.18 ± 0.12) than V5 (8.92 ± 0.12), V5/R1 (8.73 ± 0.12), and R1 (9.05 ± 0.12). Corn silage from corn treated with foliar fungicide had improved chemical composition and fermentation and has the potential for increased milk production when fed to dairy cattle.

Key Words: corn silage, fermentation, foliar fungicide

1440 Chemical and energy profiles of value added pellet products based on combination of new coproducts from biofuel/bio-oil processing, low grade of peas, and lignosulfonate chemical compound at different levels for ruminants.

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The aim of this project was to test and develop eight high-value-added pellet products based on combination of coproducts from biofuel/bio-oil processing, low grade of peas, and lignosulfonate at different levels for ruminants. Statistical analyses were performed using PROC MIXED of SAS 9.3 with significance declared at $P < 0.05$. The results showed that BPP3 (high level of carinata meal, low level of peas, and no lignosulfonate), BPP4 (high level of carinata meal and low level of peas and lignosulfonate), and BPP7 (high level of canola meal, low level of peas, and no lignosulfonate) had the higher CP ($P < 0.05$), whereas both BPP3 and BPP4 also had the higher neutral detergent insoluble CP (NDICP; $P < 0.05$) and BPP6 (low level of canola meal and high level of peas and lignosulfonate) and BPP7 and BPP8 (high level of canola meal and low level of peas and lignosulfonate) had the higher acid detergent insoluble CP (ADICP; $P < 0.05$). BPP7 and BPP8 had the higher NDF, ADF, and ADL compared with the other blend pellet products ($P < 0.05$). Energy values using the NRC summative approach indicated that BPP1 (low level of carinata meal, high level of peas, and no lignosulfonate) and BPP6 (low level of canola meal and high level of peas and lignosulfonate) had the higher truly digestible nonfiber carbohydrate (tdNFC; $P < 0.05$); BPP3 and BPP4 had higher truly digestible CP (tdCP; $P < 0.05$); BPP1 was higher in truly digestible NDF (tdNDF; $P < 0.05$); and BPP7 and BPP5 (low level of canola meal, high level of peas, and no lignosulfonate) had the higher truly digestible fatty acids (tdFA; $P < 0.05$). However, BPP1 showed the higher level of total digestible nutrient (TDN; $P < 0.05$) and BPP1, BPP3, and BPP4 had the higher NE_L, NE_m, and NE_g ($P < 0.05$). In conclusion, carinata meal–based pellet products have more available protein (higher NDICP but lower ADICP) than canola meal–based blend pellet products. Canola meal–based blend pellet products have higher levels of NDF, ADF, and ADL than carinata meal–based pellet products. Pellet products based on carinata meal combined with peas has potential to be used as a good energy and good protein source compared with pellet products based on canola meal combined with peas.

Key Words: canola, carinata, lignosulfonate.

1441 Use of short-season hybrids may enable greater use of corn silage in western Canadian feedlot diets without decreasing animal performance.

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As a result of the overall trend for an increase in corn heat units and growing season precipitation in western Canada, early maturing corn hybrids are currently being introduced where previously barley silage (BS) was the main forage used in feedlot cattle production. We hypothesized that early maturing corn silage (CS) could replace BS in backgrounding (BKGN) feedlot cattle diets, and because of its greater starch content, dietary proportion of CS could be increased and duration of the BKGN phase could be extended without compromising animal performance. A total of 160 steers (mean BW ± SD: 272 ± 22.4 kg) were assigned to 16 pens and fed BKGN diets containing either 60% (DM basis) BS (CON) or 60 (60CS), 75 (75CS), and 90% CS (90CS; 4 pens/treatment) until they reached an average pen BW of 380 (SBKGN; 2 pens/treatment) or 430 ± 15 kg (LBKGN; 2 pens/treatment) in a split-plot design. All steers were finished (FIN diet; 9% CS, 86% barley grain, and 5% supplement) to an equal-BW end point (700 ± 15 kg LW). During BKGN and FIN, DMI, ADG, and G:F were measured for all pens. Carcass data were also collected. There was no BKGN diet × duration interaction ($P > 0.05$) for most of the production measures. As dietary CS content increased during BKGN, DMI and ADG decreased (quadratic, $P \leq 0.003$) and there was also a tendency ($P = 0.078$) for a decrease in G:F at the highest level of CS. However, the BKGN diet had no effect ($P > 0.05$) on DMI, ADG, and G:F during the FIN phase. Similarly, the BKGN diet had no effect ($P > 0.05$) on carcass traits including dressing percentage and quality grade. As expected, compared with SBKGN steers, LBKGN steers took longer (105 vs. 71 d; $P = 0.001$) to reach the end of BKGN target weight. As a result of their heavier weight at the beginning of FIN, LBKGN steers also had a higher DMI (11.6 vs. 11.0 kg/d; $P = 0.045$) and reached the FIN end point earlier (116 vs. 146 d; $P < 0.001$) than SBKGN steers. However, the duration of BKGN had no effect ($P > 0.05$) on carcass traits. In summary, inclusion of up to 90% CS in cattle diets fed over a short or long BKGN phase did not compromise production performance during FIN.

Key Words: backgrounding duration, corn silage, production performance

1442 In vitro starch and neutral detergent fiber degradability of corn silage hybrids.

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This study investigated in vitro starch and NDF rumen degradability of 5 corn silage hybrids: Hubner H5333RC3P, H6191RCSS, and H5222RC3P; Masters Choice MC 5250; and Healthy Herd Genetics 42HFC15. Three of these hybrids were rated as potentially high in starch degradability, whereas the other two, Hubner 5333 and Hubner 6191, were rated low to medium in starch degradability, respectively. Samples from a corn silage hybrid trial conducted in Centre County, PA, at The Pennsylvania State University's Russell Larson Research farm were ensiled (in triplicate) in sealed 2.5-kg-capacity plastic bags. Silages were moved to a −20°C freezer on d 0, 30, 60, 120, and 150 after ensiling and stored frozen for at least 30 d before analysis. Silage subsamples were dried at 65°C for 72 h, ground through a 4- (in vitro degradability) or 1-mm (NIR and chemical analyses) sieve, and analyzed for in vitro starch and NDF degradability in 2 commercial laboratories and one university laboratory. Seven-hour starch degradability was determined by in vitro incubation with ruminal inoculum (IVSD; 2 assays) and by NIR (2 assays). Silage samples were also analyzed for NDF degradability (NDFD) by 48-h in vitro incubation with ruminal inoculum (IVNDFD), for 30-h NDFD by NIR (NIRNDFD), and for total tract NDF digestibility by NIR (TTNDFD). IVSD varied from 65.1 to 68.3% and was not affected ($P \geq 0.50$) by hybrid. Starch degradability determined by NIR was higher than IVSD, 73 to 78%. IVSD clearly increased with increasing ensiling time ($P < 0.001$), from 58.3 and 66.0 (d 0) to 69.7 and 69.3% (d 150) for laboratories 1 and 2, respectively. The NIR analysis showed similar trends. Silage hybrids varied in NIRNDFD from 56.6 to 59.9% ($P = 0.001$), but there was no difference ($P = 0.15$) in IVNDFD due to hybrid. Hybrid also had no effect on TTNDFD. All procedures indicated decreased ($P \leq 0.002$) NDFD or TTNDFD with increasing ensiling time, particularly from d 0 (63.8%) to 30 (57.8%); for some hybrids, the decrease in NDFD reached 10 percentage units. In this study, IVSD was similar among corn hybrids and hybrid had no effect on IVNDFD. These data have to be confirmed in vivo. With all hybrids, IVSD clearly increased and NDFD decreased with ensiling time, particularly NDFD from d 0 to 30. The reason for the decrease in NDFD needs to be elucidated.

Key Words: corn silage, degradability, in vitro, neutral detergent fiber, starch

1443 Evaluation of use of heat-stable α-amylase for neutral detergent fiber contents by using cellulose standard in filter bags made from different textiles add starch in samples. T. N. P. Valente*[1], E. Detmann[2], and C. Batista Sampaio[3], *[1]IFGoiano, Posse, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil*.

The objective of this study was to evaluate the efficiency of using nylon textiles (50 μm), F57 (Ankom), and nonwoven textile (NWT; 100 g/m^2) on laboratory evaluation of NDF by using quantitative filter paper as purified cellulose standard (12.5 cm Ø; ashless with 0.0086% of ash and 96.53% of DM; code 050154; Vetec) by simulating composition of samples with additions of corn starch (Sigma S-5296; 91.62% DM). The quantitative filter paper was processed in a knife mill with a 1-mm screen sieve and the procedures for analyses of NDF contents were performed in a fiber analyzer (Ankom^{220}). The experiment was performed with additions of different ingredients into the filter paper: corn starch added at the levels of 15 or 50% of DM. The ratio 20 mg of DM/cm^2 of surface was followed. The treatment was based in the use or not of heat-stable α-amylase. The experiment was performed according to a completely random design using 3 textiles × 2 levels of starch × 2 using or not heat-stable α-amylase factorial arrangement. The recovery bias of NDF was NRF = (Mo − Me/Me) × 100, in which NRF = NDF recovery bias (%), Me = the expected mass of NDF or mass of cellulose standard (g), and Mo = the observed mass of NDF or the residue obtained after analysis (g). The bias estimates were obtained as described above based on assumption that the cellulose standard presents 100% of NDF. Statistical procedures were performed using by SAS. For type I error, 0.01 was adopted as the critical limit, using a Tukey–Kramer test. When heat-stable α-amylase was not used, the NDF contents were overestimated ($P < 0.01$) and presented similar biases for both starch levels. The biases varied from +3.89 to +9.88% observed for all types of filter bags. Such a pattern corroborates the interference of starch on laboratorial evaluation of NDF. The biases were generally lower for nylon than for F57 and NWT ($P < 0.01$) when 50% of starch was considered. The biases for both starch levels were not significant ($P > 0.01$) when α-amylase was used, which brings into evidence the removal of contaminant starch from insoluble residue. The use of F57 and NWT resulted in accurate estimates of NDF contents. For samples containing starch, use of heat-stable α-amylase is recommended in the evaluation of NDF contents. Thanks for financial support to IFGoiano, FAPEG, and CNPq.

Key Words: F57, nonwoven textile, nylon

1444 Production response of lactating cows to diets based on corn or forage sorghum silage harvested on two dates and supplemented with soybean meal or mechanically pressed cottonseed meal. J. K. Bernard*, S. Tao, and T. Smith, *University of Georgia, Tifton*.

A 6-wk randomized design trial with a 4 × 2 factorial arrangement of treatments was conducted to evaluate the production response of 48 lactating Holstein cows (140.9 ± 55.9 d in milk) to diets based on corn (CS) or forage sorghum silage (FS) harvested in the summer (S) or fall (F) and supplemented with either soybean meal (SBM) or mechanically pressed cottonseed meal (CSM). Corn was planted in April and harvested in July (CSS); a second crop was planted in August and harvested in November (CSF). Forage sorghum was planted in April, harvested in July (FSS), allowed to regrow, and harvested again in November (FSF). Ensiled forages provided 41.67% of the DM in the experimental diets. Approximately 19% of the total dietary N provided by SBM was replaced with CSM. Cows were fed a corn silage based diet for 2 wk before beginning the 4-wk experimental period. No differences ($P > 0.10$) were observed in DMI (23.6 ± 1.6 kg/d) or milk yield (35.0 ± 1.7 kg/d) among treatments. An interaction ($P = 0.03$) of forage source and protein supplement was observed for milk fat, which was lowest for CSF-CSM (3.09%) compared with the other treatments (3.64 ± 0.16%). Milk fat yield was greater ($P = 0.006$) for diets based on FS compared with diets based on CS (1.28 and 1.22 kg/d, respectively). No differences ($P > 0.10$) were observed in yield or concentration of milk protein, lactose, or SNF. An interaction ($P < 0.001$) was observed for efficiency of milk production, which was lowest for CSS-SBM (1.39) and CSF-CSM (1.39) compared with CSF-SBM, FSS-SBM, FSF-SBM, and FSF-CSM (1.54, 1.47, 1.48, and 1.58, respectively) but not different from CSS-CSM and FSS-CSM (1.44 and 1.44, respectively). Concentrations of milk urea N were lower for diets based on CS compared diets based on FS (8.50 and 11.50 mg/dL, respectively; $P < 0.001$) and for diets supplemented with CSM compared with diets supplemented with SBM (9.31 and 10.70 mg/dL, respectively; $P = 0.002$). Results of this trial indicate that diets based on CS or FS harvested in S or F can support similar performance and that CSM can be substituted for SBM without negatively affecting production.

Key Words: corn silage, forage sorghum, mechanically pressed cottonseed meal

1445 Commercial ground corn surface area is better related to rumen disappearance than geometric mean particle size. J. P. Goeser*[1,2], B. Beck[3], T. Koehler[4], D. Tanata[5], E. Reid[6], M. Kirk[7], and R. D. Shaver[8], *[1]University of Wisconsin, Madison, [2]Rock River Laboratory, Inc., Watertown, WI, [3]Witmers Feed and Grain, Columbiana, OH, [4]Landmark Cooperative, Cottage Grove, WI, [5]Medford Cooperative, Medford, WI, [6]Cooperative Feed Dealers, Conklin, NY, [7]Masters Choice, Anna, IL, [8]University of Wisconsin-Madison, Madison*.

Ground dry shelled corn is not uniform relative to animal performance. Geometric mean particle size (GMPS; μm) has been related to rumen digestion but research has evaluated only ground corns sized >700 μm GMPS. The industry has reduced GMPS to <400 μm in some cases. Furthermore, GMPS and standard deviation can be combined into a surface area measure (SA; cm^2). The objective of our work was to determine if GMPS or SA were related to rumen in situ starch disappearance (SD; % starch) for commercial dry ground shelled corns. Commercial dry, ground shelled corn ($n = 38$) samples were collected from feed mills in the Eastern and Midwestern United States. Samples were assessed for particle size by shaking eight sieves for 10 min, ranging from 2,000 μm to the pan, and determining percent weight retained on each. Geometric mean particle size and SA were determined using Kansas State University equations. Samples were assessed for starch (% DM) using the Hall 2008 AOAC procedure. Starch, GMPS, and SA mean and standard deviation were 70.6/3.2, 715/233, and 92.7/20.8, respectively. Three grams of corns were weighed into Ankom R510 bags (50-μm pores), soaked in warm water, and incubated for 0 or 7 h, in triplicate across three ruminally cannulated lactating dairy cows consuming a 60% forage, corn silage–based diet. After incubation, bags were rinsed in a commercial laundry machine, dried at 50°C for 24 h, and weighed to determine the DM disappearance. Residues were composited and starch was assessed. Corn SD at 0 (SD0) and 7 h (SD7) were determined as starch loss during incubation. The SD0 and SD7 (% starch) mean/standard deviation were 19.8/12.4 and 68.7/10.6, respectively, suggesting that a range in SD was achieved. Time point (class variable), starch, GMPS, and SA were related to SD using backward elimination and final model fit using Fit Model function within SAS JMP version 11.0. Geometric mean particle size and SA were not allowed within the same final model because GMPS is used within the SA calculation. The SA sum of squares was nearly 3 times that of GMPS (908 vs. 328), and hence only SA remained. Residual plots were assessed for normality. The final model exhibited $R^2 = 0.86$, SE = 10.3. Time, starch, and SA were ($P < 0.02$) related to SD, and time × starch showed a trend ($P < 0.06$). The parameter estimate for SA was 0.20 (SE 0.06). These observations suggest SA is better related to rumen starch disappearance than GMPS and should be considered by feed mills when evaluating ground corn and the top 15% SA here were >110 cm^2/g.

Key Words: corn, digestion, starch

1446 Effect of steam-flaked and ground corn with different particle size on dairy cow performance with high-concentrate diet. G. R. Ghorbani*, F. Ahmadi, and M. Haidary, *Isfahan University of Technology, Isfahan, the Islamic Republic of Iran*.

Eight midlactation Holstein cows were used to study the effect of steam-flaked and ground corn with different particle size on the performance of lactating cows with high concentrate. Cows were assigned to four treatments in a replicated 4 × 4 Latin square experiment. Cows were fed (ad libitum) a total mixed ration (36:64 forage:concentrate ratio, DM basis). The diets were different only in corn particle size. The treatments were ground corn with different particle size (mean particle size = 0.59, 0.68, and 0.82 mm, for treatments 1, 2, and 3, respectively) and steam-flaked corn for treatment 4 (density = 0.41 kg/L). Treatments had no effects on DMI, milk yield (MY), 3.5% fat-corrected milk (FCM 3.5%), milk protein, lactose, and SNF percentage. Milk fat percentage was significantly higher for cows receiving steam-flaked corn than for cows receiving treatment 1 and 2 diets (2.61, 2.48, and 2.70 vs. 2.75; $P = 0.003$). Rumen and urinary pH was greater for treatment 4 than for treatment 1, 2, and 3 (6.46 vs. 6.06, 5.92, and 6.05 [$P < 0.01$] and 8 vs. 7.93, 7.95, and 7.98, respectively). Feed efficiency (MY/DMI) was not affected by dietary treatments, whereas in treatment 4, 3.5% FCM/DMI was significantly ($P < 0.05$) higher than in treatment 1. Overall, these data indicate that ground corn with a mean particle size of 0.82 mm has effects similar to those of steam-flaked corn with 0.41 kg/L density.

Key Words: ground corn, Holstein dairy cows, particle size, performance, steam-flaked corn

1447 Effect of diastatic power and processing index on the feed value of barley grain for finishing feedlot cattle. G. O. Ribeiro Jr.*[1], M. L. Swift[2], and T. A. McAllister[1], *[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Hi-Pro Feeds, Okotoks, AB, Canada*.

The objective of this study was to assess the nutritional value of barley grain differing in diastatic power (DP; high vs. low, a malt trait) and processing index (PI; 75 vs. 85). One hundred sixty Angus × Hereford crossbred yearling steers (467 ± 38 kg; 144 intact; 16 rumen cannulated) were used in a complete randomized 2 × 2 factorial experiment. Steers were assigned to 16 pens, 8 of which were equipped with the GrowSafe system to measure individual feed intake. Cannulated steers (2 per pen) were randomly assigned to the 8 GrowSafe pens. Diets consisted of high- or low-DP barley grain (80.0% of diet DM) processed to an index of either 75 or 85% (PI). Ruminal pH in cannulated steers was measured over four 5-d periods using indwelling electrodes. Fecal samples were collected every 28 d from the rectum of each steer to assess digestibility using AIA as a marker. No differences ($P > 0.10$) in rumen pH were observed among cattle as measured by the indwelling pH meters. However, lower ($P < 0.05$) rumen pH was observed for steers fed low- as opposed to high-DP barley in rumen samples collected just before feeding and measured in the laboratory. Intake of DM and OM were not affected ($P \geq 0.24$) by DP but were lower ($P < 0.01$) with more severe processing (PI-75 vs. PI-85). Low-DP barley tended to exhibit higher ($P = 0.09$) total tract DM digestibility than high-DP barley. Steers fed PI-75 barley also had higher ($P = 0.06$) G:F and NE_g. Digestibility of DM, OM, CP, NDF, and starch was higher ($P < 0.05$) for PI-75 barley than for PI-85 barley. Low-DP barley increased ($P < 0.05$) carcass dressing percentage by 0.5% compared with high-DP barley, with a lower ($P = 0.06$) PI tending to increase rib eye area. Compared with high DP, steers fed low-DP diets had more ($P = 0.01$) total (41.7 vs. 19.4%) and severe liver abscesses (22.2 vs. 9.7%). Results suggest that although low-DP barley increased liver abscesses, differences in DP did not alter digestion or growth performance, but low-DP barley did improve dressing percentage. Barley with different DP responded similar to processing, with more intensive processing (PI-75) of barley improving starch digestion, feed efficiency, and NE_g without negatively affecting rumen pH.

Key Words: barley, beef cattle, malt traits, processing index

1448 Heating of ensiled high-moisture corn and aerobic loss of volatile organic compounds are delayed by inoculation with *Lactobacillus buchneri*. S. Qi, W. Rutherford, B. Smiley, B. Harman, and F. Owens*, *DuPont Pioneer, Johnston, IA*.

Volatile organic compounds (VOC) when combined with specific nitrous oxide air pollutants have been associated with smog. Volatile organic compounds are released from silage surfaces exposed for removal from storage and during feed mixing and delivery. Extent of loss of VOC depends on air exposure time and presumably is accelerated by silage heating. Inoculation of corn silage with *Lactobacillus buchneri* (LB) retards yeast growth and delays heating of corn silage exposed to air. This study was designed to measure effects of LB inoculation on heating and losses of VOC and DM from high-moisture corn (HMC). High-moisture corn from three different Pioneer hybrids was treated with 1×10^5 cfu LB/g wet material with a Pioneer brand LB inoculant or left untreated. Following treatment, samples were placed in triplicate PVC silos and allowed to ferment for 60 d. Following removal from storage, triplicate samples of each HMC were exposed to air in Honig adiabatic chambers with temperatures being continuously monitored. Wet silage samples were recovered after 24, 48, 72, 96, and 120 h of air exposure and a liquid extract was assayed for concentrations of specific VOC. Concentrations of ethanol, acetate, lactate, 2 propanediol (PD), and total VOC in fermented HMC were 0.5, 0.1, 0.8, 0.02, and 1.5% of DM for untreated HMC and 0.8, 0.5, 0.5, 0.04, and 2.0% of DM for LB-inoculated HMC, with LB silages being higher in total VOC and acetate ($P < 0.02$) but lower ($P < 0.02$) in lactate. Of the initial concentrations of total volatiles, ethanol, and lactate in fermented HMC, disappearance half-life during air exposure was shorter for control HMC (1.3, 1.4, and 1.1 d, respectively) than for LB-treated HMC (41, 11, and 300 d, respectively). Above and beyond this "hidden" loss of energy as volatiles, microbial metabolism during air exposure results in additional loss of DM. The DM lost during aerobic exposure was greater (4.92 vs. 0.3%; $P < 0.01$) for untreated HMC than for LB-treated HMC and time for silage temperature to increase by 1.7°C was shorter (55 vs. 150 h; $P < 0.01$) for control HMC than for LB-treated HMC. Results indicate that inoculation of HMC with LB postpones heating and retards release of VOC and DM from HMC. Through delaying the loss of VOC and increasing retention of DM during air exposure, inoculation of HMC with LB increased nutrient recovery from ensiled HMC.

Key Words: corn silage, *Lactobacillus buchneri*, volatile organic compounds recovery

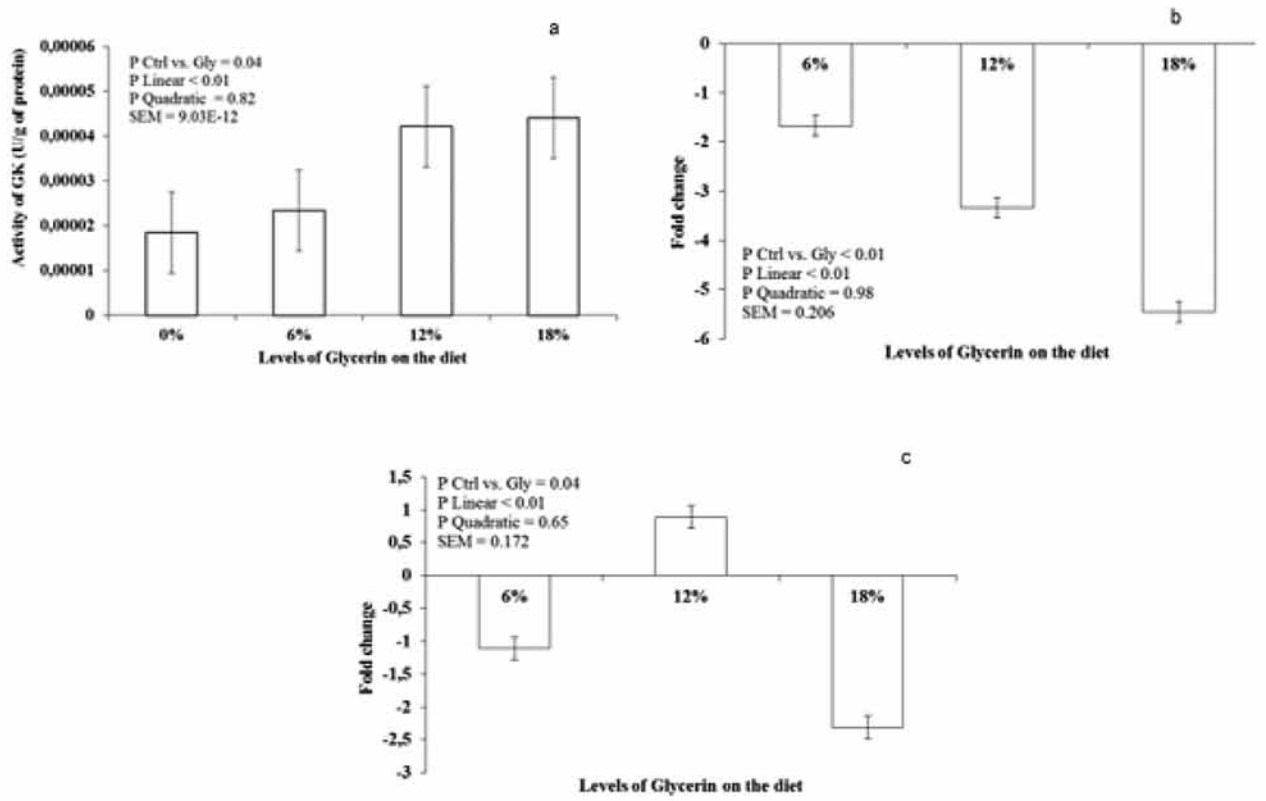

Figure 1449. Glycerol kinase activity (a), relative expression of *GK1* (b), and relative expression of *PCK1* (c) in the liver of young bulls fed with different crude glycerin concentrations.

1449 Liver gluconeogenesis in young bulls fed different levels of crude glycerin. M. M. Ladeira*[1], J. R. R. Carvalho[1], P. D. Teixeira[1], J. C. O. Dias[2], T. R. Gionbelli[1], A. C. Rodrigues[1], and D. M. Oliveira[3], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]IFNMG, Salinas, Brazil, [3]Universidade Estadual do Mato Grosso do Sul, Aquidauana, Brazil*.

This study aimed to evaluate gene expression of *glycerol kinase 1* (*GK1*) and *cytoplasmatic phosphoenolpyruvate carboxykinase* (*PCK1*) and glycerol kinase activity in the liver of young bulls fed different levels of crude glycerin. Forty-four crossbred young bulls (one-fourth Angus, one-fourth Nellore, one-fourth Senepol, and one-fourth Caracu), with initial BW of 368 ± 4 kg, were used in a completely randomized design, with four treatments (0, 6, 12, and 18% of crude glycerin in the diet, DM basis) and 11 replicates. Diets were formulated with corn silage as forage, and crude glycerin replaced ground corn. Corn gluten meal-21 was included in the diets with crude glycerin to provide similar levels of CP (13% CP). Immediately after slaughter of animals, liver samples were collected, frozen in liquid nitrogen, and stored in −80°C to analyze *GK1* and *PCK1* genes expression using RT-qPCR. In addition, same samples were used to measure glycerol kinase activity. Orthogonal contrasts were used to evaluate the linear and quadratic effects of glycerin and without-glycerin vs. glycerin diets. Liver glycerol kinase activity linearly increased ($P < 0.01$) following glycerin inclusion (Fig. 1a). On the other hand, the opposite results were detected on *GK1* and *PCK1* expressions (Fig. 1b and 1c, respectively). Expression of *GK1* in the liver was 1.61, 3.34, and 5.45 times lower when the animals were fed 6, 12, and 18% of crude glycerin, respectively, than in the liver of animals fed a diet without glycerin. Therefore, *GK1* expression was more affected by the diets than *PCK1*. In conclusion, the use of crude glycerin in feedlot diets downregulate the expression of *GK1* and *PCK1* and increases glycerol kinase activity in liver of young bulls.

Key Words: glycerol, glycerol kinase, *PCK1* gene

1450 Starch digestibility by lactating cows fed flint or dent corn silage stored two or six months before feeding. A. Laflotte[1], L. Aubry[2], B. Mahanna[3], and F. Owens*[3], *[1]U. Lorraine, Nancy, France, [2]DuPont Pioneer, Aussonne, France, [3]DuPont Pioneer, Johnston, IA*.

Starch availability from corn silage increases with duration of storage and is greater for grain from dent than from flint hybrids based on in situ or in vitro studies. This objective of this study was to determine the degree that starch digestibility by lactating cows changes during storage time from corn silages produced from one dent and one flint hybrid. Yields of DM for the dent and flint hybrid harvested and kernel processed from adjacent

1.1 ha plots in France on Oct 3 and Sep 26 at 41 and 37% DM were 16.1 and 15.1 t DM/ha, respectively; starch made up 32.5 and 27% of silage DM, respectively. Of ration DM, 53% was silage. Dietary energy levels were moderately low so that digestibility of starch from the silage could be accurately measured. Two groups of 10 lactating cows were fed each corn silage diet in a replicated crossover trial within periods that began 2 mo and again 6 mo after ensiling. Milk production and DMI were measured during 14-d periods of each segment. Fecal samples obtained from each cow on three nonconsecutive days during each segment were assayed for starch content. Milk yield, milk:intake ratio, and fecal starch concentrations all were greater ($P < 0.01$) 2 mo after ensiling, even though DMI was greater 6 mo after ensiling. Adjusted for differences in starch content of the diets, starch digestibility averaged 89 and 96% 2 mo after ensiling and 94 and 97% 6 mo after ensiling for the flint and the dent corn silages, respectively, increasing ($P < 0.05$) with silage storage time for the flint but not ($P = 0.66$) for the dent corn silage. After 6 mo of storage, starch digestibility was not different ($P = 0.17$) between the two corn silages. Averaged across periods, individual cows differed in starch digestibility being over 95.5% for 6 cows of the 20 cows but under 92% for 4 cows. Starch digestibility by individual cows was not correlated with parity, milk production, cow weight, or DM content of feces. In summary, when averaged across periods, total tract digestibility of starch was greater ($P < 0.02$) for this dent than this flint corn silage but tended to increase ($P < 0.07$) with duration of silage storage.

Key Words: corn silage, flint corn, starch digestion

1451 Ruminal in situ degradability and in vitro organic matter digestibility of peanut hulls under different incubation times with calcium oxide.

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Two experiments were conducted to evaluate the effects of calcium oxide (CaO) and different DM contents on ruminal in situ degradability and on in vitro OM digestibility (IVOMD) of peanut hulls (PH). In Exp. 1, PH were incubated in duplicate (2 consecutive years) in 20-L buckets following the treatments 1) as is, 2) 50% DM for 7 d, 3) 50% DM for 14 d, 4) 50% DM + 5% CaO for 7 d, and 5) 50% DM + 5% CaO for 14 d. After 7 or 14 d of incubation, bucket contents were dried and ground to pass a 4-mm screen. Ruminal in situ degradability of DM, OM, NDF, and ADF of PH, either treated or not with CaO, was determined by incubating nylon bags for 24, 48, and 72 h in duplicate, in 9 ruminally cannulated steers consuming bahiagrass hay. In Exp. 2, PH were incubated in 20-L buckets (2/treatment) following the treatments 1) 70% DM, 2) 70% DM + 5% CaO, 3) 50% DM, and 4) 50% DM + 5% CaO. Buckets were opened after 3, 6, 9, 12, and 15 d of incubation, when a representative sample was collected, dried, ground (2 mm), and incubated for 48 h to determine IVOMD. For Exp. 1, data were analyzed as a randomized complete block design, using bucket as the experimental unit. The model included the fixed effect of treatment and random effect of year. For Exp. 2, data were analyzed as a completely randomized design with repeated measures and the model included the fixed effects of DM content, CaO, incubation days, and their interactions. For Exp. 1, at all ruminal incubation time points, no differences ($P > 0.05$) were observed on in situ degradability of DM, OM, NDF, and ADF. For Exp. 2, no effect of DM content ($P = 0.64$), CaO ($P = 0.27$), or their interaction ($P = 0.33$) were observed; however, there was a CaO × day of incubation interaction ($P = 0.07$) where when CaO was added, IVOMD was greatest at 6 d of incubation, and up to 15 d of incubation, it decreased significantly. We conclude that treating PH with CaO was not effective at improving in situ ruminal degradability of nutrients. Moreover, regardless of moisture content, when PH was treated with CaO and incubated for more than 6 d, IVOMD was negatively affected.

Key Words: calcium oxide, digestibility, peanut hulls

1452 A comparison of Lacto-Whey to soybean meal in continuous cultures fed corn- or wheat-based diets.

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Lactate, a key intermediate in the fermentation of starch-based feeds, is either directly converted to propionate via acrylate by *Megasphaera elsdenii* or else is converted back to pyruvate and metabolized. In the latter process, more cellular carbon conversion into bacterial products should increase the assimilation of ammonia into bacterial nitrogen, primarily amino and nucleic acids. The effects of Lacto-Whey (LW), an ammonium lactate product, were investigated in dual-flow continuous culture systems ($n = 4$) using a 4 × 4 Latin square design. Lacto-Whey (+LW) was isonitrogenously dosed against soybean meal as a control (–LW) and factorialized with either a wheat- or a corn-based concentrate (formulated to have equal starch). Each individual continuous culture system was given 30 g of DM and their respective LW treatments in 2 equal feedings at 0800 and 2000 h (60 g/d). We hypothesized that the wheat +LW combination would increase propionate production while also increasing bacterial assimilation of ammonia. No differences ($P > 0.10$) were observed for total VFA or propionate production per day; however, the main effect of +LW tended ($P < 0.09$) to increase propionate at 1, 1.5, and 2 h after feeding. The main effect of corn increased

($P < 0.02$) the proportion of bacterial N derived from ammonia (as assessed using ^{15}N). No differences ($P > 0.10$) were observed in NDF or apparent OM digestibilities. Starch digestibility was moderately higher ($P = 0.09$) for corn than for wheat. To retain protozoa, the slower stirring speed probably sedimented grain and negated wheat starch from being more degradable than that from corn. An interaction between grain source and LW ($P < 0.05$) was explained by wheat without LW increasing lactate production but corn increasing lactate when combined with LW. Treatment × time interactions ($P < 0.05$) revealed higher lactate and total VFA concentrations in +LW treatments. Lactate in the LW dose disappeared by 1.5 h and was metabolized to propionate until 4 h. There were no treatment differences observed in the daily productions of methane and hydrogen, although the main effect of +LW numerically decreased methanogenesis. Under the conditions of this study, +LW supported microbial growth compared with soybean meal (–LW). Results are consistent with our expectation that Lacto-Whey should support lactate fermentation to propionate, thereby stabilizing ruminal fermentation.

Key Words: ammonium lactate, continuous cultures, starch source

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1453 Glucose precursor supplementation in Holstein and Jersey cows as a preventative treatment for ketosis in the transition period. K. E. Mitchell*, *UC Davis, Davis, CA*.

Glucogenic substances can help treat subclinical or clinical ketosis by lowering β-hydroxybutrate (BHBA) levels and raising glucose (Glu) levels. Subclinical ketosis is defined as BHBA ≥ 1.0 mmol/L and Glu < 60 mg/dL and clinical ketosis is defined as BHBA > 1.2 mmol/L and Glu < 60 mg/dL. The objectives of this study are to determine if supplementation with a glucose precursor powdered product (GP; Glucose Booster; Stuhr Enterprises, LLC) during transition would decrease subclinical or clinical ketosis and have an effect on health and milk production of multiparous Jersey and Holstein dairy cows. Holstein ($n = 106$) and Jersey ($n = 105$) cows at a commercial dairy were systematically enrolled into either a control (C; odd-numbered ear tags) or GP (even-numbered ear tags) treatments. Glucose precursor was top-dressed on the prepartum pen (PreP) TMR and postpartum pen (PPost) TMR at a rate of 300 g/cow per day and mixed in using a pushup tractor. Cows were then allowed access to the TMR. Daily feed samples were pooled weekly and sent to Analab (Agri-King, Fulton, IL) for nutrient analyses. Weekly blood samples were analyzed for Glu (mg/dL) and BHBA (mmol/L) using NovaMax (Nova Diabetes Care, Inc., Billerica, MA). Weekly milk samples were taken to approximately 21 DIM followed by monthly tests. Holstein ($n_{GP} = 52$ and $n_C = 54$) and Jersey ($n_{GP} = 53$ and $n_C = 52$) data was analyzed using the MIXED procedure of SAS (version 9.4; SAS Institute 2015) with repeated measures by cow, parity as a random effect and fixed effects treatment, previous lactation milk fat and protein yield, period of lactation, and DIM. Jersey cows did not show a response to treatment. Holstein cows supplemented with GP increased production by 4.05 kg/d milk yield ($P = 0.0011$), 0.22 kg/d fat yield ($P = 0.0002$), and 0.12 kg/d protein yield ($P = 0.0042$) while on treatment. After treatment, GP Holsteins' production was still greater than that of C Holsteins by 2.45 kg/d milk ($P = 0.0487$), 0.08 kg/d fat ($P = 0.17$), and 0.08 kg/d protein ($P = 0.055$) until 120 DIM. Total number of health events in the first 60 DIM for GP Holstein cows decreased ($N_{GP} = 32$ and $N_C = 44$) and incidence of clinical and subclinical ketosis decreased by 15%. Holsteins and Jerseys responded differently to treatment; therefore, different breeds face different issues during early lactation. Holsteins tend to have a difficult transition period and are more likely to benefit from GP. For Holsteins, supplementation with GP prevented ketosis, decreased health events, and increased milk yield and milk component production.

Key Words: ketosis, β-hydroxybutyrate, glucose

1454 Manipulation of lactating dairy cows diets using reduced-fat distillers' grains, corn oil, and calcium sulfate to reduce methane production measured by indirect calorimetry. J. V. Judy*[1], T. M. Brown-Brandl[2], S. C. Fernando[1], and P. J. Kononoff[1], *[1]University of Nebraska, Lincoln, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*.

A study using 16 multiparous (8 Holstein and 8 Jersey) (78 ± 15 DIM, mean ± SD) lactating dairy cows, was conducted to determine the effects of dietary manipulation on methane mitigation in dairy cattle. A replicated 4 × 4 Latin square design with 35-d periods (28 d of adaption and 7 d of collections) used to compare four different dietary treatments. Treatments were composed of a control (CON) diet, which did not contain reduced-fat distillers' grain plus solubles (RFDDGS), and treatment diets containing 20% (DM basis) RFDDGS (DDGS), 20% RFDDGS with 1.38% (DM basis) added corn oil (OIL), and 20% RFDDGS with 0.93% (DM basis) added calcium sulfate (CaS). Methane sampling was performed using indirect calorimeters (head boxes). Compared with CON, DMI was greater ($P = 0.030$) for DDGS but was not affected ($P > 0.05$) by either OIL or CaS. Milk production was lowest in CON ($P < 0.001$) compared with DDGS, OIL, and CaS (26.3 vs. 27.5, 28.3, and 27.6 ± 0.67 kg/d for CON vs. DDGS, OIL, and CaS, respectively). Compared with CON, fat-corrected milk was greater ($P = 0.007$) in RFDDGS and OIL (30.7 vs. 32.1, 32.4, and 31.2 ± 0.67 kg/d for the CON, DDGS, OIL, and CaS, respectively). The addition of DDGS did not affect ($P = 0.690$) total methane produced compared with the CON diet. However, the addition of CaS reduced ($P = 0.020$) methane production whereas the addition of OIL tended ($P = 0.177$) to reduce methane production compared with the CON diet (421.6, 429.5, 394.7, and 381.4 ± 14.41

L/d for CON, DDGS, OIL, and CaS, respectively). When expressed as methane per unit of fat-corrected milk, cows consuming OIL and CaS produced less methane ($P = 0.009$) compared with CON and DDGS (13.9, 13.6, 12.3, and 12.1 ± 0.49 L/kg per day for CON, DDGS, OIL, and CaS, respectively). Similarly, when expressing methane per unit of DMI, cows consuming OIL and CaS produced less methane ($P = 0.015$) compared with those consuming the CON diet (22.3, 21.4, 19.9, and 19.6 ± 0.75 L/kg per day for CON, DDGS, OIL, and CaS, respectively). Results of this study indicate that methane production may be reduced by feeding rations containing RFDDGS with added corn oil or calcium sulfate without adversely affecting milk production.

Key Words: dairy cows, dried distillers' grains and solubles, methane

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1455 Effect of particle size of a mash concentrate on behavior, rumen fermentation, and macroscopic and microscopic lesions of the digestive tract in Holstein bulls fed a high-concentrate diet.

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Twenty-four individually housed Holstein bulls (456 ± 6.9 kg of BW and 292 ± 1.4 d of age) were exposed to a 2 × 2 factorial design (ingredients ground with a hammer mill using a sieve size of 2 [HM2] or 3 mm [HM3] vs. the same sieve size for all ingredients exception for corn, which was ground using at 10 mm [HM210 or HM310]) to evaluate the effect of mash particle size in finishing diets. Concentrate (36% corn, 19% barley, 15% corn gluten feed, and 8.4% wheat; 14% CP and 3.28 Mcal/kg) consumption were recorded daily, straw consumption was recorded weekly, and animals were filmed weekly to register behavior. Bulls were slaughtered after 56 d of exposure to treatments. Digestive tract and liver lesions were recorded, and tissue samples were collected. Data were analyzed using an ANOVA. Mean meal particle size was 0.85 ± 0.01, 1.26 ± 0.06, 1.05 ± 0.08, 1.26 ± 0.05 mm and percentage of particles between 0.5 and 1 mm was 68 ± 2.9, 46 ± 1,7, 46 ± 5.0, and 39 ± 3.3% for HM2, HM210, HM3, and HM310, respectively. When ingredients were ground at 2 vs. 3 mm, bulls tended ($P = 0.07$) to perform less social behaviors (128 vs. 155 ± 10.1 min/d, respectively), whereas rumen papillae fusion and the percentage of rumens classified as dark decreased ($P < 0.05$) and the number of rumen papillae increased ($P < 0.05$). In addition, reducing sieve size from 3 to 2 mm tended ($P = 0.08$) to increase cecum total VFA concentrations. Moreover, when corn was sieved at 10 mm, time spent eating concentrate was lesser ($P < 0.05$) than when all ingredients were ground at 2 or 3 mm (81 vs. 63 ± 5.0 min/d, respectively). In the cecum, grinding corn at 10 mm tended ($P = 0.09$) to decrease crypt depth and to increase the acetate-to-propionate ratio. Straw intake was greatest with the HM210 treatment. Moreover, in the jejunum, papillae length and crypt depth, molar percentage of acetate, and pH, and in the cecum, molar percentage of butyrate and acetate were affected by a significant interaction ($P < 0.05$) between the main factors. In conclusion, the particle size of a mash in bulls fed high-concentrate diets modifies behavior and affects digestive tract macroscopic and microscopic morphology.

Key Words: behavior, bulls, digestive tract morphology, particle size of mash

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1456 Essential oils from three tropical *Citrus* species can reduce in vitro enteric methane production.

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The objective was to investigate the effects of essential oils from *Citrus sinensis* (SI), *Citrus limon* (LI), and *Citrus aurantifolia* (AU) on in vitro rumen fermentation, methane production, and digestibility of a total mixed ration (TMR). A TMR (0.5 g/sample) containing corn silage (28.5%), a ryegrass and triticale silage mixture (15.7%), and a corn–soybean–based grain mixture (55.8%) for dairy cows was treated with essential oils from SI, LI, or AU at doses of 0 (CON), 10 (Low), 20 (Med), and 30 mL/50 mL (High) of a rumen fluid–buffer inoculum (1:2 ratio) or with monensin (MON; 1.2 mg/g of TMR). Each treatment was incubated in triplicate in 120-mL gas-tight culture bottles at 39°C for 24 h. Each run was repeated thrice. Fermentation parameters, gas and methane production, and in vitro DM digestibility (IVDMD) were measured. Data for each essential oil were separately analyzed with the GLIMMIX procedure of SAS. Adding LI at Med and High doses increased IVDMD ($P < 0.05$) compared with MON (48.9 and 49.2 vs. 46.4% of DM, respectively) but had no effect compared with CON (48.9 and 49.2 vs. 48.1% of DM, respectively). All doses of SI and LI and Med and High doses of AU reduced ($P < 0.05$) methane production (mL/g of DMD). Compared with CON, gas volume (mL/g of DMD) was reduced ($P < 0.05$) by all doses of LI and by Med and High doses of AU. Ammonia N and total VFA concentrations and pH were unaffected by treatment. Compared with CON and MON, Med and High doses of LI and AU decreased ($P < 0.05$) molar proportion of acetate and increased ($P < 0.05$) that of propionate. Therefore, the acetate-to-propionate ratio was reduced ($P < 0.05$) by Med and High doses of LI (2.73 and 2.67 vs. 3.21 and 3.12, respectively) and AU (2.77 and 2.75 vs. 3.21 and 3.12, respectively) compared with CON and MON. Compared with CON, all doses of SI and LI as well as Med and High doses of AU reduced in vitro methane production

without reducing digestibility or total VFA concentration.

Key Words: citrus, essential oil, methane

1457 Enteric methane emissions from dairy cows fed a corn silage–based diet supplemented with increasing amounts of linseed oil.

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The objective of this study was to examine the effects of supplementing increasing amounts of linseed oil (LO) on intake, milk production, and enteric CH_4 emissions of dairy cows fed corn silage–based diets. Twelve lactating, multiparous Holstein cows (84 ± 28 d in milk and 42 ± 4.6 kg/d milk yield) were used in a replicated 4 × 4 Latin square design (35-d periods and 14 d of adaptation). Cows were fed ad libitum (5% orts, on an as-fed basis) a corn silage–based TMR (61:39 forage:concentrate ratio) not supplemented (control) or supplemented with 2, 3, or 4% LO (on a DM basis). Methane production was determined (3 consecutive days) using respiration chambers, and intake and milk yield were measured over 6 consecutive days. Data were analyzed using the MIXED procedure (SAS) and differences among treatments were declared significant at $P \leq 0.05$ using Dunnett's comparison test. Dry matter intake and energy-corrected milk (ECM) were not affected (23.5 and 33.1 kg/d, respectively) by supplementing LO at 2 and 3%, but they decreased (21.1 and 30.4 kg/d, respectively) when LO was added at 4%. Daily CH_4 emission averaged 515 g/d for cows fed the control diet and decreased by 8, 21, and 33% in cows fed 2, 3, and 4% LO, respectively. When adjusted for DMI, CH_4 emission averaged 21.7 g/kg for cows fed the control diet and declined in cows fed 2, 3, and 4% LO (19.7, 17.4, and 15.7 g/kg, respectively). When expressed per kilogram of ECM, CH_4 production was not affected by supplementing 2% LO (15.2 g/kg) but declined when LO was added at 3 and 4% (12.6 and 11.5 g/kg, respectively). Results of this study show that supplementing a corn silage–based diet with up to 3% of LO reduces enteric CH_4 production without adverse effects on DMI and milk production. However, a higher supplementation level (4%) impairs DMI and milk yield. These findings suggest that LO supplementation level should not exceed 3% (DM basis) in corn silage–based diets to mitigate enteric CH_4 without negatively affecting animal production.

Key Words: corn silage, linseed oil, methane

1458 Effect of different forages and concentrate levels on energy conversion, and enteric methane production of Holstein × Gyr heifers.

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The aim of this study was to evaluate the effect of diets containing corn silage (CS) or sugarcane (SC) with 30 or 50% of concentrate on energy conversion factors and methane production of Holstein × Gyr heifers. Sixteen Holstein × Gyr heifers with 12 ± 1.0 mo of age and average initial BW of 210 ± 20.2 kg were distributed in a completely randomized design using a 2 × 2 factorial scheme ($n = 4$), with two forages (CS or SC) and two levels of concentrate (30 or 50%) on a DM basis, during 112 d. For evaluation of energy losses, a digestibility assay was performed using the total collection of feces and urine over three consecutive days. The enteric CH_4 production was quantified by continuous analysis of regular samples of air excreted by the animals throughout the day, during six consecutive days. Greater ($P < 0.05$) CH_4 production as a function of DMI were observed for heifers fed SC-based diets. There was interaction ($P < 0.05$) between type of roughage and level of concentrate when CH_4 production was related to ADG and when expressed in relation to TDN, GE, and ME intakes. The increased level of concentrate in SC-based diets did not change ($P > 0.05$) CH_4 production in relation to TDN, GE, and ME intakes. Nevertheless, there was a reduction ($P < 0.05$) in CH_4 production related to ADG. The ratio between DE and TDN was influenced ($P < 0.05$) by type of roughage, and a greater ratio was observed for CS-based diets. The efficiency of the conversion from DE to ME was not influenced ($P > 0.05$) by variables analyzed in this study. However, the mean value observed in this study was above those proposed by the main systems of feed evaluation and nutrient requirements for ruminants. Therefore, we concluded that a greater inclusion of concentrate in SC-based diets can allow an improvement in CH_4 emissions per gain. The mean value suggested for the ME:DE ratio based on this study is 0.86.

Key Words: *Bos indicus*, calorimetry, methane

1459 Effects of duration of moderate increases in grain on bacterial diversity in the digestive tract of Holstein calves. S. Li[1], S. Moossavi[2], P. Azevedo[1], B. Schurmann[3], P. Gorka[4], G. B. Penner[5], J. C. Plaizier[1], and E. Khafipour*[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [2]Department of Medical Microbiology, University of Manitoba, Winnipeg, MB, Canada, [3]University of Saskatchewan,, Saskatoon, SK, Canada, [4]University of Agriculture, Krakow, Poland, [5]University of Saskatchewan, Saskatoon, SK, Canada*.

Feeding more grain to cattle alters the composition of digesta in the foregut and hindgut, including increasing its acidity, osmolality, and concentration of fermentable substrates. These changes may affect the composition and functionality of gut microbiota. In this study, effects of duration of grain feeding on the diversity of microbiota throughout the digestive tract were investigated in 25 Holstein steers (213 ± 23 kg; 5 to 7 mo of age). Animals received either a forage-based diet containing 92% hay and 8% of a mineral and vitamin pellet on a DM basis or a moderate-grain diet, obtained by replacing 41.5% percentage units of the hay in the forage-based diet with barley grain, for 7 or 21 d before slaughter. Immediately after slaughter, digesta samples were collected from the rumen, jejunum, ileum, cecum, colon, and rectum. Deoxyribonucleic acid was extracted from digesta samples and subjected to V4 sequencing of the 16S rRNA gene on an Illumina platform. Alpha-diversities of bacterial communities were calculated using various estimators. Differences in β-diversity of microbiota across treatments and time points were tested using permutational ANOVA. Across the digestive tract, the lowest α-diversity was observed in the ileum followed by the jejunum and rumen. The highest α-diversities were found in the cecum, colon, and rectum, with no differences among these three sites. Beta-diversity analyses showed that microbiota in the rumen, jejunum, and ileum were distinct ($P < 0.05$) and differed from those in the cecum, colon, and rectum ($P < 0.05$). Microbiota from the cecum, colon, and rectum were not distinct. Feeding the moderate-grain diet for 7 and 21 d reduced ($P < 0.05$) the richness of bacteria in rumen compared with feeding the forage-based diet during these periods. However, the moderate-grain diet did not affect these indices in the other sections of the digestive tract. Beta-diversity analysis indicated that the microbiota communities were altered in all sample sites on d 7 ($P < 0.05$) and did not change between d 7 and 21 of grain feeding. Overall, a moderate increase in the proportion of grain in the diet reduced bacteria diversity in the digestive tract of calves. The reduction occurred within 7 d after the increase in grain feeding and was maintained until 21 d after this change in diet.

Key Words: calf, grain, gut microbiome

1460 Muscle protein metabolism of growing Holstein × Gyr heifers. F. A. S. Silva*[1], S. C. Valadares Filho[2], L. N. Rennó[1], S. A. Santos[3], D. Zanetti[1], L. A. Godoi[1], M. V. C. Pacheco[1], H. M. Alhadas[1], P. P. Rotta[4], and L. F. Costa e Silva[4], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal da Bahia, Salvador, Brazil, [4]Colorado State University, Fort Collins*.

The aim of this study was to evaluate muscle protein metabolism of Holstein × Gyr heifers. Sixteen Holstein × Gyr heifers with an average age of 12 ± 1.0 mo and initial BW of 210 ± 20.2 kg were distributed in a completely randomized design using a 2 × 2 factorial scheme ($n = 4$), with two forages (corn silage or sugarcane) and two levels of concentrate (30 or 50%) on a DM basis, during 112 d. A total urine collection was performed from the 110th to the 112th day of the experimental period for quantification of 3-methylhistidine (3MH) excretion. Muscle protein metabolism was evaluated by the fractional synthesis rate (FSR), fractional degradation rate (FDR), and fractional accretion rate (FAR) of myofibril proteins. There was no interaction ($P > 0.05$) between type of forage and level of concentrate for any variable. Greater ($P < 0.05$) values for the daily excretion of 3MH, protein muscle gain, FSR, FDR, and FAR were observed for the animals fed 50% concentrate independent of forage type. Heifers fed sugarcane showed an increase in FSR and FDR with the increase in the concentrate level of approximately 54 and 53%, respectively. In the case of heifers fed corn silage–based diets, the increase in FSR and FDR was approximately 8 and 7%, respectively. This increase in concentrate level enabled animals consuming a sugarcane-based diet to reach protein turnover rates numerically similar to those animals consuming corn silage–based diets, even when it was associated with the inclusion of 50% concentrate. Therefore, the increase of 20% in concentrate levels using sugarcane-based diets is enough to raise the supply of nutrients and to provide a greater muscle growth in Holstein × Gyr heifers.

Key Words: dairy cattle, protein turnover, tissue deposition

1461 Effects of milk replacer feeding rate, egg yolk inclusion in milk replacer, and calf starter starch content on Holstein calf performance through four months of age. T. S. Dennis*, T. M. Hill, J. D. Quigley, F. X. Suarez-Mena, and R. L. Schlotterbeck, *Provimi North America, Brookville, OH*.

The objectives of this research were to evaluate milk replacer (MR) feeding rates, alternative protein sources in MR, and calf starter starch concentration and their effects on calf performance to 4 mo of age. Male Holstein calves (42.6 ± 1.2 kg BW; $n = 192$) were assigned at 3 d of age to 1 of 6 treatments in a randomized complete block design with a 2 × 2 × 2 factorial arrangement of treatments. Factors tested from d 0 to 56 (nursery) were low- or high-MR feeding rates, 0 or 10% inclusion of spray-dried egg yolks in MR, and low- or high-starch calf starter. Low MR rate was 0.66 kg DM fed for 39 d followed by 0.33 kg DM for 3 d. High MR rate was 0.87 kg DM fed for 5 d, 1.08 kg DM for 37 d, and 0.43 kg DM for 7 d. The MR contained 27.5% CP and 19.6% fat (DM basis) and starters contained 21.2% CP; low starch was a complete pellet with 10.2% starch and high starch was textured with whole corn and oats with 43.3% starch. From d 56 to 112 (grower), calves were randomly assigned to pens (4 calves/pen) maintaining MR rate and starch content while stratifying yolk treatments within pen. Starter was blended with chopped hay (5% of the diet) during the grower phase. Data were analyzed as repeated measures with calf (nursery) or pen (grower) as the experimental unit. Calf ADG, hip width, and BCS change were greater ($P < 0.05$) for calves fed high vs. low MR, 0 vs. 10% yolk, and high vs. low starch in the nursery. Starter intake was less ($P < 0.05$) for calves fed high vs. low MR, 10 vs. 0% yolk, and low vs. high starch. In the grower phase, calves fed low MR and high starch had the greatest ADG and hip width change compared with calves fed low MR and low starch, with other treatments intermediate ($P < 0.05$). Overall, calves fed high MR had 9% greater ADG and 4% greater hip width change than calves fed low MR, yet nutrient efficiency was similar, despite 80% more MR intake than calves fed low MR. Additionally, calves fed high-starch starter achieved 18% greater ADG and 17% greater hip width than calves fed low-starch starter overall, an over 2-fold greater response than the effect of MR feeding rate.

Key Words: calf, feeding rate, starch

1462 Effects of mineral and vitamin supplementation to pasteurized whole milk diets on growth and health of preruminant Holstein bull calves. D. Wood*[1], L. A. Krueger[2,3], M. Dehghan Banadaky[4], J. R. Stabel[5], M. A. Engstrom[6], D. C. Beitz[7], and R. Blome[1], *[1]Animix, Juneau, WI, [2]Agri-King, Inc., Fulton, IL, [3]Dep. of Animal Science, Iowa State University, Ames, [4]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, the Islamic Republic of Iran, [5]Infectious Bacterial Diseases Research Unit, National Animal Disease Center, Agricultural Research Service, USDA, Ames, IA, [6]DSM Nutritional Products, LLC, Parsippany, NJ, [7]Iowa State University, Ames*.

Our objective was to determine whether supplementation of vitamins and trace minerals (VTM), formulated to meet or exceed NRC requirements when added to pasteurized whole milk (PWM), increases challenge resolution and prevents intestinal macromolecular permeability after injection with bacterial lipopolysaccharide (LPS). Neonatal Holstein bull calves ($n = 24$) were randomly assigned to 1 of 4 dietary treatments. Calves were individually fed PWM diets for 15 d at a low (LM; 3.8 L) or high level (HM; 7.6 L) of daily intake and were supplemented (+) or not supplemented (–) with a commercial VTM premix (Animix, Inc.). No starter grain was offered. At d 13 of age, calves were subcutaneously injected with LPS of *Escherichia coli* (3 μg/kg of BW) and orally administered d-mannitol and lactulose to measure intestinal paracellular transport of macromolecules. Vitamins and trace mineral supplementation increased vitamin E in serum at d 7 compared with VTM(–) calves (2.22 ± 0.26 and 1.37 ± 0.17 μg/mL, respectively; $P < 0.05$), but vitamin E was not different among groups at the time of challenge. VTM(+) calves also demonstrated increased plasma Fe at 48 h after challenge compared with VTM(–) calves (1.11 ± 0.18 and 0.58 ± 0.08 μg/mL, respectively; $P < 0.05$). Copper (0.87 ± 0.06 and 0.72 ± 0.05 μg/mL; $P < 0.05$), Mg (19.1 ± 0.37 and 17.98 ± 0.41 μg/mL; $P < 0.05$), and P (82.7 ± 2.6 and 75.8 ± 2.4 μg/mL; $P < 0.1$) were greater in HM calves than in LM calves, respectively, throughout the study. Inflammatory acute phase protein haptoglobin was greatest in HM(–) calves ($P < 0.05$) on both d 13 and 15 (1,040.7 ± 305.4 and 782.6 ± 204.1, respectively), whereas differences in serum amyloid A and intestinal permeability were not detected. Average daily gain from d 1 to 13 was greater in HM calves than in LM calves (0.57 ± 0.03 and 0.45 ± 0.04 kg/d, respectively; $P < 0.05$) with no VTM effect. From d 13 to 15 (during LPS challenge), total gain was greater in HM(+) calves than in HM(–) calves (0.48 ± 0.04 and 0.39 ± 0.04 kg, respectively; $P < 0.1$). We conclude that VTM supplementation to PWM improved performance during challenge and affected Fe and vitamin E, whereas increased milk intake increased Cu, Mg, and P in plasma. Increased haptoglobin in HM(–) calves indicates decreased challenge resolution

when fed PWM not supplemented with VTM according to NRC guidelines.

Key Words: calf, pasteurized whole milk, vitamin E

1463 Effect of Axcelera-C on calf performance, intake, digestive development, and immune function during the first three months of life. M. Terré[1], F. Fàbregas[2], and A. Bach*[3], [1]*IRTA, Caldes de Montbui, Spain,* [2]*Department of Ruminant Production, IRTA, Caldes de Montbui, Spain,* [3]*ICREA, Barcelona, Spain*.

Ax Celera-C is a pellet based on whey concentrate and soybean meal (20% CP and 12% fat). Forty newborn Holstein female calves (40 ± 0.97 kg BW) were distributed in two feeding programs: 20 calves were offered Axcelera-C (AX) alone during the first 15 d of age and later on in combination (150 g/d Axcelera-C) with a concentrate until weaning, and 20 calves (CT) were fed the same concentrate throughout the study. Calves were fed the same milk replacer at the rate of 5 L/d at 12.5% DM concentration until 49 d age, when it was reduced to 2 L/d until weaning (56 d age). Chopped oat hay was offered ad libitum in a separated bucket. Animals were weighed weekly, and feed intake was recorded daily from 11 to 90 d of age. Humoral immunity was evaluated as the antibody response to a double injection of 0.5 mg of hen egg white lysozyme (HEWL) at 49 and 63 d of age. At weaning, rumen liquid samples and epithelium biopsies were obtained to determine pH and VFA concentration and to assess gene expression of *acat1*, *errfi1*, *hmgcs2*, *bpifa1*, and *trim40* as indicators of rumen epithelial growth, innate immunity, and inflammation. Data were analyzed using a mixed-effects model. Average daily gain was greater from 14 to 21 d of age in AX calves than in CT calves (0.50 and 0.35 kg/d ± 0.040, respectively). From 11 to 15 d of age, AX calves tended ($P = 0.10$) to have a greater DMI than CT calves (103 vs. 70 g/d ± 14.4, respectively), and as a result, the G:F was improved ($P < 0.05$) in AX calves in this period. When Axcelera-C was mixed with the starter feed, differences in DMI and performance disappeared for the remainder of the study. Primary and secondary responses to HEWL were similar in both treatments. Rumen pH and epithelium gene expression did not differ between treatments, but AX calves had greater ($P < 0.05$) rumen molar proportions of acetate and lower of propionate than CT calves at 56 d of age (60.1 and 19.5 vs. 55.5 and 24.1% ± 1.76, respectively). In conclusion, the use of Axcelera-C as a prestarter in young calves seems promising because it stimulates starter feed intake during the first 2 wk of life, but further research is needed to optimize the transition to a regular starter feed.

Key Words: calves, concentrate, performance

1464 Colostrum supplement feeding with a medium-quality bovine colostrum: Passive immunity transfer, health, and performance of dairy calves. M. R. De Paula, N. B. Rocha, E. Miqueo, F. L. M. Silva, T. Manzoni, S. Baldassin, and C. M. M. Bittar*, *University of Sao Paulo, Piracicaba, Brazil*.

The aim of this study was to evaluate the transfer of passive immunity, performance, and health of Holstein calves fed colostrum supplement associated with a medium-quality colostrum. After birth, 44 newborn male calves were blocked according to birth weight (BW) and date of birth and distributed in the following treatments: 1) 15% BW of high-quality colostrum (70.6 mg immunoglobulin/mL; $n = 15$; BW = 39.2 kg), 2) 15% BW of medium-quality colostrum (42.7 mg immunoglobulin/mL; $n = 14$; BW = 38.0 kg), and 3) medium-quality colostrum (41.7 mg immunoglobulin/mL; $n = 15$; BW = 39.1 kg) + colostrum supplement (Feedtech Colostrum Supplement; DeLaval, São Paulo, Brazil). Colostrum was fed within the first 12 h of life in two meals. For calves receiving the colostrum supplement, the product was supplied with the two colostrum meals in a dose of 15 mL each. Blood samples were taken every 12 h up to 48 h of life. Calves were individually housed, with free access to water and concentrate, and fed 6 L of milk replacer daily (12.5% solids, 21% CP, and 15% fat and 0700 and 1800 h), up to the sixth week of life, when they began to receive 4 L/d until weaned with 8 wk. Colostrum feeding protocol affected the total serum protein concentration at the first 48 h of life ($P < 0.05$), whereas the concentrations of albumin, γ-glutamyl transferase, and alkaline phosphatase were not affected during the same period ($P > 0.05$). Colostrum feeding protocol did not affect the fecal score, the number of days with diarrhea, days with fever, and days of needed rehydration ($P > 0.05$); however, animals that received high-quality colostrum were treated for a shorter number of days ($P < 0.05$). The concentrate intake and total DMI were not affected by colostrum supplement ($P > 0.05$) and increased over the weeks ($P < 0.0001$). Body weight, weight gain, feed efficiency, and growth measures were not affected by supplement ($P > 0.05$), although there was an age effect ($P < 0.0001$). The total serum protein concentration during the liquid-feeding phase was higher for animals receiving high-quality colostrum when compared with animals receiving medium-quality colostrum ($P < 0.05$). However, concentrations of albumin, glucose, and β-hydroxybutyrate were not affected ($P > 0.05$). Feeding the colostrum supplement associated with the medium-quality maternal colostrum did not affect the transfer of passive immunity, performance, or metabolism of animals during the liquid-feeding phase.

Key Words: blood parameters, colostrum supply, diarrhea, immunity, immunoglobulin Y

1465 Thermoregulation, performance, and blood metabolites in calves fed different amounts of colostrum. F. L. M. Silva*, M. D. Silva, E. Miqueo, N. B. Rocha, T. Manzoni, M. G. Coelho, and C. M. M. Bittar, *University of Sao Paulo, Piracicaba, Brazil*.

Colostrum is an important immunity supply that protects calves against infectious diseases. Additionally, colostrum is an excellent energy source for thermogenesis for the newborn calf. However, the amount of colostrum required to promote heat is not well established. The objective of this study was to evaluate the newborn thermoregulation, performance, and blood metabolites in calves fed different amounts of colostrum. Thirty newborn Holstein male calves were blocked by birth weight (BW) in a randomized experimental design and fed high-quality colostrum in 3 different volumes: 10, 15, and 20% of BW. The colostrum intake occurred immediately after birth and 6 h after the first colostrum feed, totaling the treatment. At 24 h of life, each calf was placed in a temperature-controlled chamber at 10°C, for 150 min. Rectal temperature, skin surfaces temperatures, heart and respiratory frequency, and shivering were measured every 15 min, and blood samples were taken every 30 min. After challenge, calves were individually housed, with free access to water and starter concentrate (20% CP and 80% TDN), and received 6 L/d of milk replacer (Sucelac; Agroceres; 21.6:15.5 and 12.5% solids) until the eighth week of life, when weaned. Data were analyzed as repeated measures over time by using the MIXED procedure (SAS Inst. Inc.). Feeding colostrum to newborn at 15 or 20% of their BW tended to increase ($P = 0.06$) the rectal temperature during cold challenge (37.7, 38.1, and 38.0°C). However, there were no effects on skin surfaces temperatures ($P > 0.05$). During challenge, feeding higher volumes of colostrum did not affect blood metabolites but tended to decrease ($P = 0.07$) plasma lactate concentration (46.7, 45.0, and 34.6 mg/dL). There was no difference ($P > 0.05$) among colostrum volume for shivering behavior. Concerning performance, there were no effects on growth ($P > 0.05$), but feeding colostrum at 15 or 20% of their BW increased ($P \leq 0.05$) heart girth (84.1, 86.9, and 86.6 cm). There were no effects ($P > 0.05$) on DMI and blood metabolites. As animals were growing, all parameters were significantly affected by age ($P \leq 0.05$); however, there were no treatment and age interaction effect ($P > 0.05$). Feeding newborn calves colostrum at 15 or 20% of their BW can increase thermoregulatory responses in newborns and improve some growing features during the liquid-feeding period. Supported by FAPESP.

Key Words: blood parameters, cold challenge, weight gain

1466 The effects of supplementing a ruminally protected B-vitamin complex on preweaning growth and performance of Holstein heifer calves. K. M. Wood*[1], E. Evans[2], C. L. Girard[3], H. Leclerc[4], L. Doepel[5], and G. B. Penner[6], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, [2]Technical Advisory Services, Bowmanville, ON, Canada, [3]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [4]Jefo Nutrition, St. Hyacinthe, QC, Canada, [5]University of Calgary, Calgary, AB, Canada, [6]University of Saskatchewan, Saskatoon, SK, Canada*.

For preweaned dairy calves, incomplete rumen development may limit microbial B vitamin synthesis, resulting in a mild B-vitamin deficiency. Seventy Holstein heifer calves were used to evaluate the effect of providing a B-vitamin supplement in the starter on DMI, growth, and blood parameters. Calves were individually housed and fed in 1 of 3 rooms (block) until weaning at 9 wk of age. Dietary treatments were 13 g/d commercially available palmitic acid (CON; $n = 35$) or ruminally protected B vitamins (ProB; $n = 35$), in which 5 g of a B-vitamin supplement was blended with 8 g of palmitic acid. Treatments began at 1 wk of age. The 13 g of supplement was mixed with 50 g of calf starter and fed once per day. Once the calves consumed the supplement, they were offered calf starter ad libitum. Heifers were also fed 600 g of milk replacer (150 g/L water) divided into 2 feedings. After 7 wk, milk replacer was reduced to 300 g/d and calves were weaned at the end of wk 9. Calf BW and hip and rump height were measured on a weekly basis. Blood samples were collected on d 2 and 63 and analyzed for total protein concentration and platelet, white blood cell (WBC), and red blood cell (RBC) counts. Data were analyzed as a completely randomized block design with the mixed model using fixed effects of block, treatment, time, and their interaction. Regression was used to calculate growth traits. Calf ADG was 0.71 kg/d for both treatments (SEM = 0.017, $P = 0.84$). Hip and wither heights and ADG did not differ ($P \geq 0.77$) between treatments. There were no treatment differences ($P = 0.94$) for supplement intake or total DMI (CON = 933.8 kg/d and ProB = 967.2 kg/d; SEM = 40.5, $P = 0.56$). Final blood platelet count was 484.3×10^9/L for CON and 551.5×10^9/L for ProB (SEM = 22.5) and was greater in ProB than in CON ($P = 0.035$); however, final WBC and RBC did not differ ($P \geq 0.23$). These data indicate that supplemental ruminally protected B vitamins do not affect preweaning calf growth. However, supplementation may have implications on immune function, which may have implications for overall calf health.

Key Words: B vitamins, calf, preweaning

1467 RNaseq-based whole transcriptome analysis in the jejunum of preweaned calves under different milk feeding regimes. H. M. Hammon[1], D. Frieten[2], C. Gerbert[3], C. Koch[3], G. Dusel[2], R. Weikard[1], and C. Kühn*[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]University of Applied Sciences, Bingen, Germany, [3]Educational and Research Centre for Animal Husbandry, Hofgut Neumuehle, Muenchweiler, Germany*.

An early dietary nutrition plan in calves is crucial for later appropriate heifer and cow performance. However, there is controversy about the appropriate milk supply during the first weeks of life. Currently, there is only limited knowledge about the genomewide expression pattern for the juvenile intestine. Therefore, we performed a next-generation-sequencing–based holistic whole transcriptome analysis of the jejunum in male German Holstein calves fed two different diets. Calves received colostrum for 3 d and then milk replacer (MR; 125 g powder/L). For one group of calves, MR was restricted to a volume of 6 L MR ($n = 6$), whereas the alternative group was fed on an ad libitum protocol for 8 wk ($n = 6$). Subsequently, MR intake for all calves was reduced to 2 L/d from wk 8 to 10 and maintained at this level until the end of the trial. During the entire experiment, both groups were provided hay and concentrate ad libitum. Eighty-one days after birth, the calves were euthanized, and epithelial sections of the jejunum were collected, snap frozen in liquid nitrogen, and stored at −80°C until further analyses. Total RNA was isolated with specific attention to avoid genomic DNA contamination. For each sample, an indexed, stranded sequencing library was prepared including a polyA bead-based selection step. Libraries were sequenced in a 2 × 80 bp paired-end protocol on an Illumina HiSeq2500. After demultiplexing, reads were trimmed for quality and adaptor sequences. The reads passing quality control were aligned to the bovine genome, and transcripts were assembled with an annotation-guided approach enabling discovery of yet-unannotated genes and transcripts. Differential expression between calf groups was analyzed based on expression normalized on total number of reads and length of the respective genes. On average, 56.8 million paired-end reads were obtained per sample, and the average percentage of reads mapping to the bovine genome was 88%. Between 18,395 and 20,904 genes per sample could be identified after applying a threshold of 10 read counts per gene. The number of novel transcripts amounted to 16,378. Applying a threshold of $q < 0.1$, which accounted for multiple testing, 99 genes showed a differential expression between groups. Among those, 22 were without previous annotation in the bovine genome. Our analyses provide the first comprehensive catalog of RNaseq-based whole transcriptome for the calf jejunum. Furthermore, our data prove persistent effects of differential milk diets on the jejunal gene expression pattern.

Key Words: calves, milk feeding, trancriptome

1468 Comparison of two calf-rearing programs on the performance and cost–benefit ratio. L. M. Gomez*, J. A. Henao, A. K. Amorocho, M. R. Valenzuela, C. Mesa, and P. Aguirre, *Nutri-Solla Group, Research and Development Unit, Solla S.A., Medellin, Colombia*.

There is a deep interest in assessing different kinds of calf rearing programs based on greater rates of liquid feeding to increase ADG and to decrease age at first calving. In a complete randomized design with repeated measures, two milk feeding plans (treatments) were evaluated in 57 Holstein female dairy calves (37.3 ± 3.7 kg BW and 3 d old) during 10 wk. Treatment 1 (T1) consisted of feeding 12% of weight at 3 d in whole milk and treatment 2 (T2) a consisted of a step-down program of 20 (from 0 d to 2 wk), 15 (3–4 wk), and 10% (5–10 wk) of weight at 3 d in whole milk. Calves were fed colostrum (IgG; 100 mg/mL) at 30 min of life and after that, they were left with the cow suckling ad libitum until 3 d of life without access to solid feed. Calves were housed in individual hutches with ad libitum access to T1 ($n = 28$) and T2 ($n = 29$). From the third day, calves were offered pelleted starter feed (173.1 g CP, 460.1 g NSC, and 201 g NDF per kilogram DM) in the morning at 0700 h. Water was offered ad libitum. The calves were weaned when the intake of the starter feed was over 1.000 g/d during three consecutive days, from Day 1 to 4 after weaning half of the milk amount was given and since 5 d without milk. Body weight, DMI, ADG, days to weaning (DW), feed:gain ratio, total protein and energy intake, chest girth (CG), height at withers (HW), height at sacrum (HS), and total cost of production were measured. No differences were found ($P > 0.05$) on BW, CG, and HW and HS changes during the 10 wk among treatments. At the end of the trial, no differences were detected ($P > 0.05$) in BW, ADG, DW, concentrate DMI and feed:gain ratio, CG, and HW and HS. Calves fed T2 tended ($P = 0.11$) to have greater total DMI and protein DMI (79.6 and 19 kg) than calves fed T1 (73.7 kg and 17.6 kg). Calves fed T2 had greater ($P < 0.05$) milk DMI, ME of DMI, and cost of production (33.3 kg, 341.5 Mcal, and 105.4 USD) than calves fed T1 (28.7 kg, 312.2 Mcal, and 93 USD). Feeding with a step-down program having more milk does not support improvements of performance and increases the average cost of production.

Key Words: calves, cost–benefit ratio, performance, weaning

Table 1469.

Table 1. Growth performance, ruminal fermentation, and digestibility of weaned calves feeding different forage combination

Items	AH	OH	WS	Items	AH	OH	WS
Growth performance				Ruminal fermentation			
DMI, kg/d	2.78	2.75	2.91	Acetate acid, %	64.95	64.99	65.69
Body weight, kg	112.51^{a}	114.61^{a}	109.65^{b}	Propionate acid, %	20.45^{b}	19.55^{c}	21.76^{a}
ADG, kg/d	0.93^{a}	1.00^{a}	0.89^{b}	Butyric acid, %	6.92^{b}	7.38^{a}	4.97^{c}
G/F, %	33.45	36.36	30.58	Acetate/propionate	3.18^{b}	3.33^{a}	3.02^{c}
Heart girth, cm	11.73^{b}	12.83^{a}	11.80^{b}	TVFA, mmol/L	60.97^{b}	64.95^{a}	48.39^{c}
Digestibility				Protozoal protein, mg/Ml	2.35^{a}	2.54^{a}	2.03^{b}
CP digestibility, %	71.29^{b}	73.00^{a}	69.95^{c}	Bacterial protein, mg/Ml	2.00^{ab}	2.08^{a}	1.92^{b}
P digestibility, %	69.56^{ab}	70.95^{a}	66.98^{b}	Microprotein, mg/mL	4.35^{a}	4.62^{a}	3.96^{b}
Diarrhea frequency, %	25.90	12.76	20.57				
Diarrhea rate, %	45.33	21.33	33.33				
Feces index	1.89	1.45	1.63				

AH – 100% alfalfa hay, OH – 66.7% alfalfa hay + 33.3% oat hay, WS – 66.7% alfalfa hay + 33.3% whole corn silage.

a, b – different superscript letters with the same row represent a significant difference between treatments (P<0.05).

1469 Effects of different forage combination on growth performance, ruminal fermentation, and digestibility of weaned calves. Y. Zou*, X. Zou, Z. J. Cao, Y. Wang, and S. L. Li, *State Key Laboratory of Animal Nutrition, Beijing Engineering Technology Research Center of Raw Milk Quality and Safety Control, College of Animal Science and Technology, China Agricultural University, Beijing, P. R. China*.

The effects of feeding different forage combinations on growth performance, ruminal fermentation, and digestibility were investigated in weaned calves for 35 d. Forty-five female calves weaned at 60 d with similar weight were randomly arranged into three treatments 1 wk after weaning with same pellet feed (60% of the diet); forage combinations were 1) 100% alfalfa hay (AH), 2) 66.7% alfalfa hay + 33.3% oat hay (OH), and 3) 66.7% alfalfa hay + 33.3% whole corn silage (WS). There was no significant difference (P > 0.05) among the three treatments with weaned calves in DMI. However, the BW and ADG of calves fed AH and OH were significantly higher (P < 0.05) than WS calves, with higher heart girth in OH calves (P < 0.05). Proportion of butyric acid, ratio of acetate to propionate, total VFA concentration, protozoal protein, bacterial protein, and microprotein in rumen were highest in OH (P < 0.05), AH was intermediate, and WS was lowest. Oat hay feeding increased CP and P digestibility (P < 0.05) and decreased diarrhea frequency, diarrhea rate, and feces index at the mean time. In conclusion, a forage combination of alfalfa hay and oat hay had certain advantages to promote the ruminal development of calves and reduce feed cost and diarrhea incidence. Based on this study, a feeding pattern of "26.67% alfalfa hay + 12.33% oat hay + 60% starter feed" is more suitable for 3-mo weaned calves.

Key Words: oat hay, ruminal fermentation, weaned calves

1470 Use of the Brix refractometer to evaluate milk replacer solutions for calves. H. K. Floren*[1], W. M. Sischo[1], C. Crudo[1], and D. A. Moore[2], *[1]Washington State University, Pullman, [2]Department of Veterinary Clinical Sciences, Washington State University, Pullman, WA*.

The Brix refractometer is used on dairy farms and calf ranches for several reasons including evaluation of colostrum quality (estimation of IgG concentration), estimation of serum IgG concentration in neonatal calves, and nonsalable milk evaluation of total solids for calf nutrition. Another potential use is to estimate the total solids concentrations of milk replacer mixes as an aid in monitoring feeding consistency. The purpose of this study was to evaluate the use of Brix refractometers to estimate total solids in milk replacer solutions. Five different milk replacer powders were mixed to achieve total solids concentrations from approximately 5.5 to 18%, for a total of 90 different solutions. Both digital and optical Brix refractometers were used to compare with total solids. The two types of refractometers' readings correlated well with one another (R^2 = 0.997). The Brix readings were highly correlated with the total solids percentage (R^2 = 0.94). A value of approximately 1.08 to 1.47 would need to be added to the Brix reading to estimate the total solids in the milk replacer mixes. Osmolality was correlated to the Brix reading but the relationship was different depending on the type of milk replacer. The Brix refractometer can be successfully used to estimate total solids concentration in milk replacer mixes to help monitor milk replacer feeding consistency.

Key Words: calf, milk replacer, refractometer

1471 Effect of corn wet distillers' grains inclusion in growing diets on backgrounded cattle performance. M. Arcieri*[1], P. Davies[2], D. Méndez[2], J. Elizalde[3], and I. Ceconi[2], *[1]Universidad Nacional de Córdoba, Córdoba, Argentina, [2]Instituto Nacional de Tecnología Agropecuaria, General Villegas, Argentina, [3]Private consultant, Rosario, Argentina*.

Distillers' grains (DG) can be used as energy as well as protein dietary sources. An experiment was conducted to evaluate the effect of partially replacing dry-rolled corn (DRC) and sunflower meal (SFM) with corn wet DG (WDG) in growing diets on cattle performance. One hundred ninety-two Angus calves (199 ± 3 kg initial BW) were assigned by weight to 1 of 3 blocks and group housed in 1 of 24 pens. Pens were randomly assigned to 1 of 4 diets containing (DM basis) 0% WDG, 19.4% DRC, and 20.4% SFM (CON); 10.0% WDG, 13.9% DRC, and 15.9% SFM (10-DG); 20.0% WDG, 8.0% DRC, and 11.8% SFM (20-DG); or 35.0% WDG, 0% DRC, and 4.8% SFM (35-DG). All diets contained 58.2% sorghum-sudangrass silage and 2.0% dry supplement. Diets were formulated to generate a RDP balance equal to zero and to meet or exceed MP requirements at expected ad libitum DMI and ADG. Dietary CP and lipid concentrations and IVDMD measured 12.0, 2.97, and 66.3%; 13.5, 4.00, and 66.8%; 15.1, 5.04, and 67.3%; and 17.3, 6.61, and 68.2% for CON, 10-DG, 20-DG, and 35-DG, respectively. Calves were fed once daily for 85 d and held off feed for 16 h to record initial and final individual BW. Data were analyzed as a generalized randomized complete block design. Cattle ADG was greater ($P < 0.01$) for calves fed the 20-DG diet (913 ± 20 g) compared with those fed the CON (682 ± 20 g) or 10-DG (829 ± 20 g) diets, although it was similar ($P = 0.93$) to those fed the 35-DG (915 ± 20 g) diet. Conversely, DMI was similar ($P > 0.65$) between cattle fed the CON (6.01 ± 0.27 kg/d), 10-DG (5.97 ± 0.27 kg/d), and 20-DG (5.93 kg/d) diets and smaller ($P < 0.01$) compared with cattle fed the 35-DG (5.41 ± 0.27 kg/d) diet. Consequently, G:F improved ($P < 0.01$) with increasing WDG dietary inclusion (114.4, 139.5, 154.2, and 169.6 ± 6.7 for CON, 10-DG, 20-DG, and 35-DG, respectively). Greatest lipid concentration in the 35-DG diet may have decreased fiber digestibility, which, in turn, could relate to reduced DMI. Additionally, ADG quadratic response ($P < 0.01$) may have resulted from greater NEg concentration and from DMI quadratic response ($P < 0.01$) with increasing WDG dietary inclusion. Including 35% WDG in a silage-based diet resulted in greatest G:F and growing-according ADG.

Key Words: backgrounding, cattle performance, distillers' grains

1472 Effects of *Saccharomyces cerevisiae* fermentation products on intestinal villi integrity in neonatal calves naturally infected with *Cryptosporidium* spp. S. Vázquez Flores[1], M. de Jesús Guerrero Carrillo[2], M. F. Scott[3], J. Hamann*[3], S. Barrera Almanza[1], C. Guizar Bravo[1], A. Patricia Baños Quintana[1], and P. Jazmin Aranda Vargasb[2], *[1]ESIABA-Tecnológico de Monterrey-Campus Querétaro, Querétaro, Mexico, [2]Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro, Querétaro, Mexico, [3]Diamond V, Cedar Rapids, IA*.

The objective of this study was to characterize the integrity of intestinal villi in neonatal bull calves naturally infected with *Cryptosporidium* spp. This study took place on a commercial dairy near Querétaro, México (1,100 cows in production). At birth, all calves received a colostrum substitute and were randomly allocated to one of three treatments: maltodextrin (placebo control [C]), SmartCare + Original XPC (T1), or Biomos (T2). All calves showed satisfactory levels of serum IgG as determined by a commercial serum radio-diffusion kit (C = 1,367.5 ± 292.1, T1 = 1,492.3 ± 48.2, and T2 = 1,572.8 ± 106.5). Calves were then given UV-purified whole milk and calf starter until d 28. On d 28, all calves were humanely sacrificed within the university premises for postmortem analysis and intestinal sample collection (duodenum, jejunum, and ileum). All samples were formalin fixed, and the histopathological smears were stained with hematoxylin–eosin. Villi scores (length and width) were measured twice by 2 different trained analysts using 10 fields per smear with an optic microscope (40x). Oocyst concentration was made using a modified concentration technique (Arrowood, 1987), with Sheather's solution at 1.12 specific gravity, in fecal samples collected on d 0, 7, 10, 14, and 28. Villi integrity was characterized as normal, fragmented, atrophied, or blunt. Statistical analysis was performed using parametric (Hsu's MCB) and nonparametric (Wilcoxon) analyses in JMP 11.1.0. In general, the number of intestinal villi per field varied from 10.1 to 12.5. There were no differences in duodenal villi scores between treatments. Villi were less ($P < 0.05$) fragmented and atrophied for T1 compared with C and T2 in the jejunum and ileum. Compared with C, T1 and T2 had larger ($P < 0.001$) crypts present in the ileum. *Cryptosporidium* spp. was present in 100% of the bull calves and ranged in concentration from 8×10^4 to 4×10^9 oocysts/mL. The use of *Saccharomyces cerevisiae* fermentation products shows promising results in maintaining intestinal villi integrity in spite of the protozoan infection

Key Words: intestinal villi integrity, neonatal calves, *Saccharomyces cerevisiae* fermentation product

1473 Evaluation of Brix refractometer to assess immunoglobulin G concentration of first and second colostrum from Jersey cows. D. Rolle, S. Rodríguez, A. Valldecabres, and N. Silva-del-Rio*, *Veterinary Medicine Teaching and Research Center, University of California Davis, Tulare*.

The objective of this study was to evaluate if concentration of IgG in first and second colostrum from Jersey cows may be estimated using Brix refractometry on farm. Colostrum samples and total weight of first (n = 136) and second (n = 70) milking after calving were collected from multiparous Jersey cows on a 3,500-cow California herd. The first colostrum was collected at 9.4 ± 3.8 h after calving and the second colostrum at 21.0 ± 3.7 h after calving. Fresh colostrum samples were evaluated for Brix percentage by using a handheld electronic refractometer (Reichert Inc., Depew, NY). Colostrum samples were aliquoted in 2-mL vials and frozen before IgG analysis by radial immunodiffusion (RID). The association between Brix percentage and IgG concentration was evaluated with the CORR procedure of SAS. The GLM procedure of SAS was used to describe the regression equation between Brix percentage and IgG concentration. Observations above the maximum Brix reading (>32%) were removed. Concentration of IgG was higher (P < 0.001) for first colostrum, averaging 83.8 g/L (range: 23.7 to 172.9 g/L), than for second colostrum at 46.9 g/L (6.2 to 100 g/L). Similarly, Brix percentage was higher (P < 0.001) for first colostrum, with an average of 25.4% (range: 16.2 to 37.1%), than for second colostrum with an average of 18.4% (range: 13.1 to 29.1%). Readings of Brix percentage were highly correlated with concentration of IgG in first (r = 0.81) and second (r = 0.77) colostrum. Harvested colostrum weighed 3.9 ± 2.6 kg at first milking and 4.2 ± 2.1 kg at second milking. Based on the regression equation, the most adequate Brix percentage cut points to define colostrum quality (50 g of IgG/L) were 19.1 and 18.7% for first and second colostrum, respectively. For first colostrum, sensitivity of Brix refractometer was 96.1%, specificity was 60.0%, and positive and negative predictive values were 96.8 and 54.5%, respectively. For second colostrum, sensitivity of Brix refractometer was 78.6%, specificity was 79.5%, and positive and negative predictive values were 73.3 and 83.7%, respectively. Our results indicate that Brix measurements can be used to rapidly estimate IgG concentration on first and second milking colostrum from Jersey cows. To identify colostrum samples with >50 IgG g/L, the most adequate cut point was slightly inferior to the 21% Brix reading that previous studies suggested.

Key Words: Brix refractometer, colostrum immunoglobulin G, Jersey cow

1474 Effects of lactose inclusion in calf starters on starter intake, growth performance, and digestive organ development. K. Inouchi*[1], A. Saegusa[2], Y. Inabu[3], T. Sugino[3], and M. Oba[4], *[1]ZEN-RAKU-REN, Nishi-shirakawa, Japan, [2]ZEN-RAKU-REN, Fukushima, Japan, [3]Hiroshima University, Higashi-hiroshima, Japan, [4]University of Alberta, Edmonton, AB, Canada*.

The objective of this study was to evaluate the effects of lactose inclusion in calf starters on starter intake, growth performance, and digestive organ development. Sixty Holstein bull calves were raised on an intensified nursing program using milk replacer containing 28% CP and 15% fat and fed the texturized calf starter containing lactose at 0 (Control), 5.0 (LAC5), or 10.0% on a DM basis (LAC10; n = 20 for each treatment). All calf starters were formulated for 23.1% CP. As the pellet portion contained lactose and all adjusted ingredients, treatment calf starters differed only in the pellet. Ethanol soluble carbohydrate concentrations of Control, LAC5, and LAC10 were 7.3, 12.3, and 16.8% (DM), respectively. Starch concentrations of Control, LAC5, and LAC10 were 29.7, 27.0, and 21.4% (DM), respectively. All calves were fed treatment calf starters ad libitum, and their hay intake was limited to 150 g/d. Body weight, hip height, withers height, body length, hip width, and heart girth were measured weekly. Fifteen calves were killed at the age of 62 d, and 45 calves were killed at the age of 80 d. Digestive organs were harvested, emptied, rinsed and weighed. Starter DMI intake was 267 ± 45 (Control; mean ± SE), 216 ± 20 (LAC5), and 283 ± 31 g/d (LAC10) before weaning (d 7–56); 1,516 ± 156 (Control), 1,344 ± 105 (LAC5), and 1,622 ± 127 g/d (LAC10) during weaning transition (d 49–63); and 2,778 ± 164 (Control), 2,636 ± 109 (LAC5), and 2,812 ± 164 g/d (LAC10) after weaning (d 56–80). Average daily gain was 0.64 ± 0.03 (Control), 0.64 ± 0.03 (LAC5), and 0.71 ± 0.34 kg/d (LAC10) before weaning (d 7–56); 1.02 ± 0.76 (Control), 1.03 ± 0.08 (LAC5), and 1.17 ± 0.08 kg/d (LAC10) during weaning transition (d 49–63); and 1.41 ± 0.06 (Control), 1.40 ± 0.06 (LAC5), and 1.34 ± 0.06 kg/d (LAC10) after weaning (d 56–80). Wet mass of the reticulorumen was 1.37 ± 0.14 (Control), 1.49 ± 0.04 (LAC5), and 1.60 ± 0.09% BW (LAC10) at d 62 and 2.21 ± 0.08 (Control), 2.03 ± 0.07 (LAC5), and 1.97 ± 0.16% BW (LAC10) at d 80. None of the response variables above were significantly different (P > 0.05). In addition, treatments did not affect (P > 0.05) the other primary response variables including body height, body length, heart girth, and wet mass of the other digestive organs. These results indicate that inclusion of lactose in calf starters up to 10% of DM may not affect starter intake, growth performance, and digestive organ development.

Key Words: calf, lactose, starter

1475 Bioavailability of different sources of zinc using stable isotopes in male Holstein calves.

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Trace minerals are an important component of ruminant nutrition. Furthermore, understanding the bioavailability of various trace mineral sources is essential for accurate dietary formulation. The objective of this trial was to determine bioavailability of Zn when provided in either an inorganic or an organic form. Sixteen weaned male Holstein calves (BW = 60 ± 2 kg [mean ± SE]) were used in a randomized compete block design. Calves were individually fed a common texturized starter formulated to meet NRC nutrient requirements. Calves were orally administered 4 or 8 mg of Zn from 2 sources: ^{67}Zn oxide and ^{70}Zn-methionine hydroxy analog chelate (^{70}Zn-MHAC). Blood was collected via catheters before isotope administration and 0.25, 0.5, 0.75, 1, 2, 4, 6, 8, 10, 12, 16, 20, 24, 36, 48, and 72 h after isotope administration for determination of isotope enrichment. Calves were euthanized 72 h after isotope administration, and target tissues were weighed and sampled for determination of isotope enrichment. Plasma area under the curve (AUC) for isotope enrichment was significantly ($P < 0.01$) greater with ^{70}Zn-MHAC (2.02 ± 0.12 ppm) compared with ^{67}Zn oxide (1.20 ± 0.12 ppm). When dose was considered, plasma AUC for isotope enrichment was significantly ($P < 0.01$) greater with 8 mg of labeled Zn (2.34 ± 0.12 ppm) compared with 4 mg (0.87 ± 0.12 ppm). Isotope enrichment was significantly ($P < 0.01$) greater with ^{70}Zn-MHAC compared with ^{67}Zn oxide for all tissues with the exception of omasal tissue, which tended ($P = 0.07$) to be greater. When dose was considered, isotope enrichment was significantly ($P < 0.01$) greater with 8 mg of labeled Zn compared with 4 mg for all tissues except muscle ($P = 0.17$) and tibia ($P = 0.42$). The slope for ^{70}Zn-MHAC was significantly ($P \leq 0.01$) higher compared with that of ^{67}Zn oxide for abomasal tissue (0.036 vs. 0.011; $r^2 = 0.88$), duodenal tissue (0.070 vs. 0.043; $r^2 = 0.90$), ileal tissue (0.069 vs. 0.028; $r^2 = 0.95$), jejunal tissue (0.072 vs. 0.024; $r^2 = 0.93$), liver (0.096 vs. 0.012; $r^2 = 0.83$), muscle (0.016 vs. −0.031; $r^2 = 0.89$), pancreas (0.076 vs. 0.003; $r^2 = 0.82$), thymus (0.023 vs. −0.003; $r^2 = 0.85$), and tibia (0.007 vs. −0.003; $r^2 = 0.86$). Together these data demonstrates using stable isotopes as a valid technique to measure bioavailability and greater bioavailability was observed from Zn-MHAC when compared with zinc oxide.

Key Words: bioavailability, stable isotopes, zinc

1476 Endocannabinoid concentrations in plasma associated with feed efficiency and carcass composition on crossbreed steers.

V. M. Artegoitia*[1], A. P. Foote[2], R. M. Lewis[3], D. A. King[2], S. D. Shackelford[2], T. L. Wheeler[2], and H. C. Freetly[2], *[1]University of Nebraska, Lincoln, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [3]University of Nebraska-Lincoln, Lincoln*.

Endocannabinoids, including anandamide (AEA) and 2-arachidonoylglycerol (2-AG), are a class of endogenous lipid mediators that activate cannabinoids receptors and may be involved in the control of feed intake and energy metabolism. The objective of this study was to quantify AEA and 2-AG in plasma and identify possible associations with production traits and carcass composition in finishing beef steers. Individual DMI and BW gain was measured on 140 crossbred steers for 105 d on a finishing ration. Blood samples were collected on d 84 of the experiment, which was 40 d before slaughter. Variables were analyzed using Pearson CORR procedure of SAS. Mean endocannabinoid concentrations in plasma were 4.48 ± 1.82 and 0.43 ± 0.24 ng/mL for AEA and 2-AG, respectively. The AEA concentration was positively correlated with G:F ($r = 0.20$, $P = 0.02$), indicating that more efficient animals were correlated with higher AEA plasma concentration. Nevertheless, AEA concentration was negatively correlated with metabolic BW at the midpoint of the experiment ($r = −15$, $P = 0.07$) and initial BW ($r = −0.19$, $P = 0.03$). In addition, AEA concentration was negatively correlated with the 12th rib fat thickness ($r = 0.17$, $P = 0.07$), but no correlation was found with USDA-calculated yield grade ($r = −0.14$, $P = 0.11$) or marbling score ($r = 0.05$, $P = 0.54$). The concentration of 2-AG was positively correlated with AEA ($r = 0.21$, $P = 0.01$); however, 2-AG concentration was not correlated with parameters of feed efficiency or carcass composition. In summary, the present study is the first to report plasma concentration of endocannabinoids in steers. These results provide evidence that plasma concentration of a key endocannabinoid, AEA, was favorably correlated with feed efficiency and fat thickness on crossbred steers at finishing. The USDA is an equal opportunity provider and employer.

Key Words: anandamide, 2-arachidonoylglycerol, ultra-performance liquid chromatography tandem mass spectrometry

1477 The phenotypic relationship between residual feed intake and ultrasound carcass traits in Santa Gertrudis steers. C. R. Branton*, *Stephen F. Austin State University, Nacogdoches, TX*.

Numerous studies have been conducted characterizing phenotypic and genetic variation in RFI in beef cattle, but limited studies have examined effects of diet and/or stage of maturity on phenotypic reranking of cattle for feed efficiency traits. For this study, 2 trials were conducted with Santa Gertrudis steers (N = 233). Steers were fed a roughage-based diet (2.1 Mcal ME/kg DM) during the growing phase and a high-grain diet (3.0 Mcal ME/kg DM) during the finishing phase. Steers were weighed at 14-d intervals and DMI was measured (Calan gate or GrowSafe) for 70 d during both the growing and finishing phases, with ultrasound measurements obtained on Day 70 of each feeding phase. RFIp was calculated as the difference between actual DMI and expected DMI based on regression of DMI on ADG and mid-test $BW^{0.75}$. Stepwise regression revealed that final back fat depth (BF) accounted for additional variation in RFI in both the growing (R^2 = 0.43 vs. 0.46) and finishing (R^2 = 0.54 vs. 0.56) phases. Therefore, RFIc was computed for both phases based on regression of DMI on ADG, mid-test $BW^{0.75}$, and final BF depth. During the growing phase, RFI_p was positively correlated ($P < 0.01$) with DMI (0.75), feed:gain ratio (0.49), and final BF depth (0.13) but not with ADG or BW. Feed:gain ratio was negatively correlated ($P < 0.01$) with ADG (−0.70) but was not correlated with DMI. During the finishing phase, RFI_p was positively correlated ($P < 0.01$) with DMI (0.65), feed:gain ratio (0.51), and final BF depth (0.17) but not with ADG or BW. Feed:gain ratio was negatively correlated ($P < 0.01$) with ADG (−0.69) but was not correlated with DMI. Correlations between RFIp and RFIc were 0.91 and 0.92 during the growing and finishing phases, respectively. Spearman rank correlations revealed that ADG and feed:gain ratio measured during the growing phase were weakly associated with ADG (0.21) and feed:gain ratio (0.12) measured during the finishing phase, whereas rank correlations were moderate for DMI (0.47), RFIp (0.45), and RFIc (0.28) measured during the growing and finishing phases. Although these results indicate that a moderately positive rank correlation exists between RFI measured when steers are fed high-roughage vs. high-grain diets, these two feed efficiency traits may not be biologically similar. It is unclear as to whether the lack of a strong correlation between RFI measured during growing vs. finishing phases was due to influences of diet and/or stage of maturity.

Key Words: carcass composition, residual feed intake, Santa Gertrudis steer

1478 Using indigestible rare earth markers and internal markers to predict dry matter intake and residual feed intake. K. A. Weld* and L. E. Armentano, *University of Wisconsin – Madison, Madison*.

Residual feed intake (RFI) is a feed efficiency measure that requires multiple animal individual intakes. The objective of this trial was to determine the plausibility of using a known daily dose of a rare earth marker combined with an inherent, internal total mixed ration (TMR) indigestible component and spot fecal sampling to predict DMI and RFI of lactating dairy cattle. Fifteen lactating Holstein cows (107 ± 20 d in milk) were maintained on a single diet for 5 wk in tie stalls. Milk production and DMI were recorded daily, and milk samples and BW were taken weekly. Indigestible rare earth markers were administered orally by 3 methods: once daily by bolus (ytterbium), once daily by top-dressing TMR (samarium), or twice daily by bolus (lanthanum). Cows received all external rare earth markers the last 10 d of the trial with the final 3 d being used to collect 10 fecal samples. Fecal samples were composited and analyzed for concentrations of rare earths by inductively coupled plasma mass spectrometry (CV mean ± SD: 3.8 ± 1.7) and indigestible NDF (CV: 3.6 ± 4.3) and indigestible DM (CV: 5.4 ± 4.6) using a 288-h in situ incubation. Combining one of the three rare earth external markers with one of the two diet internal markers allows prediction of DMI and RFI as a 3 × 2 factorial. There was a significant correlation between measured DMI in the final week and DMI predicted using 1x bolusing ($r > 0.60$, $P < 0.02$) but not using top-dressing ($r > 0.42$, $P > 0.08$) or 2x bolusing ($r = 0.33$, $P = 0.22$). Phenotypic RFI was calculated as the difference between individual cow DMI and regression estimated DMI where the regression included $BW^{0.75}$, BW change (deltaBW; BW in kg), and milk energy (Mcal). Individual regressions were calculated for measured DMI and the 6 marker predicted DMI. The solutions from these regressions differed: (coefficient [±SE]; 5 wk of intakes: DMI = 0.50 (±0.10) × milk energy + 0.57 (±0.04) × $BW^{0.75}$ − 0.28 (±0.45) × deltaBW − 1.51 (±7.56); 1 wk intakes: DMI = 0.39 (±0.09) × milk energy + 0.11 (±0.03) × $BW^{0.75}$ − 0.37 (±0.39) × deltaBW − 11.47 (±6.51); and predicted DMI 1x/iNDF: DMI = 0.53 (±0.12) × milk energy − 0.07 (±0.05) − $BW^{0.75}$ + 1.48 (±0.55) × deltaBW + 23.57 (±9.27)).There was a correlation between the RFI calculated from the actual DMI in the last week and the RFI calculated from 5 wk of data ($r = 0.61$, $P < 0.05$).The actual RFI, from observed DMI of 5 wk or 7 d, were not correlated with the RFI calculated using the marker predicted DMI.

Key Words: digestibility marker, intake prediction, residual feed intake

Table 1479.

Item	Equation	R^2	P
DMVI	4.6733 (STIR) + 4.7374	.7011	<.0001
DMD	6.6871 (STIR) + 401.52	.1292	= .003
DDMI	2.6198 (STIR) - 0.7004	.5301	<.0001

1479 Short-term intake technique to predict dry matter intake and digestibility in forages.
F. M. Ingentron[1,2], B. C. Lentz[1], N. P. Stritzler[1], C. N. Rabotnikof[1], M. Menghini[3,4], and H. M. Arelovich*[3,4,5], *[1]Fac. Agronomia, Universidad Nacional de La Pampa, Santa Rosa, Argentina, [2]CONICET, Santa Rosa, Argentina, [3]CIC, Bahia Blanca, Argentina, [4]Dto. Agronomia, Universidad Nacional del Sur, Bahia Blanca, Argentina, [5]CERZOS, Bahia Blanca, Argentina*.

The objective of this study was to evaluate short-term intake rate (STIR) to predict DM voluntary intake (DMVI) and digestibility (DMD) in rams when offered different grass species usually grazed in semiarid Argentina. The evaluated forages were 3 warm-season grasses—fingergrass (F; *Digitaria eriantha eriantha* cv. Irene), kleingrass (K; *Panicum coloratum* cv. Verde), and switchgrass (S; *Panicum virgatum* cv. Alamo)—at vegetative (ve) and deferred (d) stages plus 4 small grains—wheat (W; *Triticum aestivum*) oats (O; *Avena sativa*), rye (R; *Secale cereale*), and triticale (T)—and alfalfa hay (AH; control forage for STIR). In separate experiments, 6 Pampinta rams (56 kg mean BW) were individually fed indoors ad libitum each forage in 2 daily meals (1000 and 1600 h) for 7 d of adaptation plus 7 d of DMVI observations and total fecal collection in bags. Simultaneously, a different group of 6 rams of similar BW were used to measure STIR. This group was fed once daily at maintenance level with AH. After 4 h of fasting, the animals were allowed active consumption of each forage for a 4-min period, controlled by an independent observer standing by each ram. Both DMVI and STIR were determined by subtracting refused from offered DM. Dry matter digestibility was calculated from DMVI and feces output, and digestible DMI (DDMI) was computed as well. The range of variable means and SE across grass species were 21.2 ± 2.3 (Sd) to 127.7 ± 7.2 (O), 34.3 ± 5.8 (Sd) to 69.1 ± 2.4 (AH), and 7.7 ± 1.5 (Sd) to 63.5 ± 3.3 (AH) for DMVI (g/kg $W^{0.75}$ per day), DMD (%), and DDMI (g/kg $W^{0.75}$ per day), respectively. The association between STIR and the variables DMVI, DMD, and DDMI (n = 6 for each forage) was studied by regression against the mean STIR value. Linear regression equations describing these relationships are shown in the table. There is strong positive association between STIR and DMVI; however, when a quality factor, such as DMD alone or linked to DMVI, is included, the STIR prediction potential seems to become weaker. Other factors such as palatability and leaf:stem ratio may have an influence not determined by this study.

Key Words: intake prediction, forages, sheep

1480 Effects of a blend of essential oils on milk yield and feed efficiency of lactating cows.
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The objective of this study was to assess the effect on milk yield and feed efficiency of a combination of essential oils for lactating dairy cows. A 56-d experiment was conducted involving 40 Holstein cows (688 ± 87 kg BW, yield 29.1 ± 73.0, and 220 ± 5.2 DIM) and 2 treatments. The study followed a randomized complete block design and lasted 8 wk. Treatments were either no supplementation (Control) or a supplementation of 1 g/d of Agolin Ruminant (Agolin, Switzerland) (AGR). Agolin Ruminant is combination of microencapsulated essential oil compounds (containing coriander oil, geranylacetate, and eugenol). All cows were fed a common TMR containing 15.3% CP, 34.6% NDF, and 1.53 Mcal of ENl/kg that was delivered twice daily. Treatments were applied in the milking parlor using a precision feeding system. The control cows received 300 g of soybean meal at each milking, and AGL cows received 300 g of soybean meal containing 1.66 g/kg of Agolin Ruminant at each milking (twice daily). Individual milk production, milk composition, and feed intake were recorded daily, and feed efficiency was then calculated (as kg of milk/kg of DMI). Treatment was individually applied, and cow was the experimental unit (n = 20). Data were analyzed with a mixed-effects model with repeated measures. Cows on AGL produced more (P < 0.05) milk (31.1 ± 1.02 kg/d) between 25 and 56 d of study than Control cows (29.7 ± 1.02 kg/d), but overall, there were no differences between treatments in milk yield. Milk fat (3.90 ± 0.08%) and milk protein (3.94 ± 0.08%) were not affected by treatment. There were, overall, no differences in DMI (24.8 ± 0.67 kg/d) between treatments, but AGL cows tended (P = 0.06) to consume less feed (24.2 ± 0.94 kg/d) than Control cows (24.8 ± 0.94 kg/d) in several days during the last 23 d of study. As a result, feed efficiency was greater (P < 0.01) in AGL cows (1.33 ± 0.05) for most days after 33 d of study than in Control cows (1.25 ± 0.05). It is concluded that Agolin Ruminant increases milk production after about 3 wk of treatment, and because feed intake does not change or even tends to decrease, feed efficiency increases.

Key Words: essential oil, milk efficiency, yield

1481 Repeatability of feed efficiency in beef cattle offered grass silage and zero-grazed grass.
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The objective of the study was to examine the within-animal repeatability of intake, growth, and feed efficiency between two consecutive feeding periods in beef cattle fed grass silage followed by zero-grazed grass. One hundred eighty-three steers comprising 94 Charolais (CH) and 89 Holstein-Friesian (HF) were used. Individual DMI and growth were measured over two consecutive 70-d feeding phases. Each feeding phase was preceded by a dietary adaptation period. For phase 1, steers were offered first-harvest grass silage (DM 290 g/kg and DM digestibility 700 g/kg) ad libitum, and for phase 2, they were offered zero-grazed grass (DM 196 g/kg) ad libitum. The grass herbage was harvested (without chopping) twice daily from *Lolium perenne* dominant swards using a "zero-grazer." The residuals of the regression of DMI on ADG and mid-test metabolic BW, within each breed, were used to compute individual residual feed intake (RFI) coefficients for each feeding phase. Repeatability between the two feeding phases for ADG, DMI, G:F, and RFI was estimated using Pearson correlation coefficients. Mean BW (SD) and age (SD) at the start of phase 1 were 485 kg (38.0) and 373 d (18.0) and 401 kg (43.3) and 399 d (7.6) for CH and HF, respectively. Corresponding BW at the start of phase 2 were 519 (38.3) and 441 (39.2) kg. During phase 1, overall ADG, DMI, G:F, and RFI (SD) for CH were 0.40 kg (0.17), 6.5 kg/d (0.57), 0.06 kg BW gain/kg DM (0.03), and −0.01 kg DM/d (0.35). Corresponding values for HF were 0.46 (0.17), 7.1 (0.60), 0.07 (0.02), and −0.02 (0.48). For phase 2, respective values were 1.31 (0.19), 9.1 (0.55), 0.14 (0.02), and −0.03 (0.34) and 1.25 (0.22), 9.5 (0.56), 0.13 (0.02), and −0.02 (0.43). For CH, correlations between the two feeding phases for ADG, DMI, G:F, and RFI were $r = 0.13$ ($P > 0.05$), $r = 0.70$ ($P < 0.001$), $r = 0.07$ ($P > 0.05$), and $r = 0.40$ ($P < 0.001$), respectively. Corresponding values for HF were −0.03 ($P > 0.05$), 0.51 ($P < 0.001$), 0.04 ($P > 0.05$), and 0.30 ($P < 0.01$). We conclude that DMI and, to a lesser extent, RFI are repeatable traits when cattle are offered grass silage and zero-grazed grass.

Key Words: beef cattle, feed efficiency, repeatability

1482 Repeatability of feed efficiency in steers offered a high-concentrate diet.
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The objective of the study was to examine the within-animal repeatability of intake, growth, and feed efficiency between the growing and finishing stages for beef cattle fed the same diet. One hundred sixty-seven steers comprising 90 Charolais (CH) and 77 Holstein-Friesian (HF) were used. Following a dietary adaptation period, individual DMI and growth were measured over two 71-d feeding phases 300 d apart. Mean BW (SD) and age (SD) at the start of phase 1 were 395 kg (37.8) and 283 d (18.3) and 294 kg (42.3) and 306 d (7.7) for CH and HF, respectively. Corresponding BW at the start of phase 2 were 675 (49.8) and 611 (49.3) kg. During both feeding phases, steers were individually offered the same concentrates (860 g/kg rolled barley, 60 g/kg soya bean meal, 60 g/kg molasses, and 20 g/kg minerals and vitamins) ad libitum plus a restricted allowance of grass silage daily. Throughout the interim period, they were all offered either grass silage or fresh grass herbage. The residuals of the regression of DMI on ADG and mid-test metabolic BW, within each breed, were used to compute individual residual feed intake (RFI) coefficients for each feeding phase. Repeatability between the two feeding phases for ADG, DMI, G:F, and RFI was estimated using Pearson correlation coefficients. During phase 1, overall ADG, DMI, G:F, and RFI (SD) for CH were 1.26 kg (0.26), 8.4 kg/d (0.82), 0.15 kg BW gain/kg DM (0.03), and −0.02 kg DM/d (0.51). Corresponding values for HF were 1.40 (0.22), 8.8 (0.84), 0.16 (0.02), and −0.05 (0.50). For phase 2, respective values were 1.39 (0.26), 11.5 (1.11), 0.12 (0.02), and −0.01 (0.69) and 1.31 (0.37), 12.5 (1.30), 0.11 (0.03), and −0.08 (0.95). For CH, correlations between the two feeding phases for ADG, DMI, G:F, and RFI were $r = 0.21$ ($P > 0.05$), $r = 0.63$ ($P < 0.001$), $r = 0.07$ ($P > 0.05$), and $r = 0.35$ ($P < 0.001$), respectively. Corresponding values for HF were 0.22 ($P = 0.06$), 0.56 ($P < 0.001$), 0.08 ($P > 0.05$), and 0.29 ($P < 0.05$). We conclude that DMI and, to a lesser extent, RFI are repeatable traits when cattle are offered a high-concentrate diet.

Key Words: beef cattle, feed efficiency, repeatability

1483 NADH dehydrogenase (ubiquinone) Fe-S protein-1 (NDUFS1), a core subunit of mitochondrial complex I, is not differentially expressed in peripheral blood mononuclear cells of beef steers with divergent residual feed intakes.
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Mitochondrial complex I (NADH:ubiquinone oxidoreductase) plays a crucial role in energy production and is intrinsically linked to animal bioenergetics. Several studies suggest mitochondrial protein complex subunits are differentially expressed in tissues and cells of chickens and cattle with divergent residual feed intake (RFI). The objective was to evaluate differences in mitochondrial complex I in peripheral blood mononuclear cells (PBMC) as a marker to identify different

RFI phenotypes. Crossbred steers fed corn- or roughage-based diets were RFI tested during the growing phase at the University of Missouri and shipped to Iowa State University where they were fed corn- or byproduct-based diets until harvest. Blood samples were collected on d 59 of the finishing phase from 37 steers that represented low and high extremes in growing phase RFI (n = 8 and 11 and mean RFI = −1.25 and 1.20 kg for corn-based diet and n = 10 and 8 and mean RFI = −1.67 and 1.25 kg for roughage-based diet, respectively). The PBMC were isolated and lysate proteins (50 μg total protein/lane) were separated by PAGE and blotted onto nitrocellulose membranes. A polyclonal antibody against NADH dehydrogenase (ubiquinone) Fe-S protein-1 (NDUFS1), a marker of complex I, was used to determine relative abundance of the protein in PBMC. Primary antibody binding specificity was confirmed with a commercially available bovine heart mitochondria lysate, which was also the positive control. Antibody binding was determined by chemiluminescence after blots were incubated with a horseradish peroxidase conjugated secondary antibody. The NDUFS1 band signal intensities were adjusted relative to the signal intensity of the positive control for each gel and normalized to total protein in the lane. There were no effects of diet (P = 0.50) or RFI phenotype (P = 0.45) on relative abundance of NDUFS1 protein in PBMC of steers. Examination of data from only steers with low RFI suggested a tendency, a slight positive relationship (r = 0.36, P = 0.14), between NDUFS1 protein abundance and low RFI, regardless of diet. A similar response was not evident in steers with high RFI (P = 0.79). Relative expression of the protein NDUFS1 is not clearly related to RFI of steers fed corn- or roughage-based diets and cannot be used as a marker for selection of efficient animals. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30214 from the USDA National Institute of Food and Agriculture.

Key Words: NDUFS1 protein, residual feed intake, steer

1484 Dry matter intake prediction of heifers under tropical conditions. M. I. Marcondes*[1] and A. L. Silva[2], [1]*Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Brazil,* [2]*Universidade Federal de Vicosa, Vicosa, Brazil*.

The objective was to develop a model able to predict DMI of heifers raised under tropical conditions as well as to test the effect of breed (Holstein purebred vs. Holstein × Gyr crossbreed) on DMI. A database composed of 389 individual animal observations, from 14 experiments, was used to develop the model for DMI. Only experiments that had concurrent information about DMI, average BW, ADG, and breed were used. Animals that had ≥87.5% Holstein crosses were considered pure breeds and the others were considered crossbreeds. The data were analyzed following a meta-analysis procedure, where each experiment was considered a random sample for large populations. The model used to fit the DMI was $DMI = \beta_0 + \beta_1 \times BW + \beta_2 \times BW^2 + \beta_3 \times ADG + \beta_4 \times ADG^2$, in which DMI = dry matter intake (kg/d); BW = average body weight (kg); ADG = average daily gain (kg/d); and β_0, β_1, β_2, β_3, and β_4 are equation parameters. To test the random effects of independent variables on the intercept and slope, the variance components (VC), heterogeneous first-order autoregressive (ARH (1)), and unstructured (UN) matrices of (co)variance were tested. All statistical procedures were performed using the MIXED procedure of SAS and Akaike's information criteria was used to indicate the best (co)variance matrix. Breed effect was tested every equation parameter. Observations with Studentized residuals > |2.5| were considered outliers. For all statistical procedures, a significance level of 5% was adopted for fixed effects and a level of 20% was adopted for the random (study) effect. Heifer DMI values were linearly affected by BW and ADG and quadratically affected by ADG. Genetic group affected the BW and ADG coefficients, demonstrating that this is an important source of variation and that different models should be used to estimate the DMI of Holstein purebred and crossbred heifers. The fitted models were $DMI_{Holstein} = -0.2092 + 0.0169 \times BW + 2.5833 \times ADG - 0.5126 \times ADG^2$ and $DMI_{Crossbred} = -0.2092 + 0.0179 \times BW + 2.3048 \times ADG - 0.5126 \times ADG^2$, in which $DMI_{Holstein}$ = DMI of Holstein heifers (kg/d), $DMI_{Crossbred}$ = DMI of crossbred heifers (kg/d), BW = average body weight (kg), and ADG = average daily gain (kg/d). It can be concluded that DMI in heifers is affected by BW and ADG and different equations should be used to estimate DMI in Holstein purebreds and Holstein × Gyr crossbred dairy heifers raised under tropical conditions.

Key Words: dairy heifers, growing animals, Holstein × Gyr

1485 An improved model for predicting dry matter intake in prepartum dairy cows. F. A. Paiva*[1], F. Peñagaricano[1], J. K. Drackley[2], and J. E. P. Santos[1], [1]*University of Florida, Gainesville,* [2]*University of Illinois, Urbana*.

The objective was to develop a mathematical model to predict DMI in prepartum Holstein cows. Data on daily DMI, parity, BW, body condition (BCS), and chemical composition of diets fed ad libitum to 1,451 Holsteins during the final 21 d of gestation in 31 experiments were compiled. Cows were grouped according to parity prepartum as nulliparous (n = 290), primiparous (n = 510), or multiparous (n = 660) and BCS as thin (BCS < 3.00), moderate (3.00–3.50), or fat (BCS > 3.50). Body weight was used as percentage of the mean BW within parity for nulliparous (620 kg), primiparous (690 kg), and multiparous (760 kg) and day relative to calving (DRC) was used as a categorical variable. Dietary factors included NE for lactation, CP, ruminal degradable and undegradable protein, ash, fat, NDF, ADF, nonfibrous carbohydrates, percent dietary forage, forage NDF, Ca, P, Mg, and

Table 1485.

Table 1. Comparison of prediction models for DMI of prepartum dairy cows

Variables	Hayirli et al. (2003)[1]	NRC (2001)	Cross-validation	Final[2]
Observed mean (Y)	11.58	11.58	11.58	11.58
Predicted mean ($\hat{Y}$)	12.69	12.31	11.54	11.55
Bias (Y-$\hat{Y}$)	-1.11	-0.73	0.04	0.03
R^2	0.11	0.11	0.20	0.22
MSPE	13.31	12.57	9.86	9.53
Root MSPE (kg/d)	3.65	3.55	3.14	3.09
Root MSPE (% Y)	31.49	30.61	27.11	26.62
Mean bias, % MSPE	9.22	4.13	0.02	0.02
Slope bias, % MSPE	9.13	9.15	0.66	0.19
Dispersion error, % MSPE	81.65	86.71	99.32	99.80
Concordance correlation coefficient	0.28	0.29	0.36	0.38

[1] Hayirli et al. (2003): J. Dairy Sci. 86:1771-1779.

[2] DMI, kg/d = 6.8591 + (BW% x 3.8748) + (NDF% x -0.1146) + (DCAD mEq/Kg x 0.006618) + Null (0) / Prim (2.5684) / Mult (2.2892) + Thin (0.4825) / Mod (0.3655) / Fat (0) + DRC (estimates)

dietary cation–anion difference (DCAD). Models were built with parameters entered in sequence using the MIXED procedures of SAS and R. Initial model included the random effects of study and cow nested within parity and study and the fixed effect of DRC. Each cow-level or diet-level factor was individually analyzed and fixed effects with $P < 0.05$ were used to build multivariable models. Multicollinearity among diet-level factors was assessed and parameters with high collinearity were individually evaluated in separate models. The final model was built using only significant variables and best fit assessed according to lowest Akaike's (AIC) and Bayesian (BIC) information criteria. The final model was DMI (kg/d) = intercept + [BW (% mean parity BW) × estimate] + [NDF (% of DM) × estimate] + [DCAD (mEq/kg) × estimate] + parity estimates + BCS category estimates + DRC estimates. The model was rerun 31 times excluding 1 of the 31 experiments each time, which was used to evaluate predictive ability using cross-validation (cross-validation model). Therefore, 31 different models were generated and the excluded experiment was used to evaluate the prediction of DMI. The final model was contrasted with other prediction models for DMI (Table 1). Of the total variance in DMI, the random effects accounted for 46.1%, the fixed effects accounted for 21.2%, and the residual accounted for 32.7%. The final model reduced the root of mean square of the predicted error by 0.46 to 0.56 kg/d, therefore more accurately predicting DMI of prepartum cows compared with currently used models.

Key Words: dry matter intake, model, prepartum

1486 The use of artificial neural network to estimate feed intake in lactating cows through milk mid-infrared spectra of individual cow milk samples.

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Feed intake is one of the most important components of feed efficiency in dairy systems. It is, however, a difficult trait to measure in the field. The use of milk spectrum from mid-infrared (MIR) spectroscopy previously has been used to estimate milk traits and could be an alternative to direct measurement of DMI. The objective of this study was to develop a Fourier transform MIR-based milk analysis method coupled with artificial neural networks (ANN) to estimate DMI in lactating Holstein cows. Five hundred ninety-nine milk samples from 189 lactating cows housed at either the Emmons Blaine Dairy Cattle Research Center (Arlington, WI; $n = 129$ cows) or the Dairy Forage Research Center (USDA, Prairie Du Sac, WI; $n = 60$ cows) were analyzed for MIR spectra. Individual DMI was periodically recorded from cows housed in a free-stall barn equipped with 32 Insentec electronic feeding gates (Arlington) or directly measured on tie-stall barn (USDA). The spectra absorbance values were used as input variables to develop and optimize the ANN configuration. Wavelengths with less than 10% of CV among samples were not used. The ability of the resulting one-hidden-layer ANN model was compared with a linear predictive model developed through partial least squares (PLS) regression. Four ANN models were developed considering 5, 10, 15, and 20 neurons. A 7-fold cross-validation method was used to assess the predictive ability of the models. The r^2 of cross-validation increased as the number of neurons increased from 5 to 20 ($r^2 = 0.31$, 0.43, 0.45, and 0.48, respectively). The root mean square error (RMSE) decreased as the number of neurons increased up to 15 (RMSE = 4.13, 3.61, 3.30, and 3.38 kg/d, respectively). In contrast, the PLS model (7 factors) resulted in lower $r^2 = 0.14$ and greater RMSE = 4.41 kg/d. Compared with established statistical method (PLS), the proposed ANN model demonstrates the potential to provide improved prediction of DMI. Future research should be conducted to investigate alternative ANN architectures and to assess its performance using test validation in an independent data set.

Key Words: artificial neural network, intake, mid infrared

1487 Effects of supplementing lactating dairy cow ration with sodium sesquicarbonate on reticulorumen pH, rumination, and dry matter intake.

1488 Toxicity of antibiotics on rumen protozoan *Entodinium caudatum* and its associated microbes.
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Rumen ciliate protozoa play important roles in rumen function. However, knowledge on the metabolism and physiology of rumen protozoa is limited, mostly because of lack of axenic cultures of rumen ciliate protozoa needed to generate direct evidence. Antibiotics alone and in combination with physical separation have been successfully used in generating axenic cultures of free-living aerobic ciliate protozoa, such as species of *Tetrahymena* and *Paramecium*. However, no effort has been successful in developing axenic cultures of rumen protozoa. Rumen protozoa have lived together with a high density of rumen bacteria and other groups of microbes for many millions of years, and killing of the associated bacteria and/or archaea resulted in loss of viability of rumen protozoa. The objective of this experiment was to evaluate the toxicity of different antibiotics to *Entodinium caudatum*, a major species of *Entodinium*, which, as a genus, accounts for more than 90% of the total rumen protozoa in cattle and sheep fed high-concentrate diets. Based on the mode of action, eight antibiotics were selected that each has a broad spectrum to kill or to inhibit bacteria. *Entodinium caudatum* cells grown in a culture were filtrated and washed to remove most of the free-living bacteria and methanogens. The washed *E. caudatum* cells were then fed a protozoal feed containing ground wheat, alfalfa, and grass and incubated for 72 h with 4 different concentrations and three replicates per antibiotic treatment. After incubation, *E. caudatum* cell counts, optical density, and electron microscopy (both scanning and transmission) were used to determine *E. caudatum* viability, growth of contaminating bacteria, and changes of intracellular structure of *E. caudatum* cells. Except ampicillin, all the tested antibiotics decreased *E. caudatum* growth in a concentration-dependent manner. Chloramphenicol appeared to be the most toxic to the viability of *E. caudatum*. Scanning electron microscopy and transmission electron microscopy revealed few ecto- or endosymbiotic microbes of the *E. caudatum* cells irrespective of the antibiotic treatments. Damages to the intracellular structures were detected by scanning electron microscopy, especially among the *E. caudatum* cells treated with chloramphenicol. Transmission electron microscopy is underway to further examine cellular damages, and several antibiotics cocktails are being evaluated for their usefulness to kill the associated microbes and generate an axenic *E. caudatum* culture.

Key Words: axenic culture, electron microscopy, *Entodinium caudatum*

1489 Effect of diets containing different levels of crude glycerol on nutrient intake in lambs.
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Crude glycerin is a byproduct of biodiesel production that represents a potential ingredient for use in animal nutrition. The objective of this study was to evaluate the effect of diets containing different levels of crude glycerin on nutrient intake in male lambs. The experiment was conducted in the animal metabolism laboratory of Universidade Estadual de Londrina. Four castrated male lambs (25 ± 2.6 kg) were used in a 4 × 4 Latin square design. Animals were identified and individually allocated to metabolic cages containing a feeder and a water trough. The experiment was divided in 4 periods of 13 d, with the first 7 d for diet adaptation and 6 d of sample collection. A basal diet (50:50 forage to concentrate) consisting of chopped *Brachiaria dictyoneura* hay, ground corn, soybean meal, urea, and a mineral and vitamin premix was provided throughout the experiment. Crude glycerin was added to the basal diet at either 0, 5, 10 or 15% of diet DM. Diets were made isocaloric and isonitrogenous by the addition of ground corn and urea, respectively. Daily intake was measured based on individual orts. Samples of offered diets and orts were analyzed for DM, OM, CP, NDF, ADF, ether extract (EE) and total carbohydrates (TC). Data was submitted to ANOVA and regression with a 5% significance level. The inclusion of crude glycerin influenced the intake of nutrients ($P < 0.01$) when expressed as grams per day, percent BW, and grams per kilogram$^{0.75}$, with a quadratic response for all parameters evaluated. Overall, the highest theoretical nutrient intake in kilograms per day was between 3.81 and 5.14% glycerol inclusion. Only CP and EE, when expressed as percent BW and grams per day, resulted in higher theoretical intake for diets containing glycerin at 10.88 and 7.91% inclusion, respectively. Nutrient intake for all treatments was sufficient to meet the nutritional requirements and to keep the BCS within the desired to maintain the physiological status of the animals during the experimental period. Crude glycerin, when fed to lambs in a 50:50 forage-to-concentrate diet, can be included up to 5.14% of diet DM without negatively affect the intake of nutrients in grams per day and grams per kilogram$^{0.75}$.

Key Words: byproduct, energy, small ruminants

1490 Effects of corn particle size and neutral detergent fiber:starch ratio on in vitro neutral detergent fiber degradability.
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Reducing particle size is the most common technique to increase starch digestibility, especially for corn, and both the

amount and the size of starch source may affect the rumen environment. The objective of our study was to verify the effects of specific ranges of corn particle size and NDF:starch ratios on starch and NDF degradability (NDFd). The same batch of corn was milled using a Wiley mill with either a 1- or a 2-mm screen. The corn was sieved and separated using the following sizes: <250, 250 to 500, 500 to 1,180, and 1,180 to 2,000 μm. All sizes were analyzed for starch, CP, EE, and NDF. Oat hay and alfalfa were used separately to evaluate the effects of particle size on NDFd using the NDF:starch ratios of 1:1 and 1:1.25. Ratios were adjusted for each size class based on actual starch and NDF contents of both corn and forages. Higher ratios were excluded because the buffering capacity of the medium avoided changes in pH and NDF digestibility. Residual starch and NDF of the fermented samples were obtained at 3, 6, 9, 12, 24, and 48 h. Rates of digestion (kdStarch and kdNDF) were calculated using a first-order decay model and estimated indigestible starch and NDF using the 48 and 240 h fermentation residuals, respectively. Indigestible starch was numerically different across sizes. Data were analyzed according to a randomized complete block design with a factorial arrangement of treatments. The main tested effects were size, ratio, forage, and their interactions. Fermentation run was considered a random effect. With increasing particle size, starch decreased from 79 to 55%, NDF increased from 3.4 to 33.1%, EE increased from 2.17 to 3.78%, and CP increased from 6.40 to 8.21%. Both forage type and NDF:starch ratio did not have any effect ($P > 0.45$) on ivSD and kdStarch. As expected, kdStarch linearly increased ($P < 0.01$) with smaller particle size with no interaction with either forage or NDF:starch ratio, from 0.14 to 0.47 h^{-1}. Interaction was present ($P < 0.01$) between forage and particle size for ivSD and kdStarch, with more starch degraded for the two smallest sizes and alfalfa. Particle size, and not amount, affected NDF digestibility for both forages ($P < 0.01$), with consistently higher NDFd and kdNDF for the largest size. Particle size affected NDF fermentation more than amount for corn, even if the medium might have decreased the effect of larger amount of starch.

Key Words: in vitro, neutral detergent fiber, particle size, starch

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1491 Associations between residual feed intake and metabolite profiles and feeding behavior traits in feedlot cattle. M. D. Miller*[1], G. E. Carstens[1], J. M. Thomson[2], J. G. Berardinelli[2], M. R. Herrygers[2], J. White[2], L. O. Tedeschi[1], and P. K. Riggs[1], *[1]Texas A&M University, College Station, [2]Montana State University, Bozeman*.

Objectives of this study were to evaluate the effects of residual feed intake (RFI) classification on performance and feed efficiency in steers fed a high-grain diet and to examine associations between RFI and blood metabolite profiles and feeding behavior traits to identify RFI biomarkers. Performance, DMI, and feeding behavior traits were measured for 70 d in Angus crossbred steers ($N = 168$) using a GrowSafe system. Steers were classified into low- ($n = 52$), medium- ($n = 64$), and high- ($n = 52$) RFI groups based on ±0.5 SD from the mean RFI of 0.00 (SD = 0.82). Low-RFI steers consumed 17% less ($P < 0.0001$) DMI (9.05 vs. 10.89 ± 0.14 kg/d), had 18% lesser ($P < 0.0001$) feed:gain ratio (5.05 vs. 6.11 ± 0.10), and generated $95 per head more ($P < 0.001$) profit compared with high-RFI steers, even though ADG and carcass value were not affected by RFI classification. Blood samples were collected from steers with lowest RFI ($n = 25$) and highest RFI ($n = 24$) on Day 70 of the trial, and serum metabolite concentrations were analyzed using ^{1}H-NMR spectroscopy. Partial least squares (PLS; MetaboAnalyst) were used to examine associations between RFI and metabolites and feeding behavior traits. Of the 12 feeding behavior traits evaluated, 4 traits had variable of importance in projection (VIP) scores > 1.0, which included head-down (HD) duration, bunk visit (BV) duration, nonfeeding interval (NFI) duration, and head-down–to–meal duration ratio (HD:MD). The first 2 components of PLS accounted for 54% of between-animal variance in RFI. Steers with low RFI had longer ($P < 0.001$) NFI duration (less time at the bunk), 45% lower HD duration, 35% lower BV duration, and 32% lower HD:MD than high-RFI steers. Of the 44 metabolites detected by ^{1}H-NMR, 5 metabolites had VIP scores > 2, which included glycine, betaine, tyrosine, valine, and leucine. The first 2 components of PLS accounted for 34% of between-animal variance in RFI. Steers with low RFI had higher ($P < 0.001$) concentrations of glycine and lower ($P < 0.06$) concentrations of betaine, tyrosine, valine, and leucine than high-RFI steers. These preliminary results reveal that metabolomic profiling and feeding behavior traits may provide opportunities to identify biomarkers that are predictive of RFI in beef cattle.

Key Words: feedlot cattle, metabolites, residual feed intake

1492 Effects of acidity and silage type on lysine retention among two lipid-coated ruminally protected lysine products. J. N. Reiners* and D. W. Brake, *South Dakota State University, Brookings*.

Milk protein secretion among cattle consuming corn-based diets can be limited by metabolizable Lys. Therefore, ruminally protected AA (RPAA) are commonly included in cattle diets to increase metabolizable Lys intake. Previous data suggest that Lys associated with lipid-coated RPAA is reduced by greater diet moisture content. Effects of silage type and acidity on Lys associated with lipid-coated RPAA products (EB and EC) were evaluated over time. Crystalline Lys and Lys mixed with lipid in amounts equal to either EB or EC served as negative controls. Controls and each lipid-coated RPAA (4 g) were placed in mesh bags (10 by 20 cm; pore size = 50 mm) and mixed with

Table 1493. Effect of DIM on fecal composition and nutrient digestibility.

	Low DIM, AM	Low DIM, PM	High DIM, AM	High DIM, PM	SED	*P* values		
						Group	Time	Group × Time
Fecal nutrient								
Dry matter	11.96^{B}	11.61^{B}	13.43^{A}	13.30^{A}	0.46	0.01	0.46	0.74
Crude protein	17.85^{A}	16.49^{B}	17.57^{A,B}	17.01^{A,B}	0.60	0.73	0.03	0.36
ADF	29.82^{B}	32.62^{A}	31.57^{A,B}	32.22^{A,B}	0.67	0.40	0.001	0.01
NDF	46.19^{B}	49.59^{A}	47.55^{A,B}	48.06^{A,B}	0.94	0.91	0.01	0.03
Starch	8.63^{A}	6.93^{A,B}	6.66^{B}	7.31^{A,B}	0.84	0.26	0.36	0.06
Ash	10.11^{B}	11.04^{A,B}	11.06^{A,B}	11.45^{A}	0.37	0.14	0.01	0.26
Apparent digestibility								
pdNDF	67.85	68.25	68.83	70.13	2.69	0.57	0.62	0.79
NDF	51.50	52.28	52.22	53.74	2.60	0.67	0.47	0.81
Protein	65.19	67.99	66.84	66.99	1.66	0.70	0.29	0.33
Starch	89.13^{B}	91.43^{A}	91.97^{A}	90.87^{A,B}	1.06	0.25	0.42	0.03

either alfalfa silage or corn silage at 2 different levels of acidity (pH = 4.6 or pH = 6.6) for 0, 6, 12, or 24 h. Silage pH was modified by mixing with 10% (wt/wt) NaOH. After removal, mesh bags were rinsed with cold water and contents of each bag were lyophilized. Lipid-associated Lys was subsequently determined by analyzing total free Lys content after removal of triacylglycerols and free fatty acids with hexane:methanol. Dissociation kinetics were calculated using the nonlinear procedure of SAS, and data were analyzed as a completely randomized design. As expected, the proportion of Lys that dissociated after initial contact (ID) from the negative controls was complete (100 ± 2.5%) and indicated that Lys analyses reflected measures of lipid-associated Lys. The ID from RPAA was less ($P = 0.02$) for EB (20.4 ± 2.8%) than for EC (31.3 ± 2.8%). Additionally, ID increased as acidity increased when RPAA was mixed with corn silage; however, ID was not affected by acidity when mixed with alfalfa silage (silage × pH ≤ 0.01). Amounts of Lys that slowly dissociated (SD) from RPAA during silage incubation were greater ($P = 0.01$) for EB (59.6 ± 4.8%) than for EC (38.4 ± 4.8%). Furthermore, SD increased with greater acidity in corn silage but did not differ among alfalfa silage with either greater or lesser acidity (silage × pH = 0.01). Rate of Lys dissociation was not different among either RPAA ($P = 0.40$; 10.9 ± 1.9%/h) and was not affected by acidity ($P = 0.73$) or silage type ($P = 0.62$). Lipid-associated Lys remaining at 24 h for EB (20.1 ± 5.7%) was not different ($P = 0.24$) compared with that for EC (30.3 ± 5.7%).

Key Words: amino acid, cattle, lysine

1493 Relationship of days in milk to nutrient digestibility in lactating multiparous cows.

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The objective was to determine if differences in days in milk (DIM) affect apparent nutrient digestibility in lactating multiparous cows fed the same ration. Of 136 cows in a multiparous, high-producing pen on a 1,000-cow commercial dairy, 24 were selected for sampling based on differences in DIM and milk yield (Low DIM: $n = 12$, milk = 64 ± 6 kg, and DIM = 85 ± 6; High DIM: $n = 12$, milk = 55 ± 4 kg, and DIM = 158 ± 15). Milk, fecal, and TMR samples were collected once daily for 10 consecutive days. Samples were collected in the morning on 6 d and the afternoon on 4 d. Individual cow milk and fecal samples were composited into one daily milk or fecal sample per DIM group and analyzed for nutrient composition. In addition, daily fecal composite and TMR samples were analyzed for apparent digestibility of potentially digestible NDF (PdNDFd), NDF (NDFd), protein (Protd), and starch (Starchd). Fecal nutrient composition and apparent digestibility data were analyzed using the Glimmix procedure of SAS. The model included fixed effects of group, sampling time, and their interaction. Day was included as a repeated measure. The CORR and REG procedures were used for comparing daily variations in digestibility with milk yield and composition. For fecal nutrient composition, DIM × sampling time was significant for ADF and NDF, due to sampling time differences in the low-DIM group (Table 1). There was a group effect on fecal DM in which DM was lower in low-DIM cows. Time effects were also observed, with CP being higher before noon and ADF, NDF, and ash being higher after noon. There was no effect of DIM on PdNDFd, NDFd, Protd, or Starchd. There was an effect of DIM × sampling time on Starchd ($P = 0.03$) due to higher Starchd at the before-noon sampling for high-DIM cows ($P = 0.03$). There were no significant correlations of digestibility measures with milk yield. A 1% increase in PdNDFd ($P = 0.02$) and NDFd ($P = 0.006$) was associated with a 0.04 and 0.05% increase, respectively, in milk fat percentage. A 1% increase in Starchd ($P = 0.003$) was associated with a 0.03% increase in milk protein percentage. Because DIM had minimal effects on digestibility measures, it is likely not necessary to consider DIM when selecting cows for estimation of nutrient digestibility within a high-producing pen.

Key Words: days in milk, fecal composition, nutrient digestibility

1494 Effects of animal and diet characteristics on digestibilities of dry matter, fiber, and starch in lactating cows. R. A. De Souza*[1], R. J. Tempelman[1], M. S. Allen[1], J. K. Bernard[2], B. Weiss[3], and M. J. VandeHaar[1], *[1]Michigan State University, East Lansing, [2]University of Georgia, Tifton, [3]The Ohio State University, Wooster*.

Our objective was to determine the effects of DMI, BW, and diet characteristics on total tract digestibilities of DM, NDF, and starch (DMD, NDFD, and StarchD, respectively) in high-producing cows. The database was constructed with individual observations of digestibilities, ingredients, and chemical composition of diets; BW and DMI; experimental design; and treatment arrangement. The data set contained 1,942 observations on 635 cows from 56 studies with >6 observations per treatment in Michigan, Ohio, and Georgia. Forage sources included corn, alfalfa, wheat straw, and orchardgrass. Nutrient digestibility means were 66 ± 6, 42 ± 11, and 93 ± 5% for DMD, NDFD, and StarchD, respectively. Diet nutrient contents (% DM) were 31 ± 5% NDF, 27 ± 6% starch, 2.6 ± 1.2% FA, and 17 ± 1.4% CP. Dry matter intake and BW were 23 ± 5 and 669 ± 79 kg, respectively. Data was analyzed using a mixed model with HPMIXED procedure of SAS. The full model included linear and quadratic effects of diets, $BW^{0.75}$, DMI, and all possible 2-way interactions between diet variables and DMI as fixed effects. Cow, block, period, and study were used as random effects. Best fitting reduced models were generated using backward and stepwise regression procedures. Interactions were not significant. A simplest model was generated using only DMI and the random effects. The backward, stepwise, and simplest models were cross-validated using five folds, and the resulting correlations coefficients across studies (CORR) were compared by *t* test. The model that resulted in the highest CORR and lowest number of variables was accepted as the best fitting model for each nutrient digestibility. The best fitting prediction equations were DMD = 69 − 0.20 × DMI (MSE = 8.5, r^2 = 0.68, CORR = 0.20); NDFD = 32 + 0.26 × grass + 0.46 × starch + 3.4 × FA + 0.83 × DMI − 0.020 × $starch^2$ − 0.34 × FA^2 − 0.030 × DMI^2 (MSE = 26, r^2 = 0.80, CORR = 0.41); and StarchD = 97 − 0.30 × DMI (MSE = 3.1, r^2 = 0.84, CORR = 0.22); grass, starch, and FA are expressed as percentage of DM and DMI is expressed as percentage of $BW^{0.75}$. Our results confirm that digestibility was reduced as DMI increased but at a lower rate than the previous equation used by NRC (2001). Digestibility of DM and StarchD can be predicted based on only DMI; however, NDFD required diet characteristics in addition to DMI. Starch levels > 25% and FA > 5% dramatically reduced NDFD.

Key Words: digestibility, intake, model, neutral detergent fiber, starch

1495 Effects of silage type and inclusion level on ruminal characteristics and feeding behavior of feedlot steers. P. R. B. Campanili*[1], J. O. Sarturi[1], S. J. Trojan[1], M. A. Ballou[1], L. A. Pellarin[1], J. D. Sugg[2], L. A. Ovinge[1], A. Alrumaih[1], and A. A. Hoffman[1], *[1]Texas Tech University, Lubbock, [2]Angelo State University, San Angelo, TX*.

Silage type and level of inclusion on beef cattle finishing diets ruminal fermentation and degradability, digestibility, and feeding behavior were evaluated. In Study 1, beef steers (*n* = 6; BW = 363 ± 23 kg) fitted with ruminal cannula were used (6 × 4 unbalanced Latin square design). Treatments (*n* = 4) consisted of silage type (corn = BH8895 and sorghum = AF7401) and silage inclusion (10 or 20%, DM basis). Each period consisted of 14 d for adaptation and 7 d for collections. Steers were individually fed ad libitum once daily. Silage degradability was studied by in situ technique. In Study 2, the same technique was used to study the degradability of intact ensiled sorghum grain (*n* = 10; 18.9-L units; 112 d of storage; 2 sites). Beef steers (*n* = 3; BW = 547 ± 56 kg) fed a growing diet were used. Data were analyzed using Glimmix procedure of SAS (day as repeated measure). Steers fed 20% sorghum silage had greater DMI (P = 0.03) and total VFA (P = 0.01) but tended (P = 0.07) to the least propionate molar proportion compared with other treatments. Steers fed 10% corn silage had the greatest (P = 0.04) ruminal butyrate and the least (P < 0.01) ruminal pH average compared with other treatments, which reached nadir at 5.62 (P < 0.01) 12 h after feeding. Additionally, the 10% corn silage treatment tended (P = 0.09) to have the least in vitro methane production. Starch digestibility tended (P = 0.08) to peak for steers fed 10 and 20% corn silage (98%) and bottom for steers fed 20% sorghum silage (92%). Steers fed corn silage had greater ($P \leq 0.01$) total tract apparent digestibility (11% DM and 32% NDF), lower (P < 0.01) acetate/propionate, and 34% greater (P < 0.01) silage ruminal degradation and tended (P = 0.07) to chew 1.1 h/d less compared with steers fed sorghum silage diets. Steers fed 20% silage chewed and ruminated more ($P \leq 0.04$), degraded more (P < 0.01) NDF, and had greater (P < 0.01) acetate/propionate but less DM digestibility than 10% silage-fed steers. Sorghum grain ruminal degradability reached 52% at 96 h. Replacement of corn silage with sorghum silage in beef finishing diets requires adjustments to balance dietary energy. Sorghum material induced a desirable roughage effect in feeding behavior but also offered potential to be improved regarding fiber digestibility and intact grain ruminal degradability.

Key Words: corn, silage, sorghum

1496 Identification of biological pathways involved in residual feed intake in Hereford cattle through gene set enrichment analysis. J. L. Mutch*[1], M. Neupane[1], C. M. Seabury[2], H. L. Neibergs[1], P. C. Tizioto[3], D. J. Garrick[4], M. S. Kerley[3], D. W. Shike[5], J. E. Beever[5], J. F. Taylor[3], U. S. Feed Efficiency Consortium[3], and K. A. Johnson[1], *[1]Department of Animal Sciences, Washington State University, Pullman, [2]College of Veterinary Medicine, Texas A&M University, College Station, [3]University of Missouri, Columbia, [4]Department of Animal Science, Iowa State University, Ames, [5]University of Illinois, Urbana*.

Understanding the biological differences between animals with different feed efficiency phenotypes enhances our understanding of the trait. The objective was to use gene set enrichment analysis-SNP (GSEA-SNP) to identify gene sets (GS) associated with the residual feed intake (RFI) phenotype in Hereford cattle. Feed intake and BW gain were measured on 847 steers and heifers at Olsen Ranches in Harrisburg, NE. Animals were genotyped using the Illumina BovineSNP50 (n = 358) or BovineHD BeadChips (n = 459). BovineSNP50 genotypes were imputed with Beagle 4.1 to the density of the Illumina BovineHD BeadChip using the BovineHD genotyped Herefords as a reference. Genomewide association analysis (GWAA) was performed using GRAMMAR mixed model software, and the most significant SNP for each of 19,723 genes from the UMD-3.1 reference assembly were selected as a proxy for that gene. Gene proxies were considered only for SNP that were located within 8.5 kb of a gene, as this is representative of the average haplotype block size in Herefords (determined by a haplotype block analysis). Following GWAA, GSEA-SNP was conducted with 4,389 GS from Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), Reactome, Biocarta, and Panther. Significance was calculated using the null distribution estimated from 10,000 permutations for each GS using GenABEL in R. An enrichment score was calculated for each GS using a modified Kolmogorov–Smirnov statistic and normalized (NES) based on the size of each GS. The GS associated (NES > 3.0) with RFI were centrosome (37 leading edge genes [LEG]) and cytoskeleton (97 LEG) from GO and peroxisome from KEGG (30 LEG). The centrosome GS is involved in mitosis and cell cycle regulation and the peroxisome GS is involved in lipid homeostasis. The cytoskeleton organization GS contained four differentially expressed LEG: *Type I keratin 19* (*KRT19*), *α 1 actin I* (*ACTA1*), *α 1 actinin* (*ACTN1*), and *cysteine and glycine-rich protein 3* (*CSRP3*). These genes were previously found by this consortium to be differentially expressed between the high- and low-RFI groups of Herefords. In the low-RFI group, expression of *KRT19* in the liver was greater than in the high-RFI cattle. Low-RFI Herefords also had reduced expression of *ACTA1* in the liver and pituitary, *ACTN1* in the hypothalamus, and *CSRP3* in the liver. Alterations in lipid metabolism and cell cycle regulation are associated with the RFI phenotype. This project was supported by AFRI Competitive Grant no. 2011-68004-30214 from the USDA National Institute of Food and Agriculture.

Key Words: cattle, gene set enrichment analysis, residual feed intake

1497 Updating equations to estimate dry matter intake of Nellore and beef crossbred cattle. L. F. Costa e Silva*[1], S. C. Valadares Filho[2], P. P. Rotta[3], J. A. G. Azevedo[4], F. F. Silva[1], A. C. B. Menezes[1], and B. C. Silva[3], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [4]Universidade Estadual de Santa Cruz, Ilheus, Bahia, Brazil*.

Dry matter intake is the most important variable that affects animal performance, mainly in beef cattle due to economic impact and its complex gastrointestinal system with peculiar metabolic functions. A database with 1,459 animals, being 1,188 Nellore and 271 beef crossbred cattle, was developed to generate equations estimating DMI for animals raised on feedlot. Variables such as DMI, BW, metabolic BW (mBW), ADG, and level of concentrate (LC) were collected. First of all, a PROC CORR was used to evaluate which variables are significantly correlated with DMI. The variables mBW, LC, and ADG presented the highest correlation with DMI, and those were chosen to be part of the equations generated. The range of DMI in this database was from 2.96 to 12.3 kg/d whereas LC was from 0 to 100% and ADG was from −0.36 to 2.26. After all, statistical models were fitted by the cross-validation procedure. Also, differences between genetic group (Nellore and beef crossbred cattle) were evaluated, which allowed us to develop two different equations. Then, the following equations were developed to estimate DMI of Nellore and beef crossbred cattle, respectively: for Nelore cattle, DMI $= -2.406 + 0.064 \times LC - 0.00065 \times LC^2 + 0.070 \times BW^{0.75} + 4.384 \times ADG - 1.255 \times ADG^2$ ($R^2 = 0.797$), and for beef crossbred cattle, DMI $= -4.355 + 0.0598 \times LC - 0.00049 \times LC^2 + 0.128 \times BW^{0.75} + 3.974 \times ADG - 1.128 \times ADG^2$ ($R^2 = 0.717$). From this, if we derive these equations in function of level of concentrate, we can know at which amount of concentrate each genetic group is able to reach the maximum DMI. Therefore, Nellore cattle reach maximum DMI when 49.2% of concentrate is provided in diet whereas beef crossbred cattle reach this amount for 61.0% of concentrate. This statement proves that Nellore cattle are more sensible to high amounts of concentrate than beef crossbred cattle. Moreover, if we derive these equations in function of ADG, we are able to know at which ADG the animals reach maximum DMI. For Nellore and beef crossbred cattle, the maximum DMI is reached when

ADG is 1.75 and 1.76 kg/d, respectively. Therefore, Nellore cattle are more sensible when level of concentrate is increased in diet when compared with beef crossbred cattle.

Key Words: beef crossbred cattle, cross-validation, level of concentrate, Nellore

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1498 Rumen bacterial species associate with residual feed intake in beef cattle.

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Residual feed intake (RFI) describes an animal's feed conversion efficiency independent of phenotypic performance. The objective of this study was to quantify differences in ruminal bacteria between the most efficient animals and the most inefficient animals and any interaction with rumen sample fraction. One-hundred fifty Red Angus cattle were allocated to three groups according to sex and herd origin. Animals were fed in confinement for at least 78 d to determine the RFI category for each. Within each contemporary group, the two most efficient (n = 6) and least efficient animals (n = 6) were selected. Rumen solids and fluid were collected immediately after slaughter. Bacterial DNA extraction from the solid fraction included mechanical homogenization followed by enzymatic and bead beating lysis for all samples. Real-time quantitative PCR was used to examine the relative abundance of specific ruminal bacteria compared with the geometric mean of two universal 16S rRNA primers. Data were analyzed using the MIXED procedure of SAS 9.3. Fixed effects in the model included RFI category, rumen fraction, RFI × fraction, and sex. Individual animal was the experimental unit and incorporated into the statistical model as a random effect nested within group. Of the nine species evaluated, *Succinivibrio dextrinosolvens* was the most abundant, averaging 1.8% of 16S rRNA copy number. Results indicated most efficient cattle had a 6-fold decrease (P = 0.04) in relative abundance of *S. dextrinosolvens* and also had a 4-fold reduction (P = 0.02) in *Anaerovibrio lipolytica*. Although most efficient cattle tended (P = 0.09) to have greater relative abundance of *Eubacterium ruminantium*, a tendency (P = 0.10) for an RFI × fraction effect indicated the greatest differences were between the solid fraction of most efficient and least efficient cattle. Fraction effects were observed for *Butyrivibrio proteoclasticus* (P < 0.001) and *Selenomonas ruminantium* (P < 0.001) as each were increased within the solid fraction compared with the liquid. An RFI × fraction effect (P = 0.01) also was observed for *Fibrobacter succinogenes*, with a greater relative abundance in the liquid compared with the solid fraction for least efficient cattle. No effect of RFI or fraction was observed for *Megasphaera elsdenii* or *Prevotella bryantii*. These findings indicate large differences in RFI phenotypes in beef cattle are associated with bacterial species in the rumen, and they may have a role in conferring feed efficiency.

Key Words: bacteria, residual feed efficiency, rumen

1499 The association between body condition score, residual feed intake, and hyperketonemia.

F. M. Tiberio*[1], R. S. Pralle[1], C. A. Getschel[1], R. C. Oliveira[1], S. J. Bertics[1], K. A. Weigel[1], R. D. Shaver[1], L. E. Armentano[2], and H. M. White[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]University of Wisconsin – Madison, Madison*.

The transition period in dairy cows is associated with the onset of negative energy balance and body fat mobilization. Mobilized lipids can lead to excessive ketone production. The objective of this trial was to characterize the relationship between hyperketonemia (HYK) and milk production, BCS, and residual feed intake (RFI). Blood and milk samples were collected twice weekly from cows 5 to 18 d in milk (DIM) for a total of 4 samples. Hyperketonemia was diagnosed using the Precision Xtra Meter and defined as blood β-hydroxybutyrate (BHBA) ≥ 1.2 mmol/L. Cows were treated on diagnosis. Dry period (−28 DBCS), calving, and final blood sampling BCS was recorded. Previous midlactation production and DMI were used to calculate RFI by subtracting predicted energy intake from the observed energy intake. Effect of milk composition, milk yield, lactation number, BCS, and previous RFI on the observed maximum BHBA concentration (MAXBHBA) was determined using PROC MIXED of SAS 9.4. Least squares means ± SE are reported. Of the 570 cows sampled, 19.7% were diagnosed with HYK. Mean DIM at the first positive HYK test was 9 ± 0.9 d and the average BHBA concentration at the first positive HYK test was 1.53 ± 0.14 mmol/L. MAXBHBA was greater ($P \leq 0.05$) for multiparous cows compared with primiparous cows. Milk fat content was increased (4.33 vs. 4.69 ± 0.05%; $P < 0.0001$), milk protein content was decreased (3.60 vs. 3.40 ± 0.02%; $P < 0.0001$), somatic cell count was decreased, and milk yield was increased (44.02 vs. 47.47 ± 1.46 kg/d; $P < 0.0001$) in the first 30 DIM for cows positive for HYK compared with negative cows. Cows with a DBCS ≥ 4.0 had greater MAXBHBA (0.88 vs. 1.28 ± 0.08 mmol/L; $P \leq 0.05$) than cows with lower BCS. Cows that lost >0.75 BCS units after calving had greater ($P \leq 0.05$) MAXBHBA than cows that lost ≤0.75 BCS units. MAXBHBA was not significantly correlated to RFI. Prompt diagnosis and treatment of HYK appears to prevent HYK-associated decreases in milk production. Avoiding overconditioning of dry cows and excessive fat mobilization during the transition period may decrease HYK incidence; however, previous lactation RFI does not appear to be correlated to developing HYK.

Key Words: body condition score, hyperketonemia, residual feed intake

1500 Effects of arginine infusion through jugular vein on the milk performance and casein synthesis in midlactation cows. M. Z. Wang*, *Yangzhou University, Yangzhou, P. R. China*.

Previous studies show that milk protein yield increases with arginine infusion (Doepel and Lapierre, 2011). Our previous in vitro work by Chen et al. (2013) demonstrates that arginine increases casein protein synthesis in bovine mammary epithelial cells and that arginine plays an important role in the transcriptional regulation of casein genes and mTOR-related genes in bovine mammary epithelial cells (Wang et al., 2014). Subsequently, our Wistar rats feeding trail found that a 2x Arg group had significant effects on the mammary gland development and its casein protein synthesis (Hu et al., 2015). But whether arginine promotes the growth of the cow mammary tissue and casein expression is unknown. Therefore, this study was performed to investigate the responses of milk yield and milk composition for arginine infusion by midlactating Holstein cows. Six healthy lactating cows at similar lactation stages with similar weights, parities, milk yields, and body conditions were divided into 3 groups (2 for each group), casein model group (control group), arginine infusion group (37.66 g arginine contenting 12.10 g N/d), and alanine isonitrogen group (77.24 g alanine containing N 12.13 g N/d), respectively, in a 3 × 3 Latin square trail with a 7-d infusion plus a 15-d interval per period. The milk performance, casein content, and casein gene expression were detected. The results showed that at Day 5, the arginine infusion group was higher than the casein model group in the contents of milk protein and nonfat milk solids ($P < 0.05$), whereas at Day 6, the arginine infusion group was higher in milk fat content compared with the alanine isonitrogen group ($P < 0.05$). As for the milk casein contents, α-casein in the casein model group was lower than these in the other 2 groups ($P < 0.05$), β-casein had no difference between groups ($P > 0.05$), and κ-casein of the arginine infusion group was the highest among the groups ($P < 0.05$). In addition, arginine the infusion group had significantly higher expression in genes CSN1S1 and CSN1S2 ($P < 0.05$), and numerically higher expression in gene CSN3 compared with the other 2 groups. We therefore concluded that for the first time, arginine infusion increases the contents of α-casein and κ-casein in milk as well as their gene expressions in mammary tissue from dairy cows, which is contributed to the improvements of milk protein content and milk quality.

Key Words: arginine, casein, jugular infusion, milk performance

1501 Diet starch content and fermentability affects feed intake and milk yield of cows in the postpartum period. R. I. Albornoz*, *Michigan State University, East Lansing*.

The objective of this study was to evaluate the effects of diet starch content and fermentability fed during the postpartum (PP) period on DMI, yields of milk (MY) and milk components, and body reserves. Fifty-two multiparous Holstein cows were used in a randomized block design with a 2 × 2 factorial arrangement of treatments. Diets were formulated to 22 (LS) or 28% (HS) starch with dry ground corn (DGC) or high-moisture corn (HMC) as the primary starch source. Treatments were fed from 1 to 23 d PP and then switched to a common diet until 72 d PP to measure carryover (CO) effects. Treatment period (TP) diets were formulated for 22% forage NDF and 17% CP, and starch concentration was adjusted by substitution of corn grain for soyhulls. The diet for the CO period was formulated to 20% forage NDF, 17% CP, and 30% starch. Throughout the experiment, both DMI and MY were measured daily, and milk components, BCS, and back fat thickness (BFT) were measured weekly. During TP, DGC increased DMI by 2.2 kg/d compared with HMC ($P < 0.01$) but tended to increase DMI more with HS (3.4 kg/d) than LS (1 kg/d; interaction, $P = 0.12$). Treatments also interacted over time; DGC increased DMI throughout the TP for HS but only after the first week for LS compared with the HMC treatments ($P < 0.01$). There was no main effect of starch content on DMI. The effect of corn source diminished over time during the CO period ($P = 0.03$), with no main effects of treatment on DMI. Dry ground corn increased yields of milk by 2.6 kg/d ($P = 0.12$), 3.5% fat-corrected milk (FCM) by 4.3 kg/d ($P = 0.02$), fat by 165 g/d ($P = 0.03$), and protein by 165 g/d ($P = 0.01$) compared with HMC, with no effect of starch content throughout the TP. Starch source and content interacted ($P < 0.05$) to affect yields of fat and FCM during the CO period, which were greater for DGC-HS and HMC-LS (1.78 and 52.1 kg/d, respectively) than for DGC-LS and HMC-HS (1.62 and 48.6 kg/d, respectively). Dry ground corn tended to decrease BCS loss until the third week of TP ($P < 0.15$) compared with HMC but had no effect overall. No effects of treatment were detected for BFT during TP but HMC increased BFT 0.1 mm ($P = 0.04$) during the CO period. Ruminal fermentability of starch is an important consideration for diets of cows in the PP period.

Key Words: dry corn, fresh cows, high-moisture corn

Table 1503.

Item	LMP55	LHMP55	HMP43	SE
wk -6 to calving				
DMI, kg/d	14.6^{by}	14.6^{by}	16.4^{ax}	0.3
Plasma total protein, g/dL	7.5	7.4	7.7	0.1
Plasma urea nitrogen, mg/dL	11.0^{cz}	13.4^{by}	14.8^{ax}	0.4
wk 1 to 12				
DMI, kg/d	25.7	24.7	24.9	0.5
Milk, kg/d	51.3^{x}	47.5^{y}	47.8^{xy}	1.2
Solids-corrected milk, kg/d	50.9	47.9	49.3	1.1
Fat, %	4.08	4.14	4.34	0.10
True protein, %	3.08	3.17	3.19	0.04
wk 1 to 2				
Plasma total protein, g/dL	7.1	7.1	7.3	0.1
Plasma albumin, g/dL	3.5	3.4	3.4	0.1
Plasma nonesterified fatty acid, uEq/L	547	502	584	33
Blood β-hydroxybutyrate, mmol/L	0.65	0.67	0.74	-

^{abc} $P \leq 0.05$
^{xyz} $P \leq 0.10$

1502 Effects of feeding a histidine-deficient diet on lactational performance of dairy cows.

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A 10-wk randomized complete block design study with 24 Holstein cows (87 ± 22 days in milk and 630 ± 56 kg BW) was conducted to determine the effects of feeding a His-deficient diet on lactational performance of dairy cows. Following a 2-wk covariate period, cows were blocked by days in milk, milk yield, and parity and randomly assigned to one of the following 2 treatments: His-adequate diet (HAD; digestible His [dHis] supply of 75 g/d, or 2.8% of MP requirements) and His-deficient diet (HDD; dHis supply of 50 g/d, or 2.0% of MP requirements). Both HAD and HDD were supplemented with rumen-protected (RP) Met (Mepron; Evonik Nutrition & Care GmbH) and RP Lys (AjiPro-L; Ajinomoto Co., Inc.) supplying dMet and dLys at 2.5 and 2.4% and 7.5 and 7.2%, respectively, of MP requirements. At the end of the study, HDD was supplemented with RP His (an experimental product supplying 9.3 g/d of dHis; total dHis supply of 62 g/d, or 2.5% of MP requirements) for 9 d. The diets consisted of (DM basis) 45% corn and 20% alfalfa silages and 35% concentrates. Diets contained 16.3 and 16.2% CP, respectively, and supplied MP and NE_L in excess of cow requirements. Dry matter intake and yields of milk, energy-corrected milk, and milk protein were decreased ($P \leq 0.02$) by HDD (25.4, 37.6, 34.4, and 1.07 kg/d, respectively) compared with HAD (27.1, 40.5, 37.4, and 1.18 kg/d, respectively). Milk urea nitrogen was decreased ($P < 0.01$) by HDD vs. HAD. Feed and energy-corrected milk feed efficiencies, milk nitrogen efficiency, milk fat and protein concentrations, milk fat yield, and BW change of the cows were not affected by treatments ($P \geq 0.12$). Blood hemoglobin concentration was 5.4% lower ($P < 0.01$) in cows fed HDD compared with cows fed HAD, suggesting a provision of about 24 g of His from this endogenous depot during the 8-wk experimental period. Plasma His concentration was decreased ($P < 0.01$) by HDD vs. HAD. Supplementation of RP His increased DMI (26.6 vs. 25.1 kg/d; $P < 0.01$) but did not affect milk yield (36.0 vs. 34.8 kg/d; $P = 0.28$) compared with HDD during the last 9 d of the study. Overall, feeding a diet deficient in His but supplying adequate MP, Met, and Lys had negative effects on DMI and lactational performance of dairy cows. The effect on DMI was reversed when RP His was supplemented.

Key Words: dairy cow, dry matter intake, histidine

1503 The effect of metabolizable protein supply for dry Holstein dairy cows on periparturient feed intake, metabolism, and lactation performance.

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Some nutritionists increase MP supply for dry cows to improve subsequent lactation performance and health based on field observations. This study determined the effect of MP supply during the dry period on DMI, metabolism, and early lactation performance. Eighty Holstein cows that had completed ≥1 lactation were randomly assigned to treatments: 1) a 55-d dry period with approximately 84 g MP/kg DMI in the far-off (13.1% CP, 9.4% starch, and 51.7% NDF) and close-up (12.9% CP, 14.9% starch, and 47.0% NDF) diets (LMP55), 2) a 55-d dry period with approximately 84 g MP/kg DMI in the far-off diet (13.1% CP, 9.4% starch, and 51.7% NDF) and approximately 108 g MP/kg DMI in the close-up diet (14.5% CP, 15.1% starch, and 43.0% NDF; LHMP55), and 3) a 43-d dry period with approximately 108 g MP/kg DMI in a 1-group

diet (14.5% CP, 15.1% starch, and 43.0% NDF; HMP43). Close-up diets were fed for 3 wk before expected calving. Dry diets supplied ≥29 g Met/d and ≥91 g Lys/d. A fresh diet (15.6% CP, 21.7% starch, and 33.5% NDF) was fed for 2 wk and then a high diet (15.2% CP, 26.1% starch, and 30.2% NDF) was fed for 10 wk. Diets were modeled with CNCPS version 6.5. Cows were individually fed 1x/d, group housed, and milked 3x/d. Milk was sampled weekly. Coccygeal blood was collected −3 to 2 wk relative to calving. Data were analyzed as a completely randomized design by ANOVA with the MIXED procedure of SAS with model effects of treatment, time, and treatment × time. Metabolism and lactation performance were not improved by providing additional MP during the dry period compared with a lower MP diet that met the Met and Lys requirements.

Key Words: dry period, metabolizable protein, transition cow

1504 Meta-analysis to predict amino acids limiting dairy cattle performance. I. J. Lean*[1], M. B. De Ondarza[2], C. J. Sniffen[3], and K. E. Griswold[4], *[1]Scibus, Camden, Australia, [2]Paradox Nutrition, West Chazy, NY, [3]Fencrest, LLC, Holderness, NH, [4]Kemin Industries, Inc., Des Moines, IA*.

Meta-analytic methods were used to provide statistical relationships between estimated MP (EMP) AA supply (g or g/ME) and milk protein content, milk protein percentage, and milk yield in lactating dairy cows. Sixty-three research publications (258 individual observations) were identified through a search of published literature using 3 search engines and met the criteria for inclusion in the meta-analysis. An advanced nutrition model (CNCPS 6.5 with NDS platform; RUM&N Sas, Italy) was used to determine dietary nutrient parameters including EMP AA. Two approaches were used to analyze the data: 1) a mixed models weighted analysis with a random effect of study to determine whether the explanatory variables predicted cow responses and 2) a classical effect size meta-analytical evaluation of responses to treatment. Regardless of the analytical approach or method of expression (g or g/ME), EMP Met increased milk protein yield, milk protein percentage, or milk yield, confirming that it can be first limiting in lactating dairy cow diets. With a difference of 0.07 units EMP His (g/ME) (1.13 vs. 1.20 for control and treatment, respectively), effect size analysis determined that each additional unit of EMP His (g/ME) increased milk protein yield by 1.72 kg, identifying His as a possible limiting AA. Milk yield increased by 3.28 kg/unit of EMP Trp (g/ME) (0.60 vs. 0.616 for control vs. treatment, respectively). Milk true protein yield was improved by EMP Leu (g). Estimated MP Lys (g or g/ME) did not increase responses in production outcomes. However, mean EMP Lys supply was lower than typically recommended and the change with treatment was minimal (157 vs. 162 g; 6.36 vs. 6.38% MP). This meta-analysis supports other research indicating the positive impact of Met and His as limiting AA for protein synthesis and suggests Leu, Trp, and Lys be given greater consideration in future research.

Key Words: amino acids, meta-analysis, milk protein

1505 Influence of essential amino acid balancing postpartum on lactation performance by dairy cows through a meta-analysis. L. F. Ferraretto*[1], C. S. Ballard[1], C. J. Sniffen[2], and I. Shinzato[3], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Fencrest, LLC, Holderness, NH, [3]Ajinomoto Heartland Inc., Chicago, IL*.

A meta-analysis was performed to evaluate the impact of dietary individual essential AA concentration (g of AA/Mcal of ME) on lactation performance by dairy cows during the initial 4 wk of lactation. The data set comprised 20 unpublished feeding trials evaluating the effect of lysine or lysine/methionine supplementation. Diets were formulated with CPM/CNCPS, which provided a complete dietary AA profile. Data were analyzed using Proc Mixed of SAS with treatments as fixed effects and trial as a random effect. Positive relationships between methionine and milk and milk protein yields were observed ($P < 0.10$ and $P < 0.07$, respectively) during wk 1 to 4. Actual and energy-corrected milk (ECM) yields increased ($P < 0.04$ and $P < 0.08$, respectively) along with lysine concentration on wk 1, 2, and 4 whereas milk protein yield increased ($P < 0.03$) during the 4 initial weeks of lactation. Arginine and threonine were negatively related to milk fat content and yield ($P < 0.07$ and $P < 0.10$, respectively) on wk 3 and 4. Quadratic relationships between milk or milk protein yields and dietary concentrations of leucine and phenylalanine ($P < 0.06$ and $P < 0.09$, respectively) were observed during wk 1 to 4. Isoleucine concentration was negatively related to ECM and milk protein yields ($P < 0.09$ and $P < 0.07$, respectively) during wk 3 and 4 and to milk and milk fat yields ($P < 0.09$ and $P < 0.05$, respectively) on wk 3. Dietary valine was positively related to ECM ($P < 0.10$) and negatively related to milk protein concentration ($P < 0.08$) on wk 2 and 3. On wk 3 and 4, a positive relationship between milk yield and valine was observed ($P < 0.08$). Dietary histidine was positively related to milk yield ($P < 0.07$) but negatively related to milk protein content ($P < 0.06$) on wk 2 to 4. Concentration of tryptophan was negatively related to ECM ($P < 0.07$), milk fat content ($P < 0.03$), and yield ($P < 0.02$). Overall, benefits on lactation performance were observed with increased concentrations of methionine, lysine, valine, and histidine. In contrast, isoleucine and tryptophan were negatively related to lactation performance whereas arginine and threonine depressed milk fat. These results underscore the importance of AA balancing beyond lysine:methionine ratio when formulating diets for early lactation dairy cows.

Key Words: amino acids, lactation performance, postpartum

1506 Canola meal in dairy cow diets during early lactation increases production compared with soybean meal. S. A. E. Moore*[1] and K. F. Kalscheur[2], *[1]University of Wisconsin-Madison, Madison, [2]USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI*.

Replacement of traditional protein sources such as soybean meal (SBM) with canola meal (CM) has resulted in increased milk yield for dairy cows in mid to late lactation. The objective was to determine performance of early lactation dairy cows fed diets formulated with CM or SBM as the main protein source at either a high (HI; 17.6%) or low (LO; 15.4%) CP concentration. Seventy-nine multiparous Holstein cows (mean ± SD, 2.76 ± 0.87 parity) received the treatment diet beginning at calving. Cows were blocked by calving date and maintained the same treatment assignment until the experiment ended at wk 16 of lactation. Diets were formulated to contain 39.6% corn silage, 15.4% alfalfa silage, and 45% concentrate mix on a DM basis. Canola meal was included at 19.4 and 11.9% DM, whereas SBM was included at 14.5 and 8.9% DM. Data were analyzed using the MIXED procedure of SAS. Body condition score and BW at calving and previous lactation mature equivalent 305 were used as covariates. Cows fed CM diets were has milk yield compared with cows fed SBM (mean ± SEM, 55.7 vs. 51.2 ± 0.97 kg/d; $P < 0.01$). Dry matter intake tended to be greater for cows fed CM diets (25.8 vs. 25.0 ± 0.34 kg/d; $P = 0.09$). The source of CP did not affect milk fat, protein, lactose, or total solids percentage. Decreasing dietary CP concentration increased milk fat (4.09 vs. 3.90 ± 0.07%; $P < 0.05$) and total solids (12.8 vs. 12.5 ± 0.95%; $P = 0.07$). Cows fed HI diets produced greater milk urea N (MUN) than cows fed LO diets (12.6 vs. 9.82 ± 0.22 mg/dL; $P < 0.01$). Milk urea N tended to be lower for cows fed CM compared with cows fed SBM (10.9 vs. 11.4 ± 0.22 mg/dL; $P = 0.10$). Milk fat, protein, lactose, and total solids were greater for cows fed CM in agreement with increased milk production. Dry matter intake, milk yield, milk protein percentage, and lactose percentage did not differ with varying CP concentration. Energy-corrected milk (ECM) was greater for cows fed CM compared with cows fed SBM (57.6 vs. 53.6 ± 0.95 kg/d; $P < 0.01$). Cows fed CM exhibited a trend in feed efficiency (ECM/DMI) compared with cows fed SBM (2.27 vs. 2.16 ± 0.38; $P = 0.06$). These data suggest milk yield and feed efficiency can be improved in early lactation with the inclusion of CM.

Key Words: canola meal, early lactation, transition period

1507 The effects of heat stress on protein metabolism in lactating Holstein cows. S. Gao[1], J. Guo[1], S. Quan[2], X. Nan[1], L. H. Baumgard[3], and D. Bu*[1,4,5], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P. R. China, [2]The Animal Physiology and Biochemistry Laboratory of the Ministry of Agriculture in Nanjing Agriculture University, Nanjing, P. R. China, [3]Iowa State University, Ames, [4]Hunan Co-Innovation Center of Animal Production Safety, CICAPS, Changsha, P. R. China, [5]CAAS-ICRAF Joint Laboratory of Agroforestry and Sustainable Animal Husbandry, World Agroforestry Centre, East and Central Asia, Beijing, P. R. China*.

Independent of decreased feed intake, heat stress (HS) decreases the synthesis of milk protein, but the mechanisms responsible for the decrease are not clear. To research the direct (not mediated by feed intake) effect of HS on the synthesis of milk protein, four multiparous, lactating Holstein cows (101 ± 10 DIM, 574 ± 36 kg BW, and 38 ± 2.4 kg milk/d) were randomly assigned to four environmental chambers and divided into two groups, for two experimental periods of 18 d (a 9-d control period and a 9-d trail period). A crossover design was used and period 1 and 2 were separated by 30 d. Cows in the control period of both period 1 and 2 were exposed to constant thermal neutral (TN) conditions (20°C, 55% humidity, temperature–humidity index [THI] = 65.5, and 12 h light and dark cycles) and allowed to eat ad libitum for 9 d. The trial period of both period 1 and 2 included a HS ($n = 2$) group and a pair-fed TN (PFTN; $n = 2$) group and two groups exposed to HS (36°C from 0600 to 1800 h, 32°C from 1800 to 0600 h, 40% humidity, THI = 84.5, and 12-h light and dark cycles) and TN, respectively. The pattern and magnitude of reduced feed intake in the PFTN cows mirrored that of the HS cows. Compared with PFTN, HS decreased milk protein yield (17.7%) and content (4.1%) ($P < 0.05$). Heat stress increased before-feeding rumen liquid NH_3–N concentration compared with PFTN. Microbial CP, estimated by urinary excretion of purine derivatives, absorbed by intestine was not different between HS and PFTN cows. Heat stress decreased plasma AA (total AA and 5 specific of free AA) ($P < 0.05$) and plasma glucose ($P < 0.1$) and tended to increase BUN and increased urea nitrogen in urine and decreased NEFA. The decrease in plasma AA could have resulted from an increase in nonmammary AA oxidation or an increase in AA utilization for the synthesis of ligands involved with an acute phase protein response. Regardless, it appears blood AA utilization is reprioritized away from milk protein synthesis during HS.

Key Words: heat stress, milk protein, milk protein precursor, protein metabolism, restricted intake

1508 The effect of fructose infusion on dry matter intake in dairy cattle. R. Yair* and M. S. Allen, *Michigan State University, East Lansing*.

Loading of fructose or its analogs in mammals resulted in the accumulation of fructose 1-phosphate in the liver, sequestering organic phosphate (Pi), preventing ATP production, and most likely, as a consequence, increasing feed intake. The objectives of this work were to determine the effects of fructose and Pi infusions on feeding behavior of dairy cows to link hepatic ATP synthesis and feeding behavior and better understand the mechanisms controlling feed intake. Eight Holstein cows from 4 to 8 d postpartum (PP) were used in a duplicated 4 × 4 Latin square design experiment with one block each of multiparous and primiparous cows. Periods were 24 h, including a 2-h infusion and a 22-h recovery period. Treatments were arranged in a 2 × 2 factorial with fructose and Pi infusions as main effects. Cows were infused through a jugular catheter with 0.6 mol/h of fructose or glucose and 0.3 mol/h of NaCl or NaH_2PO_4. Effects of treatment on DMI were analyzed by ANOVA with repeated measures. Both fructose and Pi had hyperphagic effects; fructose increased DMI by 23.11% in the first 0.5 h of infusion compared with glucose (4.16 vs. 3.38 kg; $P < 0.01$) but the effect diminished over time with no effect detected by 1 h following the start of infusion. An interaction was detected between Pi and block ($P = 0.06$); NaH_2PO_4 increased DMI over the 2-h infusion period by 36.9% compared with NaCl for multiparous cows (8.41 vs. 6.14 kg; $P < 0.001$) but did not affect DMI for primiparous cows. Although effects of fructose on DMI hints at a connection between ATP synthesis and intake, Pi infusion was expected to reduce the effect of fructose by providing Pi for ATP synthesis rather than increasing intake. It is possible that the infused phosphate did not enter the liver and, therefore, did not have the expected effect. Reducing dietary P is essential to limit P excretion. Previous works showed that feeding P levels similar to this work (0.37% of DM) does not reduce DMI; however, such level might be insufficient specifically for cows in the PP period. Accordingly, further research to understand the hyperphagic effect of Pi might have implications for diet formulation for cows in the PP period. Better understanding the effects of Pi and fructose on hepatic ATP synthesis should provide insights on the connection between ATP synthesis and feeding behavior in dairy cows.

Key Words: dry matter intake, fructose, phosphate

1509 Effects of maternal nutrient restriction and melatonin supplementation on vascularity in ovine maternal and fetal jejunum. G. Jia*, *North Dakota State University, Fargo*.

Mounting evidence from previous studies suggests that melatonin, a neurohormone secreted by the pineal gland, likely plays a role in regulating nutrient delivery by regulating blood flow and improving vascular development. Therefore, this study was conducted to investigate the effect of maternal nutrient restriction and melatonin supplementation on vascular development of maternal and fetal small intestine in sheep. Thirty-one primiparous ewes were randomly assigned to receive 5 mg of melatonin/d (MEL) or no melatonin (CON) and 100 (adequate fed [ADQ]) or 60% (restricted [RES]) of nutrient recommendations from d 50 to 130 of gestation. At d 130 of gestation, ewes were euthanized and small intestinal (jejunal) tissues were collected from the dam and fetus. Intestinal capillaries were stained using Anti-CD31 (Abcam) followed by fluorescently labeled goat anti-rabbit secondary antibody (Alexa Fluor 633; Abcam). A DAPI stain was used to counterstain cell nuclei. Z-stacks of 15-μm-deep optical sections of jejunal tissues including intact villi were obtained using a confocal laser-scanning microscope (Zeiss AxioObserver Z1 with LSM700). Rendered 3D images were analyzed for capillary volume, which was expressed as a percentage of the total villous volume by using Imaris 7 software (Bitplane, South Windsor, CT). Data were analyzed as a completely randomized design, with a 2 × 2 factorial arrangement of treatments. In the maternal jejunum, there was no effect of maternal melatonin treatment or nutritional level on capillary volume density ($P > 0.59$); however, due to the large decrease in jejunal mass (RES only 0.69 of ADQ; $P < 0.001$), total jejunal vascularity was decreased ($P = 0.02$) in RES ewes vs. ADQ ewes. For the fetal intestine, neither capillary volume density nor total intestinal vascularity was affected by MEL supplementation or nutritional level, and a melatonin × nutrition interaction was not observed. Our data suggest that nutritional level affects maternal jejunal mass and total vascularity. However, neither melatonin supplementation nor nutritional level affected capillary volume density of maternal jejunum or capillary volume density or total vascularity of fetal intestine. Future research is needed to investigate whether maternal melatonin supplementation or nutritional level, or both, postnatally affect vascularity of the intestine.

Key Words: intestine, maternal melatonin treatment, vascularity

1510 Production level of dairy cows affects the extent of diet-induced milk fat depression. Y. Sun*, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing*.

The interaction between diet and milk production level on the risk of diet-induced milk fat depression (MFD) was evaluated in a crossover design experiment with a covariate period. Thirty-two mid- and late-lactation multiparous Holstein cows (14 rumen cannulated and 18 noncannulated), with a wide range and uniform distribution of milk yield (25 to 60 kg/d), were randomly assigned to treatment sequence within level of milk yield. Treatment diets and composition (% DM) were 1) control diet (CON), containing 24% starch, 33% NDF, 22% forage NDF, and 3% fatty acids, and 2) MFD-inducing diet (MFDI), containing 30% starch, 28% NDF, 17% forage NDF, and 4% fatty acids. Treatment periods were 28 d with the last 7 d for data and sample collection. The statistical model included the random effect of cow and fixed effects of period, treatment, cannulation block, and the interactions of cannulation block and treatment and of treatment and period. Linear and quadratic effects for the interaction between covariate milk yield and treatment were added to evaluate responses to treatment by level of milk yield. The MFDI decreased milk fat concentration (3.31 vs. 3.69%; $P < 0.01$) and tended to decrease milk fat yield (1.21 vs. 1.28 kg; $P < 0.10$) and 3.5% fat-corrected milk (35.6 vs. 37.0 kg; $P < 0.10$) compared with the CON. There was no main effect of treatment on DMI but treatments interacted with covariate milk yield ($P < 0.01$); MFDI decreased DMI for higher producing cows but increased DMI for lower producing cows. Linear interactions ($P < 0.10$) were detected between treatment and covariate milk yield for milk fat content and yields of milk fat and 3.5% fat-corrected milk; compared with CON, MFDI decreased content and yield of milk fat and 3.5% fat-corrected milk to a greater extent in higher producing cows than lower producing cows. The MFDI treatment decreased mean ruminal pH compared with CON (6.00 vs. 6.13; $P < 0.01$), and treatments interacted with covariate milk yield ($P < 0.10$), with less difference between CON and MFDI in higher producing cows than lower producing cows. Compared with CON, MFDI increased BCS change (0.18 vs. 0.11; $P < 0.01$) but response was not related to covariate milk yield. In conclusion, higher producing cows were at higher risk for milk fat depression induced by a high-starch, low-forage NDF diet containing supplemental fat.

Key Words: milk fat depression, production level, rumen pH

1511 Effect of production level and parity on responses of milk fat to supplementation with 2-hydroxy-4-(methylthio)butanoate. M. Baldin*[1], H. A. Tucker[2], and K. J. Harvatine[1], *[1]Penn State University, University Park, PA, [2]Novus International Inc., St. Charles, MO*.

We previously reported that high-producing cows are at higher risk of biohydrogenation-induced milk fat depression (MFD) and that 2-hydroxy-4-(methylthio)butanoate (HMTBa) reduced MFD in high-risk situations. The objective was to determine the relationship between production level and parity and responses of milk fat to supplementation with HMTBa (ALIMET; Novus International, Inc., St. Charles, MO). Twelve primiparous and 24 multiparous Holstein cows were used in a crossover design preceded by a 14-d pretrial period. The 35-d treatment periods included 28 d of a low-risk diet (31% NDF, 27% starch, and 4.2% EE) followed by 7 d of a moderate-risk diet (29% NDF, 30% starch, and 1% soybean oil). Treatments were control (corn carrier) and HMTBa (0.1% of diet DM). At the end of pretrial period, cows averaged 127 ± 33 DIM (mean ± SD) and 41 ± 9 kg milk/d (minimum 27 kg/d and maximum 61 kg/d). Milk yield and DMI were measured daily, and milk was sampled every 7 d and analyzed for fat and protein concentration. Data were analyzed using PROC MIXED with repeated measures, with cow by treatment as the subject, and the effect of treatment was tested at each time point. During the low-risk phase, no overall effect of treatment or treatment × time interactions were observed for DMI, milk yield, and milk fat and protein yield and concentration ($P > 0.2$ for all). Additionally, no treatment × parity or treatment × parity × time interactions were observed for milk fat concentration ($P = 0.2$) and yield ($P = 0.9$). During the moderate-risk phase, no overall effect of treatment or treatment × time interactions were observed for DMI, milk yield, and milk protein concentration and yield ($P > 0.4$ for all). 2-Hydroxy-4-(methylthio)butanoate supplementation maintained higher milk fat concentration (3.67 vs. 3.86; $P < 0.001$) and yield (1.37 vs. 1.47; $P < 0.001$) at the end of the moderate-risk phase. No treatment × parity or treatment × parity × time interactions were observed for milk fat variables ($P > 0.4$ for both). On d 35, responses (HMTBa; control) of milk fat concentration and yield correlated positively with pretrial milk yield (0.35 [$P = 0.03$] and 0.38 [$P = 0.02$], respectively). In conclusion, HMTBa maintained milk fat yield when cows were fed a diet with moderate risk of biohydrogenation-induced MFD and milk fat response to treatment was correlated with production level but not affected by parity.

Key Words: HMTBa, milk fat

1512 The timing of feed availability entrains the circadian rhythm of milk synthesis in dairy cattle. I. J. Salfer*, J. Y. Ying, and K. J. Harvatine, *Penn State University, State College, PA*.

Dairy cows have well-recognized natural daily rhythms of feed intake and milk synthesis. However, little is known about the regulation of these circadian rhythms. Variation in feed intake throughout the day results in a daily pattern of nutrient absorption, which may entrain the rhythm of milk synthesis. The objective of this study was to investigate the effect of the timing of feed availability on the daily rhythm of milk synthesis. Sixteen cows were randomly assigned to one of two treatment sequences in a crossover design. All cows were fed the same total mixed ration ad libitum for 16 h/d either during the day (DF) or the night (NF). Cows on the DF treatment had feed available from 0700 to 2300 h, whereas NF cows were offered feed from 1900 to 1100 h. Treatment periods were 17 d, and cows were milked every 6 h the last 7 d of each period. Milk samples were collected at each milking on the final 2 d of each period and analyzed for fat, protein, and milk urea nitrogen (MUN). Blood samples were collected on the final 3 d of each period to represent every 4 h over the day. Body temperature was monitored using vaginal temperature loggers. Data was analyzed as a crossover design in Proc Mixed and by cosine analysis to determine the phase (time at peak) and amplitude (peak to mean) of daily rhythms. Milk yield; fat and protein yield; and fat, protein, and MUN concentration displayed 24-h rhythms. Treatment modified the rhythm of milk yield, protein yield, and MUN, fat, and protein concentration ($P < 0.05$). Briefly, milk yield and lactose concentration were phase delayed by approximately 4 h in NF cows ($P < 0.05$). The daily rhythms of fat, protein, and MUN concentration of NF cows were phase advanced by 2, 10, and 3 h, respectively ($P < 0.05$). The rhythms of fat, protein, and MUN concentration exhibited a greater amplitude in NF compared with DF. Blood glucose followed a daily rhythm that was not affected by the timing of feed availability ($P > 0.10$). There was a daily rhythm of body temperature that was phase advanced 4 h by NF ($P < 0.05$). The timing of feed availability modified the rhythm of milk synthesis and body temperature in dairy cattle but did not modify the daily pattern of plasma glucose.

Key Words: circadian rhythm, food entrainment, milk synthesis

1513 Characterization of peripartum liver and skeletal muscle ceramide concentrations in lean and overweight Holstein dairy cows. S. Saed Samii*, J. E. Rico, and J. W. McFadden, *West Virginia University, Morgantown*.

Circulating sphingolipid ceramide is associated with the development of insulin resistance in overweight monogastrics. An increase in NEFA delivery to the liver can increase lipoprotein ceramide packaging and secretion. In turn, lipoprotein ceramide can antagonize insulin action in skeletal muscle. We recently discovered that ceramide concomitantly increases with hyperlipidemia in overweight cows transitioning from gestation to lactation. Considering evidence in monogastrics, our objective was to characterize the relationship between adiposity and liver and skeletal muscle ceramide concentrations. Multiparous Holstein cows were grouped by adiposity at d −28 prepartum as either lean (2.9 ± 0.1 BCS; $n = 7$; LEAN) or overweight (4.0 ± 0.2 BCS; $n = 7$; OVER). Diets were formulated to meet or exceed requirements. Blood samples were routinely collected from d −21 to 21, relative to calving, and liver and skeletal muscle biopsies were performed at d −21, −7, and 4. Liquid chromatography tandem mass spectrometry was used to quantify ceramide, monohexosylceramide (GlcCer), and lactosylceramide (LacCer). Data were analyzed as repeated measures using a mixed model with fixed effects of adiposity and time. Pearson's correlations were analyzed. Relative to LEAN, OVER experienced increased BCS loss, plasma NEFA, hepatic total lipid accumulation, and circulating ceramide (e.g., C24:0-ceramide) during the transition from gestation to lactation ($P < 0.05$). Comparable to plasma, C24:0-ceramide was the most abundant ceramide in the liver and muscle. To support a relationship between liver and plasma ceramides, plasma total ceramide and liver total ceramide were positively correlated during transition ($r = 0.39$, $P < 0.05$). Similarly, plasma C24:0-ceramide and liver C24:0-ceramide were positively correlated ($r = 0.41$, $P < 0.05$). Coinciding with an increase in circulating NEFA, hepatic total ceramide and C24:0-ceramide increased postpartum in OVER ($P < 0.05$). Liver total ceramide and C24:0-ceramide were positively correlated with plasma NEFA ($r = 0.44$ and 0.49, respectively; $P < 0.05$). Additionally, we observed an increase in postpartum hepatic C22:0-ceramide in OVER ($P < 0.05$). Hepatic total GlcCer tended to be increased postpartum for all cows ($P = 0.10$); however, hepatic total LacCer increased only in LEAN ($P < 0.05$). Muscle total ceramide and C24:0-ceramide levels were lower prepartum in OVER ($P < 0.05$). In contrast, postpartum muscle C16:0- and C24:0-ceramide were higher in OVER ($P < 0.05$). We conclude that enhanced lipolysis in overweight dairy cows increases hepatic ceramide synthesis to support ceramide accumulation in circulation. The ability of hepatic-derived ceramide to antagonize insulin action in extrahepatic tissues

during early lactation requires further investigation.

Key Words: ceramide, insulin resistance, peripartal dairy cow

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1514 Variation in rumen epithelial fatty acid metabolism and cholesterol homeostasis contributes to different responses to the high-grain diet adaptation in beef cattle. K. Zhao*[1,2], Y. Chen[1], G. B. Penner[3], M. Oba[1], and L. L. Guan[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]College of Medicine, Xi'an Jiaotong University, Xi'an, P. R. China, [3]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada*.

Ruminal digestive disorders are common during high-grain diet transition. However, little is known about the mechanism regulating this process, especially at the transcriptional level. In this study, we conducted a genomewide transcriptome comparison of ruminal epithelia when cattle were exposed to a rapid high-grain transition. Transcriptome analysis of ruminal papillae, collected from 15 beef heifers when fed 3 different dietary steps during the transition (3, 75, and 92% grain), were performed using RNA-seq. Expression of 11,044, 11,322 and 11,282 genes were detected (with reads per million [RPM] > 1 in 15 heifers of each diet) under the 3, 75, and 92% grain diets, respectively. Principle component analysis showed that the transcriptome profile of rumen epithelia between the low-grain diet (LGD; 3%) and high-grain diets (HGD; 75 and 92%) were different. During the transition from 75 to 92% grain, the ruminal pH showed varied change patterns: decreased (DG; $n = 5$) or increased (UG; $n = 5$). When the ruminal tissue transcriptomes were compared between 75 and 92% grain diets (92 vs. 75%) in each group, the expression of some ketone body and cholesterol synthesis–related genes tended to be decreased in UG (*acetyl-CoA acetyl transferase 2* [*ACAT2*], *3-hydroxy, 3-methylglutaryl CoA synthase 1* [*HMGCS1*], *HMG-CoA reductase* [*HMGCR*], and *farnesyl diphosphate synthase* [*FDPs*]) ($P < 0.1$), whereas some other cholesterol biosynthesis- and ketogenesis-related genes tended to be increased in DG (*sterol regulatory element binding transcription factor 2* [*SREBF2*] and *HMG-CoA lyase* [*HMGCL*]) ($P < 0.1$). Furthermore, the proton and cholesterol efflux–related genes were increased (Na^+/H^+ *exchanger 3* [*NHE3*] and *ATP-binding cassette 1* [*ABCA1*]) in UG ($P < 0.05$), whereas *monocarboxylate transporter 4* (*MCT4*) showed a tendency to be decreased in DG ($P < 0.1$). These results suggest DG heifers may have greater intracellular cholesterol and a reduction in intracellular pH, which might imbalance the epithelial homeostatic status. Pathway analysis showed that the differentially expressed genes in DG were involved in the "T cell receptor signaling" and "complement and coagulation cascades" pathway, whereas UG might activate cell repair function through "p53 signaling pathway" and cell cycle arrest. Overall, the different gene networks controlling fatty acid metabolism and cholesterol homeostasis among individuals might account for the animal variation in ruminal responses during high-grain diet adaptation in beef cattle.

Key Words: beef cattle, high-grain diet, rumen transcriptome

1515 Dose response effect of acetate on milk fat synthesis in lactating dairy cows. N. L. Urrutia*[1], M. Baldin[1], J. Y. Ying[2], Y. Fan[1,3], K. J. Harvatine[1], and J. Carvalho[1], *[1]Penn State University, University Park, PA, [2]Penn State University, State College, PA, [3]China Agricultural University, Beijing, P. R. China*.

Acetate is the main source of energy and substrate for milk fat synthesis in the dairy cow; however, the effect of acetate supply on milk fat synthesis has not been investigated in high-producing cows. The objective was to investigate the dose-dependent effect of acetate on milk fat synthesis. Six ruminally cannulated multiparous lactating Holstein cows were randomly assigned to treatments in a 4 × 4 Latin square design. Treatments were 0 (control), 5, 10, and 15 mol/d of acetate. Acetate was neutralized to pH 6.1 with sodium hydroxide and continuously infused into the rumen in 5 L/d for 4 d with 7-d washout periods. Milk samples were collected daily. Blood and rumen samples were collected twice (before noon and after noon) on the last day of treatment. Time course data was analyzed as repeated measures in SAS and all other data was analyzed using JMP Pro. The model included the random effect of cow and period and the fixed effect of treatment. Rumen concentration of acetate ($P < 0.01$) and acetate:propionate ratio ($P < 0.001$) linearly increased before feeding (before noon) and rumen concentration of acetate ($P < 0.001$), butyrate ($P < 0.05$), and total VFA ($P < 0.01$) linearly increased after feeding (after noon) as acetate dose increased. Acetate infusions linearly increased rumen pH before feeding ($P < 0.005$). Dry matter intake, milk yield, and protein yield and concentration were not affected by treatments. Acetate dose had a quadratic effect on milk fat yield ($P < 0.001$) and a linear effect on milk fat concentration ($P < 0.001$). Fat yield increased 7, 16, and 14% and fat concentration increased 6, 9, and 11% at 5, 10, and 15 mol/d, respectively, compared with the control. Acetate linearly increased yield and concentration of palmitic acid and yield of de novo synthetized fatty acids (both $P < 0.001$). Acetate infusions had no effect on plasma NEFA, glucose, glucagon, or insulin but linearly increased plasma βHBA after feeding ($P < 0.01$). These results demonstrate that acetate supply has an impact on milk fat synthesis under normal dietary conditions and suggest that milk fat yield and concentration may be improved through dietary strategies that increase rumen acetate production.

Key Words: acetate, milk fat synthesis, rumen infusion

1516 Lipogenic gene network expression in mammary tissue in response to abomasal infusion of casein, glucose, and acetate into feed-restricted lactating cows. M. A. C. Danes*[1,2], F. Batistel[3], G. A. Broderick[4], M. A. Wattiaux[5], and J. J. Loor[3], *[1]Federal University of Lavras, Lavras, Brazil, [2]University of Wisconsin, Madison, [3]University of Illinois, Urbana, [4]Broderick Nutrition & Research, LLC, Madison, WI, [5]University of Wisconsin-Madison, Madison*.

Nutrients that are building blocks of the main milk components also can work as regulators of the synthesis of these products through cell signaling pathways regulated at the transcriptional level. Six Holstein multiparous cows, averaging 40 kg milk/d, were used in a 6 × 6 Latin square with 14-d periods. Cows were fed the same diet for 10 d in each period, after which they were feed restricted for 4 d to 85% of ad libitum intake and abomasally infused with 1 of 6 treatments: acetate (A) or glucose (G), each at 5% of ad libitum ME intake (Mcal/d); casein (C) at 15% of ad libitum MP intake (g/d); A + C (AC); G + C (GC); or a saline solution (S; negative control). The mean milk fat yield was 1.58, 1.55, 1.42, 1.65, 1.51, and 1.41 kg/d for A, G, C, AC, GC, and S, respectively. Mammary tissue was biopsied on the last day of each period. The expression of lipogenic gene networks was evaluated via quantitative RT-PCR of 11 genes. Data were log2 transformed and analyzed using the GLIMMIX procedure of SAS. Infusion of all nutrients upregulated ($P < 0.05$) *ACSS2*, *ACACA*, and *FASN*, which are involved in acetate activation and de novo fatty acid synthesis. Surprisingly, A alone did not cause a greater effect than C and G, but when AC was infused, the expression of these genes was the greatest (approximately 2- to 3-fold greater), suggesting a role of AA in regulating fatty acid synthesis. This was even more evident in the upregulation ($P < 0.05$) by AC of *FABP3*, encoding a cytosolic transport protein required for use of fatty acids in triacylglycerol synthesis. Acetate and AC upregulated *IDH1* (approximately 2- to 5-fold), which encodes the main enzyme responsible for NADPH synthesis in mammary cells. This response agreed with the gene data indicating an overall stimulation of fatty acid synthesis especially in the AC treatment. There was no treatment effect ($P > 0.05$) on *AGPAT6*, *DGAT1*, *LPIN1*, and *PPARG*. Unexpectedly, A downregulated ($P < 0.05$) the lipogenic transcription factor *SREBF1*, which previously has been associated with fatty acid synthesis regulation in mammary tissue during milk fat depression. However, the fact that AC induced a strong tendency ($P = 0.08$) for upregulation (2-fold) of the transcription regulator *RXRA* compared with S underscores a potentially important role in the nutritional regulation of milk fat synthesis. Results underscore the role of nutrients in regulating mammary fatty acid synthesis at the transcriptional level.

Key Words: milk fat synthesis, nutrigenomics

1517 The effects of feeding increasing concentrations of corn oil on energy metabolism and nutrient balance in finishing beef steers. K. E. Hales*, A. P. Foote, T. M. Brown-Brandl, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*.

The use of added fat source is common in high-concentrate finishing diets. The objective of our experiment was to determine if feeding increasing concentrations of added dietary corn oil would decrease enteric methane production, increase the ME:DE ratio, and improve retained energy in finishing beef steers. Four treatments were used in a replicated 4 × 4 Latin square ($n = 8$; initial BW = 397 kg ± 3.89). Data were analyzed using a Mixed model with the fixed effects of period and dietary treatment and random effects of square and steer within square. Treatments consisted of 1) 0% added corn oil (Fat-0), 2) 2% added corn oil (Fat-2), 3) 4% added corn oil (Fat-4), and 4) 6% added corn oil (Fat-6). Dry matter intake or GE intake did not differ across diets ($P > 0.39$). As a proportion of GE intake, fecal energy loss and DE loss did not differ by treatment ($P > 0.27$); however, urinary energy loss tended to linearly decrease as corn oil increased in the diet ($P = 0.09$). Additionally, methane energy respired linearly decreased as corn oil increased in the diet ($P < 0.01$). No differences were detected in ME loss as a proportion of GE intake ($P > 0.98$); however, the ME:DE ratio linearly increased as corn oil increased in the diet ($P < 0.01$). No differences in retained energy or heat production as a proportion of GE intake were noted ($P > 0.59$). Dry matter digestibility did not differ across diets ($P > 0.36$). Digestibility of NDF as a proportion of intake quadratically responded, increasing from 0% corn to 4% corn oil and decreasing thereafter ($P = 0.02$). Furthermore, ether extract digestibility as a proportion of intake quadratically increased, increasing from 0 to 4% corn oil inclusion before reaching a plateau ($P < 0.01$). No differences were detected in OM digestibility across treatments ($P > 0.35$). From these data, we interpret that adding dietary fat decreases urinary energy loss and enteric methane production while decreasing NDF digestibility when included at more than 4% of dietary DM. Moreover, the ME:DE ratio linearly increases as dietary fat increases. The USDA is an equal opportunity provider and employer.

Key Words: dietary fat, energetics, finishing cattle

1518 Isolation and comparison of expression of novel glucose transporters, GLUT3 and GLUT14, in bovine uteroplacental tissues from days sixteen to fifty of gestation. M. S. Crouse*, J. S. Caton, K. J. McLean, P. P. Borowicz, L. P. Reynolds, C. R. Dahlen, and A. K. Ward, *Department of Animal Sciences, North Dakota State University, Fargo*.

Glucose transporters *GLUT3* and *GLUT14* previously have not been isolated in ruminant utero-placenta. The glucose transporter *GLUT14* is a duplicon of *GLUT3* with 95% shared homology. We hypothesized that maternal nutrition and day of gestation would impact mRNA expression of *GLUT3* and *GLUT14* in heifers and that there would be a difference in mRNA expression between the two transporters. Crossbred Angus heifers (n = 49) were synchronized, bred via AI, assigned to nutritional treatment (CON = 100% of requirements to gain 0.45 kg/d and RES = 60% of CON), and ovariohysterectomized on d 16, 34, or 50 of gestation (n = 6 to 9/d); nonpregnant (NP) controls were not bred and ovariohysterectomized on d 16 of the synchronized estrous cycle (n = 6). The resulting treatment arrangement was a 2 × 3 factorial + 1. Utero-placental tissues (caruncle [CAR], intercaruncular endometrium [ICAR], fetal membrane [chorioallantois] [FM], cotyledon [COT], intercotyledonary placenta [ICOT], and amnion [AMN]) were obtained from the pregnant uterine horn immediately after ovariohysterectomy. For NP controls, only CAR and ICAR were obtained. Comparison of expression across tissues was achieved by using NP CAR and ICAR tissues as the baseline. For FM, COT, ICOT, and AMN, NP endometrium served as the baseline. Expression of *GLUT3* was greater ($P < 0.05$) on d 50 in CAR compared with d 16 CAR. In FM, *GLUT3* was greater ($P < 0.05$) on d 16 compared with to d 50 FM. There also was a significant day × tissue interaction for *GLUT3*, which was greater ($P < 0.01$) in d 50 CAR compared with all other tissues and days. Expression of *GLUT14* in CAR was greater ($P < 0.05$) on d 50 compared with d 16 and 34. Direct comparison of the two genes showed that *GLUT14* expression was 5-fold greater ($P < 0.01$) than *GLUT3* expression across all days, tissues, and treatments. There was a significant gene × tissue interaction ($P < 0.01$), such that *GLUT14* was greater in ICAR and intermediate in CAR compared with FM and compared with *GLUT3* in all tissues. These data demonstrate that glucose transporters *GLUT3* and *GLUT14* are expressed in ruminant utero-placenta and also support our hypothesis that the magnitude of mRNA expression of *GLUT3* differs from that of *GLUT14*. There were no effects, however, of nutritional treatment or day of gestation within gene.

Key Words: early gestation, facilitated transporters, glucose

1519 Does microbial contamination affect in situ estimation of crude protein degradability of concentrate feedstuffs? A. C. B. Menezes*[1], S. C. Valadares Filho[2], P. P. Rotta[3], S. A. Santos[4], D. Zanetti[5], M. V. C. Pacheco[1], B. C. Silva[5], H. M. Alhadas[1], J. M. V. Pereira[1], and P. Pucetti[1], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Colorado State University, Fort Collins, [4]Universidade Federal da Bahia, Salvador, Brazil, [5]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*.

Microbial contamination (MC) is an important source of errors in in situ methods, thereby resulting in underestimation of CP degradability as well as overestimation of RUP content. The aim of this study was to use ^{15}N to estimate the MC of fractions soluble (a), potentially degradable (b), and the rate of digestion of the fraction b (kd) of CP as well as to estimate the necessary incubation time to estimate the RDP of energy and protein feeds considering two outflow rates (0.05 and 0.08 h^{-1}). Twelve concentrates were evaluated: six energy concentrates—wheat bran, rice meal, ground corn, ground sorghum, ground corn cob, and soybean hulls—and six protein concentrates—cottonseed meal 38% CP, soybean meal, ground bean, peanut meal, sunflower meal, and corn gluten meal. The feeds were divided into 4 groups and they were ruminally incubated in 4 crossbred bulls for 0, 2, 4, 8, 16, 24, 48, and 72 h. To estimate the MC of the incubated residues, ruminal bacteria were labeled with ^{15}N via continuous intraruminal infusion of $^{15}(NH_4)_2SO_4$. Ruminal digesta was collected for the isolation of bacteria before the first infusion of ^{15}N and after the infusion of ^{15}N during the collection period. There was no difference ($P = 0.74$) in the parameters a, b, and kd, corrected and uncorrected for MC. All the feeds followed an exponential model of degradation and the model fitted well to the data, except for corn gluten meal; probably, the maximum incubation time used here (72 h) was not long enough to allow an accurate estimation of degradation profile. The cluster analysis allowed ($R^2 = 0.944$) grouping feeds into three different groups according to the necessary incubation time to estimate RDP. The first was formed by the high-starch energy concentrates (15.4 ± 0.46 h), the second by the low-starch energy concentrates (6.8 ± 0.60 h), and the third by the protein concentrates (9.9 ± 0.41), considering kp 0.05 h^{-1}. In conclusion, the MC was low and nonsignificant, so correction of ruminal protein degradation is irrelevant for the concentrate studied. However, the chemical composition of these feeds resulted in different incubation times to estimate RDP content, and it needs to be considered in techniques used to estimate CP digestibility in the rumen and intestines.

Key Words: microbial contamination, protein, rumen degradable protein

1520 Effect of concentrate type (starch vs. fiber) and bicarbonate addition in grass silage–based diets on performance, diet digestibility, and enteric methane emissions in lactating dairy cows. A. Bougouin*, A. Ferlay, M. Doreau, Y. Rochette, S. Rudel, C. Lascoux, and C. Martin, *INRA-UMR1213 Herbivores, Saint-Genes-Champanelle, France*.

Cereals and corn silage diets are extensively used for high-yielding dairy cows and it is well established that altering dietary starch and fiber proportion results in methane (CH_4) emissions mitigation. With grass silage-based diets, quantitative evidence of CH_4 emissions reduction with high-starch concentrate is lacking. Therefore, the objective was to compare the effects of fiber-rich (F) or starch-rich (S) diets based on grass silage, supplemented or not with bicarbonate (Fb and Sb), on CH_4 emissions, diet digestibility and performance in dairy cows. Four multiparous lactating Holstein cows were used in a 4 × 4 Latin square design experiment of 4 periods of 4 wk each. Four dietary treatments were assigned based on grass silage 42%, hay 8%, and 50% F or S concentrate (DM basis), supplemented or not with sodium bicarbonate (1% DMI). Bicarbonate was used as a digestive regulator to lower the risk of ruminal acidosis appearance. Intake and milk production were measured daily and milk composition was measured weekly during the experiment. Methane production and diet digestibility were measured simultaneously for the last 5 d of each period when cows were in open respiration chambers. Feed efficiency (fat- and protein-corrected milk/DMI) was calculated using data from wk 4. Data were analyzed using mixed-effect models with cows as a random effect and period and treatments as fixed effects. Orthogonal contrasts were used to evaluate diet type or bicarbonate supplementation effects. The S and Sb diets induced less daily CH_4 emissions (417.5 and 393.9 g/d, respectively) than F and Fb diets (487.9 and 506.4 g/d, respectively) as well as a significant decrease in CH_4 intensity (−14% in g/DMI and −20% in g/FPCM). Dry matter intake was reduced by 3.5% with the starch diets compared with fiber diets ($P < 0.05$). Total tract digestibility of nutrients (DM, OM, and starch) and GE were lower ($P < 0.05$) for F and Fb diets than for S and Sb diets. Feed efficiency and milk yield and fat content were not different between starch and fiber diets ($P > 0.05$) but milk protein content was greater for the starch diets (+3%; $P < 0.05$). Bicarbonate had no effect on diet digestibility and CH_4 emissions ($P > 0.05$). However, milk fat content was higher ($P = 0.05$) with Sb than S, F and Fb diets. Feeding 50% starch-rich concentrate with grass silage diets, with or without bicarbonate, is an effective dietary approach for reducing methane emissions without altering diet digestibility and milk performance of dairy cows.

Key Words: concentrate type, dairy cow, methane emissions

1521 Validation of the GreenFeed system against model-predicted methane emissions. P. Huhtanen[1], M. Ramin[1], and A. N. Hristov*[2], *[1]Swedish University of Agricultural Sciences (SLU), Umeå, Sweden, [2]The Pennsylvania State University, University Park*.

The GreenFeed (GF) system (C-Lock Inc., Rapid City, SD) was introduced to estimate methane (CH_4) emission by measuring gas concentrations and flux when cattle visit a GF. The objective of the present study was to validate CH_4 measured with the GF system with model-predicted CH_4 emissions. Evaluation was based on 55 treatment means from dairy and beef cattle studies, in which CH_4 emission was measured by GF. Methane emission was predicted with the models of Yan et al. (2000; models Y1 and Y2), Ellis et al. (2007; E), Jentsch et al. (2007; J), and Ramin and Huhtanen (2013; R1 and R2). If the parameter values required in the models were not reported, tabulated values were used. A concentration of 18.5 MJ GE/kg DM was assumed for models based on GE intake. The evaluation was based on root mean squared prediction error (RMSPE) expressed as a proportion of observed mean. The RMSPE was divided into errors resulting from mean bias, slope bias, and random error across regression line. Observed mean (SD) CH_4 emission, DMI, and dietary concentrations of CP and NDF were 386 g/d (103), 18.4 kg/d (5.6), 172 g/kg DM (34), and 401 g/kg DM (81), respectively. Mean CH_4 emission estimated by GF was close to values predicted by models Y, J, and R that were developed from respiration chamber data (Table 1). However, observed CH_4 values were much higher than those predicted by model E, which was developed from

Table 1521. Predicted CH_4 emission (observed, 386 g/d).

					Distribution of MSE			P-value	
Model	Predicted CH4, g/d	R^2	RMSPE	% of mean	Mean bias	Slope bias	Random error	Mean bias	Slope bias
Y1	395	0.898	34.2	8.9	0.062	0.019	0.919	0.07	0.31
Y2	394	0.925	28.6	7.4	0.066	0.007	0.927	0.06	0.53
J	371	0.949	28.7	7.4	0.281	0.091	0.628	<0.01	<0.01
E	294	0.900	103.1	26.7	0.800	0.104	0.095	<0.01	<0.01
R1	382	0.952	23.2	6.0	0.034	0.037	0.929	0.18	0.15
R2	376	0.954	24.1	6.2	0.180	0.006	0.814	<0.01	0.55

data determined by different techniques. The RMSPE ranged from 6 to 9% of observed mean except model E, with most of the error due to random variation. The RMSPE was smaller when the effect of feeding level was taken into account compared with a model based only on intake (Y2 and J vs. Y1 and E). The RMSPE was further reduced when the effects of diet digestibility and composition were taken into account in addition to intake (R1 and R2 vs. the others). It is concluded that CH_4 emissions estimated by GF were consistent with values predicted by models derived from large data sets from respiration chamber studies.

Key Words: GreenFeed, methane, model

1522 Influence of colostrum on the microbiological diversity of the developing bovine intestinal tract.

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The timely acquisition of high-quality colostrum is a proven factor in promoting intestinal health in young calves, including supporting epithelial function, host metabolism, immune development, and microbial colonization. Mucosal microbial colonization is influenced by the birth environment and local factors (e.g., temperature, pH, host epithelia types, etc.). We studied the impact of colostrum on the choreography of the neonatal calf microbiome. Twelve healthy, male Holstein calves were separated from their dams immediately following birth; fed 4 L of aseptically collected, high-quality colostrum; and housed, monitored, and fed separately for the remainder of the experiment. Postpartum maternal udder and vaginal scrapings were sampled. Fecal samples were collected throughout the experiment. Three animals were euthanized for necropsy, and intestinal samples were collected after colostrum administration (Day 1) and progressively during the trial (Days 3, 7, and 21). The V3 to V4 region of the microbial 16S rRNA gene was sequenced from digesta, mucosal scrapings, and feces. Mean diversity indices were highest in maternal udder (mean 217 OTU) and vaginal scrapings (mean 152 OTU) followed by colostrum samples. In calf samples, diversity increased over time in all locations; duodenal (mean 122 OTU) and proximal jejunal samples (mean 217 OTU) had the highest diversity. Calf duodenal, middle jejunal, and ileal (Day 7) digesta samples and fecal samples were most similar to maternal colostrum samples using Bray–Curtis dissimilarity. When clustering with multidimensional scaling (MDS) by OTU abundance, there was some clustering by location of sample: intestinal samples, stomach samples, and maternal samples clustered somewhat together, respectively. The proximal jejunum had the highest diversity at the phylum level and contained phyla Acidobacteria and Actinobacteria, which were not observed in abundance elsewhere. Firmicutes increased along the digestive tract (proximal to distal), along which Bacteroidetes and Proteobacteria decreased, the latter of which was much higher in mucosal scrapings ($P < 0.05$). Shifts in community diversity were observed in the first few days after birth, and neither digesta nor mucosal microbiota had distinguished themselves by 21 d (LDA, PERMANOVA, and ANOSIM). A large proportion of genera in colostrum, udder, vagina, and intestinal samples could not be classified. In combination, these results indicate that colostrum contributes significantly to the trajectory of the intestinal microbiome of the young calf. Further studies are needed to identify the mechanism and clinical significance of these results and to explore the identity and importance of the unknown taxa.

Key Words: host-associated microbiome

1523 Effects of starch feeding on lipopolysaccharide concentrations in rumen fluid and feces in fresh dairy cows.

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The objectives of this study were to determine 1) the effect of dietary starch content on the concentrations of lipopolysaccharide (LPS) endotoxin in rumen fluid and feces of lactating dairy cows during 21 d after calving and 2) the correlation between rumen and fecal LPS concentrations. Multiparous ruminally cannulated Holstein cows ($n = 16$) were fed a close-up diet (44% NDF and 16% starch, DM basis) for 21 d before expected calving. For the first 21 d after calving, cows were fed either a low-starch diet (37% NDF and 21% starch, DM basis) or a high-starch diet (32% NDF and 27% starch, DM basis). Rumen and fecal samples were collected at 6 h after feeding on d −14, 1, 2, 3, 4, 5, 6, 7, 9, 13, 17, and 21. Data were analyzed as a completely randomized design by ANOVA with the MIXED procedure of SAS with model effects of treatment, day, and treatment × day, with day treated as a repeated measurement. Across days after calving, LPS concentrations in the rumen were higher (12,793 vs. 6,592 EU/mL; $P < 0.01$) for the cows on the high-starch diet compared with cows on the low-starch diet. Cows on the high-starch diet also had a higher LPS concentration in feces during this period (11,885 vs. 7,129 EU/mL; $P < 0.05$). Day after calving did not affect the LPS concentration in rumen fluid. However, days after calving affected this concentration in feces ($P < 0.01$) due to a relatively low fecal LPS concentration at Day 1 after calving. The concentrations of LPS in rumen fluid and in feces were positively correlated ($r = 0.35$, $P < 0.001$). Our results show that feeding higher starch during the first 3 wk of lactation increased LPS concentrations in rumen fluid and feces, indicating a greater risk for compromised rumen health and inflammation.

Key Words: fresh cows, lipopolysaccharide, starch

1524 Correlations between the abundance of specific ruminal bacteria with milk production and total tract digestibility of dairy cows fed live or killed yeast.

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Ruminal nutrient metabolism and animal performance depend on the abundance and diversity of ruminal bacteria. The objective of this study was to examine the correlation between the abundance of different ruminal bacteria and total tract nutrient digestibility and milk production of dairy cows fed diets supplemented without or with live or killed *Saccharomyces cerevisiae*. Four ruminally cannulated lactating cows (284 + 18 DIM) were assigned to 4 treatments arranged in a 4 × 4 Latin square design with four 21-d periods. Cows were fed a nonacidotic total mixed ration (46.8% corn silage, 8.5% wet brewers' grain, and 44.7% concentrate, DM basis). The diet was not supplemented with yeast or supplemented with a low dose of live yeast (5.7×10^7 cfu/d), a high dose of live yeast (6.0×10^8 cfu/d), or a high dose of killed yeast (6.0×10^8 cfu/d before heating at 80°C). Ruminal fluid was collected 0, 2, 4, 6, 8, and 10 h after the morning feeding on d 21 and strained through cheese cloth to separate solid and liquid fractions. Microbial diversity was examined by Illumina MiSeq sequencing of the V4 region of the 16S rRNA gene. Data were analyzed using R (R Core Team, 2013). In the ruminal solid fraction, the *Fibrobacter* abundance was correlated ($r = 0.60$, $P < 0.05$) with milk fat concentration. Unknown genera in family Lachnospiraceae and RFP12 were negatively ($P < 0.05$) correlated with NDF digestibility ($r = -0.52$ and -0.56, respectively). An unknown genus (UT) in family Paraprevotellaceae was negatively ($P < 0.05$) correlated with milk fat and protein content ($r = -0.56$ and -0.52, respectively) and NDF digestibility ($r = -0.65$), whereas a UT in family Clostridiaceae was negatively correlated with CP digestibility ($r = -0.59$, $P < 0.05$). In the liquid fraction, *Prevotella* was negatively correlated with DMI and milk protein and fat content ($r = -0.64$, -0.59, and -0.53, respectively; $P < 0.05$). Unknown genera in families Succinivibrionaceae and Ruminococcaceae were positively correlated ($P < 0.05$) with ADF digestibility ($r = 0.63$) and milk yield ($r = 0.49$), respectively, whereas a UT in family Lachnospiraceae was negatively correlated with DM digestibility ($r = -0.56$, $P < 0.05$). This study revealed several uncultured or unknown ruminal bacteria that appear important as candidates for future studies because of their correlation with one or more indices of dairy cow performance.

Key Words: correlation, milk production, rumen bacteria

1525 Inhibiting the growth of *Escherichia coli* O157:H7 in alfalfa silage with silage additives.

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This study examined if adding microbial inoculants or propionic acid to alfalfa silages contaminated with *Escherichia coli* O157:H7 would inhibit the growth of the pathogen during or after ensiling. Alfalfa forage was harvested at the early bloom stage, wilted to a DM of 54%, chopped to 19-mm lengths, and ensiled after treatment with one of the following: 1) distilled water (Control), 2) 1×10^5 cfu/g of *E. coli* O157:H7 (EC), 3) EC and 1×10^6 cfu/g of *Lactobacillus plantarum* (EC+LP), 4) EC and 1×10^6 cfu/g of *Lactobacillus buchneri* (EC+LB), and 5) EC and 2.2 g/kg of propionic acid (EC+ACID). Each treatment was ensiled in quadruplicate in laboratory silos for 0, 3, 7, 16, and 100 d and analyzed for EC counts, pH, and organic acids. In addition, samples from d 100 were analyzed for counts of yeasts and molds and aerobic stability. Data were analyzed using the GLIMMIX procedure of SAS. The pathogen was detected in all silages until d 7, but by d 16, it was not detected in those treated with EC+LB and EC+LP, although it was still detected in EC and EC+ACID silages. However, by d 100, the pathogen was not detected in any silage. The rate of pH decrease to 5.0 was fastest for the EC+LP silage (7 d) followed by the EC+LB silage (16 d). Nevertheless, all silages had attained a pH less than 5.0 by d 100. The rapid decrease in pH in EC+LP and EC+LB silages was associated with higher ($P < 0.05$) lactate and acetate concentrations, respectively, relative to the other silages during the early fermentation phase (d 3 to 16). Propionic acid was detected only in the EC+ACID silage. Yeast counts were lowest ($P < 0.05$) in EC+LB and EC+ACID silages. Subsamples of all d -100 silages were reinoculated with 1×10^5 cfu/g of EC immediately after silo opening. When the pathogen was subsequently enumerated after 168 h of aerobic exposure, it was not detected in silages treated with EC+ACID, EC+LB, or EC+LP, which all had pH values less than 5.0, whereas the EC silage had a pH value of 5.4 and 2.3 log cfu/g of the pathogen. Certain bacterial inoculants can hasten the inhibition of *E. coli* O157:H7 during ensiling, and like propionic acid, they can also prevent its growth on silage contaminated with the pathogen after ensiling.

Key Words: alfalfa, *Escherichia coli* O157:H7, microbial inoculants

1526 Partial replacement of ground corn by citrus pulp or steam-flaked corn fed at two concentrate levels on rumen parameters and kinetics. V. B. Ferrari*, N. R. B. Cônsolo, F. Rodriguez, J. F. Penso, M. O. Frasseto, and L. F. P. Silva, *University of Sao Paulo, Pirassununga, Brazil*.

The objective of this study was to evaluate three nonstructural carbohydrate (NSC) sources and two levels of concentrate on rumen parameters and kinetic of beef steers, having sugarcane silage as roughage source. Six rumen-cannulated Nellore steers, 345.10 ± 14 kg initial BW and` 20 mo old, were individually fed and assigned to 2 noncontemporary 6 × 6 Latin squares (LS) in a 3 × 2 factorial arrangement of treatments. Treatments consisted of three sources of NSC—ground corn (GC) and 70% of GC replaced by pelleted citrus pulp (PCP) or by steam-flaked corn (SFC)—and 2 levels of concentrate in diet (CONC)—either 60 (60C) or 80% (80C) on a DM basis. The experiment had 6 periods of 14 d. Samples of ingredients, orts, and rumen contents were analyzed for chemical composition. Rumen fluid was collected for rumen pH, short-chain fatty acids (SCFA), and ammonia nitrogen ($N\text{-}NH_3$) analyses. Statistical analysis was conducted using PROC MIXED of SAS and the model included fixed effects of CONC, NSC, and interaction (CONC×NSC) as well as random effects of period, animal(LS), and LS. Treatment effects were considered significant at $P \leq 0.05$. Increasing concentrate from 60C to 80C decreased NDF turnover rate ($P < 0.01$) and rate of passage (k_p) ($P < 0.01$). It also decreased DM and NDF intake ($P < 0.01$). Partial replacement of GC by either SFC or PCP decreased DM and CP intake ($P < 0.01$). The PCP increased NDF turnover rate ($P = 0.02$) and decreased k_p ($P < 0.01$) compared with GC. There was a CONC × NSC effect ($P < 0.05$) on rumen mass of OM, DM, and FDN, where PCP with 60C decreased these parameters. Rumen mass of iNDF was not influenced by any treatment ($P > 0.05$). Pelleted citrus pulp increased rumen pH ($P < 0.01$) and acetic acid ($P < 0.01$), decreased propionic acid ($P < 0.01$), and, consequently, increased A:P ratio ($P < 0.01$). The PCP increased total tract digestibility of DM ($P = 0.01$) and NDF ($P < 0.01$) compared with GC. Partial replacement of GC by SFC decreased acetic acid ($P < 0.01$), increased starch digestibility ($P = 0.05$), and decreased rumen $N\text{-}NH_3$ ($P = 0.03$). In conclusion, replacing GC with PCP in sugarcane silage based diets reduced intake and rate of passage but increased rumen pH and digestibility. Replacing GC by SFC increased starch digestibility and reduced rumen $N\text{-}NH_3$.

Key Words: carbohydrate source, concentrate levels, sugarcane silage

1527 Recovering lactating dairy cows from diet-induced milk fat depression using corn with different starch degradabilities. B. M. Koch, L. E. Koch*, W. C. Bridges, and G. J. Lascano, *Clemson University, Clemson, SC*.

Milk fat depression (MFD) is a condition where milk fat synthesis is impeded by ruminal biohydrogenation intermediates and continues to be a problem in the dairy industry. The objective of this experiment was to determine the effects of feeding a high- or low–rumen degradable starch diet after diet-induced MFD. Six rumen cannulated Holstein cows (416.58 ± 25.23 kg $BW^{0.75}$ and184.33 ± 29.6 DIM) were used in a crossover design consisting of covariate, induction, and recovery periods. All cows were fed a high-fiber control diet for 10 d during the covariate period and then switched to a high-PUFA and low-fiber diet for 10 d to induce MFD. After induction, cows were switched to one of two recovery diets with the incorporation of low- or high–degradable starch corn sources (LDS: 35% and HDS: 75% 7-h starch degradability) for 18 d. Samples were collected every 3 d throughout the duration of the trial. All dependent variables were analyzed using PROC MIXED of SAS including the covariate period as a fixed effect and repeated measures. Starch level was similar (25%; $P = 0.76$) in all treatments; however, crude fat level was greater for the induction diet compared with HDS and LDS (9.89 vs. 4.47 HDS and 4.92 LDS). There was no treatment effect on DMI but the effect of day on DMI was significant across treatments ($P < 0.01$). No treatment differences were detected for CP, crude fat, ADF, starch, sugar, and ash intakes but there was a significant increase of all nutrient intakes on Days 16, 22, and 28 ($P \leq 0.01$). Milk yield, protein, lactose, and solids-not-fat were not affected by treatment but were markedly decreased by day ($P < 0.01$). Milk fat decreased during induction ($P < 0.01$) and was significantly reduced by Day 7 and 10 ($P \leq 0.01$). Total fatty acids less than C16:0 and *cis*-9, *trans*-11 CLA were not affected by treatment but increased on Days 4, 7, and 10 of induction ($P \leq 0.01$). *Trans*-10, *cis*-12 CLA was not different for HDS or LDS, yet there was a tendency of days to differ ($P = 0.09$), with Day 7 and 10 of induction having a greater concentration. Milk fatty acid profiles of the recovery diets were similar, milk yield was not affected, and DMI did not vary by treatment during this experiment. This suggests that using corn sources with starch degradability of up to 75% may be incorporated into rations to recover milk fat to normal levels.

Key Words: milk fat depression, polyunsaturated fatty acids, starch degradability

1528 Effects of field pea supplementation on digestibility and rumen volatile fatty acid concentration of diets containing high- and low-quality forages. H. L. Greenwell*[1], J. L. Gramkow[2], M. L. Jolly-Breithaupt[1], J. C. MacDonald[1], and K. H. Jenkins[3], *[1]University of Nebraska-Lincoln, Lincoln, [2]University of Nebraska, Lincoln, NE, [3]University of Nebraska, Scottsbluff, NE*.

Five ruminally fistulated steers (initial BW = 202 kg; SD = 20 kg) were used in a 5 × 6 Latin rectangle to evaluate the effects of supplementation on total tract digestibility of diets containing either high- or low-quality forages. Treatments were set up as a 2 × 3 factorial (forage quality × supplement type). The first factor was high-quality forage (HQ; 50% alfalfa and 50% sorghum silage, DM basis) or low-quality forage (LQ; 50% brome grass hay and 50% wheat straw, DM basis). The second factor was one of three supplements: control (CON), dry-rolled corn (DRC), or field peas (FP). Steers were supplemented at 0.43% of BW (DM basis). Periods lasted 14 d with a 9-d adaptation period and 4-d collection period. Data were analyzed using the mixed procedure of SAS and evaluating significance at $\alpha = 0.05$. There were no interactions between forage quality and supplement type on digestibility ($P \geq 0.25$). Dry matter intake, DM digestibility (DMD), OM intake (OMI), and OM digestibility (OMD; $P < 0.01$) were greater with HQ forage (6.13 kg/d, 63.1%, 4.96 kg/d, and 64.2%, respectively) than with diets containing LQ (4.71 kg/d, 49.1%, 3.60 kg/d, and 50.1%, respectively). The FP supplement ($P \leq 0.03$) increased DMI and OMD (6.14 ± 0.512 kg/d and 61.6 ± 1.94%, respectively) over steers receiving DRC (5.33 kg/d and 56.1%, respectively) or CON (4.80 kg/d and 53.8%, respectively); DRC and CON did not differ in intake or OMD. The acetate-to-propionate ratio (A:P) was affected by both forage and supplement where HQ was less than LQ (3.61 ± 0.05 and 4.09 ± 0.05, respectively) and DRC supplement produced lower A:P (3.58 ± 0.07) than FP and CON (3.99 and 3.97 ± 0.07, respectively), which were similar. Propionate proportions differed, with HQ tending ($P = 0.06$) to have greater concentrations than LQ. There was a supplement effect ($P = 0.01$) where DRC increased propionate proportion over CON and FP (18.88, 17.96, and 17.72 ± 0.27%, respectively). Acetate proportions ($P < 0.01$) were greater for the LQ forage (72.3 ± 0.58%) than for the HQ forage diet (64.8 ± 0.58%). A supplement effect was observed for acetate ($P < 0.01$), with CON and FP values greater than DRC. Supplementing FP in low- or high-quality diets increases DMI and OMD and may be an acceptable supplement for beef cattle.

Key Words: cattle, field peas, forage quality

1529 Effect of live yeast fed to natural-program beef steers during the finishing phase. L. A. Ovinge*, J. O. Sarturi, M. L. Galyean, P. R. B. Campanili, and L. A. Pellarin, *Texas Tech University, Lubbock*.

Growth performance, carcass characteristics, nutrient digestibility, and feeding behavior were evaluated in natural-program beef cattle fed steam-flaked corn–based finishing diets with 3 inclusion levels of live yeast (ABVista Inc., United Kingdom; 0, 25, and 50 g/steer daily). Steers ($n = 144$; 341 ± 20 kg) were blocked by BW and assigned to treatments in a randomized complete block experimental design. The natural program did not include the use of implants, ionophores, and antibiotics. Live yeast was included in a premix (cottonseed meal carrier) at 1% of the diet (DM basis). Data were analyzed using the GLIMMIX procedure of SAS with pen used as the experimental unit. Feed efficiency tended to be improved (quadratic, $P = 0.08$) between d 0 and 183, with steers fed 25 g/d of live yeast having a 4.3% greater G:F than the average of other treatments. Linear increases in premium Choice ($P < 0.01$) and Choice ($P = 0.05$) carcasses were observed as live yeast increased in the diet. Total tract nutrient digestibility increased (quadratic, $P < 0.01$) as live yeast increased, with steers fed 25 g/d having greater digestible DM (5.4%), OM (4.8%), NDF (22.1%), ADF (19.9%), hemicellulose (22.7%), CP (6.2%), and ether extract (2.5%) than the average of steers in the other treatments. Rumination (11%), eating time (8%), and chewing activity (20%) were not affected by treatments (% of 24-h evaluation). Live yeast included at 25 g/d in the finishing diet of natural-program beef steers improved dietary nutrient digestibility (except starch) and carcass quality grade and tended to improve gain efficiency, without affecting feeding behavior.

Key Words: digestibility, live yeast, natural program

1530 Effects of calcium–ammonium nitrate on in vitro fermentation of bahiagrass hay with supplemental molasses. D. D. Henry*[1], F. M. Ciriaco[1], R. C. Araujo[2], M. E. Garcia-Ascolani[1], P. L. P. Fontes[1], N. Oosthuizen[1], C. D. Sanford[1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]GRASP Ind. & Com. LTDA, Curitiba, Brazil*.

A randomized complete block design was used to determine the effects of increasing amounts of calcium ammonium nitrate (CAN) on in vitro fermentation of bahiagrass hay (*Paspalum notatum*). In vitro fermentation consisted of 100 mL of a 4:1 buffer:ruminal fluid inoculum and 0.7 g of a substrate composed of 80:20 bahiagrass hay:molasses (DM basis) incubated for 48 h in 125-mL serum bottles. Three days (block) of incubation were performed. Duplicate bottles in each day were randomly inoculated and received 1 of 4 treatments: 1) negative control (no added NPN; NEG), 2) control (0.75% urea in

the substrate DM; CTL), 3) 1.2% CAN (0.38% urea and 1.2% CAN in the substrate DM; 1.2CAN), and 4) 2.4% CAN (2.4% CAN in the diet DM; 2.4CAN). Treatments CTL, 1.2CAN, and 2.4CAN were isonitrogenous. Two ruminally cannulated Angus crossbred steers (348 ± 29 kg BW) fed bahiagrass hay ad libitum and 2.27 kg (as is) of a 50:50 molasses:crude glycerol mixture, daily, were used as ruminal fluid donors. In vitro OM digestibility (IVOMD) was determined using the same amounts of substrate and inoculum from the in vitro batch culture. Data were analyzed using the mixed procedure of SAS with the fixed effect of treatment and the random effect of day. Means of duplicate bottles within day were considered the experimental unit. Contrasts were used to determine the effect of NPN (NEG vs. others), linear effects of CAN, and quadratic effects of CAN. Gas production increased ($P = 0.023$) when adding NPN (295 vs. 301 ± 2.0 mL/g of OM incubated for NEG vs. NPN, respectively) and linearly decreased ($P < 0.001$) as nitrate amounts increased. Adding NPN increased ($P = 0.015$) IVOMD, whereas a linear ($P = 0.001$) decrease occurred as nitrate increased; however, no difference ($P = 0.351$) was observed between CTL and 1.2CAN. Methane production linearly decreased ($P = 0.001$) with the addition of nitrate (4.81 vs. 0.65 ± 0.325 mmol/g substrate fermented for CTL vs. 2.4CAN, respectively). There was no effect ($P > 0.05$) of NPN or nitrate on total VFA (m*M*), acetate:propionate ratio, or molar proportions of any VFA analyzed. Added NPN improved the IVOMD of bahiagrass hay as expected in a CP-deficient forage. Inclusion of 2.4CAN reduces IVOMD and methane production, whereas 1.2CAN also reduces methane production without affecting IVOMD, implying a potential intervention to decrease methane emissions.

Key Words: fermentation, nitrate, nonprotein nitrogen

1531 A meta-analysis to estimate the net macromineral (calcium, phosphorus, magnesium, sodium, and potassium) requirements for maintenance in beef cattle. L. F. Costa e Silva*[1], S. C. Valadares Filho[2], P. P. Rotta[3], M. I. Marcondes[4], D. Zanetti[1], F. A. S. Silva[1], and M. V. C. Pacheco[1], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [4]Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Brazil*.

To predict mineral requirements for beef cattle, the factorial method has been the most used. A meta-analysis was used to estimate the net macromineral (Ca, P, Mg, Na, and K) requirements for maintenance and retention coefficient in Nellore cattle. A database composed by 278 animals from 8 studies conducted in tropical conditions was developed, being 134 bulls, 73 steers, and 71 heifers. Also, animals were from the following genetic groups: Nellore ($n = 196$), Zebu × Holstein ($n = 46$), Angus × Nellore ($n = 18$), and Simmental × Nellore ($n = 18$). Variables such as mineral intake and mineral excretion as feces and urine were collected where retained mineral was calculated by difference between mineral intake and mineral excretion. Therefore, the linear regression between retained mineral and mineral intake, as milligrams per kilogram BW, was performed to achieve the net mineral requirement for maintenance and retention coefficient where the intercept and slope were considered the net requirement for maintenance (NRM) and retention coefficient (RC) of each mineral, respectively. Then, the NRM for Ca, Na, and K were 9.85, 4.47, and 16.28 mg/kg BW, these values being below those recommended by the beef cattle NRC system of 15.4, 15.0, and 38 mg/kg BW. Considering a 300-kg animal, the NRM for Ca would be 2.95 and 4.62 g/d when estimated by this new proposal and the beef cattle NRC system. This shows that the Ca supply to meet endogenous losses is overestimated, which could reduce Ca excretion via feces to environment. Moreover, the NRM for P and Mg were 19.0 and 1.87 mg/kg BW, which are close to the recommendations of the beef cattle NRC system of 16.0 and 3.0 mg/kg BW. However, the RC for Ca, P, and Mg were 59.1, 79.6, and 23.5%, respectively, which are close to the recommendations of the beef cattle NRC system of 50, 68, and 17%, whereas the RC for Na and K were 34.2 and 48.8%, respectively, which are below those recommend by the beef cattle NRC system of 91 and 100%. Therefore, we believe that these values for the net macromineral requirement for maintenance and retention coefficient can improve the understanding of dietary mineral requirements of beef cattle.

Key Words: meta-analysis, mineral requirements, Nellore

1532 Effect of micronutrient source on mineral status and performance of steers fed low- or high-sulfur diets. S. J. Hartman*, O. N. Genther-Schroeder, and S. L. Hansen, *Iowa State University, Ames*.

The objective was to determine effects of hydroxy (HYD) or inorganic (ING) trace minerals within low- or high-S diets on mineral status and performance of beef steers. Forty-eight Angus-crossbred steers were blocked by BW (316 ± 2.8 kg) and assigned to a 2 × 2 factorial with low (0.25%; LS) and high S (0.53%; HS; additional S as $CaSO_4$). Trace minerals (TM) were supplemented as 10 mg Cu, 30 mg Zn, and 20 mg Mn per kilogram DM from ING (sulfates) or HYD (IntelliBond; Micronutrients USA LLC, Indianapolis, IN). Growing period (GP; 84 d) diets were corn silage based and finishing period (FP; 78 d) diets were corn based with 12% hay. Steers (6/pen) were fed via GrowSafe bunks, and the experimental unit was steer ($n = 12$/treatment). Plasma and liver mineral concentrations were determined at trial initiation and at the end of GP and FP. Data were analyzed as a 2 × 2 factorial using SAS; initial plasma and liver mineral concentrations were covariates in analysis.

High S decreased ($P < 0.01$) end of GP and FP liver Cu concentrations and tended ($P \leq 0.1$) to decrease plasma Cu at these times. At the end of GP, HS decreased ($P = 0.04$) plasma Zn concentrations and tended to decrease ($P = 0.1$) liver Zn concentrations. Final liver Cu concentrations were greater in ING steers than in HYD steers ($P < 0.01$). Liver Mn concentrations displayed S × TM effects ($P = 0.05$) at the end of GP and FP, where LS-HYD had greater Mn concentrations than HS-HYD, HS-ING, and LS-ING at the end of GP; however, HS-HYD final Mn concentrations tended to be greater than LS-HYD and LS-ING tended to be greater than HS-ING and LS-HYD. Growing period ADG and G:F displayed TM × S effects ($P \leq 0.06$) where LS-HYD had better efficiency and gain than LS-ING and HS-ING. Overall, HS-HYD was less efficient than HS-ING ($P = 0.02$) and LS-HYD ($P = 0.06$). Overall DMI, ADG, final BW, HCW, and marbling scores were not different ($P \geq 0.12$) due to treatment; however, steers consuming ING had larger REA ($P = 0.02$) than those fed HYD, and HS decreased ($P = 0.03$) back fat and yield grade compared with LS. In this study HS decreased markers of Cu and Zn status, and differential effects of ING vs. HYD minerals were noted, although all steers maintained adequate status.

Key Words: beef, sulfur, trace mineral

1533 Effect of anionic salts on rumen fermentation in a continuous culture system. A. L. Kenny*[1], J. L. Purdom[1], M. M. Masiero[1], J. P. Jarrett[2], T. J. Wistuba[2], and M. S. Kerley[1], *[1]University of Missouri, Columbia, [2]Phibro Animal Health Corporation, Quincy, IL*.

The objective was to determine if anionic salt products (AS), commonly used to lower dietary cation–anion difference (DCAD) in prefresh dairy cattle diets, altered ruminal digestion, microbial fermentation, or microbial yield in a single-flow continuous culture system. Two consecutive experiments were conducted using 24 fermenters inoculated with rumen fluid from two lactating Holstein cows. For Exp. 1, fermenters were fed a basal diet twice daily (47.12 g DM/d; 37% wheat hay, 26% corn silage, 12.5% soybean meal, 11% soy hulls, and 13.5% supplement on a DM basis). Treatments (0.19 g/d) were added directly to randomly assigned fermenters (4/treatment) and consisted of control (CON; basal diet only), soybean meal (SBM), urea (URE), chloride and sulfur containing AS blend (CSB), glutamic acid fermentation product (GAF), and hydrochloric acid based product (HCB). In Exp. 2, the same basal diet was used except CSB and GAF treatments were blended to the basal diet at 0.077 and 0.146 g/d, respectively, and other treatments were blended to achieve 0.19 g/d (representing approximate adjustments for equivalent DCAD content from respective AS). Diets were fed for 7 d with 4 d of adaptation and 3 d of sampling. Passage rate was 5.47% for Exp. 1 and 4.83% for Exp. 2. Fermenter samples for VFA and ammonia analysis were collected at 0 and 4 h after the morning feeding. Outflow was collected daily, and fermenter content was collected at the end of the experiment. Data were analyzed as a completely randomized design with fermenters as the experimental unit, using the MIXED procedure of SAS (version 9.3; Cary, NC). In Exp. 1, NDF digestibility (%) tended to be lower ($P = 0.088$) for GAF (31.9) and HCB (33.0) compared with the other treatments except SBM (37.4). Ammonia concentration (mg NH_3 N/dL) for URE was greater (22.2; $P < 0.01$) than for the other treatments, with CSB greater (19.5; $P < 0.04$) than SBM (18.3) and CON (18.5). These differences were not found in Exp. 2. In both experiments, there were no effects on OM, CP, or ADF digestibility; microbial efficiency; microbial flow; or VFA. Differences in NDF digestibility and ammonia concentration between Exp. 1 and Exp. 2 may be due to run-to-run variability. In conclusion, adding anionic salt products to a prefresh dairy cattle diet had no detrimental effects on ruminal digestibility or microbial fermentation and yield.

Key Words: anionic salts, continuous culture, rumen fermentation

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1534 Effects of prepartum dietary cation–anion difference and source of vitamin D on dairy cows: Vitamin D, mineral, and bone metabolism. R. M. Rodney*[1,2], N. Martinez[3], E. Block[4], L. L. Hernandez[5], C. D. Nelson[6], P. Celi[7], J. E. P. Santos[6], and I. J. Lean[1,2], *[1]University of Sydney, Camden, Australia, [2]Scibus, Camden, Australia, [3]Department of Animal Sciences, University of Florida, Gainesville, [4]Church and Dwight Animal Nutrition, Ewing, NJ, [5]Department of Dairy Science, University of Wisconsin, Madison, [6]University of Florida, Gainesville, [7]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Australia*.

This 2 × 2 factorial study evaluated the effects of feeding dairy cows diets containing either calcidiol or cholecalciferol (3 mg/11 kg of diet DM) and positive (+130 mEq/kg) or negative (−130 mEq/kg) dietary cation–anion difference (DCAD) on vitamin D, mineral, and bone homeostasis during transition. Pregnant Holstein cows ($n = 79$) were blocked by parity and milk yield and randomly allocated to treatments from 255 d of gestation until calving. All groups of cows were then fed on identical lactating cow diets until 49 d after calving. Blood samples were taken thrice weekly prepartum and after calving until d 30 of lactation, with additional samples taken at 0, 1, and 2 d postpartum, for analysis. Milk yield and composition were recorded for the first 49 DIM. Feeding calcidiol increased concentrations of calcidiol pre- (235.1 ± 6.18 vs. 60.3 ± 6.25 ng/mL) and postpartum (214.8 ± 4.85 vs. 59.13 ± 4.90 ng/mL) and calcitriol prepartum (55.66 ± 1.62 vs. 51.05 ± 1.64 ng/mL) when compared with feeding cholecalciferol. Feeding negative vs. positive DCAD increased prepartum

concentrations of calcitriol (58.0 ± 1.61 vs. 48.3 ± 1.65 pg/mL) but decreased calcidiol (136.0 ± 6.17 vs. 160.4 ± 6.26 ng/mL) and cholecalciferol (6.8 ± 0.41 vs. 9.7 ± 0.42 ng/mL) prepartum and calcidiol, cholecalciferol and calcitriol postpartum (131.3 ± 4.84 vs. 144.4 ± 4.91 ng/mL, 3.7 ± 0.28 vs. 4.9 ± 0.28 ng/mL, and 98.0 ± 4.29 vs. 117.5 ± 4.34 pg/mL, respectively). After calving, calcitriol was higher in parous than nulliparous cows. Blood calcium increased in cows fed calcidiol (2.45 ± 0.02 vs. 2.34 ± 0.02 and 2.27 ± 0.01 vs. 2.25 ± 0.01 m*M* for pre- and postpartum, respectively). Calcium concentrations in the negative DCAD group were lower before calving, compared with the positive DCAD group (2.36 ± 0.2 vs. 2.43 ± 0.2 m*M*), but higher postpartum (2.29 ± 0.01 vs. 2.23 ± 0.01 m*M*). Feeding negative DCAD lowered blood pH (7.44 ± 0.01 vs. 7.49 ± 0.01) compared with positive DCAD prepartum but not postpartum. There was no effect of vitamin D or DCAD on blood osteocalcin, PTH, adiponectin, leptin, or serotonin concentrations. Nulliparous cows had higher blood concentrations of osteocalcin and crosslaps than parous cows. Cows fed calcidiol produced 3.70 ± 1.2 kg/d more 3.5% fat- and energy-corrected milk than those receiving cholecalciferol.

Key Words: calcidiol, calcium, dietary cation–anion difference

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1535 The net macromineral (calcium, phosphorus, magnesium, sodium, and potassium) requirements for growth in beef cattle estimated by meta-analysis.

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To predict mineral requirements in beef cattle, the factorial method has been the most used. A meta-analysis was used to estimate the net macromineral (Ca, P, Mg, Na, and K) requirements for growth in Nellore cattle. A database composed by 873 animals from 21 studies conducted in tropical conditions was developed, being 411 bulls, 255 steers, and 157 heifers. Also, animals were from the following genetic groups: Nellore (n = 473), Zebu × Holstein (n = 149), and beef crossbred cattle × Nellore (n = 250). The net mineral requirement was calculated using the following allometric model: $Mi = a \times EBW^b$, in which Mi is the amount of each mineral in the body, EBW is the empty body weight, and a and b are parameters of the model. When differences were observed for sex (bulls, steers, and heifers) and genetic group (Zebu, dairy crossbred, and beef crossbred cattle), distinct equations were separately generated. For crossbreeding, differences between dairy crossbreeds and beef crossbreeds were not verified ($P > 0.05$) for any mineral, which allowed us to analyze genetic group such as Zebu and crossbred cattle. Moreover, the allometric plateau method was used to reach the empty body weight at which animals achieve maturity for mineral retention and, after this point, there are only mineral requirements for maintenance. Therefore, differences regarding sex were observed for Ca and Na, allowing us to generate different equations for bulls, steers, and heifers. Also, from the database used in this study, bulls establish their need for Ca and Na when they reach 432 and 424 kg of EBW, respectively, whereas for steers, the EBW to reach maturity of these minerals were 421 and 481 kg, respectively. For heifers, the EBW were 432 and 405 kg for Ca and Na, respectively. In the case of P, Mg, and K, differences were verified for genetic group where zebu cattle establish the need for P, Mg, and K for growth when the EBW is 522, 427, and 460 kg, respectively. Moreover, considering crossbred cattle, the estimate of EBW for reaching maturity of P, Mg, and K is 469, 433, and 492 kg, respectively. Therefore, we believe that the equations for the net macromineral requirement for growth can improve the understanding of dietary mineral requirements of beef cattle and contribute to correct supply of minerals in diet reducing losses and environment pollution.

Key Words: beef cattle, mineral, requirement

1536 The effect of decreasing dietary cation–anion difference in the prepartum diet on urine mineral excretion and blood energy metabolite concentrations in multiparous Holstein cows.

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The objective of this study was to determine the effect of decreasing dietary cation–anion difference (DCAD) in the prepartum period on prepartum urine mineral excretion and concentrations of energy metabolites in plasma in the periparturn period. Multiparous Holstein cows (n = 89) were randomly allocated to one of three prepartum diets with decreasing DCAD, CON (+18.3 mEq/100 g DM), MED (+5.9 mEq/100 g DM), or LOW (−7.4 mEq/100 g DM), beginning at 24 d before expected parturition and individually fed. Cows were fed a common postpartum diet from parturition until 63 d in milk. Urine samples collected 1x before treatment assignment and 1x/wk prepartum were analyzed for mineral and creatinine concentrations. Blood samples were collected 1x before treatment assignment, 2x/wk prepartum, 2x/24 h postpartum, and 3x/wk through 21 d postpartum. Repeated

measures analysis was conducted using the MIXED procedure of SAS with linear and quadratic effects of decreasing prepartum DCAD as contrasts. Pearson's correlation coefficient for the association between urine pH and urine Ca-to-creatinine ratio was determined using the CORR procedure of SAS. Least squares means or geometric means and 95% confidence intervals are presented. No difference in prepartum or postpartum concentrations of NEFA or β-hydroxybutyrate was observed for the treatment groups. A trend for a quadratic effect on postpartum plasma glucose was observed (CON = 50.0 mg/dL [48.6–51.4], MED = 50.8 mg/dL [49.4–52.1], and LOW = 48.6 mg/dL [47.2–50.0]; $P = 0.09$). No effect of treatment on Mg excretion was observed; however, as calving approached, the ratio of urine Mg to creatinine decreased in all groups ($P < 0.01$). A quadratic effect on mean ratio of urine Ca to creatinine was observed (CON = 0.03 [0.02–0.04], MED = 0.07 [0.06–0.09], and LOW = 0.33 [0.27–0.44]; $P < 0.01$). A quadratic effect on estimated grams of Ca excreted, based on a creatinine excretion rate of 29 mg/kg of BW per day, also was observed (CON = 0.7 g/d [0.6–0.9], MED = 1.7 g/d [1.4–2.0], and LOW = 8.2 g/d [6.8–10.0]; $P < 0.01$). Urine pH and urine Ca-to-creatinine excretion ratio were highly correlated ($r = -0.81$, $P < 0.01$). Feeding decreasing DCAD prepartum did not significantly alter concentrations of energy metabolites in plasma in the peripartum period. Urine Ca excretion greatly increased when cows were fed the lowest DCAD, suggesting greater Ca flux prepartum, which likely contributed to improved Ca status postpartum.

Key Words: dietary cation–anion difference, energy metabolism, mineral excretion

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1537 The effect of decreasing dietary cation–anion difference in the prepartum diet on plasma haptoglobin concentrations and incidence of cytological endometritis in multiparous Holstein cows. B. M. Leno*[1], C. M. Ryan[1], R. O. Gilbert[2], K. Zanzalari[3], D. Kirk[4], J. D. Chapman[4], and T. R. Overton[1], *[1]Cornell University, Department of Animal Science, Ithaca, NY, [2]Cornell University College of Veterinary Medicine, Department of Clinical Sciences, Ithaca, NY, [3]Phibro Animal Health Corp., Quincy, IL, [4]Phibro Animal Health Corporation, Quincy, IL*.

The objective of this study was to determine the effect of decreasing dietary cation–anion difference (DCAD) in the prepartum period on concentration of haptoglobin in plasma in the peripartum period and incidence of cytological endometritis. Multiparous Holstein cows ($n = 89$) were randomly allocated to one of three prepartum diets with decreasing DCAD, CON (+18.3 mEq/100 g DM), MED (+5.9 mEq/100 g DM), or LOW (−7.4 mEq/100 g DM), beginning at 24 d before expected parturition and individually fed. Cows were fed a common postpartum diet from parturition until 63 d in milk. Plasma samples were analyzed for haptoglobin concentrations at wk −1 and d 3, 5, 7, and 14. A low-volume uterine lavage was conducted at approximately 8 d in milk (range 4–12 d; first lavage) and again at approximately 50 d in milk (range 40–60 d; second lavage). Cytology slides were prepared and 200 cells (excluding erythrocytes) were counted per slide to determine the percent polymorphonuclear leukocytes (PMN). The MIXED procedure of SAS, with linear and quadratic effects of decreasing prepartum DCAD as contrasts, was used to analyze plasma haptoglobin as a repeated measure and percent neutrophils present at the first and second lavage. Geometric means and 95% confidence limits are presented. Fisher's exact test was conducted to determine associations of treatment with incidence of cytological endometritis (CE) at second lavage (>10% PMN) using the FREQ procedure of SAS. A linear trend for lower plasma haptoglobin with decreasing DCAD was observed (CON = 0.7 mg/mL [0.6–0.8], MED = 0.6 mg/mL [0.5–0.7], and LOW = 0.6 mg/mL [0.5–0.7]; $P = 0.12$). No effect of prepartum DCAD on percent PMN at first or second lavage was observed. Incidence of CE was not different between treatment groups (CON = 10/30, MED = 7/30, and LOW = 9/29; $P = 0.70$). Decreasing prepartum DCAD did not alter PMN presence in endometrial cytology or incidence of cytological endometritis but tended to reduce haptoglobin in the peripartum period, suggesting decreased inflammation in those cows.

Key Words: cytological endometritis, dietary cation–anion difference, haptoglobin

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1538 Influence of molybdenum concentration, pH, and transit time on the in vitro bioaccessibility of sulfur. J. Hawley* and E. B. Kegley, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

In vitro bioaccessibility (IVBA) methods are useful to provide knowledge on possible interactions between antagonists and the factors involved in digestion on the potential to influence the physiological solubility of minerals for absorption into the animal. This study was conducted to evaluate the influence of Mo concentration, pH, and transit time on the S IVBA of S sources frequently used in beef cattle rations. In vitro digestions ($n = 540$) were used in a 3 × 5 × 3 × 3 factorial arrangement of treatments (4 replicates/treatment) to determine the effects of Mo concentration (no additional Mo [No Mo], 1 [Low Mo] ppm Mo added, or 5 [High Mo] ppm Mo added) on the S IVBA of S sources (no S source [Control], corn gluten feed [CGF], dried distillers' grains [DDG], chemical grade sodium sulfate [Na_2SO_4–CG], or feed grade sodium sulfate [Na_2SO_4–FG]) using hydrochloric acid solutions (pH = 2, 4, or 6), transit times (0.5, 2, or 6 h), and agitation to simulate the physiologic conditions that occur in the gastrointestinal environment. Sulfur IVBA in the processed samples was estimated by dividing extractable S in the in vitro digestions by

the S concentration in the S source being assayed. Sulfur and Mo concentrations were determined by inductively coupled plasma spectroscopy. Sulfur IVBA differed ($P < 0.0001$) by S source (0.0, 44.7, 42.9, 106.1, and 102.9% S for Control, CGF, DDG, Na_2SO_4–CG, and Na_2SO_4–FG, respectively). A Mo concentration× S source interaction was observed for S IVBA ($P < 0.0001$). The addition of High Mo to CGF and DDG decreased S IVBA, whereas the S IVBA of Na_2SO_4–CG was not affected by Mo concentration. Increased transit time for No Mo and Low Mo increased S IVBA and was greatest for Low Mo at 6 h; however, High Mo was not affected by transit time ($P < 0.0001$; Mo concentration × transit time interaction). A S source × transit time interaction was observed for S IVBA ($P < 0.0001$). Increased transit time increased the S IVBA of CGF and DDG, whereas the S IVBA of Na_2SO_4–FG was not affected by transit time. These findings indicate a complex interrelationship exists between the physiochemical properties of S sources, Mo antagonism, and ruminal factors on S bioaccessibility.

Key Words: antagonism, in vitro bioaccessibility, sulfur

1539 Bovine hair mineral concentrations as potential indicators of mineral status. J. Hawley* and E. B. Kegley, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

This study was designed to assess the efficacy of bovine hair mineral concentrations as an indicator of mineral status. Thirty-six primiparous beef heifers of predominantly Angus breeding were stratified by BW, BCS, and anticipated calving date and assigned to 12 pens (3 heifers/pen) for a 260-d maternal nutrition study. Pens were randomly assigned to 1 of 4 treatments (2 × 2 factorial): 1) 0.15% S and 6 mg Cu/kg, 2) 0.15% S and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$), 3) 0.55% S (from Na_2SO_4) and 6 mg Cu/kg, or 4) 0.55% S (from Na_2SO_4) and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$). A cracked corn and soybean meal basal ration delivered each treatment starting at 170 ± 16 d of gestation through 150 ± 16 d in lactation. Heifers had ad libitum access to mixed grass pasture. Heifer blood, hair, and liver samples were collected on d 55 and 112 ± 16 relative to parturition, and progeny blood, hair, and liver samples were collected on d 59 and 114 ± 6 relative to birth. Point-biserial correlation (r_{bp}) analysis was used to determine the correlation between hair mineral concentrations and age. Pearson's correlation (r) analysis was performed to determine the correlation between bovine hair mineral concentrations and traditional mineral status indices. Indices that showed significant correlation were analyzed by simple linear regression to determine the working relationship between indices. Age influenced hair mineral concentrations. Progeny exhibited greater hair Cu ($r_{pb} = 0.47$, $P < 0.0001$) and Zn ($r_{pb} = 0.38$, $P < 0.0001$) concentrations. Heifer hair Cu concentrations were positively correlated with plasma Cu ($r = 0.70$, $P < 0.0001$) and liver Cu ($r = 0.59$, $P < 0.0001$) concentrations. Progeny hair Cu concentrations were negatively correlated with plasma S ($r = -0.55$, $P < 0.0001$) and positively correlated with liver Cu ($r = 0.32$, $P < 0.05$) concentrations. Regression equations revealed heifer hair Cu concentrations accounted for 49 and 35% of the variability in plasma and liver Cu concentration, respectively. Progeny hair Cu concentrations accounted for 30 and 10% of the variability in plasma S and liver Cu concentrations, respectively. Results suggest that bovine hair mineral concentrations alone do not provide sufficient information to assess mineral status; however, they may be useful when combined with other traditional mineral status indices to assess mineral status with greater precision.

Key Words: beef cattle, hair, mineral concentrations

1540 Effects of diets containing either traditional anionic salts or a commercial anionic supplement on feed intake and energy balance of prepartum dairy cows. F. S. Strydom*[1], J. N. Nothnagel[1], and J. P. Swiegers[2], *[1]Nova Feeds, Malmesbury, South Africa, [2]Ruminant Nutrition Consultancy, Bethlehem, South Africa*.

Anionic supplements are fed to prepartum (PP) dairy cows to reduce dietary cation–anion difference (DCAD) and improve calcium status at calving. Traditional anionic salts (AS) can reduce DMI, presumably due to poor palatability. Commercial

Table 1540.

DMI, kg/d (LS Mean)	AS	SC	AS v SC (Adj P value)
3rd week PP	12.6	13.5	1.00
2nd week PP	11.4	13.2	0.622
1st week PP	9.7	11.7	0.053
3 week average	11.4	12.8	0.0004
EB, Mcal/d (LS Mean)			
3rd week PP	-0.02	+0.99	1.0000
2nd week PP	-1.74	-0.29	1.0000
1st week PP	-6.22	-2.82	0.122
3 week average	-2.68	-0.51	0.0039

Table 1541.

Table 1. Effect of level of prepartum DCAD and duration (Dur) of feeding on intake and blood measures

	Treatment					P value		
Prepartum	S -60	S -160	L -60	L -160	SEM	Dur	DCAD	Dur x DCAD
DMI (-21 to -1), kg/d	12.1	9.9	11.4	10.0	0.6	0.45	<0.01	0.29
Urinary pH	6.19	5.38	6.41	5.47	0.09	0.10	<0.01	0.47
Blood pH	7.419	7.382	7.413	7.384	0.007	0.80	<0.01	0.58
Blood HCO_3^-, m*M*	26.2	22.6	25.7	23.8	0.5	0.49	<0.01	0.13
Base excess, m*M*	1.62	-2.40	1.04	-1.43	0.63	0.75	<0.01	0.21
Blood iCa, m*M*	1.26	1.29	1.25	1.28	0.01	0.44	<0.01	0.93
Postpartum								
Blood pH	7.448	7.452	7.444	7.454	0.003	0.74	0.05	0.47
Blood pCO_2, mm Hg	41.9	41.7	41.6	42.5	0.5	0.73	0.49	0.34
Blood HCO_3^-, m*M*	29.3	29.1	28.6	30.1	0.4	0.59	0.07	0.02
Base excess, m*M*	5.17	5.51	4.56	6.11	0.37	0.99	0.01	0.10
Blood iCa, m*M*	1.12	1.13	1.13	1.13	0.02	0.81	0.66	0.70

anionic supplements purportedly are more readily consumed, but there is little research to support this assertion. Twenty-nine pregnant multiparous Holsteins were used to examine the effects of AS or a commercial anionic supplement (SoyChlor [SC]) on DMI and energy balance (EB) during the last 3 wk of pregnancy. The AS supplement consisted of 55% ammonium chloride, 29% magnesium sulfate, and 16% ammonium sulfate. At dry off, each cow entered a communal pen and was accustomed to a Calan gate feeder. The far-off dry period diet was a total mixed ration without anionic supplementation. At 21 d before expected calving date, cows were alternately assigned to a treatment. The AS or SC was incorporated into the diet to yield a calculated DCAD [(Na + K) − (Cl + S)] of −120 mEq/kg. Urine pH was monitored to ensure similar metabolic acidification among the two PP groups. Individual DMI was measured daily. Diet energy content (estimated using the CNCPS version. 6.5 model) and DMI allowed calculation of EB. Data were analyzed using the Mixed procedure of SAS. Post hoc testing of means was done using Bonferroni's procedure. Overall treatment and treatment by week effects for each of the three PP weeks were examined. Least squares means are in the table. Over the entire PP period, cows supplemented with SC had higher DMI ($P < 0.001$) and EB ($P < 0.004$) than cows supplemented with AS. Dry matter intake and EB declined for both groups as the PP period progressed toward calving.

Key Words: anionic supplement, dry matter intake, energy balance

1541 Effect of level of dietary cation–anion difference and duration of prepartum feeding on calcium and measures of acid–base status in transition cows. C. Lopera*[1], R. Zimpel[1], F. R. Lopes Jr.[1], W. G. Ortiz[1], B. N. Faria[1], M. R. Carvalho[1], A. Vieira Neto[1], M. L. Gambarini[2], E. Block[3], C. D. Nelson[1], and J. E. P. Santos[1], *[1]University of Florida, Gainesville, [2]Federal University of Goiás, Goiânia, Brazil, [3]Church and Dwight Animal Nutrition, Ewing, NJ.*

Objectives were to determine the effects of extending the feeding of acidogenic salts prepartum at two levels of negative dietary cation–anion difference (DCAD) on mineral metabolism and acid–base status in dairy cows. One hundred twelve Holstein cows at 230 d of gestation were blocked by lactation (1 vs. >1) and 305-d milk yield and, within each block, randomly assigned to one of four treatments arranged as 2 × 2 factorial with two levels of DCAD (−60 vs. −160 mEq/kg) and two durations (DUR) of feeding the negative DCAD, short (S; 21 d) or long (L; 42 d). Cows in S received an isonitrogenous and isocaloric diet with a DCAD of +130 mEq/kg from 233 to 254 d of gestation. Therefore, during the first 21 d of the experiment, cows were fed one of three DCAD diets, +130, −60, or −160 mEq/kg, whereas during the last 21 d of gestation, they were fed either −60 or −160 mEq/kg. Urine was collected twice weekly, and pH was measured. Cows were weighed and their BCS was assessed once weekly prepartum. Intake of dry matter (DMI) was measured daily. Blood was sampled from the jugular vein at 250, 269, and 272 d of gestation and on d 0, 1, 2, 3, and 4 postpartum and analyzed for concentrations of ionized Ca (iCa), blood gases, pH, base excess, and bicarbonate (HCO_3^-). Data were analyzed by ANOVA with repeated measures using the MIXED procedure of SAS. Intake of DM

in the first 21 d in the experiment decreased ($P < 0.01$) by reducing the DCAD and averaged 11.8, 10.9, and 10.4 kg/d for cows fed +130, −60, and −160 mEq/kg, respectively. Similarly, urinary pH decreased ($P < 0.01$) with a reduction in DCAD and averaged 8.11, 6.59, and 5.67 for cows fed +130, −60, and −160 mEq/kg, respectively. Results for the last 21 d of gestation and first 4 d postpartum are depicted in Table 1. Reducing the level of negative DCAD from −60 to −160 mEq/kg reduced DMI, induced a more exacerbated metabolic acidosis prepartum, and increased the concentration of iCa in blood. Extending the duration of negative DCAD had minor impacts on blood iCa and measures of acid–base status.

Key Words: acidogenic salts, dietary cation–anion difference, prepartum

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1542 Effects of concentrate type and chromium propionate supplementation on insulin resistance parameters, milk production, and reproductive outcomes in lactating dairy cows consuming excessive energy.

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This experiment compared insulin resistance parameters, milk production, and reproductive outcomes in lactating dairy cows consuming excessive energy and receiving, in a 2 × 2 Latin square design, the following treatments: 1) concentrate based on ground corn (CRN; $n = 13$) or citrus pulp (PLP; $n = 13$) and 2) supplemented ($n = 14$) or not ($n = 12$) with 2.5 g/d of chromium propionate. Twenty-six multiparous, nonpregnant, lactating Gir × Holstein cows (average 80 d in milk on d 0) were offered corn silage for ad libitum consumption (d 0 to 180). Cows individually received concentrate formulated to allow diets to provide 160% of their daily NE_L requirements. Cow BW, BCS, and milk production were recorded weekly. Blood samples were collected weekly before the morning concentrate feeding. Glucose tolerance tests (GTT) were performed on d 0, 60, 120, and 180, by infusing cows with 0.5 g of glucose/kg of BW. Follicle aspiration for in vitro embryo production was performed on d 0, 80, and 160. No treatment differences were detected ($P \geq 0.25$) for BW and BCS during the experiment. Milk production and milk fat and solid concentrations were similar ($P \geq 0.24$) between treatments. However, CRN had greater ($P = 0.01$) milk protein compared with PLP cows (3.54 vs. 3.14%, respectively; SEM = 0.08). Within weekly samples, concentrations of serum insulin and glucose as well as revised quantitative insulin sensitivity check index and insulin:glucose ratio were similar among treatments ($P \geq 0.40$), whereas CRN had less serum NEFA concentrations compared with PLP cohorts (0.178 vs. 0.219 mmol/L; SEM = 0.008). No treatment differences were detected ($P \geq 0.35$) on number of viable oocytes collected and embryos produced within each aspiration. During the GTT, no treatment differences were detected ($P \geq 0.16$) for serum glucose concentration, glucose clearance rate, glucose half-life, and insulin:glucose ratio ($P \geq 0.16$). Serum insulin concentrations were less ($P = 0.05$) in CRN cows supplemented with chromium propionate compared with nonsupplemented CRN cohorts (9.01 vs. 13.61 ng/mL, respectively; SEM = 1.73), whereas chromium propionate supplementation did not impact serum insulin within PLP cows ($P = 0.68$). In summary, concentrate type altered milk protein content and serum NEFA concentrations in lactating dairy cows consuming excessive NE_L and impacted the effects of chromium propionate supplementation on serum insulin response to a GTT but did not influence milk yield or reproductive responses.

Key Words: chromium, dairy cows, energy intake, insulin resistance

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1543 Regulatory effect of dietary intake of chromium propionate on function of monocyte-derived macrophages from Holstein cows in mid lactation.

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Chromium (Cr) has been reported to improve insulin sensitivity and cattle performance. However, its effect on bovine macrophage metabolic and inflammatory response is unknown. The objective was to characterize the effect of dietary Cr on cow performance and the immunometabolic response of polarized macrophages ex vivo. Twelve healthy primiparous and 16 multiparous Holstein cows (143 ± 37 DIM) were enrolled. Cows were fed a common diet once daily that was top-dressed with 200 g of ground corn containing no Cr (CTL) or chromium propionate (CrP; 8 mg of Cr/cow per day) for 35 d. Cows were weighed at 0, 17, and 35 d of supplementation. On the same days, blood monocytes were isolated and cultured to obtain 3 monocyte-derived macrophage phenotypes: M0 (nonstimulated), M1 (interferon-γ polarized), and M2 (interleukin-4 polarized). The experiment was set in a randomized complete block design. Neither DMI nor milk yield were affected by CrP or its interactions. Similarly, plasma concentrations of glucose, insulin, and NEFA were not affected by CrP or its interaction with parity. Across parities, CrP increased expression of *IGFI* (fold change [FC]: 1.7; $P = 0.03$) in M0 and increased expression of *CXCL11* (FC: 2.2; $P = 0.07$) and *SLC2A3* (FC: 2.1; $P = 0.06$, only at 17 d of feeding) in M2. For primiparous cows, CrP compared with CTL tended to reduce the production of nitrate in M2 (266 vs. 532 n*M*; $P = 0.14$) and to increase the expression of *IGFI* in M2 at 17 d of supplementation (FC: 3.4; $P = 0.06$). For cows supplemented with CrP but not with CTL, primiparous cows compared with multiparous cows tended to have greater BW gain (37.8 vs. 0.6 kg; $P = 0.07$), better efficiency of BW gain ($P = 0.08$), greater blood monocyte number

(1.31 vs. 0.85 × 10^3/μL; $P = 0.10$), greater glucose in media in M2 ($P = 0.11$), and lower tumor necrosis factor-α in media in M1 (24.6 vs. 61.1 pg/mL; $P = 0.12$). In addition, at 17 d of supplementation, *SLC2A5* expression tended to be greater in M1 (FC: 10.6; $P = 0.13$) and in M2 (FC: 8.8; $P = 0.07$) and IGFI tended to be greater in M2 (FC: 3.5; $P = 0.06$). Regardless of parity, the minor effects observed may indicate potential regulatory mechanisms of Cr on the immunometabolic response of monocyte-derived macrophages via regulation of insulin and IGF-I on glucose transporters.

Key Words: chromium, lactating cows, macrophage

1544 Influence of supplementary zinc- and chromium–amino acid complexes on growth performance and carcass characteristics of finishing cattle fed zilpaterol hydrochloride.

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Eighty bullocks (528.27 ± 26.81 kg) were used to determine the influence of supplementary chromium (Cr) and zinc (Zn) from AA complexes on growth performance and carcass characteristics of cattle during a finishing period, which included feeding zilpaterol hydrochloride (ZIL). Bullocks were individually weighed and blocked by weight at study initiation. Groups of five bullocks were placed in 16 dirt-floor pens (6 by 12 m). Pen was the experimental unit. Pens within a block were randomly assigned to treatments as follows: 1) basal diet (13.5% CP and 2.15 Mcal NE_m/kg DM) that provided 30 mg of inorganic Zn/kg DM from $ZnSO_4$ plus an additional 40 mg Zn/kg DM from $ZnSO_4$ provided through a hand-fed supplement (control; CTR), 2) basal diet plus 40 mg Zn/kg DM provided from Zn methionine complex (ZnM; ZINPRO 120; Zinpro Corp., Eden Prairie, MN), 3) CTR plus 0.40 mg Cr/kg DM provided from Cr methionine complex (CrM; Micróplex; Zinpro Corp., Eden Prairie, MN), and 4) basal diet plus 40 mg Zn/kg DM from ZnM and 0.40 mg Cr/kg DM from CrM (ZCM). Diets provided equivalent supplemental levels of 70 mg Zn/kg DM. All bullocks were supplemented with 0.15 mg ZIL/kg BW (Zilmax; Merck Animal Health, Summit, NJ) for 30 d with a 3-d withdrawal before harvest. Zilpaterol, ZnM, and CrM were top-dressed in the feed bunk. Data were analyzed by ANOVA as a mixed model, for a randomized complete block design with a 2 × 2 factorial arrangement of treatments. The model included the random effect of block and fixed effects of ZnM, CrM, and ZnM × CrM interaction. Bullocks receiving ZnM gained faster than CTR ($P = 0.04$; 1.87 vs. 1.55 kg/d, respectively) and exhibited an improved ($P = 0.05$) gain:DM feed efficiency ratio (0.21 vs. 0.16 kg). Dietary ZnM tended ($P = 0.06$) to improve the observed/expected ratio of NE_m (1.21 vs. 1.01) and NE_g (1.27 vs. 1.02) compared with CTR, respectively. Zinc source had no effect on DMI ($P = 0.97$). Feeding CRM had no effect on performance variables ($P > 0.15$). The HCW was similar for bullocks fed $ZnSO_4$ or ZnM (366 and 372 kg, respectively). Carcass dressing percentage tended ($P = 0.10$) to be increased by ZnM compared with CTR (64.5 vs. 63.7%, respectively). The results suggest that ZnM supplementation may contribute to an incremental improvement in growth performance of finishing beef cattle fed ZIL.

Key Words: feedlot performance, zilpaterol hydrochloride, zinc

1545 Effect of peripartum source of dietary calcium and magnesium and postpartum level of magnesium on dry matter intake, performance, and plasma minerals in multiparous Holstein cows.

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The objective of this study was to determine the effect of source of dietary Ca and Mg in the peripartum period and level of Mg postpartum on DMI, milk production and composition, and plasma macromineral concentrations. Multiparous Holstein cows ($n = 41$) were randomly assigned to one of two prepartum diets beginning at 21 d before expected parturition in which supplemental Ca and Mg were provided primarily from common sources (C; calcium carbonate and magnesium oxide) or MIN-AD (M; Papillon Agricultural Company, Inc., Easton, MD). At calving, cows remained on the same source assignment and were further randomized to receive Mg at 0.45 (C-HM, $n = 11$; M-HM, $n = 9$) or 0.30% of DM (C-LM, $n = 11$; M-LM, $n = 10$). Cows were fed individually through 42 d in milk (DIM), and blood samples were collected 2x/wk prepartum and daily from d 0 through 7 postpartum. Repeated measures data were analyzed with the MIXED procedure of SAS. Actual postpartum Mg intake, based on 21-d average DMI and diet analyses, were 84, 71, 103, and 71 g/d for C-HM, C-LM, M-HM, and M-LM, respectively. Prepartum, cows fed M had increased DMI (17.9 ± 0.3 vs. 17.0 ± 0.3 kg/d; $P = 0.05$) and energy balance (10.0 ± 0.4 vs. 8.7 ± 0.4 kg/d; $P = 0.03$). An interaction of source, level, and week was found for postpartum DMI in wk 1 to 6 ($P = 0.03$), reflecting increased DMI during wk 2 for cows fed M-HM. No effects on postpartum energy balance were observed. There was no effect on milk yield postpartum. A source × time interaction for fat yield ($P = 0.01$), 3.5% fat-corrected yield ($P = 0.03$), and energy-corrected yield ($P = 0.02$) was detected such that cows fed M had higher yield, especially in wk 1 postpartum. No effects of treatment on plasma Ca concentrations were observed. Cows fed higher Mg tended to have higher plasma Mg postpartum (1.71 ± 0.03 vs. 1.64 ± 0.03; $P = 0.09$) and cows

fed M tended to have higher plasma P postpartum (4.67 ± 0.14 vs. 4.35 ± 0.13; $P = 0.09$). Overall, cows fed M had increased DMI in parts of the transition period and increased fat- and energy-corrected yield. Plasma Ca was not influenced by dietary source and level of Mg; however, plasma Mg was increased by feeding higher Mg postpartum and plasma P was increased by feeding M in the transition period.

Key Words: magnesium, mineral source, transition cow

1546 Effects of mineral supplementation on pre- and postpartum primiparous beef heifer performance and progeny preweaning performance.

J. Hawley*, E. B. Kegley, and J. G. Powell, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

A study was conducted to determine the effect of mineral supplementation on primiparous beef heifer pre- and postpartum and progeny preweaning performance. Thirty-six primiparous beef heifers (20 ± 0.5 mo of age) of predominantly Angus breeding were stratified by BW (398 ± 24.9 kg), BCS, and anticipated calving date and assigned to 12 pens (3 heifers/pen) for a 260-d study. Pens were randomly assigned to 1 of 4 treatments (2 × 2 factorial): 1) 0.15% S and 6 mg Cu/kg, 2) 0.15% S and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$), 3) 0.55% S (from Na_2SO_4) and 6 mg Cu/kg, or 4) 0.55% S (from Na_2SO_4) and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$). A cracked corn and soybean meal–based supplement delivered each treatment starting at 170 ± 16 d of gestation through 150 ± 16 d in lactation. Heifers grazed mixed grass pasture and were provided access to predominantly fescue hay in quantities sufficient to ensure ad libitum forage intake. A 7-d controlled internal drug release $PGF_{2\alpha}$ protocol was used to synchronize estrus. Heifer BW and BCS were collected on d −113, −112, −85, −57, −29, 1, 27, 56, 85, 113, 149, and 150 ± 16 relative to parturition. Calf BW was collected on 0, 31, 59, 86, 115, 141, and 150 ± 6 d relative to birth. Orthogonal contrasts were used to determine the effects of Cu vs. S supplementation. Gestation length was not influenced ($P = 0.52$) by mineral supplementation. Mineral supplementation did not influence ($P \geq 0.40$) heifer BW, ADG, or BCS. Synchronized estrus response was not influenced ($P \geq 0.68$) by mineral supplementation; however, reproductive tract scores (Cu main effect, $P = 0.09$) and synchronized conception rates (Cu main effect, $P = 0.07$) tended to be greater for heifers supplemented with Cu. For calf birth weight, progeny from heifers fed 0.15% S and supplemented with Cu tended to have greater birth weights; however, supplemental Cu decreased birth weights for progeny from heifers fed 0.55% S (Cu × S interaction, $P = 0.09$). Progeny ADG trended to be greater from heifers supplemented with Cu (Cu main effect, $P = 0.13$). Results of this study suggest mineral supplementation may influence primiparous beef heifer postpartum reproductive and progeny preweaning performance.

Key Words: beef heifers, mineral supplementation, progeny

1547 Effects of mineral supplementation on pre- and postpartum primiparous beef heifer mineral status and progeny preweaning mineral status.

J. Hawley*, E. B. Kegley, and J. G. Powell, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

A study was conducted to determine the effect of mineral supplementation on primiparous beef heifer pre- and postpartum and progeny preweaning mineral status. Thirty-six primiparous beef heifers (20 ± 0.5 mo of age) of predominantly Angus breeding were stratified by BW (398 ± 24.9 kg), BCS, and anticipated calving date and assigned to 12 pens (3 heifers/pen) for a 260-d study. Pens were randomly assigned to 1 of 4 treatments (2 × 2 factorial): 1) 0.15% S and 6 mg Cu/kg, 2) 0.15% S and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$), 3) 0.55% S (from Na_2SO_4) and 6 mg Cu/kg, or 4) 0.55% S (from Na_2SO_4) and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$). A cracked corn and soybean meal–based supplement delivered each treatment starting at 170 ± 16 d of gestation through 150 ± 16 d in lactation. Heifers had ad libitum access to mixed grass pasture. Heifer mineral status was assessed in blood samples collected on d −113, −85, −57, −29, 1, 27, 56, 85, 113, and 150 ± 16; in liver biopsy samples collected on d −113, −57, 1, 56, and 113 ± 16; and in colostrum samples collected 24 h relative to parturition. Heifer Se status was assessed in blood samples collected on d −113 ± 16, −13 ± 13, and 150 ± 16 relative to parturition. Progeny mineral status was assessed in blood samples collected on d 0, 31, 59, 86, 115, 141, and 150 ± 6 and in liver biopsy samples collected on d 7, 59, and 115 ± 6 relative to birth. Progeny Se status was assessed in blood samples collected on d 150 ± 6. Orthogonal contrasts were used to determine the effects of Cu vs. S supplementation. Heifers supplemented 0.55% S exhibited lower plasma and liver Cu concentrations (S main effect, $P < 0.05$). At parturition, heifers supplemented with 0.55% S exhibited lower plasma Cu concentrations (S main effect, $P < 0.01$). Supplemental Cu tended to increase colostrum Cu concentrations in heifers fed 0.55% S but lower colostrum Cu concentrations in heifers fed 0.15% S (Cu × S interaction, $P = 0.08$). Progeny from heifers supplemented with 0.55% S exhibited lower plasma Fe, serum Se, and liver Cu concentrations (S main effect, $P < 0.05$). Results of this study suggest mineral supplementation may influence primiparous beef heifer pre- and postpartum and progeny mineral status.

Key Words: beef heifers, mineral status, progeny

1548 Relative bioavailability of selenium sources for beef cattle. M. A. Zanetti*[1], J. S. Silva[2], J. C. D. C. Balieiro[1], and J. A. Cunha[2], *[1]University of São Paulo – USP/FZEA, Pirassununga, Brazil, [2]FZEA-USP, Pirassununga, Brazil*.

Recent research conducted at FZEA-USP, Pirassununga, Brazil, demonstrated that it is possible to reduce the cholesterol in bovine meat using high levels of organic selenium (Zanetti et al., 2014). This study aimed to compare the bioavailability of high levels of organic and inorganic selenium using muscle concentration. The study used 63 Nellore cattle of approximately 24 mo of age and 350 kg live weight, in a feedlot during 84 d, in individual pens. The animals (9/treatment) were submitted to one of the seven diets: control diet without additional supplementation of selenium, control diet + 0.3 mg Se kg DM in the form of sodium selenite, control diet + 0.3 mg of Se kg DM in the form of organic selenium, control diet + 0.9 mg Se kg DM in the form of sodium selenite, control diet + 0.9 mg Se kg DM in the form of organic selenium, control diet + 2.7 mg Se kg DM in the form of sodium selenite, and control diet + 2.7 mg Se kg DM in the form of organic selenium. The organic selenium used was yeast selenium. Diets were formulated according to NRC (1996) recommendations, and the roughage:concentrate ratio was 30:70. Corn silage was used and the concentrate was a mixture of corn grain and soybean meal. The control diet had 0.065 mg of Se/kg of DM. Animals were weighed at the beginning of the experiment and every 28 d. Food intake was monitored daily and offered in amounts to leave 10% orts. At the end of the experiment (84 d), the animals were slaughtered and muscle samples were taken for selenium analysis, according to Whetter and Ullrey (1978). The bioavailability was calculated by the technique of slope ratio assay (Ammerman et al., 1995). Linear regression was performed with the general linear models procedure (Proc GLM) of SAS (2004) to characterize muscle Se concentrations. The slopes estimation with SE were 0.028 ± 0.005 for the sodium selenite and 0.123 ± 0.005 for the yeast source. The difference between the slopes was significant ($P < 0.0001$). The relative bioavailability estimated by muscle selenium concentration for the yeast selenium in relation to the sodium selenite was 4.39 or 439%, when using diets high in concentrate and with high selenium levels. Acknowledgments: FAPESP.

Key Words: feedlot, muscle selenium, sodium selenite, yeast selenium

1549 Hydroxy trace mineral supplementation lowers proportion of low-quality embryos in postpartum dairy cows. A. H. Souza*[1], C. D. Narciso[2], G. E. Higginbotham[3], E. Martinez[2], R. Ruggeri[2], and E. O. S. Batista[4], *[1]Ceva Animal Health, Libourne, France, [2]Sequoia Veterinary Services Inc., Tulare, CA, [3]Micronutrients, Indianapolis, IN, [4]University of Sao Paulo, Pirassununga, Brazil*.

Objectives of this study were to test whether type of mineral source fed after calving (0 to 70 DIM) could improve quality of in vivo produced embryos from superovulated dairy cows. Postpartum Holstein cows (n = 82) received the same basic TMR (NRC 2001) composed (DM kg/d) of alfalfa hay (3.6), corn silage (3.2), haylage (1.4), wheat silage (1.5), flaked corn (4.4), canola meal (2.7), distillers' (1.7), almond hulls (2.7), corn gluten feed (2.0), EnergII (0.1), and mineral source (0.6). Animals were blocked by parity and calving date and randomly assigned to 2 dietary treatments differing only in type of supplemented mineral source, as follows: 1) hydroxy (HYD) (hydroxyl sources of Cu, Mn, and Zn) and 2) combination (COM) (sulfate sources of Mn, hydroxyl sources of Cu, and 75% zinc sulfate/25% organic Zn). Data was analyzed with the PROC GLIMMIX of SAS and cows were treated as a random experimental unit. Cows were superovulated with a modified 5-d double Ovsynch protocol associated with 400 mg/cow of FSH (Folltropin), and uterine content was flushed 6 d after synchronized ovulations. A single batch of FSH and frozen semen from a single sire (15×10^6 sptz/straw from Select Sires Inc.) were used to minimize variation due to FSH batch and service sire. In addition, a single treatment-blinded technician graded all embryos. There were no overall differences between groups in CL number, fertilization efficiency, or production of transferable embryos. Surprisingly, HYD supplementation significantly reduced the proportion of degenerated embryos in relation to all structures (HYD = 27.3 ± 4.5 vs. COM = 44.4 ± 6.2; $P = 0.03$) or fertilized structures (HYD = 34.8 ± 5.7 vs. COM = 52.2 ± 6.9; $P = 0.04$). In addition, further analysis indicated that HYD increased the proportion of cows that yielded more than 80% of good quality, freezable embryos (HYD = 32.4% vs. COM = 16.6%; $P = 0.04$). These results were unrelated to level of milk production and/or parity number of the superovulated cow. Also, conception results after transferring HYD (59.2%; n = 71) or COM (56.4%; n = 55) embryos to Holstein recipient heifers did not differ (P = 0.72). In conclusion, these findings support the hypothesis that feeding hydroxy minerals can improve embryo quality in postpartum dairy cows. Future research is needed to explore a possible positive impact of hydroxy mineral supplementation on conception results of artificially inseminated cows.

Key Words: dairy cow, embryo quality, hydroxy mineral

1550 Effects of zinc amino acid complex on mammary epithelium and dairy food chemistry.

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Objectives of this study were to determine effects of supplemental zinc level and source on mammary epithelial barrier integrity and milk chemistry in dairy cattle. In a mouse model, moderate zinc deficiency was shown to dramatically impact milk secretion and mammary gland involution. In addition, through multiple pathways, zinc is known to impact apoptosis in mammary and other epithelial tissues. To test for similar effects in cattle, 12 multiparous Holstein cows in mid to late lactation (132 ± 21 DIM) were blocked by milk production and randomly assigned to treatment sequence in a replicated 3 × 3 Latin square experiment. Each treatment period lasted 21 d (17 d of acclimation and 4 d of sampling). Treatments consisted of 1) 0.97 g zinc/d provided as $ZnSO_4$ (approximately 30 mg zinc/kg diet DM; 30-ZS), 2) 1.64 g zinc/d as $ZnSO_4$ (60-ZS), and 3) 0.55 g zinc/d provided as $ZnSO_4$ plus 1.13 g zinc/d provided as a zinc methionine complex (60-ZM; Zinpro Corp., Eden Prairie, MN). Treatments were also balanced for metabolizable methionine using Smartamine M (Adisseo Inc., France). Cows were housed in individual tie stalls, given ad libitum access to water, and fed a balanced basal ration twice daily. Treatments were provided daily in an oral bolus and contained all supplemental trace minerals except for selenium, which was included in the grain mix. Measurements were analyzed with a mixed model using fixed effects of treatment, period, and their interaction and the random effect of cow. Significance was declared at $P < 0.05$ and tendencies at $P < 0.10$. Feed intake tended to increase for 60-ZS cows ($P = 0.06$) and 60-ZM cows tended to have increased milk fat percentage ($P = 0.08$) compared with 30-ZS cows. No other effects on milk composition, yield, or production efficiency were observed. No effects of treatments were observed on heat coagulation time or the percent of NPN in the milk. Plasma electrolyte, lactose, and α-lactalbumin levels as well as transcript abundance of genes implicated in zinc transport (ZnT2), tight junction formation (occludin), and apoptosis (clusterin) were also unaffected by treatment. In conclusion, zinc supplementation of dairy rations at 60 ppm as opposed to 30 ppm did not appear to impact the integrity of the blood milk barrier or dairy food properties of milk.

Key Words: epithelial integrity, trace mineral, zinc

1551 Effects of sulfur on the nutrition value of dried distillers' grains with solubles for beef cattle.

L. He*, *China Agricultural University, Beijing, P. R. China*.

To investigate the effects of sulfur levels and sources on the nutrition value of corn dried distillers' grains with solubles (DDGS) for beef cattle, in vitro cultivation setting three sulfur levels (0.346, 0.692, and 1.038%) and four sulfur sources (Na_2SO_4, Na_2SO_3, $Na_2S_2O_3$, and Na_2S) without regard of interactions was conducted for 72 h with rumen fluid collected from Simmental × Limousin steers in triplicate and monitoring the fermentation parameters (DM digestibility [DMD], gas production [GP], VFA, and ammonia nitrogen [NH_3–N]) and model predicted indicators (OM digestibility [OMD], ME, NE, microbial protein [MP], and gas yield [GY]). The results showed that the sulfur content of DDGS used in livestock ranged from 0.346 to 1.038% on a DM basis; high sulfur level (0.692 and 1.038%) only decreased ($P < 0.05$) asymptotic gas production (b). As to the effects of sulfur sources, Na_2SO_4 and Na_2S produced more GP ($P < 0.05$) along with a faster rate ($P < 0.01$) than those of Na_2SO_3 and $Na_2S_2O_3$, whereas Na_2SO_3 had the highest b and the inverse for Na_2SO_4 ($P < 0.01$); Na_2SO_4 and Na_2S also had a higher ($P < 0.01$) OMD, ME, NE (for maintenance and growth), and GY_{24} and a lower ($P < 0.01$) DMD_{24} and MCP than those of Na_2SO_3 and $Na_2S_2O_3$; no significant response of VFA and NH_3–N to sulfur levels and sources was found ($P > 0.05$). These results suggest that DDGS with different sulfur content ranging from 0.346 to 1.038% have a similar feed value and that dietary sulfur source exerts a great effect on its nutrition value for beef cattle.

Key Words: dried distillers' grains with solubles, in vitro fermentation, sulfur

1552 Effects of sulfur on the in vitro fermentation profile of dried distillers' grains with solubles.

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This study was conducted to investigate the effects of sulfur on the nutrition values of dried distillers' grains with solubles (DDGS) for beef cattle by in vitro rumen fermentation. In vitro cultivation was conducted in triplicate with the rumen fluid collected from 3 Simmental steers, and the gas production (GP) was recorded until 72 h of incubation, setting DDGS as the fermentation substrate with different sulfur levels (0.346, 0.692, and 1.038%, on a DM basis) and various sulfur sources (Na_2S, $Na_2S_2O_3$, Na_2SO_3, and Na_2SO_4). The filtrate of the fermentation fluid was used to determine ammonia nitrogen (NH_3–N), VFA, and DM digestibility (DMD), finally calculating OM digestibility (OMD), ME, NEm and NEg, and microbial CP production (MCP) with the monitored parameters. The results showed that in vitro gas production parameters (b and c) of DDGS were significantly influenced by its sulfur

source ($P < 0.01$) but not sulfur level ($P > 0.05$), being that the sulfur from Na_2SO_3 developed the slowest gas production rate (c) (0.018/h) with the highest asymptotic gas production (b) (60.20 mL/g) and the inverse for Na_2SO_4 (0.049/h and 42.77 mL/g). What is more, sulfur from Na_2SO_4 and Na_2S produced higher ($P < 0.05$) GP than those of Na_2SO_3 and $Na_2S_2O_3$ at 12, 24, and 48 h, whereas there was no difference ($P > 0.05$) found in different sulfur levels. Sulfur from Na_2SO_4 and Na_2S also had higher ($P < 0.01$) DMD, OMD, ME, NEm, and NEg than that of Na_2SO_3 and $Na_2S_2O_3$. As to the VFA profile, sulfur from Na_2SO_4 tended ($P = 0.09$) to produce a lower total VFA (29.10 mmol/L) than the others (37.34, 39.10 and 37.98 mmol/L), and there was no difference ($P > 0.05$) in the individual fatty acid proportion. These results suggest that DDGS with different sulfur concentration ranging from 0.346 to 1.038% have a similar in vitro rumen fermentation profile, whereas its sulfur source exerts a great effect on the fermentation, indicating that the valence state of sulfur in DDGS makes a big difference to its nutrition value for beef cattle.

Key Words: dried distillers' grains with solubles, in vitro fermentation, sulfur

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1553 Supplementation with a blend of capsicum and artificial sweetener alters milk yield and nutrient partitioning in lactating dairy cows. E. H. Wall* and D. M. Bravo, *Pancosma, Geneva, Switzerland*.

Supplementation of lactating dairy cows with capsicum oleoresin (CAPS) or with SUCRAM (SUC; Pancosma, Geneva, Switzerland) increases milk and component yield; however, responses to the two additives fed in combination have not been described. Therefore, the objective of this experiment was to determine the effects of a CAPS-SUC blend on lactation performance of dairy cows. Primi- and multiparous lactating Holstein dairy cows were housed together in a free-stall pen and were milked using an automated milking system (AMS). During a 10-wk period, CAPS-SUC was blended with a carrier and was dispensed at the AMS for CAPS-SUC cows (n = 91) at a rate of 0.22 kg/d (doses of CAPS and SUC: 100 mg/d and 3.2 g/cow per day, respectively); control cows received no additive (n = 102). All cows were supplemented with 300 mg/d of monensin. Individual cow milk production and composition, milking frequency, and BW were recorded daily. Average DMI of the pen was monitored daily and did not change throughout the study. Supplementation with CAPS-SUC did not affect milking frequency (3.5 milkings/d; $P > 0.60$). There was a parity × treatment interaction for milk yield characterized by a decrease with CAPS-SUC in primiparous animals (34.7 vs. 32.1 kg/d; $P < 0.001$) but an increase in multiparous animals (41.4 vs. 44.6 kg/d; $P < 0.001$). Yield of milk fat (1.6 kg/d) and protein (1.2 kg/d) was not affected by treatment ($P > 0.10$). There was a treatment × parity × stage of lactation interaction for BW such that in cows less than 100 DIM, BW was increased with CAPS-SUC only in primiparous animals (590 vs. 616 kg; $P < 0.001$) whereas there was no effect in multiparous animals ($P > 0.30$). The prevalence of subclinical ketosis, indicated by milk fat-to-protein ratios, was decreased with CAPS-SUC (20 vs. 15%; $P < 0.01$). The decrease in milk yield of primiparous cows together with a corresponding increase in BW indicates that CAPS-SUC may have altered nutrient partitioning to support skeletal growth or accretion of tissue stores in those animals. This, taken together with the decreased incidence of ketosis and changes in milk production, reveals that CAPS-SUC can shift nutrient partitioning and consequent milk production performance of lactating dairy cows.

Key Words: feed additive, phytonutrient, SUCRAM

1554 Supplementation with rumen-protected capsicum oleoresin increases milk production and component yield in lactating dairy cows. E. H. Wall* and D. M. Bravo, *Pancosma, Geneva, Switzerland*.

Insulin responses in peripheral tissues of dairy cows are shifted so that availability of glucose is prioritized for milk synthesis during lactation. Supplementation of dairy cows with rumen-protected capsicum oleoresin decreased insulin responses and improved milk production performance. The objective of this experiment was to test the hypothesis that supplementation of rumen-protected capsicum oleoresin (RP-Caps; NexUlin; Pancosma) would increase milk production of dairy cows. Primi- and multiparous lactating Holstein cows were housed together in a free-stall pen and were milked using an automated milking system (AMS). During a 6-wk period, cows were blocked by stage of lactation (1–99 DIM, n = 67; 100–199 DIM, n = 63; and 200+ DIM, n = 66) and were randomly assigned to RP-Caps or control treatments. Rumen-protected capsicum oleoresin was blended with a carrier and was dispensed at the AMS for RP-Caps cows (n = 97) at a rate of 0.22 kg/d (100 mg/cow per day of RP-Caps); control cows (n = 99) received no additive. All cows were supplemented with 300 mg/d of monensin. Individual cow milk production and composition, milking frequency, and BW were recorded daily. Prevalence of subclinical ketosis was estimated by milk composition (fat/protein > 1.5). Average DMI of the pen was monitored daily and did not change throughout the study. Supplementation with RP-Caps did not affect milking frequency (3.6 milkings/d; $P > 0.50$). There were no parity × treatment interactions detected; however, there was an interaction between stage of lactation and treatment ($P < 0.001$) such that only cows in the 1 to 99 DIM group responded to RP-Caps whereas there was no effect of treatment in the other two groups ($P > 0.50$). In that group, milk production was increased in RP-Caps cows (40.7 vs. 44.4 kg/d; $P < 0.001$). Rumen-protected capsicum oleoresin had no effect on fat (4.5 vs. 4.4) or protein (3.09 vs. 3.10) percentages; therefore, the increase in milk production was accompanied with an increase in component and energy-corrected milk yield (46.2 vs. 50.0

kg/d; $P < 0.001$). The increase in milk and milk component yield was not accompanied by changes in BW (673 vs. 669 kg; $P > 0.30$) or prevalence of subclinical ketosis (22.1 vs. 23.9%; $P > 0.50$), indicating that metabolic status was maintained despite the increased nutrient output into milk. Responses to RP-Caps may be mediated by postruminal effects on insulin responses and augmented glucose sparing during early and peripeak lactation.

Key Words: feed additive, phytonutrient, postruminal effects

1555 WS Effects of increasing sugar beets on steer backgrounding performance. I. McGregor*, C. M. Page, W. C. Stewart, and M. Van Emon, *Montana State University, Bozeman*.

The objective of this study was to evaluate the effects of sugar beets on steer backgrounding performance. Forty-eight Angus steers (260.7 ± 3.43 kg) were used in a completely randomized design for a 50-d study. On d −1, steers were weighed and assigned to 1 of 8 pens (6 steers/pen) equipped with GrowSafe units and one of four dietary treatments on d 0 ($n = 12$ steers/treatment; 2 pens/treatment): 1) 0SB, a control diet with no sugar beets; 2) 15SB, 15% sugar beets substituted for barley on a DM basis; 3) 30SB, 30% sugar beets substituted for barley on a DM basis; and 4) 45SB, 45% sugar beets substituted for barley on a DM basis. Sugar beets directly replaced rolled barley on a DM basis. All dietary treatments were formulated to meet or exceed the nutrient requirements of a 295-kg steer gaining 0.91 kg/d. The MIXED procedure of SAS was used for statistical analysis. Initial BW, mid BW, final BW, period 1 and 2 ADG, and period 1 and 2 G:F were not different ($P \geq 0.33$) due to dietary treatment. There was a significant treatment × day interaction ($P < 0.001$) for DMI. On d 3, 19, 21, 23, 33, 44, and 45, 0SB DMI was reduced ($P \leq 0.05$) and increased ($P \leq 0.05$) on d 12, 20, and 47 compared with 15SB. On d 3, 19, 21, 33, 35, and 50, 0SB DMI was reduced ($P \leq 0.03$) and increased ($P \leq 0.01$) on d 9, 12, and 20 when compared with 30SB. On d 19, 21, 27, 33, 37, 38, and 45, 0SB DMI was reduced ($P \leq 0.05$) and increased ($P \leq 0.04$) on d 9, 24, and 35 when compared with 45SB. On d 35 and 37, 15SB DMI was reduced ($P \leq 0.002$) and increased ($P \leq 0.05$) on d 9 and 36 when compared with 30SB. On d 37 and 47, 15SB DMI was reduced ($P \leq 0.02$) and increased ($P \leq 0.03$) on d 1, 9, 44, and 46 when compared with 45SB. On d 45, 30SB DMI was reduced ($P \leq 0.03$) and increased ($P \leq 0.04$) on d 24 when compared with 45SB. These data suggest that backgrounding steers can be fed diets with up to 45% sugar beets on a DM basis without negatively impacting performance.

Key Words: backgrounding, steers, sugar beets

1556 Effects of red grape pomace to adapt beef cattle to finishing diets and spoilage mitigation strategies. L. A. Pellarin*[1], J. O. Sarturi[1], P. R. B. Campanili[1], L. A. Ovinge[1], B. C. Bernhard[1], B. J. Johnson[1], J. C. Brooks[1], and E. W. Hellman[2], *[1]Texas Tech University, Lubbock, [2]Texas A&M AgriLife Extension and Texas Tech University, Lubbock*.

The effects of red grape pomace to step-up beef steers to steam-flaked corn–based finishing diets on growth performance, carcass characteristics, nutrient digestibility, feeding behavior, and mitigation of pomace spoilage were evaluated. In Study 1, crossbred yearling steers ($n = 48$; 364 ± 41 kg) were blocked by BW and randomly assigned to 1 of 2 adaptation strategies, 1) traditional roughage sources (alfalfa hay/cottonseed hulls based) and 2) red grape pomace based, in a randomized complete block design. Both adaptation strategies decreased roughage as steam-flaked corn gradually increased in diets. Steers were fed once daily, following standard operations of the Burnett Center (Idalou, TX), a series of 5 diets consisting of four 7-d step-up diets and 1 common finishing diet (160 d), which did not contain pomace. In Study 2, red and white grape pomace were ensiled (18.9 L units; $n = 6$/treatment) following 1 of the 4 spoilage mitigation strategies: 1) control, 2) molasses, 3) inoculant (*Lactobacillus buchneri*), and 4) inoculant + molasses in a completely randomized design (2 × 4 factorial treatment arrangement). Data were analyzed using the GLIMMIX procedure of SAS. Intake, gain, and efficiency of steers during either adaptation or finishing phases were not ($P \geq 0.16$) negatively affected by red grape pomace when compared with a traditional adaptation strategy. Total tract apparent digestibility of DM, OM, EE, NDF, and ADF evaluated during the finishing phase was not ($P \geq 0.53$) affected by adaptation strategies, except by a subtle (99.46 vs. 99.03%) increase ($P = 0.01$) in starch digestibility for steers fed pomace when compared with a traditional adaptation strategy, respectively. Feeding behavior was not ($P \geq 0.21$) affected by adaptation strategies, except by steers fed the traditional strategy spending 17.3 and 18.4% more time ruminating and chewing on step-up diet 3 compared with the pomace strategy in the same phase ($P = 0.04$ and $P = 0.01$, respectively). After storage period (169 d), red grape pomace lost less DM compared with white pomace (7.87 and 11.37%, respectively; $P < 0.03$), whereas no differences among mitigation treatments were observed ($P = 0.52$). Red grape pomace strategy adapted beef steers to finishing diets without detrimental effects on growth performance and nutrient digestion when compared with a traditional alfalfa hay/cottonseed hulls approach. Grape pomace can be stored for long periods under anaerobic conditions with modest amount of DM losses; however, spoilage mitigation after silo opening must be further studied.

Key Words: adaptation, grape pomace, storage

1557 Effects of thyme (*Thymus vulgaris*) essential oil on feed intake and feeding behavior of Nellore steers. L. C. Roma Junior*[1], E. S. Castro Filho[2], |J. M. Bertocco Ezequiel[3], M. Almeida[4], and E. H. C. B. Van Cleef[2], *[1]Sao Paulo's Agency for Agribusiness Technology – APTA, Ribeirao Preto, Brazil, [2]Sao Paulo State University – UNESP, Jaboticabal, Brazil, [3]UNESP, São Paulo State University, Department of Animal Science, Jaboticabal, São Paulo, Brazil, [4]São Paulo State University, Jaboticabal, São Paulo, Brazil*.

The objective of this study was to evaluate the effects of increasing amounts of thyme (*Thymus vulgaris*) essential oil (TEO) on feed intake and feeding behavior of Nellore steers. Four ruminally cannulated steers (701 ± 37 kg BW) were assigned to a 4 × 4 Latin square design and were fed a total mixed ration containing 40% corn silage, 10% bermudagrass hay, and 50% commercial concentrate. Treatments consisted of a daily ruminal infusion of 0 (T0), 2 (T2), 4 (T4), or 8 (T8) g/animal per day of TEO. Each period lasted 21 d (13 d of adaptation and 8 d of data collection) and animals were fed once daily (0700 h). Feed delivered and feed refused were monitored every morning to calculate DMI. Feeding behavior observations were performed by 4 trained observers who recorded, each 5 min during 12 h (from 0600 to 1800 h), the following activities: interaction with feed bunk (IB), interaction with waterers (IW), ruminating standing (RS), ruminating laying (RL), standing still (SS), laying (LA), stereotypies (ST), and other activities (OA). The chewing activity was also evaluated with observations of number of chews per feed bolus, time spent chewing each feed bolus, and chews per time. Data were analyzed using the MIXED procedure and orthogonal contrasts were used to determine the linear, quadratic, and cubic effects of TEO and of T0 vs. TEO treatments. The infusion of TEO did not affect DMI of steers (average = 8.6 kg/d). Also, no effects of treatments were observed for IB, IW, RS, RL, LA, ST, and OA, and the averages were 183.3, 10.0, 37.5, 283.5, 92.5, and 112.5 min, respectively. The time spent on activity SS was linearly increased ($P = 0.03$) with increasing inclusion of TEO, showing a 20% increase from T0 to T8. Regarding the chewing activity, no alterations were observed, and the treatments' averages were 46 chews/feed bolus, 56 s/feed bolus, and 0.82 chews/s. Although TEO has known powerful antibacterial properties, it does not affect DMI, or most of the animal behavioral activities, when infused up to 8 g/d. (Financial support: FAPESP 2014/01212-4.)

Key Words: additive, medicinal plant, thymol

1558 Effects of functional oils or monensin on dry matter digestibility, milk yield, and composition of Holstein cows. F. P. Rennó*[1], E. F. Jesus[2], T. A. Del Valle[1], G. D. Calomeni[1], T. H. Silva[1], C. S. Takiya[1], T. H. A. Vendramini[1], P. G. D. Paiva[2], G. G. Silva[1], A. Saran Netto[3], and J. Torrent[4], *[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, University of Sao Paulo, Pirassununga, Brazil, [4]Oligo Basics Agroindustry, Cascavel, Brazil*.

Cashew nut shell liquid (CNSL) and castor oil have been defined as functional oils (FO) due to their antimicrobial, anti-inflammatory, antioxidative, and gastroprotective properties. Twenty-four multiparous cows (150.24 ± 61.43 d in milk and 29.1 ± 4.01 kg/d of milk yield) were used in a replicated 3 × 3 Latin square experiment with 21-d periods to compare the effects of FO or monensin (MON) supplementation on DM total apparent digestibility and milk yield and composition. Cows were assigned to one of these treatments: no additive (CON), supplementation of 500 mg/kg DM of FO (CNSL and castor oil as active ingredients; Essential; Oligo Basics, Cascavel, Brazil), and supplementation of 22 mg/kg DM of MON (Rumensin; Elanco Animal Health, São Paulo, Brazil). Diet was offered as a total mixed ration twice daily. Orts were weighed daily to determine feed intake, and samples of ingredients, orts, and feces were collected on Days 16, 17, and 18 of each period. Feces were collected every 9 h. All samples were analyzed for DM and indigestible NDF (iNDF) content. To obtain iNDF content, samples of ingredients, orts, and feces were placed in bags of nonwoven textile, incubated during 288 h in the rumen of two cows, and submitted to neutral detergent treatment. Fecal excretion was calculated based on iNDF intake and its concentration in feces. Cows were milked twice daily. Milk samples were automatically collected on Days 15, 16, and 17 of each period and analyzed fresh for fat, protein, and lactose by infrared methodology (Lactoscan; Entelbra, São Paulo, Brazil). Data were analyzed using PROC MIXED of SAS, and when treatment effects were significant, the PDIFF test was applied. Treatments did not affect DM intake or digestibility. Functional oils and MON increased ($P < 0.01$) milk (25.92, 27.17, and 27.13 kg/d for CON, MON, and FO, respectively), protein (0.78, 0.81, and 0.81 kg/d for CON, MON, and FO, respectively), and lactose (1.17, 1.22, and 1.22 kg/d CON, MON, and FO, respectively) yields. Cows supplied MON showed lower milk fat percentage compared with CON and milk fat from FO cows was not different from any of treatments (3.66, 3.46, and 3.60% for CON, MON, and FO, respectively). Cows supplemented MON produced milk with lower lactose concentration compared with FO cows. Monensin increased milk production with a decrease in milk fat percentage and FO increased milk production without affecting

milk fat percentage.

Key Words: castor oil, functional oil, ionophore.

1559 Effect of rumen-protected *Capsicum* oleoresin on immune responses in lactating dairy cows experimentally challenged with lipopolysaccharide.

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The objective of this experiment was to investigate the effects of rumen-protected *Capsicum* oleoresin (RPC) on immune responses in lactating dairy cows experimentally challenged with lipopolysaccharide (LPS). Nine multiparous Holstein cows (100 ± 9.1 d in milk and 665 ± 83.3 kg BW) were used in a replicated 3 × 3 Latin square design experiment balanced for residual effects with three 28-d periods. Treatments were 0 (control), 100, and 200 mg RPC/cow per day. Rumen-protected *Capsicum* oleoresin was mixed with a small portion of the total mixed ration and top-dressed. The basal diet consisted of (DM basis) 44% corn silage, 12% alfalfa silages, and 41% concentrate feeds and contained 16.1% CP and 30.9% NDF, and the NE_L and MP of the basal diet met the requirements of the cows. Bacterial LPS was intravenously administered at 1.0 μg/kg BW and blood samples were collected at 0, 2, 4, 8, and 24 h after administration. Dry matter intake, milk yield, and white blood cells including neutrophils, lymphocytes, monocytes, and eosinophils were decreased ($P < 0.01$) and rectal temperature, hemoglobin, and serum concentration of cortisol and haptoglobin were increased ($P < 0.01$) by LPS. Plasma concentration of thiobarbituric acid reactive substances, red blood cells, and platelets were not affected ($P \geq 0.13$) by LPS. Dry matter intake (25.7 kg/d; SEM = 1.73), milk yield (35.7 kg/d; SEM = 2.44), and milk composition were not affected ($P \geq 0.25$) by RPC after LPS challenge. Rectal temperature, white blood cells, red blood cells, hemoglobin, and platelets were also not affected ($P \geq 0.20$) by RPC, except lymphocyte counts were quadratically increased ($P = 0.02$) by RPC at 0 h. Compared with the control, RPC decreased ($P \leq 0.04$) serum concentrations of cortisol and haptoglobin and increased ($P < 0.01$) concentration of thiobarbituric acid reactive substances in plasma following LPS challenge. Collectively, feed intake, milk yield, rectal temperature, white blood cells, and red blood cells were not affected by RPC in dairy cows challenged by LPS. However, RPC increased concentration of thiobarbituric acid reactive substances in plasma and decreased cortisol and haptoglobin concentrations in serum. Data suggest that dietary supplementation of RPC increased oxidative stress in plasma and alleviated acute phase responses induced by LPS in lactating dairy cows.

Key Words: acute phase response, capsicum, lipopolysacharride

1560 Effects of cinnamaldehyde on performance of postweaned Holstein dairy heifers.

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Essential oils are secondary metabolites obtained from plants and are gaining interest because of their functions similar to ionophores. The objective of this 70-d study was to determine the effects of the essential oil cinnamaldehyde compared with the ionophore monensin sodium on performance of postweaned Holstein dairy heifers. Eighty-four 12-wk-old Holstein heifers (109 ± 7.50 kg) were housed in a naturally ventilated curtain side-wall barn in 12 pens with 7 heifers/pen (3.98 m^2/hd). Heifers were randomly assigned to 1 of 4 treatments in a completely randomized design: 1) control (CON; carrier, 908 g of ground corn), 2) monensin sodium (MON; 1 mg/kg of BW + carrier), 3) cinnamaldehyde (CIN1; 1 mg/kg of BW + carrier), or 4) cinnamaldehyde (CIN2; 2 mg/kg of BW + carrier). The treatments were mixed into a 20% CP whole shell corn and protein pellet mix fed daily at 2.27 kg/head per day. Heifers had access to free choice hay and water daily. Initial BW and hip heights (HH) were taken at the start of the study and biweekly thereafter until calves reached 22 wk of age. Blood samples were also taken on each weigh day to determine blood urea nitrogen, glucose, and insulin-like growth factor-1 (IGF-1) concentrations. Fecal samples were taken from 3 heifers/pen initially and then at wk 4, 8, and 10 of the study to determine coccidia count. There were no performance effects ($P > 0.05$) of cinnamaldehyde on growth, hay intake, HH, or blood metabolites compared with heifers offered MON or CON. Average daily gains were 0.98, 0.99, 1.01, and 1.03 kg/d and average hay intakes per pen were 17.08, 16.34, 18.11, and 17.60 kg/d for CON, MON, CIN1, and CIN2, respectively. Fecal samples by pens indicated the presence of viable coccidia, but the number of counts was low and not consistent across heifers within each pen. Feeding monensin sodium to postweaned dairy heifers did not affect any of the performance parameters measured when compared with the control. Under the conditions of this study, there were also no benefits of supplementing cinnamaldehyde into grain mixes for postweaned heifers. Increasing the dose of cinnamaldehyde or changing the way it was administered to feed may have resulted in a different outcome.

Key Words: cinnamaldehyde, heifer, monensin sodium

1561 Effects of essential oils and exogenous enzyme in feedlot finishing diets high in flint ground corn at different particle sizes during the adaptation period. M. A. P. Meschiatti[1], J. M. M. D. Moraes[1], T. S. Acedo[2], L. F. M. Tamassia[2], C. S. Cortinhas[2], V. N. D. Gouvea*[2], J. R. Dórea[3], and F. A. P. Santos[4], *[1]USP, Sao Paulo, Brazil, [2]DSM Nutritional Products SA, Sao Paulo, Brazil, [3]University of Wisconsin, Madson, [4]University of São Paulo, Piracicaba, Brazil*.

The objective of this study was to evaluate the interaction between two feed additives—MON (sodium monensin; Tortuga) vs. CRINA-RUM (the combination of essential oils: Crina Ruminants, DSM, and α-amylase; Ronozyme RumiStar)—and two different ground flint corn particle sizes—ground corn (GC = 1.82 mm average particle size) or coarsely ground corn (CGC = 2.53 mm average particle size)—on performance of finishing Nellore bulls during the adaptation period, the first 30 d. Two hundred fifty-six Nellore bulls (initial BW = 360 kg ± 38) were fed diets containing 82.5% ground corn (1.82 or 2.53 mm), 8.5% sugarcane bagasse, 5% soybean meal, 3% minerals and vitamin supplement, and 1% urea. Animals were blocked based on initial BW and randomly allocated in 48 pens. Treatments were GC + MON (1.82 mm ground corn and sodium monensin; 26 mg/kg DM), GC + CRINA-RUM (1.82 mm ground corn and the combination of essential oils [90 mg/kg DM] + α-amylase [560 mg/kg DM]), CGC + MON (2.53 mm ground corn and sodium monensin; 26 mg/kg DM), and CGC + CRINA-RUM (2.53 mm ground corn and the combination of essential oils [90 mg/kg DM] + α-amylase [560 mg/kg DM]). The DMI, ADG, and feed efficiency (G:F) were evaluated after 30 d of adaptation. The data were analyzed using PROC MIXED of SAS in a 2 × 2 factorial arrangement (2 ground corn particle sizes and 2 feed additives). Pen was considered the experimental unit. No interactions between feed additives and flint corn particle size were observed ($P > 0.05$). There was no effect ($P > 0.05$) of ground flint corn particle sizes on performance of the animals during the adaptation period. Animals fed with CRINA-RUM had 7.89% greater DMI (8.36 vs. 7.70 kg; $P < 0.05$) and 11.9% greater ADG (1.26 vs. 1.11 kg; $P = 0.08$) compared with animals fed MON, respectively. In conclusion, the use of essential oil combined with α-amylase improved animal performance during the adaptation period for animals fed ground flint corn grain.

Key Words: beef, Nellore, starch

1562 Effects of essential oils and exogenous enzymes on intake, digestibility, and rumen fermentation in finishing Nellore cattle. M. A. P. Meschiatti[1], L. A. Pellarin[1], C. D. A. Batalha[2], T. S. Acedo*[3], L. F. M. Tamassia[3], C. S. Cortinhas[3], V. N. D. Gouvea[3], F. A. P. Santos[2], and J. R. Dórea[4], *[1]USP, Sao Paulo, Brazil, [2]University of São Paulo, Piracicaba, Brazil, [3]DSM Nutritional Products SA, Sao Paulo, Brazil, [4]University of Wisconsin, Madson*.

The objective of this trial was to evaluate the combination of essential oils and exogenous enzymes on intake, digestibility, and ruminal fermentation in finishing Nellore cattle. Five Nellore steers (427 ± 52 kg BW) were fed isonitrogenous and isocaloric diets containing 82.5% corn, 8.5% sugarcane bagasse, 5% soybean meal, 3% mineral and vitamin supplement, and 1% urea. The treatments were MON (sodium monensin; Tortuga; 26 mg/kg DM), CRINA (essential oils; Crina Ruminants; DSM; 90 mg/kg DM), CRINA$^+$MON (90 and 26 mg/kg DM, respectively), CRINA$^+$RUM (CRINA + α-amylase; Ronozyme RumiStar; DSM; 90 and 560 mg/kg DM, respectively), and CRINA$^+$RUM+P (CRINA + RUM + protease; Ronozyme Proact; DSM; 90, 560, and 840 mg/kg DM, respectively). The experimental design used was a 5 × 5 Latin square. The 20-d experimental periods consisted of 15 d for adaptation followed by 5 d for collections. Data were analyzed using PROC MIXED of SAS and means were compared by Tukey test considering animal and period as random effects and treatments as fixed effects. Cattle fed CRINA$^+$RUM presented greater ($P < 0.01$) DM and total nutrient digestible (TND) intakes compared with MON (9.77 vs. 7.69 kg and 7.73 vs. 5.89 kg, respectively). CRINA increased ($P = 0.02$) total CP digestibility compared with MON (74.9 vs. 65.3%, respectively). The combination of CRINA$^+$RUM+P also increased ($P < 0.01$) total CP and the total carbohydrate digestibility in comparison with MON (75.0 vs. 65.3% and 91.0 vs. 84.8%, respectively). Total starch digested (kg) was greater ($P < 0.05$) for cattle fed CRINA$^+$RUM in comparison with MON (5.44 vs. 4.19 kg, respectively), although no difference ($P = 0.12$) in fecal starch was observed between the treatments. No difference in total NDF ($P = 0.73$) and EE ($P = 0.60$) digestibilities, ruminal pH ($P = 0.84$), and molar concentration of acetate ($P = 0.14$) were observed among the treatments. Animals fed CRINA$^+$RUM presented greater molar concentration of propionate ($P = 0.02$) and lower acetate-to-propionate ratio ($P = 0.04$), compared with CRINA$^+$RUM+P (41.5 vs. 27.7 m*M* and 1.48 vs. 2.2, respectively). Ruminal ammonia nitrogen was lower ($P = 0.05$) for animals fed CRINA$^+$RUM in comparison with animals fed CRINA$^+$MON (12.4 vs. 20.26 mg dL^{-1}). In conclusion, the use of essential oils and their combination with amylase increases the DM and TDN intakes and the amount of starch digested in the total tract compared with sodium monensin, presenting minor effects on fermentation parameters.

Key Words: amylase, protease, starch

1563 Effect of inclusion of *Acacia mearnsii* tannin extract on nitrogen and energy balance in growing beef cattle fed a low-protein corn silage diet.

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The study of tannins in animal feeds has primarily focused on the effects on digestibility, intestinal nutrient flow, and/or performance of ruminant animals; however, the overall impact on energetic efficiency in growing animals is not known. Eight Holsteins steers (BW = 332 ± 32.3 kg) were used in a replicated 4 × 4 Latin square design experiment to evaluate the effect of *Acacia mearnsii* tannin extract on energy metabolism and nitrogen balance. The experimental diets consisted of corn silage plus concentrate (10%) at 2 levels of intake with and without *A. mearnsii* tannin extract (3.9 g/kg of total dietary DM). The basal diet (DM basis) was formulated to be 36.2% DM, 8.1% MP, and 12.4% CP. The treatment structure was a 2 × 2 factorial: intake, 1.2 vs. 1.8 × NEm, and tannin addition vs. control. Each experimental period was 21 d with fecal and urine collections occurring Days 15 to 21. Respiratory gasses were measured d 19 to 21 by replacing the feed bunk with a respiration hood. Measures of inspired O_2 and expired CO_2, and CH_4 were continuously collected with samples analyzed at 9-min intervals. Whole-body heat production (HP) was calculated using the equation proposed by Brouwer. Data were analyzed for effects of intake, presence of tannin, and the interaction of intake × tannin. Treatment effects were considered significant at $P \leq 0.05$. Tannin extract addition did not affect ($P > 0.10$) any measure of nitrogen or energy balance. Tannins bind proteins, which are recovered in the fiber fraction of feces as such, and usually shift the N excretory pattern from urine to feces, being positive from the environmental point of view; however, this effect was not observed in the present study. As designed, all variables were higher with high intake ($P < 0.001$). There was no interaction between intake and tannin extract. More studies are needed to evaluate the mode of action of this phenolic compound on the use of energy in growing animals.

Key Words: heat production, intake, phenolic compounds

1564 Effects of condensed tannins on the ensiling and aerobic stability of purple prairie clover (*Dalea purpurea* Vent.) silage.

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Effects of condensed tannins (CT) on ruminal fermentation have been well documented, whereas little information is available on the effects of CT on ensiling. The objective of this study was to assess the effects of CT on ensiling and aerobic stability of whole-plant purple prairie clover (PPC) silage. The PPC contained approximately 55 g CT/kg DM, was harvested from 3 plots at the flowering stage, and was wilted in the field to DM of 35%. Forage was chopped to a theoretical length of 5 cm, divided into 2 portions, and ensiled without (Control) or with polyethylene glycol (PEG) in PVC laboratory silos (5/treatment). The PEG specifically inactivates the biological activity of CT. The silos were opened after 76 d of ensiling and the silage was subsampled for chemical characterization as well as assessed for aerobic stability over 14 d. Compared with PEG treated silage, Control silage had higher ($P < 0.001$) pH (5.02 vs. 4.61) and water soluble carbohydrates (2.40 vs. 0.26 g/kg DM) but contained less lactic acid (52.6 vs. 79.9 g/kg DM; $P < 0.01$), propionic acid (0.17 vs. 0.85 g/kg DM; $P < 0.05$), soluble N (0.29 vs. 0.40 g/kg DM; $P < 0.01$), NPN (0.35 vs. 0.44 g/kg DM; $P < 0.01$), ammonia N (2.7 vs. 3.3 g/kg DM; $P < 0.01$), and ochratoxin A (10.0 vs. 40.0 μg/kg DM; $P < 0.01$). Both silages had similar ($P > 0.05$) concentrations of total VFA, acetic acid, and deoxynivalenol. These results indicate that CT in PPC reduced protein degradation and decreased the activity of both lactic acid– and ochratoxin A–producing microorganisms. After 14 d of aerobic exposure, internal temperature of PEG-treated silage started to rise 12 h earlier than that of Control silage. This suggests that CT decreased microbial activity and improved the aerobic stability of PPC silage. This study demonstrated that plant CT could be used to improve silage quality by decreasing protein degradation and the activity of mycotoxin-producing microorganisms while improving the aerobic stability of silage.

Key Words: aerobic stability, condensed tannin, purple prairie clover, silage

1565 Effect of purple prairie clover (*Dalea purpurea* Vent.) and its condensed tannins on nutrient intake, digestibility, and growth performance of lambs. K. Peng*[1,2], D. C. Shirley[3], Z. Xu[2], Q. Huang[2,4], T. A. McAllister[5], A. V. Chaves[3], S. Acharya[2], S. Wang[1], and Y. Wang[2], *[1]College of Engineering, China Agricultural University, Beijing, P. R. China, [2]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [3]The University of Sydney, Faculty of Veterinary Science, School of Life and Environmental Sciences, Sydney, Australia, [4]College of Animal Science and Technology, Northwest A&F University, Yangling, P. R. China, [5]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, Lethbridge, AB, Canada*.

This study evaluated the effects of purple prairie clover (PPC; *Dalea purpurea* Vent.) hay and its condensed tannins (CT) on feed intake, nutrient digestibility, and growth performance of lambs. Alfalfa and PPC were harvested at full flower, sun cured to <12% moisture, baled, and stored in a shed for 120 d. Purple prairie clover contained about 5% CT at harvest. Thirty-six individually fed lambs were randomly allocated into three groups and fed TMR containing 40% (DM basis) of pelleted barley grain–based concentrate and 60% of alfalfa hay (Alf), PPC hay (PPC), or PPC hay along with polyethylene glycol (PPC-p) for 77 d. Polyethylene glycol (PEG) dissolved in water was sprayed onto TMR to neutralize PPC CT activity. Lambs were fed once daily, DMI was measured weekly, and ADG was determined biweekly. Fecal samples were collected in the fifth week for 5 d to estimate nutrients digestibility using AIA as a marker. The Mixed procedure of SAS was used to analyze the data with treatment as a fixed effect and lamb as a statistical unit. Alfalfa and PPC hay had similar DM, OM, N, NDF, and ADF content at feeding. Lambs fed the PPC-p diet exhibited greater DM (68.8 vs. 59.8 vs. 66.7%; $P < 0.01$), OM (71.2 vs. 60.8 vs. 66.9%; $P < 0.001$), and N (76.5 vs. 61.0 vs. 65.5; $P < 0.001$) digestibility than those fed the Alf or PPC diets and greater NDF (59.3 vs. 42.9; $P < 0.001$) and ADF (51.0 vs. 43.3; $P < 0.05$) digestibility than those fed the Alf diet. Digestibilities of OM and DM were greater ($P < 0.05$) for PPC than for the Alf diet, whereas N, NDF, and ADF digestibility were similar. Addition of PEG to the PPC diet increased ($P < 0.05$) N and NDF digestibility and tended ($P = 0.07$) to increase ADF digestibility but did not affect DM or OM digestibility. Although PPC hay had greater DM and OM digestibility than alfalfa hay, CT reduced the fiber digestibility of PPC hay. Lambs consuming Alf, PPC, and PPC-p diet had similar ($P > 0.05$) ADG (187.1 vs. 187.1 vs. 185.3 g/d) and feed efficiency (0.151 vs. 0.151 vs. 0.147) but lambs consuming PPC tended ($P = 0.093$) to eat less (1.10 vs. 1.18 vs. 1.18 kg DM/d). Purple prairie clover hay had superior nutritive value to alfalfa hay owing to its greater DM and OM digestibility but did not improve lamb growth performance, possible due to the detrimental impact of CT on N and fiber digestion.

Key Words: digestibility, growth performance, lamb, purple prairie clover

1566 Effect of dietary polyphenol, protected amino acid, and crude protein levels on in vitro rumen fermentation and crude protein digestibility. B. Choi*[1], J. Yang[1], C. Ryu[1], S. J. Shin[1], Y. Kim[1], J. Heo[2], S. Cho[3], and N. J. Choi[1], *[1]Chonbuk National University, Jeonju-si, the Republic of Korea, [2]Microbial Institute for Fermentation Industry, Sunchang-gun, the Republic of Korea, [3]CALS Co., Ltd., Seongnam-si, the Republic of Korea*.

The present study investigated the effect of polyphenol (PP), protected AA (PA), and CP levels on in vitro rumen fermentation to improve protein utilization efficiency of dairy cattle. Dietary polyphenol extracted from sweet chestnut and protected methionine and lysine were used. Two CP levels of basal diets were designed to 16 and 18%. A factorial experimental design ($2 \times 2 \times 4$) was used to evaluate the effect of PP, PA, CP, and their interactions on rumen fermentation. Four different levels of PP (0, 0.5, 1.0, and 1.5% in diet) and two levels of PA (0 and 2.5% in diet) were mixed with two basal diets. A total of 16 different experimental diets were prepared and subjected to in vitro rumen simulated fermentation. After 24 h of incubation, rumen fermentation parameters and CP digestibility were determined. Significant main effects of factors were detected ($P < 0.05$) in gas production parameters. Factors of CP level and PA elevated gas production, and gas production decreased as levels of PP increased. However, there was no significant interaction between these factors. The factors of CP level and PP showed significant main effects on methane production ($P < 0.05$). Methane production in 18% CP diets was greater than in 16% CP diets, and methane was decreased when PP levels increased. Total VFA (TVFA) production was affected ($P < 0.05$) by the levels of CP and PP. Higher CP levels showed greater TVFA production. Total VFA production was decreased when PP levels were increased. However, TVFA production was not changed until PP levels reached 0.5%. All factors showed significant main effects on in vitro DM digestibility (IVDMD) ($P < 0.05$), and significant interactions were detected between CP × PP and PA × PP ($P < 0.05$). In vitro DM disappearance was decreased when PP levels were increased. However, these decreasing patterns were altered by the levels of CP and PA. Increasing CP or PA levels slowed the decrement of IVDMD by PP, and CP digestibility showed patterns similar to those of IVDMD. Significant main effects were found for the levels of CP and PP ($P < 0.05$), and a significant interaction was detected between PA and PP ($P < 0.05$). When PP and PA were added in the diet together, they both decreased CP digestibility. These results indicate that polyphenol can alter the rumen fermentation, and 0.5% of polyphenol in a diet can increase

protein bypass to the intestine from the rumen without negative effects on rumen TVFA production.

Key Words: crude protein, in vitro, polyphenol, protected amino acid, rumen bypass

1567 The effect of addition of mulberry leaves silage in the diet of beef cattle on their growth and slaughter performance. H. Wu*, Q. Meng, L. Ren, and Z. Zhou, *China Agricultural University, Beijing, P. R. China*.

The objective of the present study was to evaluate the effect of adding different levels of ensiled mulberry leaves to the diet of beef cattle on their growth and slaughter performance. Eighty-eight beef cattle (44 Limousine crossbred cows and 44 local breed bulls) at the age of 30 ± 3.2 mo and with an initial BW of 468.0 ± 10.0 kg were divided into 4 groups (n = 22) in a randomized complete block design with sex as a block. Four levels of ensilaged mulberry (0, 7.5, 15.0, or 22.5% DM) were tested using the basal diets, with all the treatment groups being isonitrogenous and isoenergetic. The trial lasted for a total of 100 d including 10 d for adaptation and 90 d for data collection. At the end of the feeding trial, eight cattle from each treatment group were randomly selected and slaughtered for measurement of slaughter performance including HCW, bone weight, net meat weight, back fat thickness, and rib eye area. All statistical analyses were performed for a completely randomized block design using general linear models (GLM) procedures of SAS (2000). The differences between means were assessed by the Student–Newman–Keuls test and statistical significance was defined at $P < 0.05$. The results showed that the additions of ensilaged mulberry leaves at the tested levels did not results in significant ($P > 0.50$) difference in final BW, ADG, DMI, or feed conversion efficiency. The additions of ensilaged mulberry leaves were not accompanied by a significant ($P > 0.20$) change in carcass parameters except for increases in hot dressing percentage and rib eye area ($P < 0.01$), which were 54.0% and 62.2 cm^2, 57.1% and 75.5 cm^2, 56.8% and 75.4 cm^2, and 56.1% and 75.5 cm^2 for addition level from low to high, respectively. These results indicated that although ensiled mulberry silage may not significantly improve feed utilization, growth, or major carcass characteristics of beef cattle, it can be used as a resource of nutrients for beef cattle feeding.

Key Words: beef cattle, growth performance, mulberry leaves silage

1568 Supplementation of Korean honeysuckle (*Lonicera vesicaria*) extract in timothy hay on in vitro ruminal fermentation. I. D. Lee*[1], S. K. Lee[2], S. J. Lee[2], S. Y. Yang[3], S. S. Lee[1], and J. S. Eun[3], *[1]Division of Applied Life Science, Gyeongsang National University, Jinju, the Republic of Korea, [2]Institute of Agriculture and Life Science, Gyeongsang National University, Jinju, the Republic of Korea, [3]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan*.

Korean honeysuckle (*Lonicera vesicaria*; KH) is a traditional shrub and used as folk medicine in Korea. The KH is a rich source of ascorbic acid and phenolic components, particularly anthocyanins, flavonoids, and phenolic acids. These compounds reportedly have multiple biological activities, including strong antioxidant activity and antibiotic properties. Therefore, we performed an in vitro experiment to assess the effects of KH extract (KHE) on ruminal fermentation characteristics. Milled timothy hay (0.3 g DM) was incubated with buffer, ruminal fluid, and KHE at 0 (control) 3, 5, 7, or 9% DM. The experiment was conducted in a completely randomized design with 3 replications to test the 5 dose rates (DR) of KHE. Batch culture fermentation was conducted for 12, 24, and 48 h separately to measure gas production (GP), degradability of DM, methane (CH_4) production, and ammonia N (NH_3–N) concentration at the 3 predetermined time points. Degradability of DM linearly decreased (P = 0.02) with increasing DR of KHE at 24 h, with 2.5 percentage unit decreases at 7 and 9% KHE, but there was no effect of KHE on the DM degradability at 12 and 48 h. Production of GP was generally similar to the pattern of DM degradability, having a linear decrease (P = 0.01) mainly due to 9% KHE at 24 h. Concentration of NH_3–N linearly increased because of increasing KHE supplementation at 12 h, whereas it tended to decrease in a quadratic manner (P = 0.07) at 24 h. Supplementing KHE quadratically decreased ($P < 0.01$) CH_4 production at 12 h, and it elicited linear decreases ($P < 0.01$) on CH_4 production at 24 and 48 h. However, KHE supplementation greater than 5% did not further decrease CH_4 production. These collective results demonstrate that KHE supplementation affected in vitro ruminal fermentation in a dose-dependent manner and that KHE has a potential to function as a ruminal fermentation modifier to suppress CH_4 production with minimal effects on nutrient digestion in the rumen. The positive effects on NH_3–N and CH_4 may have been resulted from combined effects from condensed tannins and saponin in KHE.

Key Words: in vitro batch culture, Korean honeysuckle extract, methane

1569 Effects of an extract of plant flavonoids from *Citrus aurantium* on performance, eating and animal behavior, ruminal health, and carcass yield in Holstein bulls fed high-concentrate diets.
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This study evaluated the effects of an extract of plant flavonoids from *Citrus aurantium* (Bioflavex CA; 24% naringin) on performance, eating pattern, behavior, and carcass quality of Holstein bulls. Ninety-nine bulls (201.8 ± 3.30 kg BW and 154 ± 0.83 d of age) were randomly allocated to 1 of 6 pens and assigned to a control (C) or Bioflavex CA (BF; 0.4 kg/ton of Bioflavex CA added to the concentrate). Each pen (6 by 12 m) had one drinker, one separate straw feeder, and one single space feeder with lateral protections where concentrate (40% corn, 14% barley, 11% wheat, 23% corn gluten feed, 15% CP, and 2.88 Mcal of ME/kg) was offered. Concentrate intake was recorded daily, and BW and animal behavior by visual scan were registered fortnightly. Animals were slaughtered after 168 d of study (12 periods of 14 d), and HCW and carcass quality were recorded. Data were analyzed using a mixed-effects model with repeated measures. Throughout the study, 4 C and 1 BF bulls were removed, 2 of the 4 C bulls due to lameness. Concentrate intake (6.9 ± 0.12 kg/d for C and BF), concentrate efficiency (0.23 ± 0.031 kg/kg), and carcass weight (262 ± 2.3 kg for C and BF) were not affected by treatments. The ADG (1.67 and 1.63 ± 0.042 kg/d for C and BF, respectively) and final BW (487 and 478 ± 3.6 kg for C and BF, respectively) tended ($P = 0.07$) to be greater in C bulls than in BF bulls. An interaction between treatment and time was observed for most behavior parameters. During the growing phase (periods 1 to 8), C bulls performed more self-grooming and attempted less mounts ($P < 0.05$) compared with BF bulls. During finishing (periods 9 to 12), an interaction in meal duration ($P = 0.01$) was observed; meal duration was greater (periods 9 to 11) in BF bulls compared with C bulls. Moreover, during finishing, nonagonistic interactions, such as oral nonnutritive and social behaviors, were greater ($P < 0.05$) in C bulls than in BF bulls. In addition, agonistic interactions (fighting, butting, and chasing) and sexual behaviors (flehmen and complete mounts) were greater ($P < 0.05$) in C bulls than in BF bulls. In conclusion, when bulls were supplemented Bioflavex CA, meal duration increased and animals' agonistic and sexual interactions were less frequent compared with non-supplemented bulls during the finishing period.

Key Words: behavior, bulls, flavonoids, performance

1570 A blend of cinnamaldehyde, eugenol, and capsicum oleoresin improves milking performance in lactating dairy cows.
C. Oguey* and E. H. Wall, *Pancosma, Geneva, Switzerland*.

Supplementation with a blend of eugenol, cinnamaldehyde, and capsicum oleoresin (ECC; XTRACT Ruminant; Pancosma, Geneva, Switzerland) was previously shown to modulate rumen function and improve feed conversion efficiency in growing ruminants. This trial aimed to determine the productive implications of this response in dairy cows. Primi- and multiparous lactating Holstein dairy cows (mean parity = 2.43; mean DIM at trial start = 125 d) were housed together in a free-stall pen and were milked using an automated milking system (AMS). For 8 wk, ECC was blended with a carrier and was dispensed at the AMS for ECC cows ($n = 97$) at a rate of a rate of 0.22 kg/d (dose of ECC = 1,000 mg/cow per day); control cows ($n = 104$) received no additive. All cows were supplemented with 300 mg/d of monensin. Individual cow milk production and composition, milking frequency, and BW were recorded daily. Average DMI of the pen was monitored daily and did not change throughout the study. Data were analyzed using the mixed procedure of SAS with repeated measures. Regardless of parity, milk production was increased with ECC (35.5 vs. 37.5 kg/d; $P < 0.001$). There was a parity × treatment interaction for the effect of ECC on milk composition such that protein percent was decreased in primiparous animals (3.2 vs. 3.1%; $P < 0.001$) but not affected in multiparous animals ($P > 0.30$). Still, ECC increased protein yield (1.1 vs. 1.2 kg/d; $P < 0.001$) and did not affect fat yield (1.4 vs. 1.4 kg/d; $P > 0.50$). Therefore, there was an increase in energy-corrected milk with ECC (38.2 vs. 39.3 kg/d; $P < 0.001$). There was no effect of ECC on BW (673 vs. 674 kg; $P > 0.70$) or prevalence of subclinical ketosis (5.1 vs. 5.5%; $P > 060$). Interestingly, there was a parity × treatment interaction for number of milkings per day. In primiparous cows, ECC increased milking frequency (2.9 vs. 3.2; $P < 0.01$), whereas there was no effect in multiparous animals (3.5 vs. 3.6; $P > 0.30$). These findings reveal that supplementation with ECC, even on top of an ionophore, improves milk production performance of lactating dairy cows.

Key Words: automated milking system, performance, XTRACT

1571 Evaluation of a proprietary blend of essential oil and cobalt on a commercial dairy. O. J. Kuester*, *South Dakota State University, Brookings*.

A field trial was conducted for 7 mo on a commercial dairy equipped with two Lely robotic milking units to evaluate the response of feeding a proprietary essential oil and cobalt product (EOC) on the lactational performance of lactating Holstein dairy cows. Cows were divided between two pens (57 ± 2 cows and 59 ± 3 cows for treatment [EOC] and control [C] pens, respectively), based on cow parity (2.65 ± 1.52 and 2.33 ± 1.20), days in milk (DIM) (184 ± 103 and 154 ± 94.2), and milk production (35.4 ± 11.3 and 36.9 ± 11.3 kg/d) before study initiation. Cows were group fed either an EOC or C total mixed ration (TMR) 2x/d, and pen diets were switched after 4 mo of data collection. Production data was collected daily from Lely Time for Cows (T4C) robotic milking software and was reduced to weekly observations for each cow. Management level milk production was not different (P = 0.92) between EOC and C treatments (41.5 ± 1.91 and 41.4 ± 2.05 kg/d, respectively). Fat and protein percentages were not different between EOC and C treatments (P = 0.55 and 0.56, respectively) but were numerically higher for EOC-fed cows than for C-fed cows (3.39% fat and 2.99% protein vs. 3.36% fat and 2.97% protein, respectively). Total feed intake was not different between treatments (P = 0.16) but was numerically lower for EOC-fed cows (25.7 kg/d) than for C-fed cows (25.9 kg/d). Feed efficiency (FE) was not different between treatments (P = 0.73) but was numerically lower for cows fed EOC than for cows fed C (1.60 FE and 1.62 FE, respectively). Feeding the proprietary EOC product on a commercial dairy operation that used robotic milking units did not increase management level milk production or FE but numerically increased milk percentages of fat, protein, and total feed intake.

Key Words: cobalt, commercial dairy, essential oil, robotic milker

1572 Effects of feeding functional oils or monensin on feedlot performance and carcass traits of Nellore cattle. A. C. Melo*[1,2], M. C. Pereira[3], A. L. Rigueiro[1], D. H. M. Watanabe[1], M. M. Squizatti[1], L. A. Tomaz[1], J. V. Dellaqua[1], O. A. Souza[1], P. F. Santi[1], A. L. J. Lelis[1], A. F. Toledo[1], and D. D. Millen[1], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]Grant provided by São Paulo State Foundation (FAPESP), São Paulo, Brazil, [3]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil*.

This study, conducted at the São Paulo State University feedlot, Dracena campus, Brazil, was designed to test the effects of adding functional oils (Essential) or monensin (MON) on feedlot performance and carcass traits of Nellore cattle fed high-concentrate diets. Ninety-six 22-mo-old Nellore yearling bulls (377.9 ± 32.0 kg) were assigned to 24 pens (4 animals/pen) and used in a completely randomized block with 2 × 2 factorial arrangement of treatments, replicated 6 times. Factors were inclusion (DM basis) or not of functional oils or MON, at a dose of 500 or 27 ppm, respectively. Animals were adapted for 16 d to the high-concentrate diets fed. The finishing diet contained 68.5% cracked corn grain, 14.0% sugarcane bagasse, 14.1% cottonseed meal, 2.1% supplement, 0.8% urea, and 0.5% limestone (DM basis). Cattle were fed ad libitum three times daily for 105 d, and DMI was recorded daily. No significant (P > 0.10) functional oils main effect or interactions between functional oils and MON were observed for any of the feedlot performance and carcass traits variables evaluated: final BW (without functional oil = 503.6 kg and with functional oil = 505.1 kg), DMI (without functional oil = 9.6 kg and with functional oil = 9.6 kg), ADG (without functional oil = 1.2 kg and with functional oil = 1.2 kg), G:F (without functional oil = 0.126 kg/kg and with functional oil = 0.126 kg/kg), HCW (without functional oil = 280.9 kg and with functional oil = 281.0 kg), and dressing percentage (without functional oil = 55.8% and with functional oil = 55.5%). Also, no significant (P > 0.10) MON main effect was observed for final BW, ADG, HCW, and dressing percentage. However, the addition of MON reduced (P = 0.001) the DMI (without MON = 10.3 kg and with MON = 8.9 kg) and improved (P = 0.01) G:F (without MON = 0.117 kg/kg and with MON = 0.136 kg/kg). Cattle fed MON performed better than those animals not fed MON. On the other hand, feeding functional oils did not improve feedlot performance and carcass traits in this study.

Key Words: additives, feedlot, Nellore

1573 Influence of tannins extract and monensin supplementation on performance of feedlot heifers in Argentina. C. Cabral[1], A. Lopez Da SIlva[2,3], J. J. Couderc[3], D. Colombatto[4], and R. Barajas*[5], *[1]Indunor, S.A., Buenos Aires, Argentina, [2]Feedlot Don Corral de Corijunio S.A., Buenos Aires, Argentina, [3]Nowet S.A, Buenos Aires, Argentina, [4]Universidad de Buenos Aires, Buenos Aires, Argentina, [5]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico*.

Tannins extract and monensin have activity against several rumen bacteria that participate in feed-protein degradation; it was hypothesized that its effects could be synergistic. Three hundred forty-eight Angus heifers (207 ± 13.4 kg) were used to determine the influence of tannins extract and monensin supplementation on performance of feedlot heifers. The heifers were individually weighed and blocked by weight at study initiation. Groups of 29 heifers were placed in 12 dirt-floor pens (50 by 70 m). Pen was the experimental unit. Pens within a block were randomly assigned to treatments as follows: 1)

Table 1574. Effect of corn processing and dietary protein level on nitrogen (N) metabolism.

Items, g/d	SFC[1]			FGC		SEM	Contrast[1]		
	HP	LP		HP	LP		P	CP	P×CP
Intake N	698.40	619.60		736.00	670.20	21.33	<0.01	<0.01	0.66
Milk N	218.65	212.58		219.04	210.92	6.83	0.85	0.06	0.77
Fecal N	264.20	258.60		293.00	255.45	13.52	0.32	0.10	0.22
Urinary N	165.89	154.93		172.70	159.16	6.02	0.06	<0.01	0.65
Pollution N	430.09	413.53		465.70	415.52	15.22	0.14	0.01	0.18
Absorbed N	434.20	361.00		443.00	413.23	24.78	0.20	0.03	0.35
N efficiency, %	31.50	34.47		29.80	31.62	1.08	0.02	0.01	0.52

[1]Contrasts for P (corn processing effect), CP (protein level effect), and interaction (P×CP).

basal diet (14.1% CP and 1.75 Mcal NE_m/kg DM) plus 3.1 g of tannins extract (TE)/kg DM provided by ByPro (Indunor-Silvafeed; Buenos Aires, Argentina), 2) basal diet plus 35 mg of monensin (MON)/kg DM from Rumensin 200 (Elanco Animal Health, Indianapolis, IN), and 3) basal diet plus 3 g of TE and 35 mg of MON/kg DM (TEMO). Tannins extract and MON were top-dressed in the feed bunk. Data were analyzed by ANOVA as a mixed model, for a randomized complete block design. The model included the random effect of block and fixed effects of treatments (TE, MON, and TE + MON). Possible influence of initial weight was explored by covariance analyses. Heifers receiving TE had higher final weight than those received MON (P = 0.05; 316 vs. 306 kg) and gained faster (P = 0.04; 1.41 vs. 1.22 kg/d). Dry matter intake was not affected by treatments (P = 0.43). The gain:DM feed efficiency was better in heifers fed TE than in MON-supplemented heifers (0.17 vs. 0.15 kg). The observed:expected diet NE ratio was higher (P = 0.05) in TE heifers than in MON heifers (NEm, 0.97 vs. 0.93, and NEg, 0.96 vs. 0.90, respectively). The mean values of final weight, daily gain, DMI, feed efficiency, and NE exhibit by TEMO heifers were intermediate and not significantly distinct (P > 0.10) from those obtained by TE and MON heifers. The results suggest that TE supplementation may contribute to an incremental improvement in growth performance of beef cattle.

Key Words: feedlot performance, monensin, tannins

1574 Effects of different protein levels and corn processing methods on nitrogen metabolism in dairy cows and environmental pollution.
G. R. Ghorbani*, H. Rafiee, and M. Alikhani, *Isfahan University of Technology, Isfahan, the Islamic Republic of Iran*.

Eight midlactation Holstein cows averaging 105 ± 9 d in milk and 47.2 ± 3 kg of milk/d were assigned to a replicated 4 × 4 Latin square design (2 × 2 factorial) to study the effects of corn processing and protein level on nitrogen metabolism. Experimental diets contained either finely ground corn (FGC) or steam-flaked corn (SFC) based on either a low protein (LP; 14.8%) or a high protein (HP; 16.2%) content. Diets consisted of 40% forage, including 15% alfalfa hay and 25% corn silage. The concentrate contained soybean meal and urea as protein sources. Cows fed diets with a greater protein concentration had 11.2% greater N intake (717.2 vs. 644.9 g/d; P < 0.01), 7.8% greater urinary N (169.3 vs. 157.0 g/d; P < 0.01), 13.3% greater absorbed N (438.6 vs. 387.1 g/d; P < 0.01), and 8% greater pollution N (447.9 vs. 414.5 g/d; P = 0.01). Cows fed HP diets had lower milk N efficiency (30.6 vs. 33.0%; P = 0.01). Cows fed FGC rather than SFC had 6.7% greater N intake (703.1 vs. 659.0 g/d; P < 0.01), tended to have 3.4% greater urinary N excretion (165.9 vs. 160.4 g/d; P = 0.06), and had lower milk N efficiency (30.7 vs. 33.0%; P = 0.02). Results indicate that cows fed LP diets and SFC diets had greater N efficiency and reduced N loss.

Key Words: ground corn, level of protein, steam-flaked corn

1575 Eelative availability for lactating dairy cattle of methionine from two sources of ruminally protected methionine.
M. Ardalan*[1], C. F. Vargas Rodriguez[1], G. I. Zanton[2], M. Vázquez-Añón[3], E. C. Titgemeyer[1], and B. J. Bradford[4], *[1]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [2]USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI, [3]Novus International, Inc., St. Charles, MO, [4]Kansas State University, Manhattan*.

Our objective was to evaluate lactational responses of dairy cows to methionine (Met) provided from 2 rumen-protected (RP) Met sources. Twenty-one Holstein dairy cows (11 primiparous [137 DIM, 634 kg BW, and 3.6 BCS] and 10 multiparous [parity 2, 142 DIM, 670 kg BW, and 3.2 BCS]) were assigned to a treatment sequence in 4 replicated 5 × 5 Latin squares with 14-d periods. Treatments included 1) control; 2) and 3) 7.5 and 15 g/d, respectively, of a RP product (NTP-1401; Novus International, Inc., St. Charles, MO); and 4) and 5) 7.5 and 15 g/d, respectively, of a rumen-protected dl-Met product (Smartamine; Adisseo, Alpharetta, GA). By evaluation with CNCPS 4.0, the diet met MP and energy requirements when DMI was 25.6 kg/d for lactating Holstein cows

producing 45 kg/d milk with 3.5% fat and 3.0% true protein. Diets contained 16.1% CP and were predicted to be deficient in metabolizable Met (1.85% of MP) but sufficient in lysine (6.8% of MP). Feed intake and milk production were measured on d 11 to 14. Blood was collected on d 14. Dry matter intake, milk yield, energy-corrected milk (ECM), milk fat yield and percentage, and efficiencies of milk and ECM production were not affected by treatment ($P \geq 0.14$). Milk protein percentage and milk protein yield linearly increased with supplementation ($P < 0.01$), without differences between Met sources or interactions between source and level. Linear regressions of milk protein percentage and milk protein yield against supplement amount within source led to slope ratios (NTP-1401/Smartamine) of 95% for protein percentage ($P = 0.65$ for difference from 100%) and 84% for protein yield ($P = 0.60$ for difference from 100%), suggesting no differences between sources for increasing milk protein. Plasma Met concentrations were linearly increased ($P < 0.001$) by Met supplementation, with the increase being greater for Smartamine than for NTP-1401 ($P < 0.001$). Plasma d-Met was increased only by Smartamine. Plasma 2-hydoxy-4-methylthio-butyric acid (HMTBA) was increased only by NTP-1401. The sum of plasma Met and plasma HMTBA was linearly increased by Met supplementation ($P < 0.01$) with no difference between sources ($P = 0.89$). Our data demonstrated that supplementation of Met can improve milk protein percentage and yield. The 2 methionine sources did not differ in their effect on lactation performance or milk composition.

Key Words: dairy, methionine, milk protein

1576 Effects of rumen undegradable protein supplementation and ambient temperature on growth performance and blood metabolites in Korean cattle steers. H. J. Kang*, M. Y. Piao, H. J. Kim, and M. Baik, *Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Seoul, the Republic of Korea*.

Under heat stress, RUP can have positive effects on milk production of dairy cow. This study was performed to evaluate whether rumen RUP supplementation and ambient temperature affects growth and blood metabolic parameters in Korean cattle. In Exp. 1, 14 Korean cattle steers (average 20.5 mo of age and 231.3 kg of BW) were divided into a conventional control diet group ($n = 7$) and a 0.55% RUP supplementation group ($n = 7$). Steers were allowed to receive daily an early fattening stage concentrate diet with the amount of 1.5% of BW using an automatic feeding station for 4 mo from July through October 2015, and they were allowed to receive a tall fescue with the amount of 0.75% of BW. Temperature data were analyzed by using one-way ANOVA, and growth and blood data were analyzed by using repeated-measured two-way ANOVA. Maximum ambient temperature and maximum temperature–humidity index (THI) were higher in July (30.6°C and 81.8, respectively), August (32.9°C and 80.7, respectively), and September (28.8°C and 80.3, respectively) than in October (19.8°C and 63.7, respectively). Blood was collected at starting day and at every 4 wk after 8 h fasting. Ruminally undegradable protein supplementation did not affect total feed intake, ADG, and feed efficiency (FE), although ambient temperature or month affected feed intake, ADG, and FE. Ruminally undegradable protein supplementation tended ($P = 0.08$) to decrease serum glucose concentrations, but it increased ($P = 0.006$) serum high-density cholesterol (HDL) concentrations. Ambient temperature or month affected ($P < 0.001$) both glucose and HDL concentrations. In Exp. 2, six Korean cattle steers (average 20.6 mo of age and 230.7 kg of BW) were raised in metabolic cages in a temperature-controlled room with air conditioning and heating system. Animals were divided into a conventional control diet group ($n = 3$) and a 0.55% RUP supplementation group ($n = 3$). In Exp. 2, steers were allowed to receive a same amount of the concentrate and the hay as that of Exp. 1. Experimental period 1 (P1) was 8 d with high temperature and period 2 (P2) was 8 d with normal temperature. Blood was collected at d 1 and 8 after 8 h fasting. Maximum ambient temperature and THI (34.4°C and 86.0) of P1 was higher ($P < 0.001$) than that (19.6°C and 67.0) of P2, respectively. In Exp. 2, RUP supplementation did not affect feed intake, ADG, FE, and blood parameters at both P1 and P2. In conclusion, RUP supplementation and ambient temperature affected blood parameters, although they did not significantly influence growth performance of Korean cattle.

Key Words: ambient temperature, beef cattle, blood metabolites, growth, rumen undegradable protein

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1577 Guanidinoacetic acid as a precursor for creatine in steers. M. Ardalan*[1], M. D. Miesner[2], C. D. Reinhardt[1], D. U. Thomson[3], C. K. Armendariz[1], and E. C. Titgemeyer[1], *[1]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [2]Department of Clinical Sciences, Kansas State University, Manhattan, [3]Department of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan*.

Guanidinoacetic acid (GAA) can be methylated to produce creatine. Because GAA supplementation bypasses the regulatory step in creatine formation, it may increase creatine availability. However, unregulated consumption of methyl groups may be problematic. We studied GAA supplementation in 7 steers maintained under conditions where methionine (Met) supply was purposefully limiting. Steers were limit-fed a soyhull-based diet and received abomasal infusions of AA to make methionine the solely limiting AA. Ruminal infusions of VFA and abomasal infusions of glucose provided energy. Factorial treatments (abomasally infused) included 0, 7.5, and 15 g/d GAA and 0 and 6 g/d l-Met. The experimental design

Table 1578. Dairy and Beef TMR CP and TAA population statistics.

Type	Parameter	n	Mean	St.Dev.	Min.	Max.
Beef	CP	9	13.2	1.2	11.2	14.7
Beef	TAA	9	11.1	1.1	9.3	12.7
Dry	CP	47	15.3	1.9	11.5	19.4
Dry	TAA	47	11.9	1.4	9.2	15.8
Lactating	CP	76	17.3	1.6	13.7	22.3
Lactating	TAA	76	14.0	1.2	10.4	18.7

was a split-plot, with Met main-plot treatments assigned in three 2 × 2 Latin squares. Subplot treatment was GAA, with amounts assigned to three 10-d subplot periods within each main-plot cell. Two steers received the same treatment sequence. Steers were housed in metabolism crates for measuring N retention over d 5 to 10. Jugular blood was collected on d 6, 8, and 10. Plasma GAA concentrations were increased by GAA supplementation ($P < 0.01$) but unaffected by Met ($P = 0.84$). Plasma creatine concentrations were increased by GAA supplementation ($P < 0.01$) but decreased by Met ($P < 0.01$). Plasma creatinine concentrations were unaffected by treatments ($P > 0.32$). Nitrogen retention was increased by Met ($P < 0.01$) but was not affected ($P > 0.28$) by GAA. There was, however, a tendency ($P = 0.10$) for N retention to demonstrate a Met × GAA interaction, with GAA linearly increasing N retention when 6 g/d Met was provided but decreasing N retention when no Met was supplemented. Urinary excretions of creatine and GAA did not demonstrate main effects of Met or GAA; however, both tended ($P < 0.10$) to be increased by GAA supplementation in the absence of supplemental Met but not affected by GAA when 6 g/d Met was supplemented. Urinary excretion of creatinine tended ($P < 0.10$) to be increased by GAA supplementation but was unaffected by Met. These data demonstrate that GAA can serve as a precursor to creatine in cattle and that metabolism of GAA and creatine are affected by methionine status. Supplementation of GAA did not affect N retention of growing steers, suggesting that either endogenous GAA production was adequate or longer periods may be required before responses are established.

Key Words: creatine, guanidinoacetic acid, methionine

1578 Total amino acid content variation for a commercial total mixed ration and relationship to crude protein. J. P. Goeser*[1,2], D. Sawyer[2], and G. A. Broderick[3], [1]*University of Wisconsin, Madison,* [2]*Rock River Laboratory, Inc., Watertown, WI,* [3]*Broderick Nutrition & Research, LLC, Madison, WI.*

Dairy cattle AA nutrition has evolved with NRC, CPM, and CNCPS model improvements. Ingredients rich in AA are added to dairy diets in precise amounts to better meet nutrient needs; however, animal health and performance still varies relative to expected responses when balancing for AA. The objective of this project was to describe total AA (TAA) population statistics and to determine if TAA varied relative to CP, for commercial TMR. Commercial TMR, $n = 141$, were selected from samples submitted to Rock River Laboratory for further analyses. Samples represented by dry, lactating dairy, finishing beef, and unknown TMR were dried using a microwave oven technique and ground (1 mm). TMR CP was determined as N × 6.25 after assaying N by a combustion technique. Total AA were determined after acid hydrolysis using *o*-phtaldialdehyde colorimetry. Type of TMR (beef, lactating, dry, and unknown) and CP were related to TAA using Fit Model function within JMP version 11.0; TMR type was considered random. Interactions and quadratic effects were tested. Residuals were visually assessed for normality using a residual by predicted plot. Commercial TMR CP and TAA (% of DM) and population statistics for all TMR except unknown are described in Table 1. Linear and quadratic relationships between CP and TAA were detected ($P < 0.05$). The quadratic effect was unanticipated and suggests a nonlinear relationship between TAA and CP. The model $R^2 = 0.78$, SE = 0.83, and parameter estimates (and SE) are as follows: 3.48 + CP × 0.58 (SE 0.04) + CP^2 × −0.02 (SE 0.01). That the slope estimate was <1.0 may partly be due to non-AA nitrogen in the form of urea, NH_3–N, or amide N present as glutamine and asparagine, all of which contribute N to CP but not to TAA equivalence. Results presented here demonstrate the variation in TAA contents of commercial farm TMR and may be useful when considering future model development and validation parameters. Furthermore, knowing TMR TAA in addition to CP may help improve on farm nutrition and troubleshooting.

Key Words: amino acid, protein, total mixed ration

1579 Impact of a rumen-protected methionine prototype on dairy cow performance, milk composition, and milk casein. A. M. Barnard*[1], B. A. Barton[2], C. A. Zimmerman[2], R. S. Ordway[2], and T. F. Gressley[1], [1]*University of Delaware, Newark,* [2]*Balchem Corporation, New Hampton, NY.*

Differences in the formulation of the protective matrix of methionine products may impact rumen degradation and intestinal availability. The objective of this study was to determine the effect of a rumen-protected methionine prototype on milk, milk protein, and casein yields. The study was conducted as a replicated 5 × 5 Latin square design in which 10 lactating,

Table 1579. Effect of methionine supplementation on production measures.

	Treatment						
		Methionine prototype					
	–Con	Met1	Met1.5	Met2	+Con	SEM	*P*-values
DMI, kg/d	28.17	28.76	28.48	28.47	29.28	0.71	0.59
Milk, kg/d	52.65	52.86	53.23	54.23	54.48	1.69	0.75
Fat, %	3.72	3.81	3.63	3.61	3.71	0.14	0.62
Fat, kg/d	1.97	1.99	1.92	1.94	1.99	0.07	0.84
Protein, %	2.64^{C}	$2.70^{A,B,C}$	2.72^{A}	$2.66^{B,C}$	$2.70^{A,B}$	0.02	0.05
Protein, kg/d	1.41^{B}	$1.43^{A,B}$	1.45^{A}	$1.43^{A,B}$	1.45^{A}	0.01	0.04
Casein, %	2.13^{C}	$2.18^{A,B,C}$	2.19^{A}	$2.14^{B,C}$	$2.18^{A,B}$	0.02	0.06
Casein, kg/d	1.14^{B}	$1.15^{A,B}$	1.17^{A}	$1.15^{A,B}$	1.17^{A}	0.01	0.06
Lactose, %	4.83	4.82	4.79	4.80	4.79	0.01	0.11
MUN, mg/dL	13.90	13.85	13.07	13.40	13.38	0.40	0.23
SCC	157.86	57.94	229.93	118.49	120.94	89.10	0.42

multiparous Holstein cows were assigned to either a methionine-deficient control ration (–Con), –Con supplemented with 0.09% Smartamine M (Adisseo, Antony, France; +Con), or the –Con supplemented with a rumen-protected methionine prototype (Balchem Corporation, New Hampton, NY) to provide either 1 (Met1), 1.5 (Met1.5), or 2 (Met2) times the amount of methionine supplied by Smartamine M. The ration was balanced with AMTS version 4.1.4 assuming 50.0 kg/d milk, 3.70% fat, 3.00% protein, and 740 kg BW. The –Con was formulated to have MP, MP methionine, and MP lysine balances of −32.5, −15.3, and +4.9 g/d, respectively. Supplementation of Smartamine M to the –Con resulted in formulated MP, MP methionine, and MP lysine balances of −16.2, +0.1, and +4.9 g/d, respectively. Periods were 14 d, and milk samples were collected on Days 11 to 14 of each period. Data collected during the last 4 d of each period were averaged by cow and analyzed using the Glimmix procedure of SAS. Data from two cows were removed before analysis due to illness. The model included a covariate (data collected during a 2-wk standardization period), fixed effects of treatment and period, and random effects of cow and cow within block. There were no treatment effects on DMI, milk yield, fat percentage, fat yield, lactose percentage, milk urea nitrogen (MUN), or somatic cell count (SCC) (Table 1). Treatment affected protein percentage ($P = 0.05$) and yield ($P = 0.04$) and tended to affect casein percentage ($P = 0.06$) and yield ($P = 0.06$). Relative to –Con, +Con and Met1.5 increased protein percentage by 0.06 ($P = 0.04$) and 0.08 ($P = 0.01$) units, respectively; protein yield by 0.04 kg/d for both treatments ($P = 0.01$); casein percentage by 0.05 ($P = 0.05$) and 0.06 ($P = 0.06$), respectively; and casein yield by 0.03 kg/d for both treatments ($P = 0.02$). The results suggest that Met1.5 was as effective at restoring methionine levels as +Con.

Key Words: bovine, methione, prototype

1580 Effects of feeding canola meal or wheat dried distillers' grains with solubles alone or in combination as the major protein sources on ruminal function and production in dairy cows.

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Canola meal (CM) is a good-quality protein supplement that is readily available and is used extensively in dairy cow diets in Canada and the United States. On the other hand, major growth of the ethanol industry in western Canada has resulted in large quantities of wheat dried distillers' grains with solubles (WDDGS) being available as an alternative protein supplement for dairy cows. Canola meal is an excellent source of limiting essential AA (e.g., lysine, histidine), whereas WDDGS has a greater CP content but is a poorer source of lysine; therefore, it is reasonable to consider that a judicious combination of CM and WDDGS as protein supplements may provide an optimal profile of essential AA that would improve milk production. The objective of this study was to determine the effects of feeding CM or WDDGS alone or in combination as the major sources of protein on ruminal fermentation characteristics and production in dairy cows. Fifteen lactating dairy cows (697 ± 46 kg BW and 76 ± 16 d in milk at the beginning of the experiment) were used in a replicated 5 × 5 Latin square design with 28-d periods (20 d of dietary adaptation and 8 d of measurements). Five cows in one Latin square were ruminally cannulated to facilitate ruminal sampling. The dietary treatments were 1) 100% CM as the major protein supplement, 2) 75% CM and 25% WDDGS, 3) 50% CM and 50% WDDGS, 4) 25% CM and 75% WDDGS, and 5) 100% WDDGS. Diets were isonitrogenous (17.6% CP) and were fed as TMR containing 50% forage and 50% concentrate. Dry matter intake (mean = 30 kg/d) was unaffected by diet. Milk production (40.4, 41.0, 41.2, 40.4, and 40.2 kg/d for the 100, 75, 50, 25, and 0% CM diets, respectively) was unaffected by diet. Milk composition was unaffected by diet; however, milk urea nitrogen linearly decreased ($P = 0.05$) as the dietary

proportion of CM decreased. Ruminal pH and concentrations of total and individual VFA were unaffected by diet. These results show that when dairy diets are formulated to contain 17.6% CP, CM or WDDGS can be fed alone or in combination as the major sources of protein and can support similar levels of milk production.

Key Words: canola meal, dairy cow, milk production, wheat dried distillers' grains with solubles

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1581 Relative bioavailability of l-carnitine delivered by ruminal or abomasal infusion or by encapsulation in dairy cattle. K. E. Olagaray*[1], J. E. Shaffer[1], C. K. Armendariz[2], A. Bellamine[3], S. Jacobs[3], E. C. Titgemeyer[1], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [3]Lonza, Inc., Allendale, NJ.*

These studies evaluated the relative bioavailability of l-carnitine delivered by different methods in dairy cattle. In Experiment 1, 4 Holstein heifers were used in a split-plot design to compare ruminally or abomasally infused l-carnitine. The study included 2 main-plot periods, with infusion routes allocated in a crossover design. Within main-plot periods, each of 3 subplot periods consisted of 4-d infusions separated by 4-d rest periods. Subplot treatments were infusion of 1, 3, and 6 g l-carnitine/d. Doses increased within a period to minimize carryover. Treatments were delivered in two 10-h infusions daily. Blood was collected before the start of infusions and on d 4 of each infusion to obtain baseline and treatment l-carnitine concentrations. There was a dose × route interaction ($P < 0.05$) and route effect ($P < 0.01$) for increases in plasma carnitine above baseline, with increases above baseline being greater across all dose levels when abomasally infused compared with when ruminally infused. Results demonstrated superior bioavailability of l-carnitine when ruminal exposure was physically bypassed. In Experiment 2, 56 lactating Holstein cows (143 ± 72 DIM) were used in a randomized complete block design (blocked by parity and milk production) to evaluate 2 rumen-protected products compared with crystalline carnitine. Treatments were 1) control, 2) 3 g/d crystalline l-carnitine (crystalline), 3) 6 g/d crystalline, 4) 5 g/d 40COAT (40% coating and 60% l-carnitine), 5) 10 g/d 40COAT, 6) 7.5 g/d 60COAT (60% coating and 40% l-carnitine), and 7) 15 g/d 60COAT. Treatments were top-dressed to diets twice daily. The 14-d experiment included a 6-d baseline-measurement period with the final 2 d used for data and sample collection and an 8-d treatment period with the final 2 d used for data and sample collection. Plasma, urine, and milk samples were analyzed for l-carnitine. Crystalline ($P < 0.001$) and 40COAT ($P = 0.01$) linearly increased plasma l-carnitine, and 60COAT tended to linearly increase plasma l-carnitine ($P = 0.08$). Total daily excretion (milk + urine) of l-carnitine averaged 1.52 ± 0.04 g/d in controls, linearly increased with crystalline and 40COAT, and quadratically increased with 60COAT (all $P < 0.05$). Crystalline increased plasma l-carnitine and milk + urine l-carnitine more than 40COAT and 60COAT (all $P < 0.05$). In conclusion, preventing ruminal degradation of l-carnitine increased delivery of bioavailable carnitine to cattle, but effective ruminal protection and postruminal availability is challenging.

Key Words: bioavailability, dairy cow, l-carnitine

1582 Comparison of three levels of a rumen-protected methionine product on performance of lactating dairy cows. A. M. Barnard*[1], B. A. Barton[2], C. A. Zimmerman[2], R. S. Ordway[2], and T. F. Gressley[1], *[1]University of Delaware, Newark, [2]Balchem Corporation, New Hampton, NY.*

Because methionine is one of the limiting AA in the majority of dairy cow rations, rations are commonly supplemented with rumen-protected methionine products. The objective of this study was to evaluate the effect of a newly developed product, AminoShure-M (Balchem Corporation, New Hampton, NY), on performance of cows fed a methionine deficit ration. In a replicated 5 × 5 Latin square design, 19 multiparous cows were assigned to either a methionine-deficient control ration (–Con), the control ration supplemented with 0.09% Smartamine M (Adisseo, Antony, France) to serve as a positive control (+Con), or AminoShure-M to provide either 1.5 (ASM1.5), 1.75 (ASM1.75), or 2 (ASM2) times the amount of methionine supplied by Smartamine M. Periods were 14 d, and milk samples were collected on Days 11 to 14 of each period. Data collected during the last 4 d of each period were averaged by cow and analyzed using the Glimmix procedure of SAS. The model statement included a covariate (data collected during a 2-wk pretreatment period) and fixed effects of treatment and period. Cow and cow within block were included as random effects. There were no effects of treatments on milk yield, DMI, fat percentage, fat yield, lactose percentage, energy-corrected milk (ECM), ECM/DMI, fat-corrected milk (FCM), milk urea nitrogen (MUN) or somatic cell count (SCC). There was an effect of treatment on milk protein percentage ($P = 0.0001$) and protein yield ($P = 0.0001$). Compared with –Con, +Con increased protein percentage (2.77 vs. 2.66%; $P < 0.0001$) and yield (1.33 vs. 1.26 kg/d; $P < 0.0001$). ASM1.5 ($P = 0.003$), ASM1.75 ($P = 0.002$), and ASM2 ($P < 0.0001$) increased protein by 0.05, 0.06, and 0.08 percentage units, respectively, compared with –Con. ASM1.5 ($P = 0.001$), ASM1.75 ($P = 0.001$), and ASM2 ($P < 0.0001$) increased protein yield by 0.04, 0.04, and 0.05 kg/d, respectively, compared with –Con. +Con also increased protein by 0.06 and 0.05 percentage units compared with ASM1.5 ($P = 0.002$) and ASM1.75 ($P = 0.004$), respectively, but was not different from ASM2. +Con also increased protein yield by 0.03 kg/d compared with ASM1.5 ($P = 0.005$) and ASM1.75 ($P = 0.01$). Similar to protein percentage, ASM2 was not significantly different from +Con, suggesting that this ASM treatment was as

effective at restoring methionine levels as +Con.

Key Words: bovine, methionine, milk protein

1583 Evaluation of *Brassica carinata* meal as a protein supplement for growing beef heifers.

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Brassica carinata is a new oilseed crop in Florida with the potential of producing high-quality biodiesel for use as jet biofuel. A high-protein meal is obtained as a byproduct of oil extraction; however, this meal has not been tested as a potential supplement for growing beef cattle. The objective of this experiment was to determine the effect of supplementation with *B. carinata* meal (BCM) on animal performance, attainment of puberty, and blood profile in growing beef heifers consuming grass hay. Thirty-two Angus crossbred heifers (271 ± 42 kg initial BW) were stratified by initial BW and randomly allocated to a total of 10 pens in 2 BW blocks. Within block, pens were randomly assigned to one of two treatments: 0 (CTL) or 0.3% of BW/d (as fed) of BCM pellets. All heifers had ad libitum access to bahiagrass (*Paspalum notatum*) hay and water, and BCM pellets were supplemented daily in the pen. Body weight and blood samples were collected every 7 d for a duration of 70 d, before the daily supplementation. Plasma was collected for analysis of progesterone and blood urea nitrogen concentrations and glucose. Data were analyzed as a generalized randomized block design including block in the model as a random variable. Progesterone data were analyzed using the LIFETEST procedure of SAS to determine the effect of treatment on time to attainment of puberty. There was a difference ($P = 0.02$) in ADG between CTL (0.28 kg/d) and BCM (0.49 kg/d). Time to attainment of puberty did not differ between treatments ($P = 0.36$). Supplementing *B. carinata* meal at 0.3% of BW/d in growing heifers consuming bahiagrass hay is a viable option for increasing ADG without negatively affecting their interval to attainment of puberty.

Key Words: *Brassica carinata*, protein supplement, ruminants

1584 Effects of replacing soybean meal with canola meal or treated canola meal on nitrogen metabolism and total tract digestibility in lactating dairy cows.

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Canola meal (CM) has been shown to improve N efficiency in dairy cows when compared with soybean meal (SBM). Treating CM may increase its RUP fraction with the goal of increasing AA availability for absorption in the small intestine. The objective of this study was to evaluate the effects of feeding treated CM (TCM) on N metabolism and total tract digestibility of dairy cows. Thirty multiparous Holstein cows, averaging (means ± SD) 660 ± 55 kg BW, 119 ± 23 DIM, and 44.1 ± 7 kg milk/d, and 15 primiparous cows, averaging 592 ± 34 kg BW, 121 ± 19 DIM, and 33.5 ± 6 kg milk/d, were blocked in a randomized complete block design. Cows were fed a control diet for a 2-wk covariate period and then switched to the experimental diets for a 12-wk study; cows were individually fed in tie-stalls and had free access to water. Treatments differed only in CP source, which were SBM, CM, or TCM. The CM was treated by extrusion, with added molasses to promote the

Table 1584.

Table 1. Effect of soybean meal (SBM), canola meal (CM), or treated canola meal (TCM) on nitrogen metabolism and digestibilities

	Diet				Contrasts *P*-value	
Item	SBM	CM	TCM	SEM	SBM vs. CM+TCM	CM vs. TCM
N intake, g/d	653.0	691.9	691.9	22.7	0.17	1.00
Milk, kg/d	40.0	41.3	40.5	1.01	0.48	0.62
MUN, mg/dL	13.7	12.8	12.5	0.25	<0.01	0.43
DM digestibility, %	68.4	70.9	69.7	0.44	<0.01	0.08
OM digestibility, %	70.2	72.4	71.3	0.42	<0.01	0.07
CP digestibility, %	64.7	68.9	67.3	0.68	<0.01	0.09
NDF digestibility, %	45.1	49.1	47.1	0.80	<0.01	0.08
Fecal-N, g/d	206.5	201.9	210.2	8.01	0.96	0.47
Fecal-N, % of intake	31.6	29.2	30.3	0.45	<0.01	0.08
Urinary total N, g/d	219.4	221.3	215.5	7.25	0.92	0.57
Urinary total N, % of N intake	34.0	32.5	31.5	1.01	0.12	0.46
Urinary urea N, g/d	157.1	152.2	146.6	5.04	0.22	0.44
Urinary urea N, % of total urinary N	72.2	69.2	68.4	0.90	<0.01	0.52

browning reaction. All diets contained (DM basis) 30% alfalfa silage, 30% corn silage, 4% soy hulls, 2.4% mineral–vitamin premix, and 16% CP. The SBM diet contained 25% high-moisture corn (HMC) and 8.6% SBM; the canola diets contained 22% HMC and 11.4% CM or TCM. On the last day of wk 4, 8, and 12, spot urine and fecal samples were collected at 6 and 18 h after feeding. Data were analyzed using the MIXED procedure of SAS. Orthogonal contrasts were used to compare effects of different protein sources (SBM vs. CM + TCM and CM vs. TCM). Partial data are presented in Table 1. Compared with SBM, apparent digestibility of DM, OM, CP, and NDF was greater on both CM and TCM diets and there were trends for improved digestibilities when CM was compared with TCM. There were no differences for N intake, milk yield, and total N excreted in urine and feces; however, both canola diets decreased urinary urea N (% of total urinary N) and fecal N (% of total N intake) and decreased MUN concentration. No differences were observed between CM and TCM with regards to N utilization. Results from this experiment indicate that replacing SBM with CM or TCM in lactation diets improved digestibility and minimized environmental impact but that extrusion did not improve CM utilization.

Key Words: dairy nutrition, digestibility, nitrogen utilization

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1585 Impact of different diet crude protein levels and ruminally degradable protein:ruminally undegradable protein ratios on midlactation dairy cow performance: II. Dry matter intake, digestibility, and nitrogen balance.

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This study evaluated the impact of different CP levels and RDP:RUP ratios in the diets of 24 crossbred Holstein–Gir midlactating dairy cows. Animals were allotted for 60 d to 4 treatments on a complete random design ($n = 6$). Experimental diets were formulated using the CNCPS version 6.1 model to meet production requirements and to be isoenergetic and provide the same amount of MP. Crude protein concentrations were 12.4, 13.0, 13.6, and 15.4% on a DM basis. Ruminally degradable protein levels ranged from 5.6 to 9.7% DM and RUP ranged from 6.8 to 5.7 DM in relation to treatments with lower and higher CP levels, respectively. Soypass (Cargill) was used in substitution to soybean meal and urea to adjust RDP:RUP ratios. Parameters evaluated were DMI, CP intake (CPI), DM digestibility, nitrogen balance, microbial protein yield (MPY), and plasma urea nitrogen (PUN). Data were analyzed using PROC MIXED from SAS 9.0 on a split plot design. Dry matter intake did not differ among treatments and ranged from 20.0 to 21.6 kg/d, whereas CPI increased ($P < 0.01$) as diets' CP level increased (2.59–3.46 kg/d). Treatments did not affect DM digestibility (60.2–61.9%) but CP digestibility increased ($P < 0.04$) as RDP levels in the diets increased (58.2–67.2%). Treatments did not affect milk N (119–135 g/d) or N in feces (178–182 g/d). Urine N increased (116–247 g/d) as diets CP level increased ($P < 0.01$). Microbial protein yield was not affected by treatments. Plasma urea nitrogen values raised from 10.2 to 19.6 mg/dL as RDP levels increased ($P < 0.01$). Results show that formulating diets with more RUP sources can be an efficient tool to reduce N excretion and improve N balance. Reducing RDP and CP levels in the diets did not affect DMI and did not impair MPY.

Key Words: ruminally degradable protein, ruminally undegradable protein, nitrogen balance

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1586 Evaluation of protein supplementation in low- to medium-quality forage diets on intake and ruminal fermentation in steers.

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Four ruminally and duodenally cannulated steers (469 ± 37 kg initial BW) were arranged in a 4 × 4 Latin square to evaluate the impact of protein supplementation in low- to medium-quality forage diets on intake and ruminal fermentation. Protein supplement treatments included 1) high-fat dried distillers' grains (HDG; 10.8% fat), 2) low-fat dried distillers' grains (LDG; 5.7% fat), and 3) cottonseed meal (CSM; 3.0% fat). The basal diet (CON) consisted of low- to medium-quality chopped grass hay (8.3% CP and 64.9% NDF) fed ad libitum twice daily at h 0 and 12. Treatments were formulated to provide similar CP intake and were supplemented once daily to the basal diet: HDG at 0.8%, LDG at 0.7%, and CSM at 0.4% of BW. Each 21-d experimental period had 16 d of adaptation and 5 d of data collection. Intake data was collected d 17 to 21, and rumen fluid samples were collected on d 20 at h −2, 0, 2, 4, 6, 8, 10, and 12. Hay DMI was lower with supplementation of HDG ($P < 0.01$) verses CON and CSM but similar to LDG. However, hay DMI for LDG was not different ($P > 0.05$) than that for CON but lower ($P \leq 0.01$) than that for CSM. As expected, CP intake was greater ($P \leq 0.0001$) with protein supplementation than CON but not different among protein supplements. Fat intake was greatest to least for HDG, LDG, CSM, and CON, respectively ($P \leq 0.001$). Protein supplementation resulted in lower ($P \leq 0.05$) overall ruminal pH and over 2-fold greater ($P \leq 0.05$) ammonia concentration compared with CON. Overall ruminal pH was lowest for HDG compared with LDG, CSM, and CON (6.88, 6.23, 6.54, and 6.64 ± 0.09, respectively; $P = 0.0001$);

however, LDG and CSM were not different ($P > 0.05$) but lower ($P \leq 0.0001$) than CON. Total VFA production did not differ ($P = 0.46$) among treatments. Acetate proportions from greatest to least were CON, CSM, LDG, and HDG ($P \leq 0.03$). Propionate proportions from greatest to least were HDG, LDG, CSM, and CON ($P \leq 0.03$), with the exception of butyrate, which was not different between CSM and CON ($P = 0.26$). Supplementation of HDG, LDG, and CSM decreased ruminal pH and increased propionate while decreasing acetate proportions compared with no protein supplementation. Protein supplementation decreased hay consumption and the greatest decrease was observed with HDG supplementation.

Key Words: forage intake, protein supplementation, ruminal fermentation

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1587 The effect of increasing concentrations of different methionine forms and 2-hydroxy-4-(methylthio) butanoic acid on hepatic oxidative status and genes controlling methionine metabolism and transmethylation flux. Q. Zhang*[1], D. N. Luchini[2], and H. M. White[1], *[1]University of Wisconsin-Madison, Madison, [2]Adisseo S.A.S., Alpharetta, GA*.

The d-isomer of methionine (Met) cannot be directly utilized by the mammary gland in dairy cows; instead, it is transformed into l-Met, the proteogenic isomer, in the liver and other extramammary tissues. It remains unclear whether different Met forms and a Met hydroxy analog, 2-hydroxy-4-(methylthio) butanoic acid (HMB), are metabolized and function similarly in the liver. The objective of the present study was to examine the regulation of key genes in methionine regeneration, transulfuration, and transmethylation pathways and hepatic oxidative status in response to increasing doses of different Met forms. Hepatocytes isolated from 4 calves less than 7 d old were maintained as monolayer cultures for 24 h before addition of treatments. Treatments of (0, 10, 20, and 40 μM) d-Met, l-Met, dl-Met, dl-HMB, or a 1:1 mixture of dl-Met and dl-HMB were added to Met-free media in triplicate. After 24 h, cell lysates were collected for quantification of gene expression by quantitative PCR, and mRNA abundance was normalized to the mean of 3 reference genes. Cell culture media were collected for quantification of reactive oxygen species (ROS) by fluorometric assay. Data were analyzed with PROC MIXED of SAS 9.3. Analyses of covariance confirmed equivalent slopes of Met form and the final model included form, dose, and random effect of calf within form. Data are reported as least squares means ± SE. Neither Met form nor Met concentration affected ($P > 0.10$) ROS released from the cells. There was no main effect of Met form ($P > 0.10$) for any genes examined. The enzymes encoded by *betaine-homocysteine methyltransferase* (*BHMT*) and *5-methyltetrahydrofolate-homocysteine methyltransferase* (*MTR*) utilize betaine and 5-methyltetrahydrofolate, respectively, to regenerate Met from homocysteine. Increasing concentration of Met did not alter ($P > 0.10$) *MTR* expression (1.274, 1.269, 1.264, and 1.255 ± 0.257 arbitrary units [AU]) but decreased ($P < 0.05$) *BHMT* expression (1.308, 1.223, 1.138, and 0.968 ± 0.234 AU). Expression of glycine N-methyltransferase, the enzyme that controls transmethylation flux from S-adenosyl-methionine, was not affected (2.205, 2.157, 2.108, and 2.011 ± 0.735 AU; $P > 0.10$) by Met concentration. There was no effect ($P > 0.10$) of Met concentration on expression of cystathionine β-synthase (0.958, 0.972, 0.985, and 1.012 ± 0.168 AU), a key enzyme for the transulfuration pathway. The decrease in *BHMT* expression indicates decreased need for cellular Met regeneration with increasing Met concentration independent of Met form. The lack of differences among Met forms on regulating genes examined indicates that all Met forms were metabolized similarly within primary bovine hepatocytes and had similar sparing effects on Met regeneration in the liver.

Key Words: methionine isomer, methionine regeneration, 2-hydroxy-4-(methylthio) butanoic acid

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1588 Heat stress alters glucose homeostasis, hepatic heat shock proteins, and the immune system in lactating dairy cows. S. Quan[1,2], D. Bu*[1,3,4], Y. Zhang[2], J. Guo[1], S. Gao[1], and L. H. Baumgard[5], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P. R. China, [2]The Animal Physiology and Biochemistry Laboratory of the Ministry of Agriculture in Nanjing Agriculture University, Nanjing, P. R. China, [3]Hunan Co-Innovation Center of Animal Production Safety, CICAPS, Changsha, P. R. China, [4]CAAS-ICRAF Joint Laboratory of Agroforestry and Sustainable Animal Husbandry, World Agroforestry Centre, East and Central Asia, Beijing, P. R. China, [5]Iowa State University, Ames*.

Experimental goals were to investigate glucose homeostasis, hepatic heat shock protein profiles, and circulating immune parameters in lactating dairy cows during heat stress (HS). Holstein cows ($n = 4$; 101 ± 10 DIM, 574 ± 36 kg BW, and 38 ± 2 kg milk/d) were used in a 2 × 2 crossover design during two experimental periods (each period lasted 10 d and were separated by 30 d) while housed in environmentally controlled chambers. Pair-fed, thermal-neutral control cows (PF) were exposed to constant 20°C and 40% humidity whereas HS cows were exposed to 36°C and 60% humidity from 0800 to 2000 h and 32°C and 60% humidity from 2000 to 0800 h with 12 h light and 12 h dark cycles. Blood and milk samples were collected on d 1, 4, 7, and 10 during both periods. Glucose tolerance test (GTT) was performed on d 6 of each period. Liver tissue was collected on d 10 of each period. Heat stress reduced milk yield (21.5%; $P < 0.05$) and lactose yield ($P < 0.05$; 300 g/d) compared with PF controls. Basal serum glucose decreased (30.1%; $P < 0.05$) and the rate of glucose

disposal following the GTT increased during HS (21.4%; $P < 0.05$). Serum IgA and TNF were reduced (38.1 and 23.4%, respectively) in HS cows ($P < 0.05$) compared with the PF controls but IgG, IgM, and IL-6 were similar between environments ($P > 0.05$). Liver HSP27 mRNA increased in the HS cows (51.2%; $P < 0.05$), but HSP70, HSP90, and HSF-1 did not differ between environments ($P > 0.05$). Heat stress markedly reduced mammary carbohydrate output, and the increased whole-body glucose utilization may be indicative of both an activated immune response and fuel required to mount and sustain a heat shock response.

Key Words: heat stress, glucose disposal, heat shock protein, immune activation, lactating cow

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1589 The effect of heat stress and jugular infusions of methionine, lysine, and branched-chain amino acids in lactating dairy cattle. K. Kassube*, J. Kaufman, K. G. Pohler, and A. G. Rius, *The University of Tennessee, Knoxville*.

Heat stress (HS) affects numerous physiological processes including nutrient partitioning and protein metabolism. Heat stress decreases production of milk and milk proteins and may benefit from supplementation of essential AA. The objective of this study was to determine the effect of jugular infusion of essential AA in lactating dairy cattle experiencing HS. Twelve multiparous lactating Holstein cows were used in a crossover design to evaluate the effect of two environments (thermoneutral [TN] and HS) and the absence or presence of AA infusion (NAA or AA [methionine {12 g}, lysine {21 g}, leucine {35 g}, isoleucine {15 g}, and valine {15 g} per day]). Thermal treatments were imposed from d 1 to 14 and jugular infusion of AA was from d 7 to 14. Temperature–humidity index values during TN never exceeded 66, whereas temperature–humidity index values during HS peaked at 76 and were above 68 for 14 h/d. Milk and blood samples were collected on d 5 to 7 and d 12 to 14. Data were analyzed using the Mixed procedure of SAS and reported as least squares means ± SEM. The HS treatment increased ($P < 0.05$) respiration rates and rectal temperatures (72.1 vs. 47.0 ± 3.9 breaths/min and 39.4 vs. 38.5 ± 0.017°C, respectively). Compared with TN treatment, HS decreased ($P < 0.05$) DMI (17.4 vs. 18.9 ± 0.41 kg/d), milk yield (29.3 vs. 32.1 ± 1.09 kg/d), milk protein yield (0.87 vs. 0.98 ± 0.05 kg/d), and lactose yield (1.41 vs. 1.55 ± 0.10 kg/d). Amino acid treatment decreased ($P < 0.001$) lactose yield (1.43 vs. 1.54 ± 0.10 kg/d) but had no effect on DMI and milk yield. Heat stress decreased ($P < 0.05$) milk protein percent (2.95 vs. 3.06 ± 0.06%). Amino acid treatment increased ($P < 0.001$) milk protein percent (3.04 vs. 2.96 ± 0.06%) and decreased ($P < 0.001$) lactose percent (4.82 vs. 4.87 ± 0.04%). Compared with the NAA treatment, AA did not affect milk fat yield in the TN treatment (1.33 vs. 1.33 ± 0.09 kg/d) but decreased milk fat yield in the HS treatment (1.18 vs. 1.32 ± 0.09 kg/d; interaction, $P < 0.05$). Compared with the NAA treatment, AA treatment increased milk urea nitrogen in the TN treatment (11.7 vs. 10.9 ± 0.77 mg/dL) but did not increase milk urea nitrogen in the HS treatment (12.3 vs. 12.8 ± 0.74 mg/dL; interaction, $P < 0.01$). Plasma glucose decreased 6.7% in the AA treatment (2.8 vs. 3.0 ± 0.05 mmol/L; $P < 0.001$). Insulin, NEFA, and β-hydroxybutyrate were not affected by treatments. In conclusion, HS elicited expected decreases in production; however, the infusion of essential AA did not improve milk yield and milk protein yield during HS.

Key Words: essential amino acids, heat stress

1590 Effect of experimental design on production responses in high-producing dairy cows fed two levels of metabolizable protein. G. I. Zanton*, *USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI*.

Inferences about lactation responses to diet have been hypothesized to be affected by the use of changeover instead of continuous experimental designs; a direct test of this hypothesis has not been well studied. The objective of this study was to evaluate the effects of reducing MP on lactation performance when dairy cows are fed diets continuously or according to a changeover design. Forty-six multiparous, Holstein cows were fed a common diet for 14 d and then randomly assigned to a randomized completed block design (CONT; $n = 34$; initial mean ± SD: 2.9 ± 0.9 parity, 84 ± 30 d in milk, 720 ± 59 kg BW, and 58.1 ± 6.4 kg milk/d) or a balanced 2-treatment, 4-sequence, 4-period changeover design (CHANGE; $n = 12$; 2.7 ± 1.0 parity, 90 ± 32 d in milk, 709 ± 78 kg BW, and 56.7 ± 3.9 kg milk/d). Cows were fed once and milk thrice daily, received rBST every 14 d, and received a diet that was predicted to be either adequate (ADMP) or deficient (LOMP) in MP for 112 d or changing according to sequence for four 28-d periods. The base diet was formulated to contain (% DM) 37.5% BMR corn silage, 16% alfalfa silage, and 41% concentrate. Treatments differed by adding 5.5% expeller soybean meal to the base diet for ADMP or 5.5% soyhulls for LOMP. By design, chemical composition differed with 16.6 vs. 14.7% CP, 28.2 vs. 31.1% NDF, and 27.6 vs. 27.5% starch for ADMP vs. LOMP, respectively. Production data were analyzed for study d 22 to 28, 50 to 56, 78 to 84, and 106 to 112, corresponding to 21 d of adaptation and 7 d of measurement for cows in the changeover design. Statistical analysis was conducted using the mixed procedure of SAS as either a randomized complete block design or as a balanced changeover design where differences with $P < 0.05$ are considered significant. As shown in the table, response to dietary treatment was not different for BW, BW change, and DMI, irrespective of experimental design. Milk and protein yield and milk urea N concentration were reduced with LOMP compared with ADMP for both designs. Fat yield response to diet was not different for CONT whereas fat percent increased with LOMP. In contrast, fat yield was significantly reduced for cows fed LOMP in CHANGE with

Table 1590.

Table 1. Production responses for cows fed diets containing either adequate (ADMP) or low (LOMP) levels of MP either continuously for 112 d (CONT) or according to a 4-period changeover design (CHANGE)

	CONT				CHANGE				
	ADMP	LOMP	SEM	P_{MP}[1]	ADMP	LOMP	SEM	P_{MP}[1]	P_{CO}[1]
BW, kg	740	734	5	0.375	731	733	7	0.588	0.475
BW change, kg/28d	7.9	5.6	1.8	0.351	5.9	11.3	5.5	0.335	0.432
DMI, kg/d	28.9	30.7	0.7	0.062	30.0	30.5	0.7	0.277	0.122
Milk, kg/d	55.5	52.7	0.8	0.012	56.1	52.7	1.2	<0.001	0.961
Protein, kg/d	1.62	1.53	0.02	0.006	1.66	1.54	0.04	<0.001	0.531
Protein, %	2.93	2.92	0.02	0.860	3.03	2.99	0.04	0.099	0.356
Fat, kg/d	1.82	1.82	0.08	0.979	1.80	1.67	0.06	0.009	0.008
Fat, %	3.17	3.54	0.11	0.022	3.24	3.21	0.12	0.588	0.002
MUN, mg/dl	8.63	5.99	0.28	<0.001	8.58	5.80	0.36	<0.001	0.226

[1] P_{MP}: *P*-value for the effect of dietary treatment; P_{CO}: *P*-value for carry-over of previous treatment

no significant difference in fat percent for this design; significant carryover effect differences were observed. Under the conditions of this experiment, inferences on the response to different levels of MP were affected by the experimental design and the production variable of interest.

Key Words: experimental design, lactation, protein

1591 Meta-analysis of postruminal microbial nitrogen flows in dairy cattle.

1592 Prediction of crude protein and neutral detergent fiber content in *Pennisetum clandestinum* by near-infrared spectroscopy. A. Rivera*, *Universidad Nacional de Colombia, Medellin, Colombia*.

The objective of this study was to predict the CP and NDF content of *Pennisetum clandestinum* using near-infrared spectroscopy (NIRS).Three hundred fifty-four ($n = 354$) grass samples were collected from different dairy herds from northern Antioquia-Colombia, during 2015 and earlier 2016, which varied in soil types and fertility and grass growth stage and were analyzed at the Chemical Analysis and Bromatological Laboratory (certificate for ISOMEC 17025-2005) of the Universidad Nacional de Colombia at Medellin. Samples were dried to constant weight in a forced-air oven at 60°C for 48 h and then ground in a Wiley mill (1-mm sieve). Crude protein (N × 6.25) and NDF were analyzed following official methods. Content of CP ranged between 14 and 30.5%, with a mean of 23.07 ± 3.73%, and that of NDF ranged from 46.60 to 65.90%, with a mean of 56.22 ± 4.70%. Samples were randomized divided in two groups, and the first group ($n = 301$) was used for calibration and the second group for cross-validation ($n = 40$) and external validation ($n = 13$). Samples for calibration and cross-validation were scanned in an NIRS DS 2500 F monochromator (Foss-NIRsystem, Denmark) in the range of 1,108 to 2,492 nm for CP and 858 to 2,492 nm for NDF, with reflectance data collected every 8 nm. Modified partial least squares (MPLS) regression was applied to scatter-corrected spectra (SNV and detrend) and mathematical treatment (equation generation) was performed in the software WinISI version 4.8. The equations were selected by evaluating the statistical parameters (R^2 higher than 0.80, a SE of cross-validation [SECV] close to the SE of calibration [SEC], and a SE of reference database:SE of cross-validation [RPD] ratio greater than 3). As a result, the equation selected for CP was mathematically treated with derivative, 1; gap, 4; smooth, 3; smooth 2, 1; the mean was 22.48; SD 2,91; SEC 03253; SECV 0.439; and RPD 6.62 and correlation coefficients of calibration, cross-validation, and external validation were 0.977, 0.920, and 0.982, respectively. The equation selected for NDF was mathematically treated with derivative 1; gap, 4; smooth, 3; smooth 2, 1; the mean was 56.18; SD 4.56; SEC 1.571; SECV 1.770; RPD 2.75 and correlation coefficients of calibration, cross-validation, and external validation were 0.847, 0.727, and 0.781, respectively. According to these preliminary results, it was possible to predict reliably the CP content of *P. clandestinum*, but for NDF, further work is still needed.

Key Words: dairy, feed quality, forage analysis, near-infrared spectroscopy, nutrition

1593 Impact of metabolizable protein source on pancreatic enzyme activity in finishing cattle fed dry-rolled corn–based diets. E. J. Blom*[1], D. W. Brake[1], M. R. Fiene[1], J. A. Walker[1], F. E. Keomanivong[2], and K. C. Swanson[2], [1]*South Dakota State University, Brookings,* [2]*North Dakota State University, Fargo*.

Previous data indicate increases in MP flow from soybean meal can increase pancreatic amylase content in cattle fed corn-based diets. However, reports on effects of increased MP flows from different protein sources are limited. We evaluated effects of added MP from either dried distillers' grains or porcine blood meal and corn gluten meal to finishing cattle fed dry-rolled corn–based diets designed to meet CP requirements (CP = 13.7% DM) on pancreatic α-amylase and trypsin and duodenal maltase activity. Two hundred sixteen crossbred steers (362.3 ± 3.4 kg BW) were blocked by initial BW, randomly assigned to 18 pens, and adapted to 1 of 3 dietary treatments. Treatments were a dry-rolled corn–based diet with added urea to meet CP requirements (CON), a diet with supplemental dried distillers' grains (DGS) designed to provide an additional 200 g/d MP, and a diet designed to provide 100 g/d additional MP from blood meal and 100 g/d additional MP from corn gluten meal (BMCGM). Cattle were fed for 152 d and subsequently harvested in a commercial abattoir. At harvest, pancreata and duodenal tissues were collected from 2 steers randomly selected within each pen for enzyme analyses. Pancreatic protein concentration (114.2 ± 4.3 mg/g) was not affected (P = 0.26) by dietary treatment. Pancreatic α-amylase activity per gram tissue was less (P = 0.01) among cattle fed DGS compared with CON and BMCGM. Additionally, added MP from DGS tended (P = 0.07) to decrease pancreatic α-amylase activity per gram pancreatic protein. Greater MP flow from BMCGM increased (P = 0.02) pancreatic trypsin activity per gram tissue; however, increased MP from either BMCGM or DGS did not impact (P = 0.30) trypsin activity per gram pancreatic protein (120.9 ± 22.25 U/g). Additions of MP did not affect (P = 0.43) protein content in duodenal tissue (62.1 ± 2.67 mg/g). Similarly, duodenal maltase activity (227.6 ± 13.87 U/g duodenum and 4.30 ± 1.217 U/g duodenal protein) was not affected ($P \geq 0.29$) by additional MP from either BMCGM or DGS. These data indicate that pancreatic α-amylase and trypsin activity are impacted by amounts and source of MP in finishing cattle, which could potentially influence starch and protein digestion in the small intestine.

Key Words: cattle, metabolizable protein, pancreas

1594 Comparative effects of multiple sources of rumen-protected methionine on milk production and serum amino acid levels in midlactation dairy cows. Y. Zang[1], S. Saed Samii*[1], L. R. Tager[2], J. W. McFadden[1], and K. M. Krause[1], [1]*West Virginia University, Morgantown,* [2]*MarSyt, Elizabethtown, PA*.

Methionine (Met) and lysine (Lys) are limiting AA in dairy cow diets. Supplementation of rumen-protected (RP) Met and Lys can improve milk yield as well as yield and content of milk protein. Currently, multiple sources of RP-Met are available for supplementation; however, the comparative efficacy of these supplements to improve performance requires evaluation. Therefore, our objective was to characterize the production response of three RP-Met supplements in midlactation cows. Twelve multiparous Holstein cows (602 ± 46 kg BW and 174 ± 18 DIM) were used in a replicated 4 × 4 Latin square design with 21-d treatment periods. Dietary treatments included a corn silage and alfalfa haylage diet (control; no added Met) supplemented with one of three RP-Met sources (Novimet [Innovad], Smartamine M [Adisseo], and Mepron M85 [Evonik]). Treatments were designed to maintain a Lys:Met ratio of 2.9:1. For the control, Lys (RP-Lys; AjiPro) was added at 0.02% ration DM. For RP-Met supplementation, Met (RP-Met) was added at 0.03% ration DM. Cows fed RP-Met were provided Lys (RP-Lys) at 0.20% ration DM. Milk yields were recorded, and samples were collected during each period (d 19 to 21). Blood samples were collected on d 21 at 2, 4, and 6 h following feeding, and serum was pooled. Following solid-phase extraction, 21 serum AA were quantified using gas chromatography tandem mass spectrometry. Data were analyzed using a mixed model with repeated measures (fixed effects of treatment and period). Treatments had no effect on DMI or milk yield. Treatment did not modify milk fat, protein, or lactose yield; however, milk protein content was elevated with Smartamine M relative to control or Novimet (3.30 vs. 3.24 and 3.24% respectively; $P < 0.05$). Milk fat and lactose concentration were not modified with treatment. Treatment with RP-Met tended to increase milk urea nitrogen (P = 0.12). Smartamine M increased serum Met concentration (27.3 μ*M*) compared with the control (21.2 μ*M*), Novimet (22.7 μ*M*), or Mepron M85 (23.3 μ*M*) ($P < 0.001$). In a similar manner, Smartamine M lowered the serum Lys:Met ratio (4.5:1) compared with the control (5.2:1), Novimet (5.2:1), or Mepron M85 (5.1:1) ($P < 0.05$). Smartamine M was also able to enhance circulating glutamine relative to the control (320.8 vs. 289.5; P = 0.15). Treatment did not modify serum levels of all other AA, including Lys. We conclude that Smartamine M increased circulating Met and milk protein content more effectively than Novimet or Mepron M85.

Key Words: dairy cow, lysine, methionine

1595 Milk protein synthesis gene expression and mTOR phosphorylation in response to the "ideal" profile of Lys, Met, Thr, Phe, His, Val, Ile, and Leu in bovine mammary cells. X. Dong*[1,2], Z. Zhou[1], Z. Wang[2], B. Saremi[3], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Sichuan Agricultural University, Ya'an, IL, [3]Evonik Industries AG, 63457 Hanau, Germany*.

Essential AA (EAA) are important for milk protein synthesis and potentially could alter phosphorylation of the key proteins in the mTOR pathway. We hypothesized that the EAA profile affects the mammary transcriptome and mTOR phosphorylation/total mTOR (PmTOR/TmTOR) in bovine MAC-T cells. The specific objective was to investigate how changing the ratio of Lys to Met, Thr, Phe, His, Val, Ile, or Leu affects mRNA expression of key milk protein synthesis genes and PmTOR/TmTOR. Experiment 1 consisted (n = 5 replicates/treatment) of a control medium (i.e., the "ideal" EAA ratio [IPAA; 2.9:1 Lys:Met, 1.8:1 Lys:Thr, 2.38:1 Lys:His, 1.23:1 Lys:Val, 1.45:1 Lys:Ile, 0.85:1 Lys:Leu, and 2.08:1 Lys:Arg]) or IPAA supplemented with Met to achieve a 2.5:1 Lys:Met ratio (LM2.5) and a 2.0:1 Lys:Met ratio (LM2.0). Data were analyzed using a MIXED model in SAS. Treatment means were generated using the LSMEANS option and separated when significant with the PDIFF option. Compared with IPAA, increasing exogenous Met (LM2.5 and LM2.0) led to greater ($P < 0.01$) *SLC3A2* (l-type AA transporter) but LM2.0 led to the lowest ($P = 0.05$) *MTOR* expression and a strong tendency ($P = 0.06$) for greater *EEF2* (translation elongation factor). Although *EIF4EBP1* (translation repressor) expression did not change ($P = 0.15$), PmTOR/TmTOR was lower ($P < 0.05$) with LM2.5 and LM2.0 compared with IPAA. Experiment 2 consisted (n = 5 replicates/treatment) of IPAA or IPAA supplemented with Thr, Ile, Val, and Leu to achieve a 1.3:1 Lys:Thr ratio (LT1.3), 1.29:1 Lys:Ile ratio (LI1.29), 1.12:1 Lys:Val ratio (LV1.12), and 0.78:1 Lys:Leu ratio (LL0.78). Compared with IPAA, an increase in Thr, Ile, Val, and Leu resulted in greater ($P < 0.01$) expression of *SLC3A2*, but only an increase in Ile upregulated ($P = 0.05$) *EIF4EBP1*. Expression of *MTOR* and *EEF2* did not change ($P > 0.10$) compared with IPAA. Only the increase in Ile (LI1.29) and Val (LV1.12) led to greater ($P < 0.01$) PmTOR/TmTOR, indicating the potential for enhancing protein synthesis compared with IPAA. Overall, the data from these experiments indicate that changes in EAA profile, particularly Lys:Met, Lys:Val, and Lys:Ile, may affect mammary epithelial cell protein synthesis at least in part through regulating AA transport and PmTOR/TmTOR.

Key Words: essential amino acid profile, protein synthesis, mammary cell

1596 Nitrogen excretion of lactating dairy cows fed an alfalfa hay– or birdsfoot trefoil hay–based high-forage diet. M. Ghelich Khan[1], S. Y. Yang[1], J. S. Eun*[1], and J. W. MacAdam[2], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Plants, Soils, and Climate, Utah State University, Logan*.

Legumes that contain condensed tannins (CT) may have lower protein degradability than alfalfa. The present study investigated the effects of feeding birdsfoot trefoil (*Lotus corniculatus* L.) hay (BFTH) on lactation performance and N utilization. Eight multiparous Holstein cows in mid lactation (150 ± 10.3 d in milk) were randomly assigned to 1 of 2 rations (AH-based TMR [AHT] or BFTH-based TMR [BFTHT]) in a crossover design with 2 experimental periods. Each experimental period lasted 16 d (14 d of adaptation and 2 d of total collection), and the 2 experimental periods were separated by a 7-d washout period. On the experimental diets, AH or BFTH was included at 40% DM to AHT or BFTHT, respectively. There were no treatment effects on DMI (21.4 vs. 20.7 kg/d; $P = 0.46$), milk yield (29.4 vs. 28.1 kg/d; $P = 0.47$), milk fat concentration (3.20 vs. 3.21%; $P = 0.40$), and milk protein concentration (3.20 vs. 3.16%; $P = 0.13$) for AHT and BFTHT, respectively. In addition, dietary treatments did not affect milk yield/DMI ($P = 0.59$) and energy-corrected milk yield/DMI ($P = 0.49$). In contrast, CP digestibility increased in BFTHT compared with AHT (69.1 vs. 64.8%; $P < 0.01$). Concentration of milk urea nitrogen decreased by feeding BFTHT compared with feeding AHT (11.9 vs. 13.3 mg/100 mL; $P < 0.01$), whereas total N excretion was similar ($P = 0.54$) between the diets. However, cows fed BFTHT excreted more N in feces (194 vs. 168 g/d; $P < 0.01$), whereas urinary N excretion did not differ between the diets ($P = 0.39$), leading to a decrease in the UN:FN ratio ($P = 0.03$) in cows fed BFTHT relative to those fed AHT. Overall results in the current study suggest that feeding BFTH in a lactation high-forage diet did not affect overall lactational performance, whereas it shifted routes of N excretion evidenced by the decreased UN:FN ratio compared with feeding AH. The positive impact on environment may be attributed to a functional effect of CT as well as a unique cell wall structure of BFTH.

Key Words: alfalfa hay, birdsfoot trefoil hay, nitrogen excretion

Table 1597.

Table 1. Plasma TSAA concentrations for cows fed different RP-Met products

Item	CON	SM1	SM2	MPN	ASM	SEM	*P*-value
TSAA, μ*M*	95.4[c]	137.9[a]	142.3[a]	107.1[b]	101.7[bc]	3.7	0.001
TSAA, % of total AA – TSAA	3.93[c]	6.01[a]	5.98[a]	4.45[b]	4.39[b]	0.11	0.001

[a-c] Means within rows differ at $P < 0.05$.

1597 Determination of relative methionine bioavailability in lactating cows fed Smartamine M, Mepron, and AminoShure M using the plasma-free AA dose–response method.
N. L. Whitehouse*[1], C. G. Schwab[2], S. M. Fredin[3], and A. F. Brito[1], [1]*University of New Hampshire, Durham,* [2]*Schwab Consulting, LLC, Boscobel, WI,* [3]*Adisseo, Inc., Alpharetta, GA*.

In vivo measurements of bioavailability of Met in rumen-protected Met (RP-Met) products are critical to determine their contribution to metabolizable Met supply. The objective of this experiment was to use the plasma free AA dose–response method to compare the bioavailability of Met in Smartamine M (Adisseo, Antony, France) from the new (SM1) and original (SM2) production plants along with 2 additional commercially available RP-Met products, Mepron (MPN; Evonik Ind., Kennesaw, GA) and AminoShure-M (ASM; Balchem Corp., New Hampton, NY). Ten multiparous lactating Holstein cows, fed Met-deficient diets, were used in a replicated 5 × 5 Latin square design with 7-d periods. Treatments included a negative control with no added RP-Met (CON) or 30 g of Met supplied by the 4 RP-Met products. Milk samples were collected and DMI measurements were made on d 5, 6, and 7. Blood samples were collected 2, 4, 6, and 8 h after the morning feeding (0500 h) on d 5, 6, and 7. Plasma was pooled by cow per day for AA analysis by HPLC. Data were analyzed using the MIXED procedure in SAS. Milk yield (46.0 kg/d; SEM = 1.0; $P = 0.60$), DMI (27.4 kg/d; SEM = 0.6; $P = 0.93$), and milk fat content (3.60%; SEM = 0.11; $P = 0.95$) were unaffected by treatments. Milk protein content was greatest ($P = 0.002$; SEM = 0.04) for cows fed SM1 (2.98%) and SM2 (3.00%), intermediate for those fed MPN (2.93%), and least for ASM (2.89%) and CON (2.87%). Plasma total sulfur AA (TSAA) concentrations (μ*M*) were greatest for cows fed SM1 and SM2 and intermediate for cows fed MPN and ASM compared with cows fed CON (Table 1). Plasma TSAA concentrations were expressed as a percent of total AA; TSAA were regressed on the 0- and 30-g Met treatments. Slopes for SM1, SM2, MPN, and ASM were 0.070 (SE = 0.004), 0.070 (SE = 0.004), 0.020 (SE = 0.004), and 0.015 (SE = 0.005), respectively. The bioavailability of Met (% of total Met), calculated as the slope ratio relative to SM1, were 100, 28, and 22% for SM2, MPN, and ASM, respectively. Based on the published bioavailability of Met in SM2 (80%), the calculated bioavailabilities of Met in SM1, MPN, and ASM were 80, 23, and 17%. There was no difference in Met bioavailability between SM1 and SM2. Bioavailability of Met in MPN and ASM are less than previous estimates compared with Smartamine M.

Key Words: bioavailability, methionine

1598 Impact of three rumen-protected lysine prototypes on dairy cow performance, milk composition, and milk casein.
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Differences in formulation of the protective matrix of lysine products may impact rumen degradation and intestinal availability. The objective was to determine the effect of different formulations of lysine products on milk, milk protein, and casein yields. The study was conducted as a replicated 5 × 5 Latin square design in which 10 lactating, multiparous Holstein cows were assigned to either a lysine-deficient control ration (–Con), lysine-sufficient ration (+Con), or the –Con supplemented with either 1 of 3 different lysine prototypes (Lys1, Lys2, and Lys3; Balchem Corporation, New Hampton, NY). Rations were balanced using AMTS version 4.1.4 assuming 50.0 kg/d milk, 3.70% fat, 3.00% protein, and 740 kg BW. The +Con ration contained 1.60% porcine blood meal and was formulated to have MP, MP methionine, and MP lysine balances of −16.2, +0.1, and +4.9 g/d, respectively. The –Con ration was identical to +Con except that porcine blood meal was reduced to 0.64% with additional soybean hulls being added in its place, and –Con was formulated to have MP, MP methionine, and MP lysine balances of −42.8, +0.1, and −14.5 g/d, respectively. The lysine prototypes were supplemented at 0.21% of ration DM and contained 38% lysine, which were predicted to increase the MP lysine balance to +0.3 g/d. Periods were 14 d, and milk samples were collected on Days 11 to 14 of each period. Data collected during the last 4 d of each period were averaged by cow and analyzed using the Glimmix procedure of SAS. The model included a covariate (data collected during the 2-wk standardization period), fixed effects of treatment and period, and random effects of cow and cow within block. There were no treatment effects on DMI, protein or casein percentage or yield, lactose percentage, milk urea nitrogen (MUN),

or somatic cell count (SCC) (Table 1). There was an effect of treatment on milk yield ($P = 0.02$) and fat yield ($P = 0.03$). Lys1 increased milk yield compared with all other treatments except +Con and Lys1 increased fat yield compared with Lys3 and +Con. The positive milk response for Lys1 compared with –Con suggests that the Lys1 prototype was effective in meeting the lysine deficit in the –Con ration.

Key Words: bovine, lysine, prototype

Table 1. Effect of lysine supplementation on production measures. NO Table provided for placement!

1599 Effects of soybean meal, Fermenten, or expeller soybean meal on milk performance and intake in lactating dairy cattle.

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The objective of this study was to evaluate effects of three different dietary sources of protein on intake, milk performance, and temporal changes in BW and condition score in lactating dairy cattle. Primiparous ($n = 48$) and multiparous ($n = 144$) cows were stratified by milk production and randomly allocated into 12 pens containing 4 primiparous and 12 multiparous cows each. Cattle ranged from 60 to 180 DIM and averaged 712 kg of BW at trial start. Diets consisted of (DM basis) 42% corn silage, 13% alfalfa forage, 20% grain corn, and 25% protein premix containing either soybean meal (Diet A), Fermenten (Diet B), or a expeller soybean meal (Diet C), at a 3.5% inclusion rate. All 3 diets provided a similar level (DM basis) of aNDFom (31%), CP (14.7%), starch (26.2%), and ME (70 Mcal ME/d) as predicted by the CNCPS. The trial consisted of a 2-wk adaptation/covariate period where all cows were fed diet C and covariate measurements were taken. Pens were then randomly allocated to treatments and weekly measurements of milk production, intake, BW, and condition score were taken for 10 wk. All data were analyzed using Proc Mixed in SAS with pen as the experimental unit. In the first 6 wk of the experimental period, an increase in DMI was observed for cows fed diet B compared with cows fed diet A and C (28.1 vs. 26.8 and 26.2 kg/d, respectively; $P < 0.01$). Cows fed diet B made more energy-corrected milk (45.6 kg/d) compared with cows fed diets A and C (44.0 kg/d for both A and C; $P < 0.01$). Milk protein and fat yield was also increased in cows fed diet B. All cows gained condition score over the duration of the experiment; however, cows fed diet A gained 0.03 BCS/wk less than cows fed diets B and C ($P < 0.01$). The results from this experiment demonstrate beneficial milk performance responses to Fermenten when fed with a source of rumen available true protein. Responses are consistent with a potential decrease in ruminal CP degradation as demonstrated by previous research in our lab. Results also demonstrate the value of rumen-degradable protein vs. rumen-protected protein when fed in nitrogen-efficient diets in high-producing dairy cattle.

Key Words: Fermenten, milk performance, nitrogen, rumen degradable protein

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1600 Effect of ruminal bypass lysine on amino acid status, performance, and carcass characteristics of steers fed corn product–based diets.

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Corn and corn coproducts are the predominant sources of protein for feedlot cattle today, making up nearly 100% of diets in the Midwest. However, corn protein is a poor source of lysine, and current NRC models predict that a 45% corn, 30% DDGS, and 20% corn silage diet with 5% mineral supplement is deficient in lysine, despite the fact that the CP content of the diet (15%) exceeds requirements. Therefore, 84 steers were allotted by BW (367 ± 5.6 kg) and breed composition to 3 treatments to determine the effect of ruminal bypass lysine on blood AA, performance, and carcass characteristics. Treatments included a control with no added lysine or urea (Con), a diet that contained 0.5% Lys (AjiPro-L; Ajinomoto Inc., Chicago, IL), and a diet that contained 0.5% urea (urea). The lysine treatment was formulated to deliver 50 g/d of AjiPro-L (10 g/d of lysine). Twenty-eight steers were fed each diet and steers were housed in pens of seven (4 pens/treatment) that were blocked by BW (heavy and light). Steers were implanted with Revalor-XS at feedlot entry and were fed 300 mg of Optaflexx daily during the last 42 d of the study. Steers were slaughtered at a common BW (622 ± 13.8 kg). Data were analyzed as a randomized complete block design using the MIXED procedure of SAS. The model included the random effects of block and pen and the fixed effects of supplement and day as well as the supplement × day interaction. Total plasma AA did not differ among treatments at slaughter ($P = 0.93$); however, tryptophan tended ($P = 0.10$) to be greater (95.9, 87.8, and 103.4 μg/mL for Con, Lys, and urea, respectively) and PUN was ($P = 0.05$) greater (12.4, 12.7, 14.4 mg/dL for Con, Lys, and urea, respectively) for steers fed urea. There was no difference in DMI ($P \geq 0.62$), BW ($P \geq 0.91$), gain ($P \geq 0.73$), or G:F ($P \geq 0.75$) at any time point during the study. Treatment had no effect on HCW ($P = 0.50$), LM area ($P = 0.80$), marbling ($P = 0.93$), or any other carcass parameter ($P \geq 0.43$). In conclusion, it appears that an all corn/corn product diet provides a sufficient amounts of lysine to finishing feedlot cattle and supplemental bypass lysine may not be needed.

Key Words: beef feedlot, bypass lysine, growth

1601 Determining ruminal lysine degradability of a bypass soybean meal product and an encapsulated lysine source. J. M. Prestegaard*[1], A. L. Kenny[1], M. M. Masiero[1], and M. S. Kerley[2], *[1]University of Missouri, Columbia, [2]Division of Animal Sciences, University of Missouri, Columbia*.

A single-flow, continuous culture system was used to evaluate microbial efficiency (MOEFF), CP digestibility, VFA concentration, NH_3 concentration, OM digestibility, and lysine digestibility of a bypass soybean meal product and an encapsulated lysine source. Inoculated fermenters were randomly assigned to 1 of 3 treatments in 2 consecutive replicates (n = 24): a lysine-deficient basal diet (CON) consisting of corn, soybean meal, and corn silage; a lysine-sufficient diet (RP-SBM) containing rumen-protected soybean meal in replacement of soybean meal in the basal diet; and a lysine-sufficient diet (RP-LYS) consisting of CON supplemented with rumen-protected lysine. All treatments were balanced for similar amounts of rumen degradable protein to supply sufficient peptides and NH_3 based on microbial requirements. Fermenters were individually fed at 0800 and 1700 h for 7 d, consisting of a 4-d acclimation period to stabilize the microbial population and a 3-d sampling period. Volatile fatty acid and ammonia concentrations were analyzed in samples taken 0 and 4 h after morning feeding. Effluent was collected, composited, and frozen on the final 3 d of each replicate. Fermenter contents were collected and frozen on the final day of each replicate for bacteria analysis. No differences were observed for OM digestibility, apparent and true CP digestibility, NH_3, acetate, or propionate. In replicate 1, butyrate (mM) was greater (P = 0.01) for CON (13.63) relative to RP-SBM (9.30) or RP-LYS (9.00); however, no differences were observed in replicate 2. For both replicates, MOEFF (g effluent bacterial N/kg OM truly digested) tended to be greater (P = 0.08) in RP-LYS (21.32) than RP-SBM (17.62) and CON (17.49). Dietary lysine (g) was measured to be 0.33, 0.3,4 and 0.43 for CON, RP-SBM, and RP-LYS, respectively. Bypass dietary lysine (g) was lesser (P < 0.01) in RP-LYS (0.06) relative to RP-SBM (0.13) and CON (0.11). Lysine digestibility (%) was greater (P < 0.001) for RP-LYS (85.84) relative to RP-SBM (60.15) or CON (65.73). However, total effluent lysine (g) was statistically similar (P = 0.11) for CON (0.33), RP-SBM (0.36), and RP-LYS (0.33). Bacterial lysine in effluent (g) tended to be higher (P = 0.09) in RPLYS (0.27) relative to RP-SBM (0.23) and CON (0.22). Although dietary lysine in RP-LYS was degraded to greater extent by rumen microbes than in RP-SBM or CON, it appears the rumen microbial population compensated for lysine loss.

Key Words: continuous culture, lysine, rumen fermentation

1602 Effects of rumen-protected lysine and methionine on milk yield and milk composition in lactating Holstein cows fed two different levels of crude protein. A. Ostrensky[1], G. Negro[2], A. M. D. Santos[1], A. Anater[1], D. R. Ribeiro[1], L. F. Greco[3], M. N. Pereira[4], and R. D. Almeida*[2], *[1]Pontifícia Universidade Católica do Paraná, Curitiba, Brazil, [2]Universidade Federal do Paraná, Curitiba, Brazil, [3]Kemin South America, Indaiatuba, Brazil, [4]Universidade Federal de Lavras, Lavras, Brazil*.

Experimental objectives were to evaluate the effects of rumen-protected lysine and rumen-protected methionine (RPLM) supplementation on milk yield and composition of dairy cows. Holstein cows (n = 35) were housed in a free-stall barn and milked twice daily, received bST injections every 10 d, and were paired blocked based on milk yield, days in milk, and lactation order. The treatments consisted on four groups: 1) lower CP without RPLM supplementation (LPXX), formulated to 15.8% CP, 6.63% Lys as percent of MP, and 1.82% Met as percent of MP; 2) lower CP with RPLM supplementation (LPAA), formulated to 15.9% CP, 6.90% Lys as percent of MP, and 2.31% Met as percent of MP; 3) higher CP without RPLM supplementation (HPXX), formulated to 17.4% CP, 6.56% Lys as percent of MP, and 1.80% Met as percent of MP; and 4) higher CP with RPLM supplementation (HPAA), formulated to 17.5% CP, 6.92% Lys as percent of MP, and 2.32% Met as percent of MP. Experimental cows were fed simultaneously twice a day the same basal diet in a TMR and they were supplemented with soybean meal and/or RPLM (Lysipearl and Metipearl; Kemin, Brazil). The experimental design was a 4 × 4 Latin square with 28-d periods. Milk yield and composition were determined in the last 6 d of each period and analyzed using the mixed procedure of SAS containing the effects of milk yield in the covariate period, period, treatments (CP level, AA supplementation, and their interaction), and cow as a random effect. Milk yields were 39.26, 40.16, 39.72, and 40.25 kg/d for LPXX, LPAA, APXX, and APAA, respectively (P = 0.69 for CP level and P = 0.30 for AA supplementation). Cows fed higher CP diets showed higher (P = 0.002) protein content (3.34 ± 0.04%) than animals fed lower CP diets (3.29 ± 0.04%). The HPAA group had a tendency (P = 0.10) to produce more protein yield (1.335 ± 0.03 kg/d) than LPXX (1.283 ± 0.03 kg/d). There were no differences among treatments for all the other parameters: 3.5% fat-corrected milk, energy-corrected milk, milk energy output, fat, lactose, and total solids contents and yields. Increasing CP in the diet resulted in higher protein content in milk.

Key Words: amino acids, crude protein, metabolizable protein

Table 1604.

Table 1- Blood urea concentration and microbial protein syntheses of bulls fed with diet containing different levels of additives.

	Additives (mg/kg DM)						Contrast e P value			
	MON 30				VM	SEM	VM vs MON	L	Q	VM vs VM/ MON
Variables	0	15	25	34	34					
Blood urea (mg/KgPV)	3.23	3.23	2.70	2.87	3.06	0.15	0.41	0.14	0.06	0.39
Microbial protein (g/day)	1068	972	790	1141	862	85.05	0.12	0.39	0.61	0.04

1603 Immunometabolic gene expression in blood neutrophils (PMN) in Holstein dairy cows supplemented with rumen-protected methionine or rumen-protected choline during the peripartal period. P. Montagner[1], Z. Zhou*[1], D. N. Luchini[2], J. J. Loor[1], and M. Nunes Corrêa[3], *[1]University of Illinois, Urbana, [2]Adisseo S.A.S., Alpharetta, GA, [3]Federal University of Pelotas, Pelotas, Brazil*.

Objectives of this study were to evaluate mRNA expression of 30 genes related to neutrophil adhesion, chemotaxis and migration, oxidative stress, Toll-like receptor pathway, methionine cycle, and glutathione metabolism in response to rumen-protected methionine (MET) and choline (CHO) supplementation during the peripartal period. Forty multiparous Holstein cows were used in a randomized complete block design with 2 × 2 factorial arrangement of MET and CHO level (with or without). Treatments were control (CON), no MET or CHO; CON + MET (SMA); CON + CHO (REA); and CON + MET + CHO (MIX). From −21 d (close-up) to 30 d after calving, cows received the same diet (1.52 Mcal NE_L/kg DM) from close-up to calving. From calving to 30 d, cows were on the same diet (1.71 Mcal NE_L/kg DM) and continued to receive the same treatments through 30 d. MET supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow per day. Blood neutrophils were isolated on −10, 8, and 29 d relative to calving for quantitative PCR analysis. Data were analyzed as a factorial design with repeated measures using PROC MIXED in SAS. As expected, regardless of treatments, highest expression of proinflammatory genes (*TNFα* and *BPI*) ($P < 0.05$) were observed on 8 d, suggesting more pronounced inflammatory status compared with −10 and 29 d relative to parturition. The main effect of CHO toward greater ($P = 0.01$) expression of *cell adhesion molecule 1* (*CADM1*) and interactions of CHOL × day for PMN adhesion–related genes (*SELL*, *CXCR2*, and *ICAM1*) suggest activation of PMN in CHOL cows. In contrast, MET supplementation led to lower ($P = 0.02$) expression of *ITGAB2*, suggesting less activated status of PMN in MET cows. CHO cows also tend to have greater ($P = 0.06$) *IL10* compared with other treatments. Although *IL-10* was not changed by MET, main effect of MET was observed for lower *IRAK1*, suggesting a less pronounced inflammation in MET cows. Both *MPO* and *SOD2* were greater in MET cows whereas the main effect of CHO was not detected for *SOD2*; such changes likely were associated with reactive oxygen production in PMN. However, PMN functional study is required to confirm the proposed relationship. Overall, data indicate neutrophil gene network respond differently to peripartal supplementation with MET or CHO. Additional studies to examine the methionine and choline mechanism of action in PMN appear warranted.

Key Words: choline, methionine, transition cow

1604 Estimation of microbial protein and blood urea of confined bulls fed with diets containing virginiamycin and monensin sodium. F. R. Camilo*[1], A. M. Mobiglia[1], J. J. D. R. Fernandes[2], V. R. M. Couto[3], F. D. D. Resende[4], G. R. Siqueira[4], and R. K. Grizotto[5], *[1]CAPES Foundation, Ministry of Education of Brazil, Brasilia, Brazil, [2]UFG, Goiania, Brazil, [3]Universidade Federal de Goiás, Goiânia, Brazil, [4]APTA – Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [5]APTA – Agência Paulista de Tecnologia dos Agronegócios (São Paulo Agency of Agribusiness Technology), Colina, Brazil*.

The propose of this trial was to evaluate the effects of diets containing isolated and combined levels of virginiamycin (VM) and monensin sodium (MON) on microbial protein and blood urea of confined Nellore bulls. Fifteen Nellore bulls (536 kg of BW) with ruminal cannula were used in a randomized complete block design with five treatments in three replicates. The blocks were defined by initial BW. Treatments were defined by levels of VM and MON (mg/kg of DM) as follows: 30MON, 15VM+30MON, 25VM+30MON, 34VM+30MON, and 34VM. Animals were fed ad libitum twice daily with isonitrogenous and isoenergetic diets, with a 88:12 concentrate:roughage (sugarcane bagasse) ratio. The animals were kept in feedlot in individual pens for 28 d. The blood was

collected from the jugular vein before feeding and 2 and 3 h after feeding on the Days 0, 7, 14, 21, and 28. Spot sampling technique was realized on 28 d to estimate the daily excretion urinary of purine derivatives and then estimate microbial protein production. Data are shown in Table 1. There were effects ($P < 0.10$) on blood urea concentration between treatments and grams per day microbial protein for 34VM+30MON and 34VM treatments. The association of VM and MON resulted in greater microbial protein syntheses and effect quadratic in blood urea. In conclusion, the use of 34VM+30MON may increase of production of microbial protein, and blood urea resulted in lower concentration using 25VM+30MON on diet. Supported by Phibro/Minerva/FAPEG.

Key Words: additives, feedlot, virginiamycin

1605 Rumen fluid metabolomics analysis associated with feed efficiency on crossbred steers.

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The rumen plays a central role in the efficiency of digestion in ruminants. To identify potential differences in rumen function that lead to differences in feed efficiency, rumen metabolomic analysis by ultra-performance liquid chromatography/time-of-flight mass spectrometry and multivariate/univariate statistical analysis were used to identify differences in rumen metabolites. Individual feed intake and BW gain was measured on 144 crossbred steers for 105 d on a high-concentrate ration. Eight steers with the greatest ADG and 8 steers with the least ADG within 0.32 SD of the mean DMI were selected for the study. The DMI did not differ between ADG groups (10.10 ± 0.05 kg/d; $P = 0.41$); however, ADG was greater ($P < 0.01$) in the greatest ADG group (1.96 ± 0.02 kg/d) than the least ADG group (1.57 ± 0.02 kg/d). Rumen fluid was collected at slaughter. Metabolite identification was obtained through a mass-based bovine database search. Verification of the identities of selected metabolites was conducted by comparing tandem mass spectrometry fragmentation patterns with those from authentic compounds. Principal component analysis and *t* test on rumen fluid metabolic profile identified 90 metabolites ($P < 0.10$) that segregated with ADG group. These metabolites were primarily involved in linoleic and α-linolenic metabolism (impact value 1.0 and 0.75, respectively; $P < 0.05$); both pathways were downregulated in the greatest ADG group compared with least ADG group. Ruminal levels of four metabolites associated with ADG group were screened by receiver operating curve analysis to test their efficacy as biomarkers for ADG. Subsequently, a partial least square discriminate analysis was used to develop a predictive model to verify and optimize the exclusive biomarkers. The combination of pentadecanoic acid, eicosanoic acid, linoleic acid, and α-linolenic acid produced a good predictor of feed efficiency, AUC (95% CI) = 0.901 (0.67–1.0), representing 87.5% of sensitivity and 75% of specificity. All four metabolite levels decreased in greatest-ADG animals vs. least-ADG animals in the rumen fluid. As well, higher fold levels of small molecules in the rumen fluid were found in greatest ADG vs. least ADG ($P < 0.05$), such as folic acid (13%), malonyl-CoA (30%), pyroglutamic acid (57%), oleamide (13%), and alloxan (23%; glucose analog). This study indicates that metabolomics based on ruminal fluid can yield metabolites that can predict and classify feed efficiency. Furthermore, on the basis of the pathway analysis of biomarkers, ruminant fluid metabolomics profile give new insight into the physiology of feed efficiency. The USDA is an equal opportunity provider and employer.

Key Words: average daily gain, dry matter intake, ultra-performance liquid chromatography quadrupole time of flight tandem mass spectrometry

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1606 Enrichment of cattle rumen with bison rumen contents improves nitrogen digestion.

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This study investigated if the transfer of rumen contents from bison to cattle enhances cattle total tract fiber digestion. The experiment was a repeated measures design with two rumen transfers using 16 rumen cannulated Angus × Hereford cross beef heifers (461 ± 21 kg BW). Heifers were adapted to a barley straw diet (70/30% of DM, forage/concentrate) for 28 d before the experiment. After 46 d, 70% of rumen contents were removed from each heifer and replaced with mixed rumen contents collected after slaughter from 36 bison. This procedure was repeated 14 d later. Intake, chewing activity, apparent total tract digestion, ruminal passage rate, VFA, ammonia N, and protozoa counts were measured before the first transfer and 2 wk after the second transfer. The DMI increased ($P = 0.04$) from 1.39 to 1.50% of BW after the rumen transfers. Total chewing time did not change ($P = 0.74$; 13.9 h/d) but the chewing time per kilogram DM and NDF intake was reduced ($P < 0.001$) after rumen transfers. The DM, OM, NDF, and ADF digestibility were not affected ($P \geq 0.44$) by rumen transfers, but the total N digestibility was improved ($P < 0.001$; 68.3 vs. 70.4%). Microbial N flow (g/d) increased ($P = 0.03$); however, the efficiency of microbial N synthesis (g/kg of digested OM) was not improved ($P = 0.77$). No differences ($P > 0.14$) were observed for the ruminal rate of passage of fluids and solids. Ruminal ammonia N (m*M*) was not affected ($P = 0.77$) before feeding by rumen transfers but was greater ($P = 0.05$) 6 h after feeding. Total VFA (m*M*) and the proportion of butyrate

Table 1607.

Effects of nitrate and monensin on rumen fermentation parameters.

Daily means	0 NIT		1.25 NIT		2.5 NIT		SEM	*P*-value[1]		
	0 MON	4 MON	0 MON	4 MON	0 MON	4 MON		NIT	MON	NIT × MON
Total gas (L)	3.03	3.12	2.69	2.51	3.34	2.82	0.20	0.02	NS	NS
CH_4, mM/d	40.90	29.40	31.18	24.58	26.20	23.79	1.79	<0.01	<0.01	0.04
CO_2, mM/d	97.36	93.17	83.79	80.45	87.96	98.09	5.06	0.02	NS	NS
N_2O ($x10^{-4}$), mM/d	48	54	45	37	54	39	3.8	0.03	0.08	0.02
DMD, (g/100g DM)	69.26	69.12	69.31	69.13	68.85	69.13	1.36	NS	NS	NS
NH_3-N, (mg/dL)	23.50	22.0	17.28	18.33	15.72	15.73	1.28	<0.01	NS	NS
Protozoa, cell/mL ($x10^3$)	4.90	3.89	4.90	3.91	3.95	4.18	0.83	NS	NS	NS

[1] NS indicates P>0.10.

increased ($P < 0.001$); however, acetate and the C2:C3 ratio decreased ($P \leq 0.02$) before and 6 h after feeding as a result of rumen transfers. As a result of rumen transfer, total protozoa counts and the proportion of *Ostracodinium* increased ($P < 0.001$) whereas *Entodinium* decreased ($P < 0.001$) before and at 6 h after feeding. Overall, cattle rumen inoculation with bison rumen contents improved diet protein digestion; however, DM and NDF digestibility were not affected.

Key Words: bison, digestibility, rumen inoculum

1607 Effect of nitrate, monensin, and the combination of additives on rumen fermentation using a semicontinuous culture system. M. Capelari*[1], K. A. Johnson[2], B. Latack[1], J. Roth[1], and W . Powers[1], *[1]Michigan State University, East Lansing, [2]Washington State University, Pullman*.

A 37-d experiment was conducted to investigate the effect of nitrate (NIT) and monensin (MON) on rumen fermentation using a semicontinuous culture system. We hypothesized that the combination of additives would reduce CH_4 emissions beyond that of either additive alone, without affecting production parameters. Additives (0, 1.25, and 2.5% diet DM of NIT; 0 and 4 mg/L of MON) were tested alone and in combination (NIT+MON; 6 total treatments; 3 replicates/treatment). Buffer and water were added to eighteen 2.2-L vessels on d −8 (1.2 L of a 50:50 mixture). The first 7 d (d −7 to 0) served as a steady state phase. On d −7, rumen fluid was pooled from 5 nonadapted lactating cows fed a 50:50 forage to concentrate diet and filtered through 2 layers of cheesecloth, and 1 L was transferred to each vessel along with 30 g of solid rumen content and 20 g of a basal diet (50:50 forage to concentrate) in a 8 by 20 cm nylon bag (50 μm mesh size). On d −6, 20 g of the basal diet replaced the solid rumen content bag, and from this point onward, 2 bags, each containing 20 g of the treatment diet, were always present in the vessels for 48 h. Buffer was infused at a constant rate (70 mL/h) throughout the experiment with a peristaltic pump. Gas production was measured daily. Twice weekly, DM disappearance (DMD), pH, and ammonia nitrogen (NH_3–N) were measured. Treatment did not affect DMD (69.13 g/100 g DM; $P > 0.05$). Compared with the negative control treatment, addition of NIT reduced total gas production (2.84 vs. 3.03 L/d; $P = 0.02$), CH_4 production (28.65 vs. 40.9 m*M*/d; $P < 0.01$), and CO_2 production (87.57 vs. 97.36 m*M*/d; $P < 0.05$). Compared with the negative control, addition of MON reduced CH_4 production (29.4; $P < 0.01$). Further CH_4 reduction, compared with the negative control, was observed when NIT+MON was added (24.31 vs. 40.9 m*M*; $P = 0.04$). No treatment effects were observed for pH (7.1) or protozoa count (4.3×10^3). Addition of NIT reduced NH_3–N (16.65 vs. 23.5 mg/dL; $P < 0.01$). The combination of NIT+MON enhanced reduction of CH_4 production in a semicontinuous culture fed a 50:50 forage:concentrate diet, with no detriment to DMD.

Key Words: in vitro, methane, protozoa

1608 Metagenomic census of predominant *ureC* genes of ureolytic bacteria in the rumen of dairy cows.
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Rumen ureolytic bacteria elaborates urease to break down urea to ammonia for the synthesis of microbial protein, yet little is known about the diversity and distribution of rumen ureolytic microorganisms. The urease *ureC* gene has been chosen as the target gene for analysis of the urea-degrading microorganisms in various environments. This research investigated the predominant *ureC* genes of the ureolytic bacteria in the rumen of dairy cows using high-throughput sequencing. Six dairy cows with rumen fistulas were assigned to a two-period crossover trial. One group (Ctrl; $n = 3$) were fed the diet without urea and the other (Urea; $n = 3$) were fed rations plus 180 g urea/cow per day at three separate times. Rumen bacterial samples from liquid, solid, and wall fractions were collected for *ureC* gene amplification and sequencing using Miseq. Results showed that supplementation of urea did not change the rumen *ureC* gene abundance, whereas the wall-adherent bacteria (WAB) revealed a distinct ureolytic bacterial profile compared with solid-adherent bacteria (SAB) and liquid-associated bacteria (LAB). The *ureC* gene diversity and richness of rumen WAB was lower than that in the SAB and LAB ($P < 0.05$). The rumen predominant *ureC* gene operational taxonomic units (OTU) were gathered in clusters II, IV, and VI. Operational taxonomic units 5, 6, 15, 18, 12, 27, and 25 in the WAB; OTU 3, 4, and 1 in the LAB; and OTU 13, 19, and 21 in the SAB were predominant in each fraction, respectively. Most of the predominant OTU showed low similarity (72–91%) to the known rumen bacteria. The results suggested that the rumen of dairy cows harbors plenty of unidentified ureolytic bacteria. This survey contributes new data to existing *ureC* gene information relating to the ureolytic microbial community in ruminants and provides a basis for obtaining the regulation targets of ureolytic bacteria to mitigate urea hydrolysis in the rumen.

Key Words: diversity, rumen, *ureC* genes

1609 Rumen bacterial communities continue to shift five weeks after switching diets from conserved forage to pasture.
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Bacterial community structure is known to shift as a result of diet changes, but it is not known how long it takes for the bacterial populations to stabilize. The objective of this study was to characterize the weekly dynamics of rumen bacterial community composition of cows transitioning from an indoor diet, comprising conserved forage (CF), to a pasture. Five lactating Holstein dairy cows, maintained on a CF diet during the winter season, were switched to a pasture and followed for 5 wk. Individual rumen digesta samples were collected via esophageal intubation on wk −1, 1, 2, 3, 4, and 5 relative to the diet switch. Microbial DNA was extracted and the V1 to V3 region of the 16S rRNA gene was amplified. Sequence reads were obtained using Illumina MiSeq (version 3) and sequences were analyzed using MOTHUR (version 1.36.1). Bacterial densities ($\log_{10}$ 16S rRNA gene copies/mL rumen digesta) were quantified by real-time PCR. Data were analyzed using a repeated measures ANOVA in SAS (version 9.4). By wk 3 on pasture, bacterial densities in rumen digesta were higher when compared with CF (8.9 vs. 9.4, 9.4, and 9.5 $\log_{10}$ copies/mL for wk −1, 3, 4, and 5, respectively; $P < 0.01$). Bacteroidetes was the predominant phylum, accounting for 48 to 81% of total bacteria, followed by Firmicutes (16–47%) and TM7 (0–4%). *Prevotella* was the predominant genus of the Bacteroidetes phylum. By wk 5 on pasture, a higher abundance was observed of both bacteria of the phylum Bacteroidetes (75.3%) and *Prevotella* species (72.7%) when compared with CF (65.4 and 58.3% for Bacteroidetes and *Prevotella*, respectively; $P < 0.05$). The genus *Ruminococcus* was more abundant during wk 1 and 2 after the diet switch (3.4% for both weeks), when compared with 2.0% on wk −1 of CF ($P < 0.01$). Similarly, bacteria in the family Lachnospiraceae were more abundant during wk 1 and 2 (8.4 and 8.2%) and then became less abundant by wk 5 of cows grazing pasture (3.1%) when compared with wk −1 of cows on a CF diet (5.4%; $P < 0.05$). *Butyrivibrio* species were more abundant on wk 4 after the diet switch (3.6 vs. 1.7% for wk 4 of pasture and wk −1 of CF, respectively; $P < 0.05$) and then, on wk 5, returned to an abundance similar to CF (1.5%). In conclusion, rumen bacterial communities are highly dynamic after a diet switch and did not stabilize within 5 wk of cows grazing pasture.

Key Words: bacterial diversity, dairy cow, Illumina MiSeq

1610 Metabolome and microbiome associations after a grain and sugar challenge. H. M. Golder*[1,2], S. Denman[3], C. McSweeney[3], and I. J. Lean[1,2], *[1]Scibus, Camden, Australia, [2]University of Sydney, Camden, Australia, [3]CSIRO Animal, Food and Health Services, Queensland Bioscience Precinct, St. Lucia, Australia*.

Holstein heifers ($n = 40$) were allocated to 5 groups: 1) control (no additives), 2) virginiamycin (10 g/head·d; VM), 3) monensin (2.2 g/head·d) + tylosin (0.44 g/head·d; MT), 4) monensin (2.5 g/head·d) + yeast (Levucell SC Direct; 25 g/head·d; MY), and 5) sodium bicarbonate (200 g/head·d) + magnesium oxide (30 g/head·d; BUF). Heifers were fed twice daily a 62% forage:38% concentrate total mixed ration at 1.25% of BW DM/d for a 20-d adaptation period with their additive or additives. Fructose (0.1% of BW/d) was added to the ration for the last 10 d of adaptation. On d 21, heifers were challenged with a ration consisting of 1.0% of BW DM wheat and 0.2% of BW fructose plus their additive or additives. Stomach tube rumen samples were collected 3.6 h after consumption of the challenge ration and analyzed for pH; ammonia, d- and l-lactate, and VFA; and histamine concentrations and total bacteria. The 16S rRNA gene spanning the V4 region was PCR amplified and sequenced using an Illumina MiSeq platform. Sequence data was analyzed using the Quantitative Insights into Microbial Ecology software package (QIIME). Coinertia analysis, including Monte Carlo estimations (Ade4 package, R software) was conducted using operational taxonomic units (OTU) and rumen fermentation data from each group. A linear model was fitted to the OTU data and pairwise comparisons were performed to examine the significantly different OTU between groups ($q < 0.1$). Coinertial analysis explained 31.9% of the total variation in the associations among rumen fermentation products, bacterial community composition, and groups. Histamine and valerate concentrations explained the most variation in the microbiome. Contrasts between the control vs. BUF and control vs. MT groups showed these groups had the lowest number of significantly different OTU (14 and 23 OTU, respectively), indicating they may have similar microbiomes. The MLY vs. BUF had the highest number of significantly different OTU (826 OTU), suggesting their microbiomes had the greatest difference. New reference OTU14997 from the *Streptococcus* genus was more abundant in the control vs. MLY, VM vs. MLY, and BUF vs. MLY groups. New reference OTU20477 from the *Lactobacillus* genus was more abundant in the control vs. VM, MLY vs. VM, and BUF vs. VM groups. *Lactobacillus ruminis* was also more abundant in the MLY vs. VM and BUF vs. VM groups. *Lactobacillus mucosae* was more abundant in the BUF vs. VM group. The feed additives appeared to influence different microbial populations after the challenge.

Key Words: coinertia, feed additives, ruminal acidosis

1611 Ruminal dosing with *Megasphaera elsdenii* and strain persistence are associated with milk fat depression in Holstein cows. F. Cacite[1] and P. J. Weimer*[2], *[1]Federal Univ. of Mato Grosso, Cuiabá, Brazil, [2]USDA-ARS, Madison, WI*.

The objectives of this study were 1) to examine the effects of ruminal dosing of cows with the bacterium *Megasphaera elsdenii* (ME) on milk fat production and 2) to examine the persistence of the dosed species in the rumen. Nine cows (51–201 d in milk [DIM]) were divided into 3 groups balanced for DIM, milk production, and milk fat content and were fed the same TMR that contained corn silage, finely ground high-moisture corn, alfalfa haylage, corn oil, and monensin. The three treatments included ruminal dosing with pure cultures of one of two strains of ME (4257 and 5045, at an average of 1.9×10^{12} cells/dose) recently isolated from milk fat-depressed cows and a control dosed with sterile culture medium. To encourage persistence of ME, approximately 40% of the ruminal contents from each cow were removed just before dosing, and 108 g of sodium lactate was added for all treatments, on each of the 3 dosing days spaced 48 h apart. Milk production and composition were determined from 3x-daily milk samples collected from 8 d before first dosing to 21 d after first dosing, and ruminal fluid samples were collected for bacterial community analysis via 16 S rRNA metagenomics on the Illumina MiSeq platform. The dosing procedures resulted in a transient ruminal lactate concentration of up to 46 m*M* and a subsequent decrease in acetate:propionate ratio ($P < 0.0001$) as the lactate was metabolized. Both milk fat percentage and yield substantially varied by cow ($P < 0.001$) and were decreased ($P < 0.01$) during the week of dosing, when ME abundance was high. Data analysis of 112 ruminal samples using PROC REG of SAS revealed a negative correlation between ME relative abundance and milk fat percentage in cows dosed with ME strain 4257 ($r^2 = 0.46$, $P < 0.0001$) but not in cows dosed with strain 5045 ($r^2 = 0.056$, $P = 0.146$). Control cows dosed with lactate but not an ME inoculum displayed weak negative correlation between milk fat percentage and ME abundance ($r^2 = 0.183$, $P = 0.007$), suggesting that the native ME populations were also associated with reduced fat content. Similar results were observed for fat yield. Neither *Propionibacterium acnes* nor *Eubacterium pyruvativorans* were detected in even the most highly fat-depressed cows. The data confirm previous reports of a strong relationship between ME abundance and milk fat depression but suggest that the effect may be ME strain dependent.

Key Words: *Megasphaera*, milk fat, ruminal microbiome

1612 Potential for live yeast culture to enhance nitrate mitigation of methanogenesis in Jersey dairy cattle. R. A. Meller[1], J. M. Ashworth[1], A. M. Gehman[2], and J. L. Firkins*[1], [1]*The Ohio State University, Columbus,* [2]*Alltech, Inc., Nicholasville, KY.*

Concern over the environmental impact of dairy production has stimulated research to decrease enteric CH_4 production. One approach is feeding the electron acceptor NO_3 to be reduced by bacteria such as the selenomonads, thus outcompeting methanogens for aqueous H_2. We hypothesized that a live yeast culture (Yea-Sacc [YS]; *Saccharomyces cerevisiae*; Alltech, Inc.) would stimulate the reduction of NO_3 completely to NH_3 and thereby improve the ratio of CH_4 emission:energy-corrected milk production while decreasing blood methemoglobin concentration. Twelve lactating Jersey cows (8 multiparous and noncannulated and 4 primiparous and ruminally cannulated) were used in a replicated 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments. Cattle were fed diets either containing 1.5% NO_3 (from calcium nitrate) after an adjustment period or a control diet (containing urea isonitrogenous to NO_3) and were given a top-dress of ground corn without or with YS. All noncannulated cows were spot measured for CH_4 emission by mouth using GreenFeed (C-Lock Inc., Rapid City, SD). The main effect of NO_3 decreased ($P < 0.01$) methane 17% but decreased ($P < 0.01$) DMI by 10% (from 19.8 to 17.8 kg/d) such that the CH_4:DMI ratio tended ($P = 0.14$) to decrease by 8%. Milk and milk fat production were not affected, but NO_3 decreased ($P < 0.01$) milk protein from 758 to 689 g/d. Ruminal pH was decreased more after feeding diets without NO_3, and the acetate:propionate ratio was greater for cows fed NO_3, especially when combined with YS (interaction, $P = 0.01$). Others have noted lower palatability and lower consumption per meal, which is consistent with our observations. Methemoglobin was higher ($P = 0.01$) for cattle fed NO_3 than those fed urea but were still low (1.5 vs. 0.5% and only once exceeded 5%), documenting minimal risk for NO_2 accumulation at our feeding levels of NO_3. Although neither apparent OM nor NDF digestibilities were affected ($P > 0.15$), apparent N digestibility had an interaction ($P = 0.06$) such that, compared with those fed either diet without NO_3, N absorption was slightly higher for those fed NO_3 without YS but slightly lower for those fed NO_3 with YS. Under the conditions of this study, NO_3 did mitigate ruminal methanogenesis but was not particularly effective after considering that it depressed DMI and milk protein. Based on few interactions detected, YS had a minimal role in attenuating either of these responses.

Key Words: live yeast culture, methane, nitrate

1613 Inhibition of methanogenesis by nitrate, with or without defaunation, in continuous culture. B. A. Wenner*, B. K. Wagner, Z. Yu, N. St. Pierre, and J. L. Firkins, *The Ohio State University, Columbus*.

With regard to the focus of methane (CH_4) mitigation in ruminant production systems, nitrate (NO_3) serves as an alternative sink for aqueous hydrogen [H_2(aq)] accumulating in the rumen, producing ammonium via NO_3 reduction pathways and thereby decreasing CH_4 production. Defaunation has also been correlated in meta-analyses with decreased methanogenesis. We hypothesized defaunation might increase the CH_4 mitigation effect of NO_3 by removal of a symbiotic source of substrate to methanogens. In the present study, we applied a 2 × 2 factorial treatment arrangement in a 4 × 4 Latin square design to continuous culture fermenters ($n = 4$). Treatments were control ($-NO_3$) vs. nitrate ($+NO_3$; 1.5% of diet DM), factorialized with control (faunated [FAUN]) vs. defaunated (DEF). Fermenters were fed once daily (40 g DM; 50:50 forage:concentrate diet); four periods lasted 11 d with 3 d of sample collection. Buffer dilution and solids passage rate were maintained at 7.0 and 5.0%/h, respectively. There were no main effects of DEF or interaction of faunation status with addition of NO_3 ($P > 0.05$). The main effect of $+NO_3$ increased ($P < 0.05$) H_2(aq) compared with $-NO_3$ by 11.0 μM. The main effect of $+NO_3$ also decreased ($P < 0.05$) daily CH_4 production compared with $-NO_3$ by 8.17 mmol CH_4/d. Because there were no treatment effects on NDF digestibility ($P > 0.10$), the main effect of $+NO_3$ also decreased ($P < 0.05$) CH_4 production compared with $-NO_3$ by 1.43 mmol CH_4/g NDF digested. There were no effects of treatment ($P > 0.10$) on other nutrient digestibilities, N flow, or microbial N flow per gram of nutrient digested. These data support the existing literature that NO_3 incorporation in the diet can decrease the methanogenesis by dairy cattle. More importantly, methanogens are not necessarily inhibited by defaunation in a highly reduced environment. However, practical considerations such as nitrite toxicity and on-farm dietary adaptation to NO_3 should be considered before implementing this practice in U.S. dairy production systems.

Key Words: defaunation, methane, nitrate

1614 Does weaning age affect the development of ruminal and fecal microbiomes in dairy calves?
S. J. Meale[1], S. Li[2], P. Azevedo[2], H. Derakhshani[2], J. C. Plaizier[2], M. Steele*[3], and E. Khafipour[2], *[1]UMR Herbivores, INRA, Vetagro Sup, Saint-Genès-Champanelle, France, [2]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*.

Despite the advantages of feeding an elevated plane of nutrition to preweaned calves, this feeding strategy may increase a calf's susceptibility to depressed growth during weaning. We hypothesized that weaning at an earlier age would result in a more rapid shift in gut microbiota and consequently be the cause of this growth depression. Therefore, our study examined the effects of weaning age on ruminal and fecal microbiomes in Holstein calves fed an elevated plane of nutrition before weaning. Twenty female Holstein calves were randomly assigned at birth to be weaned at 6 (early [EW]) or 8 (late [LW]) wk. Milk replacer (150 g powder/L water) was offered at 1.2 kg/calf per day in 2 meals until a 1-wk step-down. Rumen fluid and feces were sampled at wk 5, 7, and 9, representing EW5, EW7, EW9, LW5, LW7, and LW9. Deoxyribonucleic acid was extracted, and the V4 region of the 16S rRNA bacterial gene was amplified and subjected to paired-end Illumina sequencing. The output paired-end reads were merged using the PANDASeq assembler, analyzed using QIIME, and aligned to the Greengenes database. Alpha-diversity of bacterial communities was calculated using different richness estimators. Differences in β-diversity of microbiota across treatments and age were tested using PERMANOVA. Alpha-diversity indices did not differ ($P > 0.05$) across weaning age × week in feces. However, differences ($P < 0.05$) between EW5 and EW7 calves were observed in the rumen for Shannon and inverse Simpson indices. Beta-diversity of both rumen and fecal microbiota differed ($P \leq 0.04$) between weaning age × week, indicating a more gradual shift in late-weaned calves toward a postweaned state, compared with an abrupt shift in early-weaned calves. Bacteroidetes was the dominant ruminal phyla in preweaned calves, decreasing in abundance ($P = 0.02$) after weaning, regardless of the age of weaning. A corresponding increase ($P \leq 0.09$) in Firmicutes at weaning resulted in it becoming the dominant ruminal phyla in postweaned calves. The opposite shift in dominance was observed in feces where Firmicutes was dominant before weaning and Bacteroidetes was dominant in postweaned calves. These two phyla accounted for an average 86% of total ruminal or fecal sequences regardless of age or treatment. These results indicate that late weaning at 8 wk facilitates a more gradual shift in microbiota toward a postweaned state compared with early weaning at wk 6. Hence, weaning later could reduce the adverse effects caused by feeding a high plane of nutrition before weaning.

Key Words: calves, feces, microbiome, rumen, 16S ribosomal ribonucleic acid gene sequencing, weaning

1615 Analysis methods differ in recovery of microbial glycogen. M. B. Hall*, *U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI.*

Microbial glycogen is an 1,4-,1,6-α-glucan produced from carbohydrates and stored within bacterial and protozoal cells. Enyzmatic analysis of glycogen in bacteria requires lysis of cells to make glycogen available to enzymatic attack. Lysis is typically performed with alkaline treatment. The objective of this study was to compare the detection of corn starch and of α-glucan in a fermentation pellet by 3 lysis methods from the research literature: 30% KOH boiled for 3 h (30%K), 0.2 *N* NaOH boiled 15 min (0.2N), and 0.31 *N* NaOH at room temperature for 15 min (0.31N). Fermentation pellets were prepared in an in vitro fermentation with mixed ruminal microbes in Goering and Van Soest medium, with 3 g/L of glucose, fermented for 2 h. Each fermentation vessel was quantitatively transferred into a centrifuge tube and centrifuged at 13,000 × *g* for 45 min at 5°C. Supernatants were discarded. Pellets were resuspended in 0.9% saline and recentrifuged. Supernatant was discarded and pellets were frozen at −20°C. As per individual protocols, 30%K and 0.2N were performed on undried pellets transferred into 50-mL beakers and 0.31N was performed on freeze-dried fermentation pellets. Samples were analyzed in duplicate in 2 analytical runs on 2 separate days in a randomized complete block design with fermentation pellet as the experimental unit. The statistical model for each substrate included method and fermentation run as a random variable. After incubation with alkali, all samples were neutralized with acid, and acetate buffer was added to bring the pH to 4.9 to 5.0. The 30%K and 0.2N samples received 0.1 mL of heat-stable α-amylase and 200 U of amyloglucosidase and were incubated for 2 h at 50°C. 0.31N received 0.25 mL Hazyme DCL enzyme preparation and was incubated for 16 h at 55°C. After bringing samples to volume with distilled water, samples were centrifuged to clarify and the supernatant was analyzed for glucose by a glucose oxidase–peroxidase assay. Alpha-glucan was expressed as glucose × 0.9. Recovery of corn starch was 96.7, 95.8, and 91.6% with 0.2N and 0.31N greater than 30%K, respectively ($P < 0.01$). Alpha-glucan in fermentation pellets was 29.6, 29.8, and 26.0 mg with 0.2N and 30%K greater than 0.31N, respectively ($P < 0.03$); 0.31N gave recoveries 87 to 88% of the other treatments. The pattern of starch recovery did not reflect that of microbial α-glucan recovery. With the alkaline lysis methods tested, a boiling treatment appears to be necessary for greatest microbial glycogen recovery.

Key Words: bacteria, glycogen, rumen, starch

Table 1616.

Measure	LoN-Glc	LoN-Lac	HiT-Lac	HiU-Lac
6 h Residual carbohydrate				
Glc or Lac, mg	8.28	31.0	18.9	34.3
Detected maxima				
Microbial N, mg	2.05	0.66	1.62	1.22
Glycogen, mg	18.5	0.77	1.30	1.22
Organic acid carbon, mg	19.6	16.3	19.5	11.9

1616 Utilization of lactose by mixed ruminal microbes is affected by nitrogen type and level and differs from utilization of glucose. M. B. Hall*, *U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI*.

The objective of this study was to evaluate the effects of providing lactose (Lac) at differing nitrogen (N) levels and types and glucose (Glc) at a low N level on products formed and substrate utilized by mixed ruminal microbes. The 3 N treatments were applied via modification of Goering and Van Soest medium: LoN (60% of enzymic digest of casein removed; 300 mg N/L) and HiU or HiT with urea or an enzymic digest of casein, respectively, added to LoN to give 451 mg N/L. Glucose and Lac were added at 3 g/L (79.5 mg/fermentation vial). Two replicated in vitro fermentations with mixed ruminal microbes were performed. Inoculum donors were 2 ruminally cannulated cows individually provided with 200 g each of Lac and Glc per day via their diets for 14 d before the fermentations. Vials, the experimental units, were destructively sampled hourly from 0 through 6 h of fermentation. Data were analyzed as a randomized complete block design. Organic acid carbon is the sum of carbon in acetate, propionate, butyrate, valerate, and lactate. Detected maxima and endpoints were analyzed with the factors treatment and fermentation run (random variable) in the statistical model. Orthogonal contrasts of Glc vs. all Lac, Lac LoN vs. HiN, and Lac HiT vs. HiU were evaluated. Significance was declared at $P < 0.05$ and a tendency was declared at $0.05 < P < 0.10$. Glucose was utilized more rapidly than Lac, giving less residual Glc than Lac at 6 h ($P = 0.02$); HiT tended to have a lower value than HiU at 6 h ($P = 0.07$). Maximum detected glycogen was greater for Glc than for all Lac ($P < 0.01$), which did not differ from each other ($P > 0.66$). Maximum detected organic acid carbon values did not differ among treatments, except for a tendency for a greater amount with HiT than with HiU ($P = 0.06$). Maximum detected microbial N accumulation (a proxy for cell growth) was greater for Glc than for Lac ($P = 0.04$) and tended to be greater for Lac with HiN than with LoN ($P = 0.07$). Rumen microbes utilize Glc and Lac differently; N level and type alters utilization of Lac.

Key Words: fermentation, lactose, rumen

1617 Effect of dietary energy source and level on rumen bacteria community in lactating dairy cows. D. Bu*[1,2,3], S. Li[4], Z. Yu[5], S. Gao[1], L. Ma[1], X. Zhou[6], and J. Wang[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P. R. China, [2]CAAS-ICRAF Joint Lab on Agroforestry and Sustainable Animal Husbandry, World Agroforestry Centre, East and Central Asia, Beijing, P. R. China, [3]Hunan Co-Innovation Center of Animal Production Safety, CICAPS, Changsha, P. R. China, [4]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [5]The Ohio State University, Columbus, [6]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, P. R. China*.

Increased dietary energy level and degradation rate are beneficial to rumen microbial protein synthesis and milk production by dairy cattle. This study aimed to examine the effects of dietary energy source and level on rumen bacterial community in lactating dairy cows. Eight primiparous Chinese Holstein cows were used in a replicated 4 × 4 Latin square design. Cows were allocated to four treatments arranged in a 2 × 2 factorial design with energy levels (NEL, 1.52 vs. 1.72 Mcal/kg of DM, referred to as LE vs. HE) and energy sources (steam-flaked corn or ground corn, SFC vs. GC). All cows were fed twice daily ad libitum. Each experimental period consisted of 14 d for adaptation and 7 d for sample collection. Rumen fluid was collected in the morning 3 h after feeding via stomach tubing at d 17. Total DNA was extracted from each rumen sample, and the V4 hypervariable region of 16S rRNA gene was amplified and subjected to paired-end Illumina sequencing. After merging of paired-end sequencing reads, the low-quality sequences were removed and the quality-checked sequences were clustered into operational units (OTU) using the UPARSE pipeline. The resulting OTU were taxonomically classified using the RDP classifier implemented in QIIME. The bacterial communities were profiled using α diversity measurements, whereas the effects of both energy sources and levels were evaluated based on UniFrac distance using a

permutational ANOVA method. The differences in bacterial community structure were examined using DESeq2 in R. The LE and the GC treatments decreased bacterial richness as indicated by lowered number of species detected and estimates of both Chao1 and ACE ($P < 0.05$). The lower Shannon diversity index also suggests that LE and GC treatments decreased evenness of the rumen bacterial communities ($P < 0.05$). The composition of the bacterial communities was similar at the phylum level between two types of corn, but the high-energy diet altered bacterial communities by increasing Cyanobacteria while reducing Firmicutes and Proteobacteria ($P < 0.05$). At the genus level, the SFC diet had lower relative abundance of *Papillibacter* but higher relative abundance of *Mitsuokella* than the GC diet ($P < 0.05$). In contrast, dietary energy levels affected bacterial communities more extensively, with 51 genera being affected. The results indicate that increase in dietary energy level can affect rumen bacterial community to a greater extent than energy source when provided as steam-flaked vs. ground corn ($P < 0.05$)

Key Words: energy (source and level), metagenomics, rumen bacterial community

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1618 Effect of different microbial inoculants on fermentation characteristics of *Miscanthus* silage and their rumen fermentation and digestibility.

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The present study investigated the effect of starter culture of different microbial strains on *Miscanthus* silage quality and its in vitro and in vivo digestibility. *Pediococcus pentosaceus* NJ19, *Pichia anomala* NJ22, and *Saccharomyces cerevisiae* NJ50 were used as starter culture strains. A total of 4 experimental groups including the control (without inoculation) and three treatments (with inoculation) were used. Treatment NJ19 was inoculated at 10^7 cfu/g and treatments NJ22 and NJ50 were inoculated at 10^5 cfu/g of fresh weight. Silage quality was evaluated after 30 d of fermentation. Rumen fermentation patterns were determined using in vitro rumen simulated fermentation system. The effect of starter culture on palatability of *Miscanthus* silage and apparent nutrient digestibility were estimated using 4 rumen cannulated Hanwoo steers. An in vivo trial was performed based on a replicated 4 × 4 Latin square design. Regarding silage quality, DM in NJ19 and NJ50 was significantly lower than the control ($P < 0.05$). Significantly higher CP was found in NJ19 in comparison to other strains ($P < 0.05$). All treatments showed significantly elevated lactic acid production when compared with the control ($P < 0.05$). The highest production was recorded in the NJ19 treatment ($P < 0.05$). Acetic acid in NJ19 was significantly higher than in the other treatments ($P < 0.05$), and NJ22 was significantly lower than the others ($P < 0.05$). Significant difference in in vitro DM digestibility (IVDMD) was detected at 24 h of incubation. *Miscanthus* silage with NJ19 showed a significantly higher IVDMD ($P < 0.05$). Total VFA production in NJ19 was significantly higher than that in the other treatments ($P < 0.05$). Feed intake and apparent DM digestibility of *Miscanthus* silage with NJ19 were significantly higher than in the other treatments ($P < 0.05$). No significant differences among treatments were detected in OM, NDF, and ADF digestibility. These results indicate that inoculation with *P. pentosaceus* in *Miscanthus* silage can improve its ruminal fermentation, feed intake, and DM digestibility without negatively affecting the rumen environment.

Key Words: digestibility, microbial inoculant, *Miscanthus* silage, ruminal fermentation

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1619 The effects of varying undigested neutral detergent fiber and physically effective neutral detergent fiber content of fresh cow rations on dry matter intake, rumination, and milk yield in multiparous Holstein cows.

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The objective of this study was to evaluate the effects of varying levels of undigested NDF ($uNDF_{240}$; NDF remaining after 240 h of in vitro fermentation) and physically effective NDF (peNDF) content of fresh cow rations on DMI, rumination, and milk yield. Previously unpublished data from our lab indicated that cows fed higher $uNDF_{240}$ (approximately 10.7% DM) had higher DMI and improved health status compared with cows fed lower $uNDF_{240}$ (approximately 8.3% DM) in the postpartum period. Multiparous Holstein cows ($n = 56$) were fed a common prepartum ration beginning 28 d before expected parturition and randomly assigned at calving to one of two postpartum diets differing in content of $uNDF_{240}$ and peNDF (Table 1). Treatment diets, high fiber (HF; $n = 27$) and low fiber (LF; $n = 29$), were formulated for equivalent MP and starch, with higher fiber levels achieved through the addition of straw in the HF diet. At 29 d in milk (DIM), HF cows were switched to the LF diet and all cows were fed the LF diet through 42 DIM. Repeated measures data were analyzed with the MIXED procedure of SAS with model effects of treatment, time, and treatment × time. A treatment × time interaction ($P < 0.01$) was observed for DMI when expressed as a percent of BW, such that DMI for cows fed HF was lower in wk 3 (3.05% ± 0.07 vs. 3.35% ± 0.07; $P < 0.01$) and 4 (3.13% ± 0.06 vs. 3.50% ± 0.06; $P < 0.01$) postpartum. Despite this difference in intake, total daily rumination was not different between treatments (overall mean 543.4 ± 3.5 min/d; $P > 0.10$) at any time point. A treatment × time interaction for average weekly milk yield was observed ($P < 0.01$), such

that cows fed HF had lower milk production in wk 4 (46.4 ± 1.1 vs. 50.1 ± 1.0 kg/d; $P < 0.01$). However, differences in energy-corrected milk were not different (overall mean 47.8 ± 1.4 kg/d; $P > 0.10$). Increasing $uNDF_{240}$ and peNDF content of fresh cow rations may limit intake starting in wk 2 postpartum; however, differences in milk yield were not observed until wk 4 postpartum and limiting effects were alleviated after switching to the LF diet. We speculate that the LF diet may have contributed adequate $uNDF_{240}$ in this scenario, resulting in optimal DMI, whereas the additional $uNDF_{240}$ in the HF diet may have had limiting effects.

Key Words: physically effective neutral detergent fiber, undigested neutral detergent fiber, transition cow

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1620 Bacterial diversity in the feces of lambs fed purple prairie clover (*Dalea purpurea* Vent.) and alfalfa (*Medicago sativa*). Q. Huang[1,2], D. Holman[1], T. W. Alexander[3], T. Hu[2], L. Jin[1], Z. Xu[1], T. A. McAllister[4], S. Acharya[1], and Y. Wang*[1], *[1]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [2]College of Animal Science and Technology, Northwest A&F University, Yangling, P. R. China, [3]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [4]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada*.

Our previous studies have shown that purple prairie clover (PPC) reduced the fecal shedding of *Escherichia coli* O157:H7 in lambs and generic *E. coli* in cattle, a response attributed to the presence of condensed tannins (CT). This study assessed the effect of PPC and PPC CT on the composition of the bacterial community in the feces of lambs using high-throughput 16S rRNA gene pyrosequencing. A total of 18 individually fed lambs were randomly divided into three groups and fed alfalfa (Alf), a 40:60 (DM basis; Mix) mixture of Alf and PPC, and Mix with polyethylene glycol (Mix-P) for 18 d. The Mix and Mix-P diets contained about 36 g CT/kg DM. Polyethylene glycol (PEG; MW6, 000) was sprayed onto the Mix-P diet to inactivate the biological activity of CT. Fecal samples were collected on Day 0, 13, and 18 through digital rectal retrieval. The samples were freeze-dried, DNA was extracted, and bacterial 16S rRNA gene amplicons were sequenced using the 454 pyrosequencing technology. Regardless of diet, bacterial communities were dominated by Firmicutes and Bacteroidetes, with a large proportion of OTU within these phyla remaining unclassified at the genus level after analysis. Diet had no effects on the fecal bacterial composition at the phylum level or on α-diversity metrics. Compared with the Alf diet, the Mix diet reduced the number of OTU associated with *Butyrivibrio* ($P = 0.01$), *Anaeroplasma* ($P = 0.02$), and unclassified bacteria within the families Peptococcaceae ($P = 0.03$), Christensenellaceae ($P = 0.01$), Erysipelotrichaceae ($P = 0.02$), S24-7 ($P = 0.02$), and Dehalobacteriaceae ($P = 0.03$). Similar reductions occurred within the orders RF39 ($P = 0.05$) and ML615J-28 ($P = 0.02$), but no difference was observed between Mix and Mix-P groups ($P > 0.05$). In contrast, a greater proportion of genus *Prevotella* ($P = 0.02$) was found in the Mix group compared with the Alf group. These results indicate that PPC CT up to 36 g/kg DM in the diet exert only minor effects on the composition of the fecal bacterial community of lambs.

Key Words: condensed tannins, 454 pyrosequencing, gut microbiota, purple prairie clover

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1621 Comparisons of microbial populations found in the rumen and in a dual-flow continuous culture fermentation system using high-throughput 16S amplicon sequencing. I. J. Salfer*, H. E. Larson, and M. D. Stern, *University of Minnesota, St. Paul*.

Dual-flow continuous culture fermenters are commonly used to study rumen fermentation in vitro. Previous research has shown that certain microbial populations are maintained within continuous culture at concentrations similar to in vivo values. The development of high-throughput genetic sequencing allows us to gain a global understanding of the microbial population in the rumen. The objective of this study was to use 16S amplicon sequencing to study phylogenetic differences and similarities between microbial communities found in the rumen of dairy cattle with those found in a dual-flow continuous culture fermentation system. Samples were collected from a rumen fluid, fermenter inoculum, and effluent collected directly from fermenters during 10 d of operation. Deoxyribonucleic acid (DNA) was extracted from samples, amplified to generate cDNA libraries, and sequenced using the Illumina MiSeq platform. Sequences were aligned using Mothur version 1.34.0 software and data were compared based on sample type (rumen vs. inocula vs. fermenter), inoculum donor, and day of fermenter operation. Redundancy analysis (RDA) was performed to determine correlations between fermentation measurements based on microbial community. Community differences were assessed using UniFrac metrics, analysis of molecular variance (AMOVA), and analysis of similarity (ANOSIM) based on Bray–Curtis dissimilarity matrices. Differences in taxonomic composition of different sample types were analyzed for kingdom phylum, class, order, and family taxonomic levels. Functional inferences were made by matching taxonomic data to KEGG orthology terms using PICRUSt software and analyzed by sample type. Results showed that UniFrac, AMOVA, and ANOSIM metrics were different ($P < 0.05$) between fermenters and rumen and inoculum samples. The microbial community within fermenters appeared to stabilize by Day 7 of fermenter operation. Bacteroidetes and Firmicutes made up the two most abundant phyla in rumen, inoculum, and fermenters and did not differ ($P > 0.10$) between sample types. Proteobacteria, Tenericutes, Spirochaetes, and Verrucomicrobia were found in dissimilar abundances ($P <$

0.05) between different sample types. Prevotellaceae was the most abundant family in all three sample types and did not vary ($P > 0.10$) between rumen, inoculum, and fermenter samples. PICRUSt predictions showed that AA metabolism, membrane transport, energy metabolism, and cellular processes and signaling were affected ($P < 0.05$) by sample type but that metabolism of carbohydrates, cofactors and vitamins, and lipids were not ($P > 0.10$). The overall microbial community differs between natural rumens and fermenters, but the concentrations of several prominent taxa are maintained.

Key Words: continuous culture, rumen, 16S sequencing

1622 Evaluation of in vitro and in situ starch digestibility assays. S. E. Schuling*, D. Schimek, and B. Vander Wal, *Hubbard Feeds Inc., Mankato, MN*.

The objective of this experiment was to evaluate commercial in vitro and in situ starch digestibility assays to estimate ruminal starch digestibility (RSD) and rate of ruminal starch degradation (kd). Twelve commercial dairy herds located in Wisconsin, Pennsylvania, and Missouri were used (4 free-stall and 8 tie-stall housing). Fecal samples were collected from 5 high- and 5 low-producing cows from each herd, and samples of total mixed rations (TMR) were collected after feed delivery from each pen ($n = 8$) or directly in front of each cow ($n = 80$). Corn silage (CS; $n = 13$) and corn (dry, $n = 9$, and high-moisture, $n = 7$) samples were also collected from each farm. Feed samples were thoroughly mixed and split for analysis. Fecal and TMR samples were sent to Rock River lab for starch analysis. Total tract starch digestibility (TTSD) was calculated from TMR and fecal starch content. The following equation was used to estimate RSD from TTSD: $y = 82.224 + (0.185 \times \text{ruminal})$, in which y = TTSD (Ferraretto et al., 2013). Samples of TMR, corn, and CS were sent to Rock River for 7-h in situ starch digestibility and to Dairyland lab for analysis of nutrient composition and 7-h in vitro starch digestibility. All herds tested milk through Dairy Herd Improvement Association and individual milk yield, milk fat, and milk protein content data were collected from test day closest to day of sample collection. The REG procedure of SAS was used to determine the relationship between in situ, in vitro, and in vivo RSD. In situ starch digestibility was related to in vivo RSD ($R^2 = 0.19$, $P < 0.002$). There was no relationship between in vitro and in vivo RSD ($R^2 = 0.01$, $P = 0.45$). The Cornell Net Carbohydrate and Protein System (CNCPS) uses ruminal starch kd to predict microbial protein production. Actual milk yield was related to model-predicted milk yield using model default kd for RSD ($R^2 = 0.69$, $P < 0.0001$). Ruminal starch kd was calculated for CS and corn using in situ data and entered into the CNCPS model (version 6.5; AMTS, LLC). This relationship was improved when measured in situ starch kd was entered for corn and CS ($R^2 = 0.76$, $P < 0.0001$). In conclusion, in situ starch digestibility at 7 h is a good approach for estimating RSD in vivo and using kd from this method improves milk yield predictions from the CNCPS model.

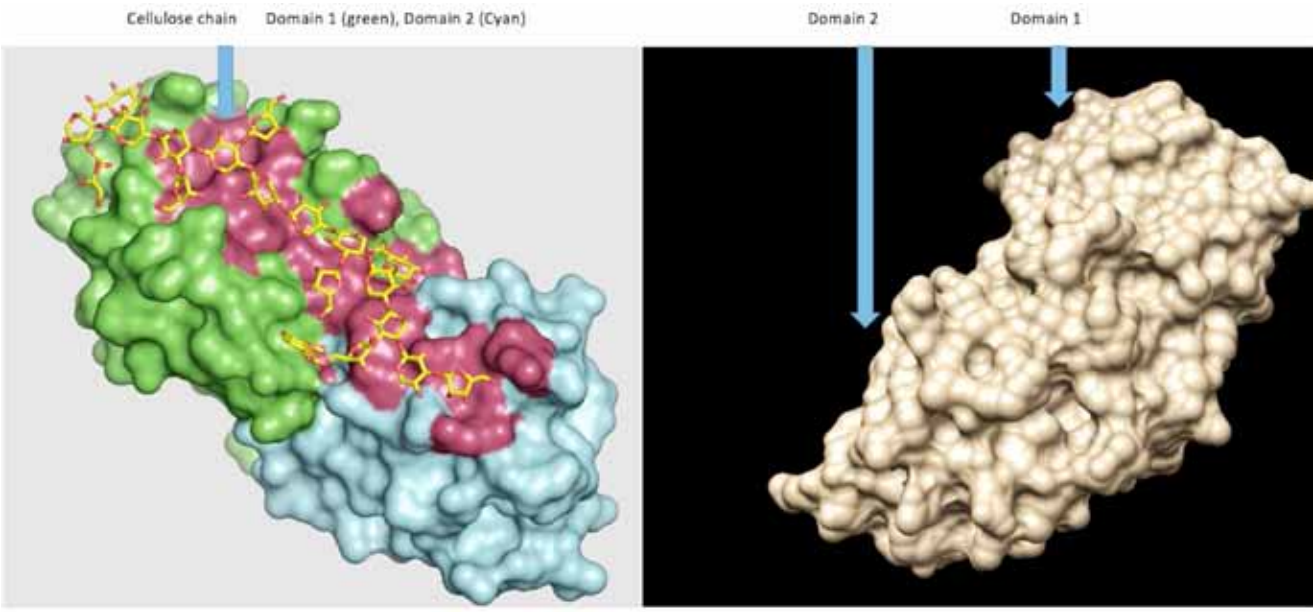
Key Words: in situ, in vitro, ruminal starch digestibility

1623 Effect of rumen acidosis and short-term feed restriction on messenger ribonucleic acid expression of genes relating to gut barrier function and immune response in Holstein steers. K. M. Wood*[1,2], R. L. A. Pederzolli[1], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]University of Guelph, Guelph, ON, Canada*.

The objective of this study was to identify whether ruminal acidosis (ACID) or feed restriction (FR) affect genes influencing barrier function (claudin [CLDN], occludin [OCLN], tight-junction protein-1 [ZO-1], and tight-junction protein-2 [ZO-2]) and immune response (toll-like receptor-2 [TLR2], toll-like receptor-4 [TLR4], and Fc fragment of IgA receptor [FCAR]). Twenty-one Holstein steers were randomly blocked and assigned to 1 of 3 treatments: control (CON), ACID, and FR. Steers were fed a common diet with a 50:50 F:C ratio once daily at 0800 h for a 5-d baseline period followed by a challenge period. Rumen acidosis was induced by restricting feed to 25% DMI for 1 d and then offering pelleted barley (30% DMI:BW) the following day. Steers on the FR treatment were restricted to 25% DMI for 5 d. Steers were killed and tissues were collected from the rumen (RUM), jejunum (JEJ), and distal colon (DC) for measurement of mRNA expression using real-time PCR. Relative fold change was calculated by the ΔΔCt method, using pairs of endogenous controls (glyceraldehyde 3-phosphate dehydrogenase, large ribosomal protein P0, or β-actin) and then normalized to the mean of the CON. Data were analyzed as a randomized complete block design using treatment as a fixed effect and block as a random effect. In the rumen, CLDN and OCLN were increased in FR over others ($P \leq 0.02$) and TLR4 was increased by 1.62- and 1.98-fold over CON ($P \leq 0.05$) for ACID and FR, respectively. In the JEJ, expression of CLDN was greater in ACID than in CON and FR ($P = 0.01$) but both ACID and FR had greater expression of OCDN ($P < 0.01$), ZO1 ($P = 0.01$), and ZO2 ($P < 0.01$) than CON. In addition, there was greater mRNA expression for FCAR in FR steers ($P \leq 0.007$) than in ACID and CON steers and greater TLR4 in FR than in CON ($P = 0.04$). In the DC, genes relating to barrier function (CLDN, OCLN, and ZO2) were greater for FR than for CON ($P \leq 0.04$). These data demonstrate that mRNA expression of genes relating to barrier function and immune response in the gastrointestinal tract are differentially affected by nutritional stressors. Nutritional challenges affect the expression of genes related to barrier function in immune response in the gastrointestinal tract. This may have implications in identifying how cattle adapt to nutritional challenges and to identify strategies to improve gut barrier function.

Key Words: acidosis, cattle, gut barrier function

Fig 1625.



1624 Use of fecal starch as an indicator of starch digestibility and starter intake in preweaned dairy calves. T. S. Dennis*, W. Hu, F. X. Suarez-Mena, T. M. Hill, J. D. Quigley, and R. L. Schlotterbeck, *Provimi North America, Brookville, OH.*

Fecal starch (FS) has been used as a tool to evaluate starch digestibility in lactating dairy cows and feedlot steers. Some on-farm advisors are also using FS in a similar way to evaluate solid feed digestibility in preweaned dairy calves. Our objective was to evaluate the relationship of FS with starter intake and starch digestibility in preweaned dairy calves. Male Holstein calves initially 43 ± 2.9 kg BW from a single farm (N = 35) were fed different amounts of milk replacer ranging from 0.66 to 1.1 kg DM daily (27% CP and 17% fat) and weaned by 7 wk of age. Starters contained 37% whole corn, 20% whole oats, 35% protein pellet, and 3% molasses and contained 43% starch (first set) and 38% starch (second set). Fecal grab samples were taken from calves at 3 (n = 20), 6 (n = 20), and 8 wk (n = 35) of age. Twelve fecal samples per calf were taken via rectal palpation over a 5-d period each week, frozen daily, combined on an equal wet-weight basis, and subsampled for analysis. Chromic oxide was used as an external digestibility marker at 3 and 6 wk, whereas AIA was used as an internal marker at 8 wk. Milk replacer and starter intakes (offered and refused) were recorded daily during collection. Linear regression analysis of starch digestibility (%) and dry feed intake (kg/d) vs. fecal starch (%) were determined using PROC REG of SAS. At 3 wk of age, starch digestibility increased ($y = 0.69x + 40.80$; $R^2 = 0.53$, $P < 0.01$) and starter intake decreased ($y = -0.01x + 1.32$; $R^2 = 0.20$, $P = 0.05$) with increasing FS. At 6 wk of age, starch digestibility ($P = 0.11$) and starter intake ($P = 0.96$) were not related to FS. At 8 wk of age after calves were weaned, starch digestibility decreased as FS increased ($y = -0.62x + 99.7$; $R^2 = 0.86$, $P < 0.01$), whereas FS and starter intake were not related ($P = 0.17$), a relationship in contrast to the previously observed result in calves still consuming milk replacer. In the current study, results suggest that FS was not a good estimate of starch digestion or dry feed intake in the preweaned calf but has promise for evaluating starch digestibility in calves after weaning.

Key Words: dairy calf, digestion, fecal starch

1625 Expression and purification of a novel bacterial expansin from *Bacillus subtilis* that synergistically degrades cellulose with fibrolytic enzymes. A. A. P. Cervantes*[1], I. Muhammad[2], C. F. Gonzalez[3], D. Vyas[1], and A. T. Adesogan[1], *[1]Dep. of Animal Sciences, IFAS, University of Florida, Gainesville, [2]University of Florida, Gainesville, [3]University of Florida, Gainesville.*

Expansin-like proteins are a recently discovered group of proteins that can change the mechanical properties of plant cell walls. Many can synergistically improve cellulose degradation by fibrolytic enzymes. This study aimed to express and purify a novel bacterial expansin-like protein from *Bacillus subtillis*. Primers were constructed based on the Expansin-Yoaj protein sequence (accession number: WP_015383820.1) and tested using genomic DNA from *Bacillus subtillis* strain, UD1022. The plasmid p15TV-LdtR was used as template and transformed in *E. coli* DH5-α. Standard methods were used for chromosomal DNA isolation, restriction enzyme digestion, ligation, transformation, and agarose gel electrophoresis. The His-tagged fusion proteins in the plasmid were overexpressed in *E. coli* BL21-Star (DE3) cells. Then the cells were lysed

using a French Press and purified with a metal chelate affinity-column charged with Ni^{2+}. The remaining fraction was dialyzed, then protein concentration and molecular weight were determined. Protein identity was confirmed by sequencing and using Phyre[2] software. To examine the protein activity and synergism with cellulase, we examined if the expansin protein increased hydrolysis of carboxymethylcellulose (10 mg/ml) by *Trichoderma reesei* β 1- 4 endoglucanase EC (3.2.1.4) beyond the increase caused by the endoglucanase alone. The experiment had 5 (treatments: Control, enzyme, enzyme + expansin-like protein at doses of 100, 200, and 300 mg/ml) × 5 (incubation durations: 0,12, 24, 36, and 48 h) factorial treatment structure with 3 replicates per treatment combination. Additionally, all expansin doses were incubated by triplicate without cellulase for 48 h. Data were analyzed using the Generalized Linear Model of R. Protein concentration ranged from 0.130 to 0.345 mg/ml with an average molecular weight of 27 kDa. The Phyre[2] software revealed a two domain structure with polar residues typical in similar non-hydrolytic proteins. Synergistic increases in cellulose hydrolysis of 6 to 10% were detected ($P < 0.05$) by adding 100 but not 200 mg/ml of expansin-like protein. Whereas, adding 300 mg/ml of expansin-like protein decreased cellulose hydrolysis. Synergistic effects were more evident at 12 and 24 h (5 to 15%; $P < 0.05$) than at 36 and 48 h. On the other hand, using expansin alone did not exhibit hydrolytic activity after 48 h regardless of the dose. The newly expressed non-hydrolytic expansin-like protein synergistically increased cellulose hydrolysis by cellulase.

Key Words: expansin, synergistic effects, fibrolytic enzymes

1626 Annual rhythms of milk, fat, and protein production in U.S. dairy cattle. I. J. Salfer*, C. D. Dechow, and K. J. Harvatine, *Penn State University, State College.*

An annual pattern of milk composition has been well appreciated in dairy cattle with highest milk fat and protein observed during the winter and lowest in the summer. However, the rhythm has not been well quantified. The cosine function is commonly used to model repeating daily and seasonal rhythms and allows determination of the amplitude (mean to peak), phase (time at peak), and period (time between peaks) of the rhythm. The objective of this study was to use cosine analysis to characterize the annual rhythm of milk, fat, and protein production using both national milk production and herd-level data. First, 10 yr of monthly average milk butterfat and protein concentration by milk market were obtained from the USDA Agricultural Marketing service database. We first determined if the data fit a cosine function with a 12 mo period using the linear form of the cosine function by random regression in PROC Mixed. A zero amplitude test was used to determine significance of the rhythm. Fat and protein concentration fit a cosine function with a 12 mo period in all milk markets. There was an interaction between milk marketing order and milk fat and protein concentration ($P < 0.01$). The phase (time at peak) ranged from October 6 to January 6 for fat and from November 21 to December 12 for protein. The amplitude of the rhythm ranged from 0.07 to 0.14% for fat production and from 0.08 to 0.12% for protein production. The amplitude of milk fat rhythm generally was lower in southern markets and higher in northern markets. Second, the annual rhythm of milk yield and milk fat and protein yield and concentration were analyzed in monthly test day data from 1684 cows from 11 tie-stall herds in Pennsylvania. Milk, fat, and protein yield and fat and protein concentration followed yearly annual rhythms. Milk and protein yield were highest in May, fat yield and concentration were highest in February, and protein concentration was highest in November. There was an interaction of herd with the rhythm of milk yield, fat yield, and fat concentration. In conclusion, there is an annual rhythm of milk yield and milk fat and protein yield and concentration that fits a cosine function and varies by geographical location and herd.

Key Words: annual rhythms, milk synthesis, yearly pattern

1627 Molecular physiology of rumen papillae following an acidosis challenge. C. E. Kent-Dennis*, J. A. Pasternak, and G. B. Penner, *University of Saskatchewan, Saskatoon, Canada.*

The objective of this experiment was to evaluate the effect of ruminal acidosis on transcript abundance and localization of proteins regulated by local inflammation in the ruminal epithelium. Seven ruminally cannulated beef cows were used in a crossover design with two periods and two treatments (acidosis or control). Heifers were fed a baseline TMR with 50:50 forage to concentrate ratio and DMI was recorded daily. The acidosis induction consisted of feed restriction (25% of DMI for 1 d) followed by a grain challenge (30% of baseline DMI) and provision of the full TMR. Ruminal pH was monitored using indwelling probes and ruminal papillae biopsies were collected on d 2 and 6 following the induction of acidosis for RNA extraction and immuno-histofluorescence. Prostaglandin-endoperoxide synthase (PTGS1) and PTGS2 facilitate prostaglandin synthesis and were selected as targets because expression is thought to be regulated by inflammation. Gene expression was measured by quantitative real-time PCR, normalized to the geometric mean of three housekeeping genes within period. Immuno-histofluorescence of toll-like receptor (TLR)-9 and TLR-4 were used to evaluate localization in a subset of samples. Statistical analysis was performed using the MIXED procedure of SAS 9.4, with treatment and period as fixed effects. A pH threshold of 5.8 was used to define the occurrence of ruminal acidosis. During the day of the grain challenge, ruminal pH for acidosis cows was below pH 5.8 for 543 min, whereas pH of controls did not fall below the threshold at any time ($P = 0.02$). Minimum and mean pH were less on the

challenge day (min: 5.4 vs. 6.2 ± 0.17 and mean: 5.9 vs. 6.6 ± 0.14, respectively; $P < 0.01$) for acidosis than control cows. Two days after acidosis induction, transcriptional abundance of PTGS1 and PTGS2 in ruminal papillae were decreased by 1.37 ($P = 0.02$) and 2.08 ($P < 0.01$) fold, respectively, relative to controls. When evaluated at d 6, no differences were observed. TLR-9 was not ubiquitously expressed, but rather was concentrated in small areas within regions of the ruminal epithelium. TLR4 was intracellularly expressed in the stratum basale, stratum spinosum, and stratum granulosum regardless of treatment. The results of this study suggest a potential acute anti-inflammatory response following acidosis, which was also tightly regulated. However, the downregulation of PTGS2 was unexpected; related transcripts are being studied to elucidate these effects.

Key Words: acidosis, inflammation, rumen papillae

1628 Endocannabinoid and lipid metabolism gene network expression in adipose tissue of peripartal cows with low or high body condition score at calving. A. S. Alharthi*[1], Z. Zhou[1], D. N. Luchini[2], and J. J. Loor[1], [1]*University of Illinois, Urbana,* [2]*Adisseo S.A.S., Alpharetta, GA.*

Our previous research revealed a strong inflammatory response within adipose tissue during the transition into lactation. Whether this localized effect is a result of oxidative stress induced by lipolysis and fatty acid oxidation or via the production of endocannabinoids remains to be determined. The objective of this study was to investigate the expression of genes composing the endocannabinoid signaling system and lipid metabolism in adipose tissue during the transition period in dairy cows. Twenty multiparous Holstein cows were retrospectively divided by prepartum body condition score (BCS) into two groups (10 cows/group): BCS $\leq$ 3.25 (LoBCS) and BCS $\geq$ 3.75 (HiBCS). Adipose tissue was biopsied at d −10, 7, and 20 relative to parturition. Tissue RNA was used to evaluate 17 target genes via quantitative real time RT-PCR. Data were log2 transformed and analyzed by the MIXED procedure of SAS. Among the endocannabinoid-related genes, a BCS × day was observed for *NAPEPLD*, *CNR2*, and *FAAH*. Expression of *NAPEPLD* and *CNR2* was greater at d 7 in LoBCS than HiBCS cows, while *FAAH* was upregulated at d 7 and 20 LoBCS than HiBCS cows. Expression of monoglyceride lipase (*MGLL*), which inactivates 2-Arachidonoylglycerol, was overall greater ($P < 0.05$) across time in LoBCS than HiBCS. In addition, LoBCS than HiBCS cows had a strong tendency ($P = 0.06$) for greater overall expression of *POMC* across time. Regarding the genes related with lipid metabolism, a BCS × day ($P = 0.04$) was observed for the mitochondrial enzyme *SOD2*, important for clearing reactive-oxygen species that cause cellular stress and inflammation, because of greater expression at d 7 in LoBCS than HiBCS. Similarly, a strong tendency ($P = 0.07$) for a BCS × day was observed for *LIPE* due to greater expression at d 7 and 20 in LoBCS than HiBCS. Among genes associated with lipolysis, LoBCS compared with HiBCS cows had overall greater expression of *ABDH5* ($P = 0.04$) and *ATGL* ($P = 0.02$), indicating a greater state of basal lipolysis over time. Although no BCS effect was detected for *CPT1A*, its expression increased sevenfold on d 20 versus −10, indicating a robust capacity of adipose for fatty acid oxidation. Overall, data indicated that cows with prepartum BCS below 3.25 experienced greater alterations in lipid metabolism and endocannabinoid signaling. A potential linkage between those pathways and risk of disorders postpartum remains to be determined.

Key Words: body condition score, endocannabinoid, lipid mobilization

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1629 Endocannabinoid network and proopiomelanocortin gene expression in peripartal bovine liver in response to rumen-protected methionine supplementation. A. S. Alharthi*[1], Z. Zhou[1], D. N. Luchini[2], and J. J. Loor[1], [1]*University of Illinois, Urbana,* [2]*Adisseo S.A.S., Alpharetta, GA.*

Results from our previous work revealed a beneficial effect of rumen-protected Met (MET) supplementation during the transition period on postpartal immune function, inflammation, and cow performance. Endocannabinoids (EC; 2-Arachidonoylglycerol, oleoylethanolamide, and anandamide) are produced on stimulation of EC receptors expressed in central nervous system and peripheral tissues. These compounds have orexigenic, anorexigenic or pro- and anti-inflammatory properties. Because MET-fed cows had a better immune and liver function postpartum, we sought to determine any changes in the EC gene network and the hormone precursor proopiomelanocortin (POMC). Twenty-two multiparous Holstein cows were fed experimental treatments consisting of a basal control diet (CON; $n = 11$) and CON plus Met (Smartamine M, Adisseo NA) (MET; $n = 11$). All cows received the same far-off diet from −50 to −22 d before expected calving, close-up diet from −21 d to expected calving, and lactation diet from calving through 30 d in milk (DIM). MET supplementation was adjusted daily from −21 d to 30 DIM at a rate of 0.08% (DM basis) of diet DM. The liver was biopsied at −10, 7, 20, and 30 d relative to parturition. RNA was extracted and used for quantitative real-time RT-PCR. Expression of each target gene was normalized by the geometric mean of three internal control genes. Data were log2 transformed and analyzed using the MIXED procedure of SAS. A strong tendency for a treatment × day effect was observed for the EC receptor *CNR2* ($P = 0.06$), the lipase *MGLL* ($P = 0.08$), the amidase *NAAA* ($P = 0.08$) and *POMC* ($P = 0.07$). These results were associated with greater expression of *MGLL* and *POMC*in MET compared with control cows on d 7, while the expression of *NAAA* was greater in MET compared with control cows on d −10 and 7. In contrast, the interaction for *CRN2* was associated

with lower expression in MET compared with control cows on d −10. There was an overall greater ($P < 0.05$) expression of the fatty acid amide hydrolase *FAAH* and the EC-synthesizing enzyme *NAPEPLD* in MET compared with control cows. Overall, results indicate that alterations in the hepatic EC signaling network in response to MET might be involved in the positive effect on performance and liver function. Additional studies to investigate the mechanism of action of MET on the hepatic endocannabinoid system appear warranted.

Key Words: endocannabinoid, liver, methionine, transition period

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1630 Substrate utilization by *Megasphaera elsdenii* strain NCIMB 41125. A. M. Mobiglia*[1], F. R. Camilo[1], and J. S. Drouillard[2], [1]*CAPES Foundation, Ministry of Education of Brazil, Brasilia, Brazil,* [2]*Kansas State University, Manhattan.*

Megasphaera elsdenii (ME) is a key lactate-utilizer in grain-fed cattle, but less is known of its competitiveness in the rumen when administered as a probiotic before feeding grains. Our objective was to evaluate capacity for ME to utilize a wide range of alternative substrates, including glucose, fructose, galactose, arabinose, xylose, maltose, sucrose, lactose, trehalose, raffinose, fructo-oligosaccaride (FOS), potato starch, soy protein, and succinate. A basal medium (NC) was prepared with yeast extract, soy peptone, minerals, vitamins, and cysteine, and used alone or amended with sodium lactate or one of the above carbon sources. Lactate medium was adjusted to pH 5.6 and all other media were adjusted to pH 6.0. Hungate tubes containing sterile media were inoculated with 2% of a fresh culture containing approximately 9.6×10^8 CFU/mL ME strain NCIMB 41125 and incubated at 39ºC for 12 h. Changes in VFA concentrations were measured by gas chromatography using a capillary column (DB-WAX; J&W Columns) and flame ionization detector. Optical density (OD), measured as absorbance at $\lambda = 600$ nm, and pH were quantified, and cultures were enumerated on agar plates to determine viable cell counts. The study was a randomized complete block with individual cell culture as the experimental unit. Data were analyzed as mixed models with substrate as the fixed effect and block as a random effect. OD readings of cultures with arabinose, galactose, lactose, trehalose, and potato starch were comparable ($P > 0.05$) to NC, indicating limited capacity for metabolism of these carbon sources. Growth was greater with fructose compared to other substrates ($P < 0.05$), followed by glucose, lactate, and maltose, all of which were greater than NC ($P < 0.05$). Growth in media with FOS, raffinose, xylose, sucrose, and soy protein were marginally greater than NC ($P < 0.05$), while succinate inhibited growth ($P < 0.05$). Changes in culture pH and VFA concentrations were consistent with changes in OD measurements. Viable cell counts were lowest ($P < 0.05$) for succinate (6.8 versus 7.9 log CFU/mL for succinate and NC, respectively), again indicating an inhibitory effect of succinate on ME. Cultures with fructose, maltose, and glucose all had low terminal pH (4.31, 4.82, and 4.85, respectively), which may have adversely affected viable cell counts (8.15, 8.27, and 8.84 log CFU/mL, respectively). This study provides evidence for metabolism of a broad range of carbon sources by *Megasphaera elsdenii* strain NCIMB 41125.

Key Words: *Megasphaera elsdenii,* NCIMB 41125, substrates

1631 16S rRNA Bacterial sequences suggest dietary intervention can be used to change microbial community structure to reduce methane emission in Holstein dairy cattle. W. Tom*, J. V. Judy, P. J. Kononoff, and S. C. Fernando, *University of Nebraska-Lincoln, Lincoln.*

The rumen microbiome plays a critical role in host nutrient acquisition, and diet has been shown to alter the composition and function of the rumen microbiome. Most microbes in in the rumen resist in vitro culturing, remaining largely uncharacterized. Recent advances in next generation sequencing (NGS) methodologies provide an excellent opportunity to better understand changes in the structure of the rumen microbiome, which may lead to novel strategies to increase animal productivity and reduce livestock greenhouse gas emissions. This study utilizes high throughput sequencing of the 16S rRNA gene to compare bacterial community structure and abundance under different dietary conditions to evaluate the effect of the rumen microbial community on methane production in Holstein dairy cows. The experiment follows a randomized row by column design (8 x 4). Eight different Holstein cows were fed four different diets; reduced fat distillers grain (RFDDGS) mix, corn oil grain mix, calcium sulfate grain mix, and a standard corn and soybean meal control. Each diet was fed for 28 d and methane emissions were measured using indirect calorimetry (headboxes). Additionally, rumen samples were collected on Day 28 via esophageal tubing for microbial community analysis. Before receiving the first treatment diet, all cows were maintained on the same common diet to reduce animal to animal variation. DNA sequencing was performed using the Illumina MiSeq™ platform. Comparisons of rumen 16S rRNA bacterial communities show a significant difference in microbiome composition both by animal and by diet (PERMANOVA, $p < 0.001$). Pairwise comparison of all diets was performed using a Wilcoxon rank-sum test revealing significant differences between corn oil and RFDDGS ($p < 0.001$), calcium sulfate and RFDDGS ($p < 0.001$), corn oil and control ($p < 0.001$), and calcium sulfate and control ($p < 0.01$). Upon examining differences in operational taxonomic unit (OTU) abundances we identified multiple OTUs showing log fold changes between diets, supporting that bacterial community composition differs based on diet. This data suggests that dietary intervention can be used to mitigate methane emission by

controlling the microbial population within the rumen.

Key Words: bacterial community, microbiome, next generation sequencing, 16S rRNA

1632 Inulin as prebiotic for *Lactobacillus salivarius* and *Enterococcus faecium* with probiotic potential in ruminants.

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Milk production in Mexico is deficient and there are diarrhea problems in nursing calves. Lactic acid bacteria (LAB) are found in the digestive tract and show an antagonistic effect against enteric pathogens. Addition of prebiotics such as inulin to diets of calves might control gastrointestinal flora. Therefore, the aim of this research was to evaluate the influence of inulin on in vitro growth performance of *Lactobacillus casei* (*Lc*), *Lactobacillus salivarius* (*Ls*), and *Enterococcus faecium* (*Ef*). In vitro incubations were performed at 37°C, replacing the MRS glucose for inulin. The experimental design was complete randomized and treatments (T) were: T1 = MRS-glucose + Ls; T2 = MRS-glucose + Ef; T3 = MRS-glucose + Lc; T4 = MRS-inulin + Ls; T5 = MRS-inulin + Ef; T6 = MRS-inulin + Lc; T7 = MRS-inulin + Ls + Ef; T8 = MRS-inulin + Ls + Lc; T9 = MRS-inulin + Ef + Lc; and T10 = MRS-inulin + Ls + Ef + Lc. Variables were growth curve, pH, lactic acid production, ammonium, strains resistance to hydrochloric acid and bile salts, and antagonism against *Escherichia coli* and *Salmonella typhimurium*. Data were statistically analyzed with PROC GLM of SAS, and Tukey test ($P < 0.05$) was used to compare treatments means. Analysis of results showed a positive effect of inulin on the growth of strains, higher absorbance readings in MRS-inulin as compared to MRS-glucose (2.35^{d}, 2.28^{d}, 2.30^{d}, 2.83^{abc}, 2.67^{c}, 2.64^{c}, 2.75^{abc}, 2.93^{a}, 2.72^{bc}, and 2.88^{ab}, from T1 to T10, respectively; $P < 0.05$) and higher bacterial count at the end of the growth curve (10.98^{d}, 10.76^{d}, 11.29^{d}, 13.11^{c}, 13.63^{b}, 13.77^{a}, 12.93^{c}, 12.74^{c}, 12.43^{c}, and 12.92^{c} Log_{10} UFC mL^{-1} from T1 to T10, respectively; $P < 0.05$), whereas no changes were found for the other variables. We conclude that LAB *Ls* and *Ef* fermented inulin with a positive effect on strains growth, without affecting their probiotic potential.

Key Words: *Enterococcus faecium*, inulin, *Lactobacillus salivarius*

1633 Moisture content influences ensiling characteristics, in situ disappearance, and in vitro digestion characteristics of reconstituted corn grain.

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Grain processing is a key factor influencing efficiency of feed utilization in feedlot cattle. Reconstitution of corn grain followed by ensiling modifies structural characteristics of grain, thereby improving starch availability and animal performance. The objective of this experiment was to evaluate changes in ensiling characteristics of corn grain reconstituted to different moisture levels, and to determine impact on in situ and in vitro digestion. Corn grain was ground to 4000 µ and subsequently mixed with water to final moisture concentrations of 27, 30, 33, and 36%. Grains were packed into 12 concrete silos (2-m dia. x 2-m height), each containing approximately 2650 kg of grain (3 silos per moisture level). Grains were allowed to ensile for 90 d, then sampled by drilling two 3-cm cores to a depth of 60 cm, which were composited to form one sample for each silo. Ensiled grains and a dry-rolled corn control (DRC) were characterized with respect to pH, moisture content, 16-hour in situ disappearance, and in vitro fermentation by mixed ruminal microbes. Grain pH was determined after steeping 25 g of grain in 100 mL deionized water for 1 h at room temperature. For in vitro fermentations, 3 g of grain (DM basis) were added to 250-mL screw-top bottles, mixed with 140 mL of artificial saliva and 10 mL of strained ruminal fluid, flushed with nitrogen, capped with Ankom gas pressure monitors, and placed into a shaking incubator at 39ºC for 16 h. Terminal pH was measured for each culture, and samples of supernatant were mixed 4:1 with 25% w/v metaphosphoric acid solution for determination of VFA profiles by gas chromatography using a flame ionization detector. In situ dry matter disappearance (ISDMD) of grains was measured over a 16-h ruminal incubation. The pH of ensiled grains was 6.3, 4.42, 4.23, and 4.15 for 27, 30, 33, and 36% moisture, respectively (linear and quadratic effects, $P < 0.01$). ISDMD were 36, 46, 43, 47, and 57% for DRC and ensiled grains with 27, 30, 33, and 36% moisture, respectively (linear, $P < 0.01$), in vitro gas production amounts were 89, 161, 163, 221, and 284 mL, respectively (linear, $P < 0.01$), and total VFA concentrations of cultures were 41, 58, 69, 86, and 100 mM, respectively (linear, $P < 0.01$). Moisture content of reconstituted, ensiled grain has a large impact on in situ and in vitro fermentation characteristics.

Key Words: corn, reconstitution, starch

1634 On the way to optimize the two stage Tilley and Terry technique for a more accurate in vitro assessment of rumen modifiers. A. Russouw[*1], E. Raffrenato[1], F. Chaucheyras-Durand[2], and E. Chevaux[2], [1]*Department of Animal Sciences, Stellenbosch University, Stellenbosch, South Africa,* [2]*Lallemand SAS, Blagnac, France.*

In vitro techniques using rumen inocula are routinely used to estimate NDF rumen and total tract digestibility values. By controlling the micro-environment of the test flask, the technique does not represent the dynamic environment of the rumen, often resulting in higher digestibility values when compared to in vivo values. Furthermore, because of the stability of the system, testing rumen modifiers in vitro may result in biased conclusions. Among the possible parameters, our objective was to assess the effects of using different buffers, NDF levels and doses of a live yeast assumed to stimulate fiber digestion, on rumen NDF and total tract OM in vitro digestibility (NDFd and TTOMd) using a modified Tilley and Terry procedure. Three buffers (Kansas State-KS; McDougall-MD; Goering and Van Soest-GV), two forages (wheat straw-WS, 83% NDF; oat hay-OH, 60% NDF) and 4 doses of yeast (0, 10^5, 10^6, 10^7 cfu/ml) were tested. Residual NDF of the fermented samples were obtained at 12, 24, and 48 h. The fermented samples followed also 48 h acid pepsin treatment for OMd estimation. NDF rate of digestion (kd) was calculated using a first order decay model and estimated iNDF using the 240 h fermentation residual. Data were analyzed according to a randomized complete block design with a factorial arrangement of treatments. The main tested effects were buffer, NDF level, and yeast dose. Run was considered random effect and response variables were NDFd and kd. The buffers resulted in different NDFd and kd ($P < 0.01$) with the KS resulting in the lowest and MD in the highest NDFd and TTOMd, for both WS and OH. Yeast interacted with both NDF level and buffer ($P < 0.01$), resulting in more effective action (higher kd) with higher NDF and GV and KS buffers. The most effective yeast dose was the 10^6 cfu/ml, when compared to the others across NDF levels and buffers, increasing kd on average 0.025 to 0.035 and 0.038 to 0.044 h^{-1} for WS and OH, respectively. Therefore, all parameters tested affected conclusions on the effectiveness of the rumen modifier tested.

Key Words: buffers, live yeast, NDF digestibility, Tilley and Terry

1635 Effect of feeding different flaxseed-based products on the rumen microbial community of dairy cows evaluated by high-throughput DNA sequencing. E. Castillo-Lopez[*1], J. Moats[1], N. D. Aluthge[2], H. A. Ramirez Ramirez[3], T. A. McAllister[4], C. L. Anderson[2], D. A. Christensen[1], T. Mutsvangwa[1], H. Lee-Rangel[5], G. B. Penner[1], and S. C. Fernando[2], [1]*University of Saskatchewan, Saskatoon, Canada,* [2]*University of Nebraska, Lincoln,* [3]*Iowa State University, Ames,* [4]*Lethbridge Research and Development Centre, AAFC, Lethbridge, Canada, Lethbridge, Canada,* [5]*Universidad Autonoma de San Luis Potosi, San Luis Potosi, Mexico.*

Four ruminally-cannulated lactating Holstein cows (mean and SD, 116.5 ± 17.5 DIM; 712.7 ± 92.3 kg BW) were used in a 4 × 4 Latin square with 28-d experimental periods to evaluate the effect of feeding flaxseed-based products on the rumen microbial population. Treatments (DM basis) were: 1) CONT, a control diet containing 51.9% of a barley-based concentrate, 20.0% alfalfa hay, and 28.2% barley silage; 2) FLAX, inclusion of 11.4% of a non-extruded flaxseed-based product which contained 55% flaxseed, 37% field peas, and 6.8% dehydrated alfalfa; 3) EF, inclusion of 11.4% of an extruded flaxseed-based product which contained 55% flaxseed, 37% field peas, and 6.8% dehydrated alfalfa; and 4) EFT, inclusion of 11.4% of an extruded flaxseed-based product which contained 55% flaxseed, 37% high-tannin faba beans (*Vicia faba*), and 6.8% dehydrated alfalfa. The flaxseed-based products used in FLAX, EF, and EFT were included (3 kg/d) by partially replacing 3 kg/d of the barley-based concentrate. At the end of each period, samples of ruminal contents were collected and DNA was extracted from samples. The V3 hypervariable region of the 16S rRNA bacterial gene was amplified and sequenced. Sequenced reads were subjected to phylogenetic classification using the pipelines UPARSE and QIIME. Data for the abundance of bacterial taxa were analyzed using the MIXED procedure of SAS. Major bacterial phyla were not affected ($P \geq 0.34$) by diet and included *Bacteroidetes* (48.8 ± 3.66%), *Firmicutes* (46.0 ± 3.92%), and *Proteobacteria* (1.3 ± 0.30%). Major bacterial families were similar ($P \geq 0.71$) across diets and were represented by *Prevotellaceae* (20.2 ± 2.82%) and *Veillonellaceae* (16.3 ± 6.19%). In addition, major genera remained unaffected ($P \geq 0.38$) and included *Prevotella* (19.3 ± 2.47%) and *Succiniclasticum* (14.5 ± 6.12%). However, compared to CONT, there were shifts in some bacterial families and genera for EF and EFT. The biohydrogenating bacteria, *Clostridium*, decreased ($P < 0.01$) resulting in 0.4, 0.1, 0.1, and 0.2 ± 0.05% for CONT, FLAX, EF, and EFT, respectively. Flaxseed extrusion and high-tannin faba beans did not affect predominant bacterial taxa; however, there were shifts in less abundant taxa including a decrease in

the biohydrogenating genus *Clostridium*.

Key Words: biohydrogenation, extruded flaxseed, rumen microbiome, tannin

1636 Effects of inoculum source and ammoniation on in vitro gas production kinetics of barley straw.

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A batch culture was conducted to assess the effects of inoculum source and ammoniation on in vitro gas production (GP) and DM digestion (DMD) kinetics of barley straw (BS). The experiment was a 2 × 2 × 2 factorial with low- vs. high-fiber digesting rumen inoculum; ammoniated vs. untreated BS; and with and without the replacement of forage with concentrate. All substrates were ground through a 2-mm screen. Inoculum was collected from two low- and two high-fiber digesting beef heifers as defined by the rate of digestion (0.021 to 0.026/h) and effective degradability (ED) of DM of BS. For the concentrate treatment (BSC), 30% BS was replaced by an equal amount of concentrate. Additional vials containing only concentrate were used to correct for its contribution to GP. The GP was recorded at 3, 6, 9, 12, 24, 36, 48, and 72 h and DMD was measured after 6, 12, 24, 48, and 72 h. The experiment was repeated three times on different days. Data were fitted to exponential models: $GP = b(1-e^{-c(t-L)})$ and $DMD = a+b(1-e^{-c\,(t-L)})$. The GP parameters were not affected by inoculum source, but lag time decreased ($P < 0.01$) with ammoniation (0.6 h) vs. untreated (1.5 h) or with BSC (0.7 h) vs. BS (1.4 h). Initial GP (ml/g OM) increased ($P < 0.01$) with ammoniation (8.1) vs. untreated (7.1) or with BSC (8.2) vs. BS (7.0). For DMD, the high- vs. low-fiber digesting inoculum decreased ($P < 0.01$) the soluble fraction, lag time and ED of DM without affecting the potentially digestible fraction or rate of disappearance of the potentially digestible fraction. Ammoniation improved ($P < 0.01$) DMD kinetics (soluble, 11 vs. 15%; potentially digestible, 50 vs. 59%; rate, 5.4 vs. 6.2%/h; lag time, 2.8 vs. 2.0 h) and ED (30 vs. 36%) of BS. The BSC compared with BS had greater ($P < 0.01$) ED (36 vs. 31%) without altering other DMD parameters. Although both inoculum source (soluble, $P < 0.05$; lag time, $P < 0.01$; and ED, $P < 0.10$) and BSC (potential digestible fraction, lag time, and ED; $P < 0.01$) exhibited an interaction with ammoniation, kinetic parameters tended to be improved by ammoniation. These results suggest that inoculum from high-fiber digesting cattle did not improve in vitro GP or DMD of BS. In addition, the study confirmed that ammoniation improved the ruminal digestion of BS.

Key Words: ammoniated straw, batch culture, inoculum source

1637 Feeding ground flaxseed to lactating dairy cows decreases the ruminal proportion of *Archaea*, but does not change the major species of cellulolytic bacteria.

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The objective of this study was to investigate the impact of incremental amounts of ground flaxseed (GFX) on ruminal microbiota of lactating Jersey cows. Twelve lactating organically-certified Jersey cows (76 ± 23 DIM and 431 ± 25 kg of BW), part of a larger feeding trial, were used in a replicated 4 × 4 Latin square design with 21-d periods (14 d for diet adaptation and 7 d for sample collection). Cows were randomly assigned to 1 of 4 treatments (DM basis) consisted of 55% mixed-mostly grass silage, 8% mixed-mostly grass hay, 2% roasted soybean and: 1) 0% GFX, 6% soybean meal (SBM), and 27% corn meal (CM), 2) 5% GFX, 4.8% SBM, and 23.2% CM, 3) 10% GFX, 3.5% SBM, and 19.5% CM, and 4) 15% GFX, 2% SBM, and 16% CM. Ruminal fluid was sampled using an esophageal tube 7 h after the morning feeding on d 17 to 19 of each experimental period, pooled, and frozen at −80°C until analysis. After DNA extraction, the 16S rRNA gene V4 variable region PCR primers 515/806 were used. Following amplification, PCR products were pooled in equal proportions based on their molecular weight and DNA concentration, purified using calibrated Ampure XP beads, and then used to prepare the DNA library for Illumina TruSeq DNA analysis (Mr. DNA Molecular Research Laboratory, Shallowater, TX). Sequencing was performed on a MiSeq and data were processed using a proprietary analysis pipeline. Final operational taxonomical units were classified using BLASTn against a curated database derived from GreenGenes, RDPII, and NCBI. Orthogonal polynomial contrasts were used to test linear and quadratic effects. Results are shown in Table 1. The ruminal proportion of archaea responded quadratically to feeding GFX. Specifically, the proportion of *Methanobrevibacter* sp. and *Methanosphaera* sp. responded quadratically, whereas that of *Methanomicrobium* sp. decreased linearly with the greatest level of GFX resulting in the lowest values. Quadratic effects were also observed for *Fibrobacter* sp. and *Prevotella* sp. with feeding GFX. Whereas the 3 major ruminal cellulolytic species (*Fibrobacter succinogenes*, *Ruminococcus albus*, and *Ruminococcus flavefasciens*) were not affected by GFX supplementation, the ruminal proportion of *Prevotella ruminicola* and *Prevotella briantii* responded quadratically

Table 1637.

Table 1. Effect of ground flaxseed (GFX) on ruminal microbiota.

	Diets (% GFX)					$P < 0.05$	
% of total	0%	5%	10%	15%	SEM	Linear	Quadratic
Archaea	5.70	4.17	4.39	3.20	0.66	<0.01	0.01
Methanobrevibacter sp.	5.49	3.99	4.21	3.04	0.67	<0.01	0.02
Methanomicrobium sp.	0.06	0.05	0.05	0.04	0.01	0.04	0.15
Methanosphaera sp.	0.14	0.12	0.12	0.11	0.01	0.04	0.04
Butyrivibrio fibrisolvens	0.14	0.15	0.13	0.14	0.02	0.82	0.62
Prevotella sp.	11.3	12.7	14.1	17.7	0.87	<0.001	<0.001
Prevotella ruminicola	0.10	0.14	0.16	0.25	0.03	<0.001	<0.01
Prevotella bryantii	0.01	0.02	0.02	0.03	0.004	<0.001	<0.001
Fibrobacter sp.	2.10	2.11	2.02	1.77	0.14	<0.01	<0.01
Fibrobacter succinogenes	0.21	0.22	0.21	0.27	0.08	0.31	0.37
Ruminococcus sp.	5.86	5.68	5.26	4.64	0.21	<0.001	<0.001
Ruminococcus flavefaciens	0.46	0.45	0.44	0.46	0.03	0.76	0.78
Ruminococcus albus	0.02	0.03	0.03	0.03	0.03	0.43	0.48

with greatest values found when feeding 15% GFX. Overall, feeding incremental amounts of GFX to lactating dairy cows decreased the ruminal proportion of methanogens, but did not affect the 3 major species of ruminal cellulolytic bacteria.

Key Words: dairy cows, ground flaxseed, ruminal microbiota

1638 Data acquisition settings of the Ankom RF system and inocula donors affect in vitro gas production.

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In vitro gas production (IVGP) provides information about the fermentation of feeds. The Ankom RF is a gas-release system that electronically acquires gas pressures. Objectives were to determine the effects of valve-opening pressure (OP) and release time (RT) on IVGP and evaluate the effects of inocula donor on IVGP of selected substrates. Settings for OP were 1, 3, or 8 psi and for RT were 250 or 500 msec. Blended inocula (strained ruminal fluid and ruminal solids blended with media) were composited from 3 steers fed high-NDF (40.3% DM; HF) or high-starch (28.3% DM; HS) diets. Data acquisition terminated early in run 4, and only IVGP for 3, 4.5, 6, 9, 12, 24, and 36 h were evaluated. Duplicate substrates and triplicate blanks were fermented for each OP and RT combination in two runs each with HF or HS inoculum. For each time, the statistical model included order of inoculation, donor (D), substrate (S), D*S, OP, and RT, with module within run as the experimental unit. Blank IVGP increased until 12–18h, then decreased linearly with a leak rate of −0.35 mL/h. Blank subtraction corrected for leakage resulting in plateau-shaped curves and differentiated lag responses for all S. Donor HF generated higher blank IVGP (4.4 mL at 9 h) than HS, which indicated more fermentable matter in HF inoculum. Blank IVGP decreased with increasing order of inoculation. Across S, IVGP differed ($p < .01$) among OP after 3 h (22.9, 0.5, and −23.7 mL/g, for 1, 3, and 8 psi, respectively). For 3 to 24 h, IVGP was higher ($p < .01$) for 500 than 250 msec RT (maximum difference of 38.1 mL/g at 9 h). Numerical derivatives of cumulative curves showed spikes when valves opened. Lower OP and shorter RT resulted in more valve openings, and also obtained lower headspace pressures. Donor HF generated lower IVGP than HS across all S, which was significant ($p < .006$) after 6 h. Up to 18 h, there was a D*S interaction ($p < .036$) with HF generating more IVGP for stover while HS was greater for corn starch. There was little difference in IVGP between HF and HS for solka floc or HMC. Results indicate that blank correction was necessary and IVGP was greater for OP of 1 psi and RT of 500 msec. Data acquisition settings may affect fermentation or create artifacts in measurements. Settings and donors should be

optimized to meet experimental objectives.

Key Words: Ankom RF, gas production, inoculum donor

1639 Effect of duration of in vitro incubation on disappearance of NDF and starch from chopped corn plants versus their resulting corn silages.

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The corn silage fermentation process and its duration can alter the extent of in vitro digestion of NDF and starch. The objective of this study was to determine whether extending in vitro incubation time will enlarge or dispel differences between fermented and unfermented corn plants in extent of in vitro digestion. Ten corn silages were prepared from Pioneer non -BMR hybrids grown at a single location and harvested on a single date at an average of 36% DM. Disappearance of NDF and starch from the unfermented chopped corn plants and from the kernel processed corn silages produced from these plants fermented for 4 mo was measured after various in vitro incubation time intervals at a commercial laboratory. Despite differences among samples in NDF and starch content, no differences among these silages for in vitro NDF digestibility or 7 h starch digestion were detected. At the longest incubation times tested, unfermented plants and corn silages had similar digestibility. But at shorter incubation times, extent of digestion of NDF and starch for the corn silages was related curvilinearly ($P < 0.05$) to those for unfermented plants. In vitro disappearance of NDF was 9, 12, 11, 10, 9, and 3% points lower for corn silages than for chopped corn plants at in vitro incubation times of 6, 12, 24, 30, 40, and 240 h. In vitro starch disappearance was 5, 9, 12, 5, 0, and 0% points greater for corn silages than for chopped corn plants at in vitro incubation times of 2, 4, 7, 12, 24, and 72 h. The correlation between unfermented plants and their silages in both NDF and starch disappearance within an incubation time interval proved weak (R2 = 0.00 to 0.36). In vitro disappearance of starch from these corn silages was not correlated with kernel processing score. Based on the typical in vitro fermentation times used commercially, corn silage fermentation for 4 mo increased in vitro digestion of starch but decreased in vitro digestion of NDF. The difference between unfermented corn plants and corn silages at various in vitro fermentation times implies that improvements in ruminal starch digestion from corn silage allowed to ferment for several months should be greatest with shorter ruminal residence times (7 h or less). However, adverse effects on NDF digestion may partially counterbalance the energy benefit from increased ruminal starch digestibility associated with longer fermentation times.

Key Words: corn silage, NDF, starch

1640 Rumen protozoal communities are dynamic after a dietary switch from conserved forage to pasture.

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Rumen protozoa shift in response to dietary factors, however, little is known about the stabilization of rumen protozoa populations after a diet change. The objective of this study was to characterize the weekly shift in rumen protozoal communities during the transition from a conserved forage (CF) to pasture. Individual rumen digesta samples were obtained from five lactating Holstein cows on weeks −1, 1, 2, 3, 4, and 5 relative to the diet switch. DNA was extracted from rumen digesta and the V3-V4 region of the 18S rRNA gene was amplified using PCR. Sequence reads were produced with the Illumina Miseq (v.3) platform and bioinformatics were performed using the MOTHUR program (v. 1.36.1). Real-time PCR was used to assess protozoal densities (cells/mL digesta). The PROC MIXED procedure of SAS (v. 9.4) was used to analyze data using a repeated measures ANOVA. On week 5 of pasture, protozoal densities were higher than CF (4.97 vs. 3.48 cells/mL digesta, respectively; $P < 0.01$). The genera *Entodinium* ranged from 2–79% abundance, *Dasytricha* from 3–71%, *Eudiplodinium* from 1–51%, *Isotricha* from 1–35%, and *Ostracodinium* from 1–17%. The genus *Isotricha* was most abundant on week 1 after the diet switch ($P < 0.05$). The abundance of protozoa belonging to the genus *Dasytricha* was higher than the CF diet by week 5 on pasture ($P < 0.05$), while protozoa of the genus *Eudiplodinium* tended to be lower after week 5 when compared to CF. In conclusion, protozoal populations were highly dynamic across weeks and within animals.

Key Words: diversity, Illumina MiSeq, protozoa densities

1641 Effects of *Bacillus subitilis* supplementation on milk production and rumen fermentation of dairy cows.

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The objective of this study was to assess the effect on milk performance and rumen fermentation of *Bacillus subtilis* C-3102 (Calsporin®; Asahi Calpis Wellness Co., Ltd., Japan). Three hundred and seventy-five lactating cows (132 primiparous, 243 multiparous; BW = 621 ± 76 kg; DIM = 145 ± 93, yield = 42.1 ± 8,1 kg/d) were randomly allocated to 3 treatments and fed a common TMR containing 15.4% CP, 39.7% NDF and 1.57 Mcal of NEl/kg. Treatments consisted of no supplementation (T0), 1.5 x 10^5 CFU/g (T1), and 3 x 10^5 CFU/g (T2) supplementation with *B. subitilis* C-3102. Calsporin® was supplemented individually during milking using a precision feeding system. At each milking, cows received either 100 g of barley (T0), or 100–150 g of barley containing Calsporin®

Table 1640.

	Diet						SE	*P* value
	Conserved Forage	Pasture						
Taxa	week -1	week 1	week 2	week 3	week 4	week 5		
Dasytricha	25.02	23.44	6.35	36.06	26.54	52.38	9.08	0.15
Eudiplodinium	18.12	16.57	30.96	21.68	9.49	4.56	4.82	0.07
Entodinium	14.93	10.61	31.61	14.77	27.06	12.80	7.16	0.52
Isotricha	5.70	21.93	3.31	3.70	10.28	9.41	3.27	0.23
Ostracodinium	9.54	3.70	3.04	3.24	5.10	1.89	1.59	0.01
Diplodinium	0.65	1.09	1.58	1.26	1.24	0.20	0.37	0.90
Epidinium	1.15	0.95	1.48	1.64	1.70	0.03	0.43	0.57
Un-Ophryoscolecidae	13.58	11.06	16.70	11.13	12.33	5.25	3.37	0.30
Un-Entodiniomorphida	2.48	1.29	0.78	1.29	0.81	1.51	1.35	0.09
Un-Trichostomatia	1.70	3.97	1.80	2.93	1.87	5.19	0.58	0.03
<1% abundance	6.03	5.09	2.39	2.30	3.57	6.79	0.90	0.01

Un = unclassified; *P*-values compare the CF diet with the average of pasture weeks 4 and 5.

to supplement either 0.3 (T1) or 0.6 g/cow/day (T2) for 105 d. Cows are milked 3 times a day. Milk production was recorded daily. Thirty cows (10 from each treatment) were sampled for rumen contents at 42 and 84 d using an esophageal tube after the morning milking. Rumen pH and VFA concentrations determined. Data were analyzed using a mixed-effects model with week as a repeated measure. Cow was the experimental unit (n = 125). Primiparous cows on T2 produced more ($P <$ 0.01) milk after wk 6 of study (35.6 ± 0.82 kg/d) than primiparous cows on T1 and T0 (34.2 ± 0.82 kg/d), whereas multiparous cows on both T1 and T2 (38.5 ± 0.82 kg/d) produced ($P <$ 0.05) more milk than multiparous cows on T0 (36.1 kg/d) after 3 wk of study. Changes in rumen fermentation profile were minor. Rumen molar proportions of propionate decreased (P < 0.05) at 84 d compared with d 42 in T1 and T2 (from 26.8 to 25.2 ± 0.48%) compared with T0, which remained constant (24.8 ± 0.48%). Molar proportions of rumen butyrate decreased ($P < 0.05$) between 42 and 84 d in T0 (from 11.5 to 9.9 ± 0.43%) compared with in T1 and T2, which remained constant (10.5 ± 0.43%). The supplementation of Calsporin® seems to exert a positive effect on milking persistency of dairy cows, with a positive response already obtained 1.5 x 10^5 CFU of *B. subtilis*/g. About 3 and 6 wk of exposure to treatments are needed for a milk response to become evident in multiparous and primiparous cows, respectively.

Key Words: probiotic, rumen, yield

1642 Effect of *Enterococcus fecalis* SROD5 supplementation on microbial communities and quantities of in vitro rumen fermentation.

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Enterococcus fecalis is one of the beneficial microorganisms, which produces fumarate reductase that converts fumarate to succinate and reduces methane production in vitro. Hence, this study was conducted to determine the effect of *E. fecalis* SROD5 supplementation on archaeal diversity and microbial population. Fresh culture of *E. fecalis* SROD5 (7.5 × 10^8 cfu/ml) at different inclusion rates (0, 0.1%, 0.5%, and 1.0%) were investigated using in vitro rumen fermentation. Ruminal samples were collected from cannulated Holstein Friesian cow and 40:60 rice straw to concentrate ratio were used as substrate at 1 g dry matter (DM) per 100 ml buffered rumen fluid. Samples from in vitro fermentation of 12 h incubation were used for determination of microbial community and quantity. Pyrosequencing of archaeal 16S rRNA gene showed that the number of operational taxonomic units (OTU) was highest in supplementation of 0.1% *E. fecalis* SROD5 (39). Shannon-Weaver index were comparable among control and treatments while Chao 1 was higher in 0.1% and 0.5% supplementation of *E. fecalis* SROD5 with 52 and 54, respectively. Meanwhile, alignment of archaeal reads showed that almost all retrieved from in vitro rumen fermenta samples fell into the phylum *Euryarchaeota*, which predominantly affiliated with family *Methanobacteriaceae* (97% to 99%) followed by *Methanomicrobiaceae*, and *Methanosarcinaceae*. Abundance of *Methanobrevibacter* was higher in non-supplementation of *E. fecalis* SROD5 with 96.54%. Higher abundance of *Methanomicrobium* was observed in 0.1% *E. fecalis* SROD5 supplementation while higher abundance of *Methanosphaera* and unclassified *Methanobacteriaceae* as well as the presence of *Methanimicrococcus* were observed in 0.5% *E. fecalis* SROD5. Supplementation of 0.1% *E. fecalis* had the highest quantities of total bacteria (2.59 × 10^8 copies/ml), total fungi (1.03 × 10^4 copies/ml), *Fibrobacter succinogenes* (1.62 × 10^5copies/ml), and *Ruminococcus flavefaciens* (1.51 × 10^3 copies/ml) while the highest methanogen quantity was observed in non-supplementation of *E. faecium* with 2.74 × 10^1 copies/ml). Addition of *E. fecalis* SROD5 changed the archaeal communities of in vitro rumen fermenta. Supplementation of 0.1% *E. fecalis* SROD5 increased microbial

population and decreased methanogen quantity.

Key Words: *Enterococcus fecalis* SROD5, in vitro, pyrosequencing

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1643 Effects of dietary neutral detergent fiber and starch ratio on rumen epithelial cell morphological structure and gene expression in dairy cows.

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Dietary neutral detergent fiber (NDF):starch ratio has been considered a potential indicator to reflect carbohydrate composition in diet formulation and could affect the composition and content of VFA in rumen of dairy cow. Rumen epithelial papilla as small bumps of the rumen mucosal epithelium could broaden the surface of the rumen, which was beneficial for improving the absorption ability of nutrients, especially for VFA. This study was designed to investigate the effect of dietary NDF:starch ratio on rumen epithelial cell morphological structure and gene expression. Eight primiparous dairy cows including 4 rumen cannulated animals were assigned to 4 total mixed rations with NDF:starch ratios of 0.86, 1.18, 1.63, and 2.34 from T1 to T4 in a replicated 4 × 4 Latin square design. The duration of each period was 21 d including a 14 d adaptation period and a 7 d sampling period. Rumen epithelial papilla was collected from rumen cannulated cows. Morphological structure of rumen epithelial papilla was detected and several genes related to the absorption and metabolism of VFA and growth of rumen epithelial papilla cell were analyzed with quantitative real-time PCR, including NHE1, NHE3, NHE4, MCT1, MCT2, MCT4, Na/KATPase, HMGCS, ACSS1, ACSS2, ACSS3, HMGCL, ACAT1, IGFBP3, IGFBP5, and IGFBP6. The results showed that the thickness of stratum spinosum and basale was linearly increased with increasing of dietary NDF:starch ratio (39.58^{a}, 42.84^{a}, 43.24^{a}, and 54.22^{b} mm for T1 to T4, $P = 0.02$), which indicated that surface of the rumen wall could be broadened and the absorption capability of VFA could be improved with the increasing dietary NDF: starch ratio. Expression of HMGCS as the limited enzyme in synthesis of ketone body metabolized by VFA was linearly downregulated ($P = 0.02$), while the expression of MCT2 positively correlated with the absorption capability of VFA was linearly upregulated with the dietary NDF:starch ratio increasing ($P < 0.01$). As dietary NDF:starch ratio increased, expression of IGFBP5 related to the growth of rumen epithelial papilla was downregulated ($P < 0.01$), while IGFBP6 expression was upregulated ($P < 0.01$), which were regulated by the short-chain fatty acids (SCFA) part of VFA. Dietary NDF:starch ratio significantly improved the thickness of stratum spinosum and basale of rumen epithelial papilla and regulated genes expression of VFA absorption and metabolism and growth of rumen epithelial cell, which may be indicative of an activated response of VFA absorption improvement with dietary NDF:starch ratio increasing.

Key Words: dairy cow, NDF: starch ratio, rumen epithelial cell morphological, gene expression

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1644 Rumen disappearance of capsaicin and dihydrocapsaicin in lactating dairy cows.

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The objective of this study was to assess rumen disappearance rate and escape of the two main active compounds of *Capsicum* oleoresin, capsaicin (CAP), and dihydrocapsaicin (DHC), in lactating dairy cows. The study involved 4 early- to late-lactation Holstein cows (24 ± 2.9 kg/d DMI; 38 ± 5.2 kg/d milk yield; 624 ± 28 kg BW) and consisted of 3, 10-d experimental periods. *Capsicum* oleoresin (CO) was administered into the rumen of the cows at 3 pulse-doses: 250, 500, and 1000 mg/cow. All cows received 250 mg CO in period 1500 mg in period 2, and 1000 mg in period 3. Chromium-EDTA was used as a rumen fluid phase passage rate marker. On day one of each experimental period, CO and Cr-EDTA solutions were administered intraruminally in each cow through the rumen cannula at the time of feeding (cows were fed once daily around 8 a.m.). Rumen fluid samples were collected at 0 (background), 0.5, 1, 2, 6, 12, and 24 h post-CO administration and analyzed for Cr, CAP, and DHC. Concentration data were fitted to a single exponential decay model using the NLIN procedure of SAS. The rate of degradation of CAP or DHC was found as: $k_{Cr} \div k_{CAP}$ or $k_{DHC} \times 100$, where k_{Cr} is the slope of decline in Cr concentration in ruminal fluid (on average 0.25 ± 0.06 h^{-1}) and k_{CAP} or k_{DHC} are slopes of decline in CAP and DHC concentrations. Rumen disappearance rates of CAP were 1.34 ± 0.711, 0.91 ± 0.248, and 1.50 ± 0.309 h^{-1} for 250, 500, and 1000 mg CO, respectively. Rumen disappearance rates of DHC were 2.22 ± 1.018, 1.82 ± 0.336, and 1.62 ± 0.372 h^{-1}, respectively. Rumen escape of CAP was estimated at 15.4, 32.6, and 17.6%, respectively, and that of DHC was 31.7, 19.3, and 16.1%, respectively. Average concentration of DHC in fecal samples was 35.6 ± 6.05 ng/g with the 1000 mg dose, whereas capsaicin was not detected in feces. CAP and DHC concentrations were 361 ± 52.6 and 203 ± 27.9 ng/mL in milk, respectively, with the 1000 mg dose, and the compounds were not detected in milk from non-treated cows. In this study, rumen escape of CAP and DHC in lactating dairy cows was

between 15.4 and 32.6%, depending on dose.

Key Words: capsaicin, dihydrocapsaicin, rumen disappearance

1645 WS Effects of capsaicin source on blood capsaicin, glucose and insulin concentrations, rumen fermentation and nitrogen balance of sheep.

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This study evaluated the bioavailability of ruminally-protected capsaicin, and potential effects on rumen microbial fermentation, diet digestibility, and N retention of sheep. Twenty-one wether lambs (36.1 ± 1.0 kg BW) were used in 2 experimental periods (19 d each) based on BW (9 and 12 lambs in period 1 and 2, respectively). From d 1 to 7 of each period, lambs were adapted to indoor individual pens, and then moved to metabolism crates from d 8 to 19. Lambs were fed twice daily alfalfa hay and 1 of 3 supplements containing no capsaicin (CON), unprotected capsaicin (DCAP), or ruminally-protected capsaicin (RPCAP). On d 14 and 19, blood samples were collected at 0, 0.5, 1, 2, 4, 8, and 12 h, and on d 19 rumen fluid samples were collected 4 h after supplement delivery. Feces and urine were collected once daily for 5 d. The experiment was a randomized complete block, and the model included treatment, h, and treatment × h. Capsaicin was not detected in serum of lambs, and no treatment × h interactions ($P \geq 0.06$) occurred for plasma glucose or insulin on d 14 or 19. Total VFA concentrations were lowest for DCAP, intermediate for RPCAP, and greatest for CON ($P = 0.05$). Acetate proportions (mol/100 mol) tended to be lower ($P = 0.06$) for DCAP than CON and RPCAP. Fecal excretions of DM, OM, NDF, and ADF were lower ($P < 0.01$), and DM, OM, NDF, and ADF digestibility (% of intake) were greater ($P < 0.01$) for lambs fed DCAP than CON and RPCAP. Nitrogen intake, fecal and urinary N, N digestibility, and N retention were not affected ($P \geq 0.15$) by treatments. Greater differences in rumen VFA concentrations between DCAP and CON than RPCAP and CON suggest that shifts in microbial fermentation were greater when capsaicin was not ruminally-protected in a prill. Undetectable capsaicin in serum of lambs receiving capsaicin, and minimal effects of RPCAP on N balance indicates the concentration of capsaicin provided may not have entered systemic circulation. This could be due to potential microbial breakdown, inability to be absorbed, or rapid post-absorptive metabolism. Further work is warranted to develop a source of absorbable capsaicin that will withstand degradation in the rumen to allow an increase in blood capsaicin to serve as a potential anti-inflammatory supplement in ruminants.

Key Words: capsaicin, ruminally-protected, sheep

Fig 1646.

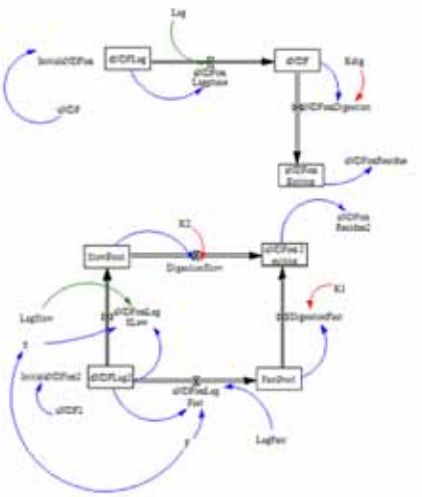

Figure 1. Multi compartment model describing in-vitro aNDFom digestion.

1646 Describing aNDFom in vitro digestion with a multi-compartment model and evaluation of predictions in the CNCPS v7.0 model.

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Models such as the CNCPS rely on having accurate values for digestion rate to aid in predicting metabolizable energy and protein yield from the rumen and subsequent milk yield and total tract digestibility. In vitro aNDFom digestion displays a sigmoidal shape, which is the result of a two-step process: the lag phase, where bacteria attach to substrate and establish digestion and the digestion phase where substrate is being degraded. In previous mechanistic models, the lag phase was discrete, meaning that aNDFom digestion could occur only after the lag phase was over. In other statistical models aNDFom digestion has been described with a multi-compartment system using γ functions. Such models can describe the sigmoidal shape of aNDFom digestion but the estimated rate of digestion were probabilistic and not deterministic. The objective of this study was to develop a mechanistic model that describes the sigmoidal behavior of in vitro aNDFom digestion, using differential equations to provide deterministic values of digestion rates. The proposed are multi-compartments models (Fig. 1), one describing aNDFom in plant by-products, where the digestible aNDFom fraction (dNDF) is unique; and the other describing aNDFom digestion in forages, where dNDF is further fractionated into fast and slow digesting pools. In both feed types a fraction remains un-digested over time (uNDF). In these models, the lag phase is a rate, the life-time of the dNDF fractions is consistent with a γ distribution, and the behavior of the system is sigmoidal. The model was fitted to 36 conserved forages, 32 fresh forages; and 15 plant by-products analyzed in-vitro. The quality of fit was evaluated with overall slope (1.03), intercept (0.01), R^2 (0.98), and an

RMSE (0.02) of the regressions of observed versus predicted. Further, the relevance of the model predictions were assessed by evaluating the RMSE of CNCPS predictions of ME allowable milk and aNDFom TTD, using information from a lactating cattle study where treatment diets were formulated to quantify the effects of aNDFom source and digestibility. Parameters of aNDFom digestion were calculated for each ingredient of the diets, and used as inputs for CNCPSv7.0. The experimental design was a 3 x 3 Latin square with 21 d adjustment and 5 d sampling periods this was used to develop the RMSE calculations. The RMSE of predictions among the three treatments were 0.8 Kg for ME allowable milk and 4% for aNDFom total tract digestibility.

Key Words: aNDFom, modeling, multi compartments model

1647 WS mammalian hormones associated with stress impact microbial fermentation of rumen fluid in vitro. L. L. Rath*, K. L. Samuelson, A. L. Salazar, F. A. Lopez, E. J. Scholljegerdes, and C. A. Loest, *New Mexico State University, Las Cruces.*

Mammalian stress hormones may negatively impact bacteria found in the digestive tract, which could be harmful to animals undergoing stress such as newly received cattle. This study evaluated the effects of epinephrine, norepinephrine, and cortisol on rumen microbial fermentation and gas production in vitro. Treatments included no stress hormone (CON), epinephrine (EPI), norepinephrine (NOR), cortisol (CORT), and a combination of EPI, NOR, and CORT (ALL). Catecholamine treatments were added to fermentation flasks at 1.125 ng/mL, and the cortisol treatment was added at 1.15 ng/mL of rumen fluid. At initiation of the study, rumen fluid was collected from two ruminally-cannulated cows, homogenized with McDougal's artificial saliva, and inoculated with one of 5 treatments for 5 consecutive periods. The rumen microbial fermentation products ammonia (NH_3) and volatile fatty acids (VFA) were sampled at h 0, 2, 4, 6, 8, and 12 during each of the first 4 periods to produce a total of 120 in vitro fermentation samples. The pH was also measured at each collection time. Gas production was measured during the final period at h 0, 0.25, 0.5, 0.75, 1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, and 12 from 24 fermentation flasks in which the 5 treatments were present in 4 replicates allowing for 4 blanks. Neither pH, NH_3, nor total VFA concentration were different ($P \geq 0.40$) among treatments. Molar percentages of acetate and isovalerate in rumen fluid were lower ($P < 0.01$) for EPI and NOR than CON, CORT, and ALL. Conversely, molar percentages of butyrate in rumen fluid were greater ($P = 0.03$) for EPI and NOR than CON, and intermediate for CORT and ALL. A treatment × hour interaction ($P < 0.01$) was observed for gas production from 8 h of incubation to the culmination of this experiment, indicating that microbial fermentation is altered by treatments.

Key Words: catecholamine, cortisol, fermentation

1648 RNA sequencing reveals differential expression of genes associated with an altered morphology of rumen papillae in lactating dairy cows fed diets with various forage sources. B. Wang[1], D. M. Wang[1], M. Liu[1], X. B. Wang[1], L. L. Guan[*2], and J. X. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Rumen epithelial wall plays an important role in nutrient absorption and animal health. However, whether forage quality affects rumen epithelial morphology is unclear. The current study was conducted to elucidate the effects of forage quality on rumen epithelial morphology and the potential underlying molecular mechanisms by determining the transcriptome of the rumen epithelium. To achieve these goals, eighteen mid-lactation dairy cows were fed three diets containing different forage sources, including alfalfa hay ($n = 6$, AH), corn stover ($n = 6$, CS), and rice straw ($n = 6$, RS), for 14 wk. The particle size of each diet, ruminal volatile fatty acids, and rumen epithelium thickness were determined, and RNA-sequencing was conducted. The dietary effect on gene expression was investigated by characterizing differential expressed genes through pair-wise comparisons (AH vs. CS, AH vs. RS, CS vs. RS). The concentration of volatile fatty acids in the rumen was greater in AH than in either CS or RS ($P < 0.05$). The thickness of the rumen papillae was greater in RS-fed cows than in cows fed AH or CS ($P < 0.05$), whereas the thickness of the papillary epithelium was reduced in CS-fed cows compared with those fed AH or RS ($P < 0.05$). In total, 37, 47, and 30 differentially expressed genes were identified from pair-wise comparisons between AH vs. CS, AH vs. RS, and RS vs. CS, respectively. Functional analysis revealed these genes involved in ion binding, proliferation and apoptotic processes, and regulation of cellular growth involving extracellular matrix proteins. Our results suggest that forages with different particle sizes and nutrients values affected rumen epithelium morphology by impacting ion binding, cell growth, and cell proliferation/apoptosis. Our findings provide insight into fundamental understanding on the effects of the dietary particle size and nutrient composition on rumen function that are needed for better management of dairy cow feeding.

Key Words: forage particle size, RNA sequencing, rumen epithelial morphology

1649 Effect of ruminal inoculum from bison or cattle on in vitro gas production, feed digestibility, and responses to exogenous enzyme supplementation.

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The objective of this study was to evaluate the effects of increasing the proportion of inoculum from bison vs. cattle with and without feed enzyme (FE) supplementation on in vitro fermentation of barley straw (BS), alfalfa hay (AH), and wheat dried distillers grain with solubles (DG). Two batch culture runs were conducted for each substrate examined. Barley straw and AH were ground through a 1-mm screen and DG was incubated as-is. In run 1, inocula were prepared by combining rumen fluid (vol/vol) of cattle fed a diet containing 70% BS and 30% concentrate (DM basis) and bison rumen fluid (unknown diet) at ratios of 100:0, 67:33, 33:67, and 0:100, respectively. The substrates were incubated for 96 h to determine gas production (GP) kinetics with gas pressure recording at 3, 6, 9, 12, 24, 36, 48, 72, and 96 h. Additionally, DM disappearance (DMD) was determined in run 2. Each run was a completely randomized design without or with FE addition at a rate of 2.0 μL/g substrate DM. The FE was a xylanase–glucanase commercial blend. Asymptotic GP (ml/g DM) of BS (254) and AH (263) was not affected, whereas that of DG responded quadratically (244, 240, 238, and 260; $P < 0.04$) with increasing bison inoculum. Rate of GP (%/h) also responded quadratically for BS (1.6, 1.6, 1.2, and 1.7%/h; $P < 0.01$) and AH (3.0, 3.0, 2.7, and 3.0%/h; $P < 0.03$) with increasing bison inoculum. Lag time of GP linearly ($P < 0.01$) decreased for BS (0.58, 0.93, 0.22, and 0.07 h), AH (0.63, 0.61, 0.29, and 0 h) and DG (0.21, 0.64, 0.11, and 0 h) with increasing bison inoculum. A quadratic ($P < 0.02$) response of DMD (31, 36, 35, and 34%) of BS to increasing bison inoculum was observed, whereas DMD of AH (55, 54, 51, and 51%) and DG (59, 58, 56, and 56%) linearly ($P < 0.01$) decreased. Addition of FE improved ($P < 0.05$) DMD of DG. Compared to cattle inoculum, bison inoculum did not enhance in vitro GP or DMD of the substrates examined. However, the mixture of cattle and bison rumen inocula did appear to synergistically reduce the lag time of GP and improve the DMD of BS. It suggests that the cattle rumen inoculum may lack certain enzymes that were present in the bison inoculum to digest BS, and that these enzymes were not provided by the FE examined.

Key Words: gas production, in vitro digestion, rumen inocula

1650 Ruminal fermentation from Nellore steers supplemented with additives in the rainy season.

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This trial aimed to evaluate the ruminal parameters (pH, ammonia-N and the VFA production) from animals fed supplements with monensin (MON), virginiamycin (VM) or both associated, in the rainy season. Twelve steers cannulated in the rumen (518.42 ± 55.40 kg) were housed in 12 paddocks (one animal on each paddock) of Brachiaria cv. 'Xaraés' and supplemented daily in 0.3% of BW. The diets were: supplement without additives (SUP), with MON (SUPM- 80 mg/kg), with VM (SUPV- 150 mg/kg) and supplement with MON and VM (SUPMV- 80 and 150 mg/kg, respectively). There were four experimental periods of 28 d (27 d for adaptation and 1 d for sampling). Animals were housed continuously in the paddocks with animals used in a trial for performance evaluating. Ruminal pH, ammonia-N, and VFA were measured on samples taken over a 12 h on Day 28 of each experimental period. Ruminal content was obtained at 0, 2, 4, 6, 8, 10, and 12 h after the period of feeding (1000 am). Data were analyzed as a completely randomly design with three replicates by treatment on each period, using the MIXED procedure of SAS. The pH, ammonia-N and VFA were analyzed as a repeated measure. The means of least squares were generated and compared ($P < 0.05$) by Tukey test. The ruminal pH from animals supplemented with additives were greater than animals supplemented without additives ($P < 0.01$), already for the concentrations of ammonia was not significant effect ($P = 0.09$). The acetate ($P < 0.01$) and propionate concentrations ($P < 0.01$) were lower in animals supplement with additives than animals supplemented without additives. However, the A:P ratio did not change ($P = 0.13$) with the inclusions of additives in supplements. The inclusion of MON, VM or both associated in supplements to fed steers on pasture in the rainy season increases the ruminal pH, decreases the acetate and propionate concentrations without affect the A:P ratio.

Key Words: monensin, pasture, propionate, ruminal pH, virginiamycin

1651 The micro gas test: A small scale in vitro system for high throughput analysis. K. Elberg[1], P. Steuer[*2], U. Habermann[2], J. Lenz[2], M. Nelles[1,3], and K. H. Südekum[4], *[1]Department of Waste Management and Material Flow, University of Rostock, Rostock, Germany, [2]Senzyme GmbH, Troisdorf, Germany, [3]German Biomass Research Center GmbH, Leibzig, Germany, [4]Institute of Animal Science, University of Bonn, Bonn, Germany.*

The evaluation of ruminal degradability of feeds and feed additives requires the knowledge of characteristic (kinetic) parameters. These parameters are mainly obtained using in vitro gas production methods. These include measurements at constant pressure (e.g., Hoheneheim gas test (HGT)), measurements at constant volume with accumulating pressure and measurements at constant volume with regular venting. To facilitate automated high throughput measurements, a small-scale system, based on pressure measurement with interval venting was developed and validated. The micro gas test [MGT] represents a cheap and versatile in vitro batch method which reduces the required inoculum volume as well as the personnel effort and space requirements significantly. The MGT is conducted in 20 mL gas chromatography vials that serve as reactors for gas production. Samples (e.g., feedstuffs) and reagents (e.g., feed additives) are accurately weighed into the vials and subsequently closed with a gas-tight sealing. The regulation of CO_2 atmospheric condition is realized through previous gas application. The ruminal fluid solution, which serves as inoculum, is prepared according to the HGT standard procedure. Incubation is performed in a heating chamber at 39°C and starts with dispensing 5 mL inoculum through a cannula into the sealed vial. Simultaneously the pressure is released through a second cannula to atmospheric pressure. For 24 and 48 h, respectively, relative pressure increase in the headspace above the sample is recorded at predefined intervals and subsequently vented. Measurements can be performed manually with manometers or automatically with adjusted autosampling systems. For the validation of the MGT a total of 14 feedstuffs, including a hay and a concentrate standard, were simultaneously incubated in the HGT and the MGT system. The same substrate-inoculum-ratio was applied for further comparison of kinetic parameters. The dried and ground (< 1 mm) feedstuffs covered a wide range of chemical compositions and digestibilities. The HGT method was prepared according to standard procedure. Compared to HGT the MGT resulted in lower ($P < 0.05$) maximum gas productions for all feedstuffs except lignocellulose. The differences were congruent to former findings on system comparisons between HGT and methods with constant volume and pressure release. However, a strong relationship between the HGT and MGT 24 h gas production could be observed. The regression analysis of mean values of both methods resulted in the equation: y = 0.87x + 1.62 with an R^2 of 0.99.

Key Words: automation, Hohenheim gas test, pressure measurement

1652 Rumen protozoal community structures are not altered in lactating dairy cows offered alternative forage crops during short-term grazing experiments. L. M. Cersosimo[*1], R. Tacoma[1], S. Greenwood[1], K. Juntwait[2], A. F. Brito[2], and J. Kraft[1], *[1]University of Vermont, Burlington, [2]University of New Hampshire, Durham.*

The objective of this study was to compare the rumen protozoal community structures and VFA in cows grazing pasture strip-tilled with alternative forage crops (AFC) or traditional grass-legume pasture mix. The study consisted of two, 21-d experiments, spring (SPR) and summer (SUM). Sixteen lactating Jersey cows (SPR: 85 ± 46 DIM; SUM: 143 ± 58 DIM) were split into two groups with eight cows assigned to the AFC (treatment, TRT) and eight cows assigned to traditional mixed grasses-legumes (control, CON). Pasture comprised 40% of the diet (DM basis), while a TMR comprised 60%. SPR AFC (2.4% of total DM) included barley, hairy vetch, rye, triticale, and wheat, and SUM AFC (10.0% of total DM) included buckwheat, oats, and chickling vetch. Milk samples were collected for four consecutive milkings (d 19–21). Individual whole rumen digesta samples (500 mL) were collected on d 20 and 21 of each experiment. Ruminal VFA samples were analyzed by GLC. Microbial DNA was extracted and the V3-V4 regions of the protozoal 18S rRNA gene were amplified via PCR. The program MOTHUR was used to perform bioinformatics analyses. A student's *t* test (JMP Pro 12) compared the LSM between groups and the PROC CORR model in SAS (v.9.4) performed Pearson correlations between rumen protozoal genera, animal performance, and VFA. Yields of milk, milk fat, and milk protein (kg/d) in SPR were: CON, 22.5; 1.08; 0.80 and TRT, 23.4; 1.15; 0.85 and in SUM: CON, 17.3; 0.74; 0.59 and TRT, 18.9; 0.92; 0.70, respectively. Total VFA (m*M*), and molar proportions of acetate (70.8%), propionate (16.0%), and butyrate (1.93%) did not differ in either experiment. The SUM TRT group had a lower ($P < 0.01$) isobutyrate proportion (0.80%) than the SUM CON group (0.98%). Abundance of protozoal taxa did not differ between groups in either experiment. The protozoal genera *Eudiplodinium* (CON: 43.0%; TRT: 49.3%) and *Entodinium* (CON: 48.1%; TRT: 37.1%) were most abundant in SPR and SUM, respectively. The protozoal genus *Diplodinium* (SPR: 6.48%; SUM: 3.28%) was positively correlated ($P < 0.001$) with milk production ($r = 0.69$), milk fat ($r = 0.64$), protein yields ($r = 0.61$), and ruminal propionate ($r = 0.38$; $P = 0.04$). The protozoal genus *Entodinium* was negatively correlated with milk yield ($r = -0.48$; $P < 0.01$). In conclusion, the rumen protozoal community structures and predominant VFA were not altered in AFC-fed cows, yet the genus *Diplodinium* was positively

correlated to animal performance and VFA.

Key Words: ciliates, *Diplodinium,* organic

1653 Metabolomics analysis reveals effect of corn silage levels on ruminal metabolic profiles in Holstein heifers.

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Controlling DMI could be one of the strategies to reduce feed cost and to increase efficiency in dairy heifer growth, whereas the metabolic mechanisms involved in control feeding have not been well examined. The objective of this study was to determine the effect of differing forage-to-concentrate ratios on the ruminal metabolite profiles in heifers under restricted feeding. Twenty-four Holstein heifers (8–10 mo and 253 ± 29 kg of BW) with similar body condition were randomly assigned into four groups and fed diets containing 20% (F20), 40% (F40), 60% (F60), and 80% (F80) of corn silage. All diets were isonitrogenous and isocaloric and provided equal amount of nutrients, and allowed for 800 g/d of ADG. The amount of feed offered was adjusted weekly based on BW. Total tract apparent digestibility of nutrients was determined with acid-insoluble ash as an internal digestibility marker with the TMR and fecal samples. Rumen fluid was sampled from each cow through a stomach tube 4 h after morning feeding at d 30 and analyzed using gas chromatography-time-of-flight/mass spectrometry. The digestibilities of DM (80.9% for F20, 79.4% for F40, 77.2% for F60, and 73.1% for F80, $P < 0.001$) and OM (84.3%, 82.3%, 80.1%, and 76.1%, respectively, $P < 0.001$) decreased linearly with increased corn silage. In total, 247 metabolites were identified from all four groups. The principal component analysis of the relative concentration of mutual metabolites revealed four separated metabolite profile clusters of four groups. The clusters derived from the F40, F60, and F80 partly overlapped with each other, whereas the cluster from the F20 was separated from the other three groups. When the mutual metabolites were used for pathway analysis, the impact values of the pathway were 0.32, 0.23 and 0.21 for pyruvate metabolism, citrate cycle and lysine degradation, respectively. These three pathways may play important roles in improvement of nutrition degradation and utilization. These indicated that lower forage level could promote rumen fermentation and provide more available nutrition for heifers.

Key Words: corn silage levels, heifers, metabolomics

1654 Response of rumen microbiota to diets containing different corn silage levels in Holstein heifers.

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Ruminants have evolved through a close symbiotic relationship with a vast ensemble of ruminal microbiota, which give important metabolic capabilities on the host. The objective of the present study was to evaluate effects of dietary corn silage levels on the changes in the microbiota of the rumen in Holstein heifers. Twenty-four half-sib Holstein heifers (8 to 10 mo of age) were blocked by BW and age in a randomized complete block design in equal numbers and assigned randomly to one of the four diets containing corn silage levels at 20, 40, 60, or 80% of DM. All diets were provided as TMR and calculated to meet the nutrition requirement of 800 g/d of ADG. The rumen contents were collected by the oral stomach tube method. Total genomic DNA of ruminal microorganism was extracted from the whole ruminal contents containing solid and liquid fractions. The V3-V4 region of the bacteria 16S rRNA gene (primers 336F and 806R), ITS1 region of the internal transcribed spacer region of fungi (primers ITS1-F and ITS2), and the partial 18S rRNA gene of protozoa (primers P-SSU-316F and GIC758R) were amplified by PCR. Paired-end sequencing was performed to sequence all libraries on an Illumina Miseq platform according to the standard protocols. For bacteria, a total of 1,544,372 valid reads and 202,189 OTUs were obtained by pyrosequencing. At the OTU level, a significant difference was found in the bacterial communities among all the treatment groups (AMOVA, $P < 0.05$), except that between the 40% and 60% forage groups (AMOVA, $P = 0.23$). The total number of valid reads and OTUs obtained for protozoa were 1,302,936 and 15,279. At the OTU level, a significant difference was found in the protozoal communities between the 20% and 60% forage groups (AMOVA, $P < 0.05$), between the 20% and 80% forage groups (AMOVA, $P < 0.05$), and between the 40% and 80% forage groups (AMOVA, $P < 0.05$). For anaerobic fungi, a total of 1,231,562 valid reads and 33,427 OTUs were obtained. At the OTU level, no significant difference was found in the fungal communities among all the treatment groups. This study demonstrated that the bacterial and protozoa communities in the rumen of Holstein heifers were altered at the OTU level by the dietary forage levels.

Key Words: forage level, heifer, ruminal microbe

1655 Effect of acetate addition and headspace gas composition on in vitro production of volatile fatty acids and gases. L. M. Judd* and R. A. Kohn, *The University of Maryland, College Park.*

The development of in vitro methods to accurately estimate gas production and volatile fatty acid (VFA) profile in rumen fermentation would enable isolation of fermentation effects from animal interactions. This experiment compared 4 headspace gas combinations with or without addition of 50 mM sodium acetate. Gas headspace treatments were: 1) CO_2 (100%), 2) CO_2–CH_4 (50/50), 3) CO_2–H_2 (95/5), and 4) CO_2–CH_4–H_2 (47.5/47.5/5). Each treatment was replicated in 4 tubes with repeated measures of VFA and gas volume taken at 0, 4, 16, 24, and 48 h. Timothy hay (0.1 g) was added to 20-mL tubes, and 0.5 mL sodium acetate solution or buffered medium were added to each tube. Tubes were equilibrated with each gas mixture before adding 9.5 mL rumen fluid. Tubes were incubated at 39°C while shaking with 20-mL syringes attached to collect and measure produced gases. Butyrate production at 4 h was affected ($P < 0.05$) by gas composition, and was: 2.96, 3.09, 2.33, and 1.44 (mM; SE ± 0.437) for treatments 1–4. Propionate production at 48 h was affected ($P < 0.05$) by gas composition, and was: 8.71, 8.97, 10.60, and 7.12 (mM; SE ± 0.789) for treatments 1–4. Gas production at 4 h was 1.08, 2.70, 0.98, and 1.43 (ml, SE ± 0.327) for treatments 1–4. Lower starting concentration of CO_2 in headspace gas may have caused CO_2 efflux from the buffer. There was a trend ($P < 0.1$) for an effect of the gas mix at 24 h on the acetate: butyrate (A:B) ratio of produced VFA. A:B ratios of produced gases were: 2.95, 2.77, 2.87, and 2.18 (mM; SE ± 0.208) for treatments 1–4. In contrast to expectation, there was a trend ($P < 0.08$) for greater acetate production with acetate addition (10.71 mM) than without (7.11 mM, SE ± 1.413). Initial gas composition of in vitro procedures can affect gas production and VFA profiles with higher percentage of CH_4 and H_2in headspace (more reduced conditions) favoring propionate and butyrate over acetate and gas production.

Key words: fermentation, gas profile, in vitro, volatile fatty acids

1656 Predicting the time course of ruminal pH from continuous reticular pH measurements. D. J. Seymour*[1], K. M. Wood[2,3], J. P. Cant[1], and G. B. Penner[2], *[1]Department of Animal Biosciences, University of Guelph, Guelph, Canada, [2]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [3]University of Saskatchewan, Saskatoon, Canada.*

While the ability to continuously measure ruminal pH has been developed, its use is limited by its on-farm practicality. Being able to predict ruminal pH with an orally bolus-dosed reticular pH probe would add increased functionality to existing technology and aid in the diagnosis of SARA. The objective of this study was to develop a model to predict the time course of ruminal pH from continuous reticular pH measurements. pH was recorded every 5 min for 15 d in both the reticulum and rumen of 4 Hereford crossbred heifers (291 ± 8kg BW) as the proportion of concentration in the diet increased every 3 d from 50 to 60, 70, 80, and 88%. Visual inspection of pH time series data revealed that fluctuations in ruminal pH were smaller and lagged behind those of reticular pH. Fitting a polynomial distributed lag model to predict ruminal pH from reticular pH produced residuals that were serially correlated. Because residuals are not available for prediction of ruminal pH with only a reticular pH probe, a novel approach to autocorrelation correction was sought. Based on the hypothesis that over- and underprediction of ruminal pH is related to similar errors in reticular pH, a penalized cubic spline function was fit to time series of reticular pH to generate a smoothed predicted reticular pH curve with residuals. Ruminal pH was then estimated from predictions and residuals of the reticular spline function using the MIXED procedure of SAS. As an alternative, ruminal pH was predicted directly from reticular pH using an unobserved components model (UCM). The predictive ability of both methods was evaluated using 10-fold cross validation. The unobserved components model was able to fit the data better compared to the alternative model (RMSE = 0.26414 vs. 0.47120) though with a higher AICc score (−10356 vs. −21021); this can be resolved by log-transforming the data before analysis. The UCM also had a smaller average error in ruminal pH prediction compared to the alternative model (0.22 pH vs. 0.35 pH) with fewer model parameters (5 vs. 11). The low error is sufficient to predict ruminal pH from continuous reticular pH measurements, allowing for a more cost-effective diagnosis of SARA in near real-time using existing reticular pH probes.

Key Words: SARA, ruminal pH, unobserved components model

1657 Changes in milk production efficiency and ruminal bacterial community composition following near-total exchange of ruminal contents between high- and low-efficiency Holstein cows. P. J. Weimer*[1], M. S. Cox[2], T. Vieira de Paula[3], M. Lin[4], and G. Suen[2], *[1]USDA-ARS, Madison, WI, [2]University of Wisconsin-Madison, Madison, [3]Federal Univ. of Mato Grosso, Cuiabá, Brazil, [4]Yangzhou University, Yangzhou, China.*

The objectives of this study were to determine if milk production efficiency (MPE) could be altered by near-total exchange of ruminal contents between high- and low-MPE cows and to characterize ruminal bacterial community composition (BCC) before exchange and over time post-exchange. Three pairs of ruminally cannulated, third-lactation cows were selected whose MPE (energy corrected milk per unit dry matter

intake [ECM/DMI]) at similar levels of ECM differed over their first two lactations when fed the same total mixed ration. At 79–279 DIM, ~95% of ruminal contents were manually exchanged between cows within each pair. Ruminal pH, and concentrations and proportions of VFA, along with BCC (as determined by 16S rRNA gene sequencing on an Illumina MiSeq) were assessed immediately before and after the exchange, and just before feeding on days −8, −7, −5, −4, −1, 1, 2, 3, 7, 10, 14, 21, 28, 35, 42, and 56, relative to the day of exchange. Where ruminal pH or mol fraction of individual VFA differed ($p < 0.01$) between cows before exchange, they returned to the recipient cow's profile within 1 d. For all 3 low-MPE (LE) cows, MPE increased over 7 d post-exchange but declined thereafter. Two of the 3 high-MPE (HE) cows displayed sharp drops in MPE following introduction of the ruminal contents from the corresponding LE cow, but one surprisingly displayed a transient increase in MPE. For all 6 cows, both liquid- and solids-associated BCC were dissimilar between individuals within a pair before contents exchange. Immediately following exchange, BCC in all three pairs for both phases were more similar to that of the received inoculum than to pre-exchange BCC for that individual. For 5 of 6 cows, the solids-associated community returned within 5–7 d to higher similarity to the pre-exchange community of that host than to the donor community. Individual variability before the exchange was greater in liquids than in solids, as was the variability in the response of their bacterial communities to the exchange. One pair showed rapid return to pre-exchange BCC within 2 d, while the other two pairs took 7–10 d to become more similar to the pre-exchange host than the donor, and continued to change until reaching similarity to the pre-exchange community by 5–7 wk post-exchange. The data suggest a role for the ruminal bacterial community as a variable in MPE.

Key Words: milk production efficiency, ruminal contents exchange, ruminal microbiome

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1658 Synergism of cattle and bison inoculum on ruminal fermentation and bacterial communities in an artificial rumen (Rusitec) fed barley straw.

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This study evaluated the effect of increasing the proportion of bison relative to cattle inoculum on fermentation and microbial populations within an artificial rumen (Rusitec) fed barley straw. The experiment was a completely randomized design with four treatments (0, 33, 67, and 100% of bison inoculum replacing cattle inoculum) replicated in two Rusitec apparatuses with 8 fermenters each ($n = 4$/treatment). The experiment lasted 15 d with 8 d of adaptation and 7 d of sampling. Fermenters were fed a diet of 70% barley straw and 30% concentrate (DM basis). True digestibility of DM (DMD) was determined after 48 h of incubation from d 13 to 15, and daily NH_3 and VFA production were measured on d 9 to 12. Protozoa counts were determined at d 9, 11, 13, and 15 and particle-associated bacteria (PAB) from d 13 to 15. Selected bacterial populations in the PAB were measured using real-time polymerase chain reaction (qPCR). Data were analyzed using the MIXED procedure of SAS. Individual fermenter was considered the experimental unit and day of sampling as a repeated measure. Increasing the proportion of bison inoculum had a quadratic effect ($P < 0.05$) on straw, concentrate and total DMD (50.3, 52.0, 52.8, and 50.3% DMD, respectively), and on straw and total NDF disappearance (NDFD). Increasing bison inoculum linearly increased concentrate NDFD, total and concentrate N digestibility, as well as total daily VFA and acetate production. A quadratic response ($P < 0.05$) was observed for daily ammonia-N, propionate, and butyrate production. Increasing the proportion of bison inoculum linearly increased ($P < 0.05$) total protozoa numbers and had a quadratic effect ($P < 0.05$) on *Fibrobacter succinogenes*, linearly increased ($P < 0.10$) *Ruminococcus flavefaciens* and decreased ($P < 0.05$) *Ruminococcus albus* 16S rRNA copy numbers. Overall, bison inoculum more readily degraded feed protein than cattle inoculum, with a mixture of inoculums synergistically increasing the DMD and NDFD of barley straw. Direct inoculation of rumen contents across ruminant species may be a means of increasing ruminal fiber digestion.

Key Words: bison, rumen inoculum, Rusitec

1659 Effect of peNDF on milk production and composition in goats fed with NNFS replacing alfalfa hay.

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The aim of this work was to evaluate the effect of physically effective neutral detergent fiber (peNDF) in diets with non-forage fiber sources (NFFS) replacing alfalfa hay on milk production and milk composition in dairy goats. The experiment was designed as 4 x 4 Latin square with 8 Alpine goats at final stage lactation. Goats were offered 1 of 4 diets with different peNDF, 2 diets with alfalfa hay (peNDF = 17.3 and 24.1%), and 2 diets with NFFS replacing alfalfa hay (peNDF = 22.3 and 26.8%). The peNDF contents were determined from the sum of the proportion of dietary DM retained either on the 2 or on the 3 sieves of the Penn State Particle Separator multiplied by the neutral detergent fiber concentration of the diet. Each period consisted of 11-d of adaptation stage and 3-d of experimental measurements. Subsequently, diets were exchanged during the other 3 periods. During the experimental days, milk production was recorded and milk fat,

Table 1659.

Table. Milk production and composition affected by peNDF of diets with NFFS replacing alfalfa hay

	peNDF					
peNDF	17.3%	24.1%	22.3%*	26.8%*	SE	P
Milk production (l/d)	1.26[b]	1.39[a]	1.21[b]	1.25[b]	0.16	0.043
Fat (%)	3.10[b]	3.22[b]	4.05[a]	4.41[a]	0.57	0.001
SNF (%)	8.63[a]	8.48[a]	8.53[a]	8.49[a]	0.17	0.397
Protein (%)	3.26[a]	3.20[a]	3.23[a]	3.21[a]	0.06	0.353

[a],[b] Between lines, means with the same letter are not significantly different

*Diets with NFFS replacing alfalfa hay

nonfat solids, and protein were determined using an infrared analyzer. Data were analyzed using GLM procedure of SAS. According to our results, milk production was higher in the diet that contained more alfalfa hay ($P = 0.043$) and milk fat was higher in both rations with NFFS ($P = 0.001$). There was no effect on milk nonfat solids ($P = 0.39$) and protein ($P = 0.353$). In conclusion, the substitution of NDF from alfalfa with NDF from NFFS modified the peNDF in rations without reduced milk production and milk fat in goats.

Key Words: dairy goats, milk production, peNDF

1660 Effects of conventional dietary adaptation over periods of 6, 9, 14, and 21 d on rumen morphometrics of Nellore cattle. D. D. Estevam[1], I. C. Pereira[1], A. L. Rigueiro[2], F. T. Pereira[2], C. L. Martins[1], M. D. Arrigoni[1], and D. D. Millen[*2], *[1]São Paulo State University (UNESP), Botucatu, Brazil, [2]São Paulo State University (UNESP), Dracena, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to determine the effects of adaptation periods of 6, 9, 14, and 21 d on rumen morphometrics, and cell death and proliferation of rumen epithelium of feedlot Nellore cattle. The experiment was designed as a completely randomized block, replicated 6 times, in which 96 20-mo-old yearling Nellore bulls (391.1 ± 30.9 kg) were fed in 24 pens (4 animals/pen) according to the different adaptation periods adopted: 6, 9, 14, and 21 d. Each of the adaptation diets containing 70.0%, 75.0%, and 80.5% concentrate were fed for 2-d, 3-d and 7-d to cattle adapted for 6-d, 9-d and 21-d, respectively. The adaptation diets containing 70.0%, 75.0%, and 80.5% concentrate were fed for 4-d, 5-d and 5-d, respectively, to cattle adapted for 14-d. The finishing diet contained: 71.5% cracked corn grain, 14.0% sugarcane bagasse, 10.5% peanut meal, 2.5% supplement, 1.0% urea, and 0.5% limestone (DM basis). After adaptation one animal per pen was slaughtered ($n = 24$) for rumen epithelium evaluations. The remaining 72 animals were harvested after 88-d on feeding. At harvest, a 1-cm^2 fragment of each rumen was collected from cranial sac. The number of papillae per cm^2 of rumen wall (NOP) was determined, as well as the mean papillae area (MPA). The rumen wall absorptive surface area in cm^2 (ASA) was calculated as follows: 1 + (NOP*MPA)–(NOP*0.002). The papillae area expressed as % of ASA was calculated as follows: (NOP*MPA/ASA)*100. The cell proliferation index (CPI) and cell death index (CDI), both expressed as % of cells proliferating or dying in the rumen epithelium, were determined by PCNA and TUNEL immunohistochemistry techniques, respectively. Orthogonal contrasts were used to evaluate linear, quadratic, and cubic relationship between adaptation periods and the dependent variable. As the adaptation period lasted longer, ASA in cm^2 was affected ($P = 0.03$) cubically (6-d = 37.7; 9-d = 32.5; 14-d = 40.9; 21-d = 39.6). An interaction was observed between adaptation periods and harvesting dates for papillae area ($P = 0.04$), CPI ($P = 0.003$), and CDI ($P = 0.02$), where cattle adapted in 14-d showed larger papillae area (6-d = 97.0%; 9-d = 96.0%; 14-d = 97.5%; 21-d = 96.8%), and smaller CPI (6-d = 58.0%; 9-d = 58.5%; 14-d = 44.8%; 21-d = 53.3%) and CDI (6-d = 62.8%; 9-d = 60.0%; 14-d = 50.4%; 21-d = 57.1%) at the end of adaptation period, but no differences were detected ($P > 0.10$) at the end of finishing period. Yearling Nellore bulls should be adapted in 14 d, because it promoted better rumen epithelium development by the end of adaptation period.

Key Words: adaptation, Nellore, rumen

1661 Pantothenic acid does not affect the concentration of biotin in plasma of Holstein bull calves. G. Ferreira*, C. L. Teets, A. N. Bladen, and A. Geiger, *Virginia Polytechnic Institute and State University, Blacksburg.*

Pantothenic acid interferes with biotin absorption in non-ruminant species. The objective of this study was to determine whether pantothenic acid affects the concentration of biotin in the blood of young calves. Weaned bull calves ($n = 16$) were fed ad libitum a pelleted starter including no B-vitamins and hay for 2 wk before the beginning and until the end of the experiment. Water was available ad libitum at all times. Two weeks after weaning, calves were blocked by age and randomly assigned to 4 treatments according to a randomized complete block design. Treatments consisted of administering, for 14 d, a daily gelatin capsule containing no B-vitamins (CON), 10 mg of biotin (Rovimix Biotin; BIO), 240 mg of pantothenic acid (Rovimix Calpan; PAN), and 10 mg biotin + 240 mg pantothenic acid (BIO+PAN). Expeller soybean meal was used as a carrier of the vitamins in the capsules.

Blood samples were collected by venipuncture of the jugular vein at Days 0 and 14. Concentrations of avidin-binding substances (ABS) in plasma (1:20 dilution) were determined by a single-step competitive enzyme-binding assay (Ridascreen Biotin kit; R-Biopharm GmbH, Darmstadt, Germany). Statistical analysis was performed using the MIXED procedure of SAS as for a randomized complete block design with repeated measures. The statistical model included the effects of treatment (fixed, df = 3), block (random, df = 3), treatment by block interaction (random, df = 9), time (fixed, df = 1), treatment by time interaction (fixed, df = 3), and the random residual error. The concentrations of ABS in plasma were similar for all treatments ($P > 0.24$) and did not change after dosing vitamins over time (3.47 and 3.07 ng/mL for Days 0 and 14, respectively; SEM = 0.7 ng/mL; $P > 0.63$). Plasma concentrations of ABS were substantially higher than those previously reported for lactating dairy cows (0.7–2.1 ng/mL). Based on these data, and contrary to our expectations, pantothenic acid did not affect the absorption of biotin in young calves.

Key Words: biotin, calves, pantothenic acid

1662 Short-term feeding of a tocopherol mix (α-, β-, γ-, and δ) alters the daily pattern of tocopherol isoforms present in milk and blood in lactating dairy cows.

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Fed over several weeks, diets supplemented with α-tocopherol will increase α-tocopherol concentrations in blood and milk. With new attention being paid to other non-α isoforms of vitamin E, how short-term supplementation of other tocopherol isoforms affects subsequent milk and blood concentrations is poorly understood. The objective of this study was to determine the daily pattern of change in the concentrations of 4 isoforms (α-, β-, γ-, and δ) of tocopherol in blood and milk of cattle supplemented with a tocopherol mixture. Four healthy, multiparous Holstein cows (DIM: 179 ± 17 d) were fed a vegetable-derived oil (Tmix) enriched with γ- and δ-isoforms of Vitamin E (9% α-, 1% β-, 62% γ-, and 24% δ-tocopherol) for 7 consecutive days (~620 g Tmix/cow·d^{-1}). Composite milk (~25mL) and whole blood (~15mL) samples were collected daily before the morning feeding. Tocopherol isoform concentrations were determined by high pressure liquid chromatography. Data were analyzed in a complete randomized design with repeated measures. Significance was declared at $P \leq 0.05$. Gamma and α-tocopherols in blood increased by d 1 and d 2, respectively, after feeding with peak concentrations achieved by d 5 (3.6 ± 0.2 μg/mL and 14.1 ± 0.5μg/mL, respectively) when compared to d 0 (0.59 ± 0.2μg/mL and 10.0 ± 0.5μg/mL, respectively). In milk, γ- and α-tocopherol concentrations were elevated by d 2 (0.26 ± 0.04 mcg/g) and d 3 (0.72 ± 0.05mcg/g), respectively, compared to d 0 (0.06 ± 0.04mcg/g and 0.52 ± 0.05mcg/g, respectively). The data illustrate that ~5 d of Tmix feeding at the level used may be sufficient to reach a higher stabilized range of concentrations of the two measurable isoforms in milk and blood in the lactating Holstein. The data establish that this experimental design is adequate toward further refinement of experiments that will be valuable toward characterizing the kinetics and biological value of α- and γ-tocopherols. Additional sampling at the gut level may be informative in determining the fate of other isoforms.

Key Words: concentration, cow, tocopherol

1663 Effect of rumen protected vitamin B complex on metabolic parameters, milk production, and d 15 conceptus and endometrium outcomes.

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The aim of this project was to determine the effects of a rumen-protected vitamin B complex supplementation (VIT B) compared with a control diet containing no supplement (CON) on: milk production and components, concentrations of BHBA, haptoglobin and progesterone in plasma, ovarian dynamics, and Day 15 conceptus and endometrial outcomes. Fifty-one multiparous Holstein cows from the herd at the UBC Dairy Education and Research Centre were enrolled into the study 3 wk before parturition and were randomly assigned to one of the two treatments. Blood samples (2/week), weekly milk samples, and daily feed intake were collected. Cows were enrolled onto a double-ovsynch protocol at 33 ± 3 days post-partum and inseminated by timed artificial insemination (AI). Ovarian structures were monitored and measured using *per rectum* ultra-sonography. The uterus was flushed on Day 15 post-AI for conceptus collection and endometrial samples were collected at the same time. Data were analyzed by ANOVA using the GLM procedure of SAS. Overall, 42 cows were flushed and 13 embryos were collected (recovery rate = 31%). Vitamin B supplementation had no affect on the size of the embryo ($P = 0.49$), ovulatory follicle size ($P = 0.51$), or CL size at embryo collection ($P = 0.51$). However, cows with third or higher parity had significantly larger embryos compared to second parity cows (9.39 ± 1.44 vs. 1.73 ± 1.76, $P < 0.05$). Milk production ($P = 0.90$), milk fat ($P = 0.86$), and protein ($P = 0.37$) values were also similar between the two groups. BHBA levels between the two groups were identical ($P = 0.94$). To understand the effect of vitamin B complex supplementation on fertility at a molecular levels, transcripts related to embryo development

(WNT, AXIN, FZD), immune system (CXCL, IL, MX), adhesion (MYH, MMP), and genes involved in the regulation of vitamin B molecules (FOLR1, TCII) are being analyzed from the endometrial biopsies. In conclusion, strategic dietary vitamin B supplementation during the transition and early lactation did not affect major outcomes of production and reproduction in lactating dairy cows. Benefits of vitamin B in fertility might potentially be linked to endometrial and conceptus gene expression; however, no major differences were observed in production or metabolic parameters.

Key Words: conceptus, cows, dairy, endometrium, gene expression, milk production, nutrition, reproduction, rumen protected, Vitamin B complex

RUMINANT NUTRITION: WESTERN SECTION

1664 WS Effect of crude protein supplementation on performance of cow-calf pairs and replacement heifers grazing late growing season forage.

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Concurrent experiments were conducted to evaluate the effect of protein supplementation to beef cattle grazing warm-season shortgrass forage during the late growing season. Cattle in all experiments grazed adjacent shortgrass pastures dominated by Buffalograss (*Buchloe dactyloides*) and Blue Grama (*Bouteloua gracilis*). Stocking rates ($\geq$ 2.3 ha/animal) were maintained such that forage availability was not limiting throughout the experiment. Precipitation in the area during the experiment was 176% of normal. For all Exp., treatments consisted of a supplemented group (1.32 kg per head of a 39% CP range cube fed 3 times a week) and a non-supplemented control group. Supplemented animals were fed a daily average of 0.22 kg of CP. In Exp. 1, 45 multiparous cow-calf pairs (initial BW 646 ± 13 kg) were individually weighed and body condition scored every 14 d. Forage clippings were taken simultaneously with BW measurements. Cow measurements and forage clippings began July 6 and concluded September 28. Cow final BW (P = 0.24) and ADG (P = 0.38) were not affected by treatment. There was no difference (P = 0.97) in cow final BCS regardless of treatment. Calf ADG (P = 0.54) and weaning weight (P = 0.45) were not affected by treatment. In Exp. 2, 26 primiparous cows (initial BW 546 ± 12 kg) were supplemented and measurements obtained in the same manner as Exp.1. Cow final BW (P = 0.39) and final BCS (P = 0.81) did not differ between treatments. Cow ADG (P = 0.07) tended to be greater when supplemented with 0.22 kg CP per day. Calf ADG (P = 0.50) and weaning weight (P = 0.11) did not differ between treatments. In Exp. 3, 25 replacement heifers (initial BW 412 ± 9 kg) were observed for BW and forage clippings were obtained every 14 d. Heifer final BW (P = 0.17) was not different between treatments. Heifer ADG (P = 0.02) was greater for supplemented heifers. Supplementing protein to cattle grazing late season medium quality forage is advantageous for increasing ADG in replacement heifers and potentially beneficial to improve condition in lactating primiparous cows. Repeating this experiment under varied precipitation patterns, as is normal for short-grass regions, would be beneficial to further examine the impact of late growing season protein supplementation on cow-calf pair/replacement heifer performance.

Key Words: beef cows, forage quality, supplementation

1665 WS Effect of corn-based supplementation on gas emissions, performance, and energetic losses of steers grazing wheat pasture.

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Thirteen Angus-cross steers (initial BW = 436 + 24 kg) were used in a crossover design to evaluate the effects of corn supplementation on gas emissions, performance, and energetic losses of steers grazing wheat pasture. Steers were allowed ad libitum access to wheat pasture (1.2 steers/ha), and were individually supplemented one of two treatments daily for two 30 d periods. Treatments included either 0.2 kg of pelleted wheat middlings (CON), or a dry-rolled corn supplement fed at 0.5% of BW plus 0.2 kg of pelleted wheat middlings (SUPP). After initial 30 d period, treatments were alternated and steers were supplemented an additional 30 d. Fecal output was determined with titanium dioxide (TiO_2) as an external marker. Beginning on d 14 of each period 15 g of TiO_2 was added to each steers supplement. In vitro analysis of wheat forage was determined to estimate DM digestibility of the wheat forage for each 30 d period. Forage intake was calculated using the determined fecal output and estimated forage digestibility. Ruminal CH_4 and CO_2 fluxes were measured using a GreenFeed (C-Lock Inc., Rapid City, SD) system. Urine energy loss was assumed to be 1.4% of GE intake. Oxygen production was estimated from CO_2 production, assuming a respiratory quotient of 1.05. Forage intake as percent of BW did not differ (P = 0.15) between CON (3.22%) and SUPP (3.61%). Average daily gain for CON and the SUPP averaged 1.4 kg and 1.3 kg, respectively, and was not influenced (P = 0.54) by supplementation. There were no differences ($P \geq 0.63$) among treatments for OM digestibility (CON: 84.9%; SUPP: 84.6%) and NDF digestibility (CON: 82.5%; SUPP: 83.1%). Carbon dioxide excreted (CON: 9.8 kg/d; SUPP: 10.5 kg/d) tended to be less (P = 0.08) for CON. No differences (P = 0.43) were observed in CH_4 emissions among CON and the SUPP supplement (334 and 351 g CH_4/d,