M27  Assessment of microbiota and short-chain fatty acids profiles in the hindgut of pre-weaned dairy calves. Y. Song1*, N. Malmuthuge1,2, M. A. Steele1, and L. L. Guan1, 1Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, 2Vaccine and Infectious Disease Organization, International Vaccine Centre, University of Saskatchewan Saskatoon, Saskatchewan, SK, Canada.

Microbial colonization in the gut during early life plays important roles in the host immunity development, metabolism, growth, and health. However, the knowledge on hindgut microbial colonization in dairy calves during the pre-weaned period is very limited. In this study, amplicon sequencing was used to characterize mucosal and digesta associated microbiota in the hindgut (cecum, colon and rectum) of newborn (at birth, n = 6), d 7 (n = 6), d 21 (n = 6), and d 42 (n = 6) Holstein bull calves. The comparison of the relative abundance of bacteria was performed with the nonparametric Kruskal-Wallis test. In total, 14 phyla were identified with Firmicutes, Bacteroidetes and Proteobacteria being the dominant phyla. At genus level, Lactobacillus and Bacteroides were the 2 predominant genera for both mucosa and digesta associated microbiota. The age effect was detected for both mucosa and digesta associated bacterial communities, while no regional effect was observed for them. Among the detected bacterial genera, the relative abundance of mucosa-attached Escherichia and Pseudomonas decreased significantly with the increase of age (P < 0.01), suggesting the initial higher prevalence of these potential pathogenic bacteria during first week of life but the prevalence lowered in healthy calves with the growth. The concentrations of total short-chain fatty acids (SCFAs), acetate, propionate, and butyrate were significantly higher at d 21 compared with d 7 (P < 0.01); however, there was no significant difference observed between d 21 and d 42 except for acetate concentration on cecum. The changing pattern of SCFA concentration was similar with the changes in the relative abundance of SCFA-producing bacterial genera such as mucosa and digesta associated Prevotella, Blautia, Ruminococcus, and mucosa-attached Fecalibacterium. This study provided the information on hindgut microbial composition and their metabolite, which may play an important role in the hindgut fermentation and health of dairy calves during pre-weaned period.

Key Words: dairy calf, hindgut, pyrosequencing

M28  Role of galectins 3 and 9 in the immunity of periparturient dairy cows. E. Asiamah1*, S. Adjei-Fremah1, K. Ekwemalor1, M. Worku1, L. Sordillo2, and J. Gandy1, 1North Carolina A&T State University, Greensboro, NC, 2Michigan State University, East Lansing, MI.

The peripartal period in the dairy cow is a crucial time influencing future fertility and milk production. Postpartal diseases like bovine mastitis can result in major economic set back in the dairy industry. Based on the hypothesis that postpartal diseases are most likely due to immune dysfunction, there is a need for the identification of candidates involved in the immuno-modulation of the peripartal immuno-competence. Galectins are multipotent, evolutionarily conserved, carbohydrate- binding proteins that, by crosslinking cell surface glyco-conjugates, trigger a cascade of transmembrane signaling events such as cell activation, cytokine secretion, migration, and apoptosis. The objective of the study was to evaluate galectin 3 and galectin 9 levels in Holstein-Friesian cows in the periparturient period. Eight Holstein-Friesian periparturient cows were used for the study. Blood was taken 2 weeks close to calving (close up), and 7 d after calving(±7). Enzyme-linked immunosorbert assay (ELISA) was used to detect and determine the concentrations of galectins 3 and 9 in the plasma of the cows. Each sample was done in triplicate. The Student t-test in SAS 9.2 was used to analyze the data obtained. The results demonstrated that galectin 3 levels decreased significantly 7 d after calving (P = 0.0362). Galectin 9, on the other hand, was observed to increase 7 d after calving but the increase was not significant compared with 2 wk before calving (P = 0.6035). This indicates that galectin levels change during the periparturient period of cows, and are differentially regulated. A better understanding of the molecular and physiological properties of galectins could help to establish its therapeutic potential in inflammatory diseases especially mastitis and other postpartum diseases in the dairy industry

Key Words: peripartal, postpartal, galectin

M29  Effects of timing of C16:0 supplementation on production and metabolic responses of early lactation dairy cows. J. de Souza* and A. L. Lock, Michigan State University, East Lansing, MI.

Fifty-two multiparous cows were used in a randomized complete block design experiment and assigned to either a control diet containing no supplemental fat (CON) or a C16:0 supplemented diet (PA) that was fed either from calving to 24 DIM (fresh period) or from 25 to 67 DIM (peak period). Fresh diets were formulated to contain (% DM) 17% CP, 30% NDF, 24% forage NDF, and 24% starch. Peak diets were formulated to contain (% DM) 17% CP, 29% NDF, 19% forage NDF, and 26% starch. The C16:0 supplement (85% C16:0), added at 1.5% of diet DM, replaced soyhulls in the CON diets. During the fresh period, PA did not affect DMI (21.5 vs. 21.6 kg/d, P = 0.92) or milk yield (47.7 vs. 46.3 kg/d, P = 0.38) compared with CON. In contrast, compared with CON, PA increased milk fat content (4.89 vs. 4.48%, P = 0.01) and yield (2.19 kg/d, P < 0.01), milk protein yield (0.40 vs. 1.53 kg/d, P = 0.03), and ECM (56.6 vs. 51.9 kg/d, P = 0.02). PA decreased BW (628 vs. 709 kg, P = 0.05), BCS (3.25 vs. 3.34, P = 0.04), plasma insulin (0.21 vs. 0.24 mg/L, P = 0.05), and increased plasma NEFA (0.65 vs. 0.59 mM/L, P = 0.03) compared with CON. A treatment by day interaction was detected for BW (P = 0.05) and BCS (P = 0.07) due to PA only decreasing these variables after 10 DIM compared with CON. During the peak period, compared with CON, PA did not affect DMI (29.9 vs. 30.2 kg/d, P = 0.68), but increased milk yield (58.0 vs. 54.6 kg/d, P = 0.01), milk fat content (3.88 vs. 3.67%, P < 0.01) and yield (2.27 vs. 2.06 kg/d, P < 0.01), milk protein yield (1.80 vs. 1.66 kg/d, P = 0.04), and ECM (62.3 vs. 57.8 kg/d, P < 0.01). Compared with CON, PA reduced plasma insulin concentration (0.25 vs. 0.32 mg/L, P = 0.05), but did not affect plasma NEFA concentration (0.35 vs. 0.32 mM/L, P = 0.41) or BW (673 vs. 684 kg, P = 0.93). There were no interactions between feeding PA and the time that supplementation started for production variables. Our results demonstrate that supplementing C16:0 during early lactation increases ECM without changes in DMI. Feeding PA may increase BW loss during the fresh period, but not during the peak period.

Key Words: body condition, palmitic acid, postpartum

Excessive adipose tissue (AT) lipolysis increases serum free fatty acids (FFA) and triggers AT inflammation predisposing cows to disease. Fetuin-A (FETA) is a FFA carrier and an acute-phase protein (APP) that enhances lipid-induced inflammation in AT of monogastrics. Little is known about its role and potential use as a biomarker in transition cows. We hypothesized that serum and AT FETA content increases as the periparturient period progresses and is enhanced by high lipolysis rate. Blood and subcutaneous AT were collected from 10 multiparous cows through the transition period at far off (FO: -51 ± 3d) and close-up dry (CU: -14 ± 2d), and early lactation (EL: 7 ± 0.5d). FETA was analyzed by ELISA in serum, and by RT-qPCR and protein blotting in AT. Contrary to our hypothesis, serum FETA concentration and AT gene and protein expression were greatest at FO compared with EL (P ≤ 0.05) when FFA concentration was the least (P < 0.01). Serum FETA concentration was 1.11 ± 0.08, 1.08 ± 0.08, and 0.98 ± 0.08 mg/mL at FO, CU, and EL (P = 0.05), respectively, and was positively associated with serum albumin (r = 0.27; P = 0.03) and calcium (r = 0.32; P = 0.05). Circulating FETA was negatively associated with FFA (r = -0.25; P = 0.05) and BCS loss (r = -0.73; P < 0.001) over the transition period, and adverse health events at EL (r = -0.42; P = 0.05). AT FETA expression dynamics through FO, CU, and EL was analogous to adipogenic and lipogenic genes PPARy, FASN, FABP4, and SCD1, and negatively correlated with AT inflammatory markers SPP1 (r = -0.46; P = 0.01) and CD68 (r = -0.38; P = 0.04). To test adipocyte inflammatory response to FETA in vitro, primary bovine adipocytes were treated with 50, 100 or 200 µg/mL of FETA (8h), or LPS (25 mg/mL; 4h). Adipocytes treated with FETA had lower CCL2 expression than LPS (P = 0.03), and reduced adipocyte IL6 transcription (P = 0.01) when treated with 100 µg/mL of FETA compared with 0. These results indicate that FETA is a negative APP inversely linked to AT lipolysis and health events in transition cows. Contrary to monogastrics, FETA plays a beneficial role in AT inflammation in cows by modulating the expression of pro-inflammatory cytokines by adipocytes.

Key Words: adipocyte marker, inflammation, lipolysis

M31 Effects of oral administration of acetylsalicylic acid after parturition on activity patterns, prevalence of diseases, mortality and culling rates in dairy cows. A. A. Barragan*, L. M. Bauman2, J. Velez2, J. D. Rozo Gonzalez2, G. M. Schuenemann1, and S. Bas1, 1Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, 2Department of Animal Sciences, The Ohio State University, Columbus, OH, 3Aurora Organic Farms, Boulder, CO.

Dystocia has been categorized as a painful event and has been associated with increased risk of cow morbidity, mortality and culling in dairy farms. Administration of NSAID drugs has been proposed to decrease postpartum discomfort. The objectives of this study were to assess the effects of oral administration of acetylsalicylic acid after calving on (1) daily activity patterns and (2) prevalence of diseases, mortality and culling rates in lactating dairy cows. Cows from 3 organic dairy herds were enrolled in the present study. Immediately after parturition, cows were blocked by parity and calving ease [eutocia (EUT); dystocia (DYS)] and were randomly assigned to 2 treatment groups: (1) ASP (n = 278): at approximately 12 h after parturition cows received 4 consecutive treatments with acetylsalicylic acid (100 mg/kg; 2 boluses) 12 h apart; or (2) placebo (PLC; n = 285): at approximately 12 h after parturition cows received 4 consecutive treatments with gelatin capsules (2 capsules) filled with water 12 h apart. Activity monitors were placed on the rear leg of a subset of cows (ASP = 48, PLC = 47) at enrolment, and were removed 7 d later. Overall, there was no difference in lying and standing time between ASP and PLC groups. Cows in the ASP group tended (P = 0.05) to have more steps compared with PLC (ASP = 3514 ± 129 steps/d; PLC = 3162 ± 129 steps/d). Furthermore, cows that experienced DYS spent more time lying (P < 0.05; DYS = 590 ± 17 min/d; EUT = 511 ± 17 min/d), less time standing (P < 0.05; DYS = 850 ± 17 min/d; EUT = 929 ± 17 min/d), and had less steps (P < 0.05; DYS = 3089 ± 126 steps/d; EUT = 3587 ± 133 steps/d) than EUT cows. Additionally, ASP cows that experienced EUT tended (P = 0.06) to spend less time lying and more time standing, and had more (P < 0.05) steps compared with PLC cows that experienced EUT. No difference was found on the incidence of health events, culling and mortality rates between groups. The results of this study suggest that activity patterns of cows that experience DYS are different from cows that experience EUT, and that administration of ASP after calving may increase activity of dairy cows.

Key Words: acetylsalicylic acid, activity, calving ease

M32 Preliminary evaluation of the DeLaval Cell Counter’s ability to quantify somatic cell counts in nonlactating bovine mammary secretions. B. D. Enger*, C. E. Crutchfield, S. C. Nickerson, C. L. M. Parsons, and R. M. Akers, Virginia Polytechnic Institute and State University, Blacksburg, VA, University of Georgia, Athens, GA.

Measurement of milk somatic cell count (SCC) is often used to screen lactating dairy cows for mastitis. Many methods have been developed to rapidly measure SCC in milk from lactating cows but few validated tools are available to quantify SCC in secretions from nonlactating mammary glands. The objective was to quantify SCC in nonlactating secretions by direct microscopic examination and determine if these measures correlate with the SCC produced by a commercial SCC counter designed for lactating cows, the DeLaval Cell Counter (DCC). Mammary secretions (n = 90) collected from 6 dry, non-pregnant, Holstein cows (1 to 3 lactations; 53 to 64 d dry) were diluted 1:4 in PBS containing 2.2% BSA and used to make duplicate secretion smears for microscopic quantification and measured in duplicate by the DCC. Each smear was enumerated by 2 independent counters. Duplicate secretion smears produced a within-sample coefficient of variation of 12.8%. Average values were used for further evaluation. Mean microscopic SCC ranged from 1.56 to 131.0 × 10^6 cells/mL (mean = 20.0 × 10^6 cells/mL; SD = 22.4 × 10^6 cells/mL). Secretion SCC enumerated by counter 1 (mean = 19.8 × 10^6 cells/mL) were lower (P = 0.0045) than those produced by counter 2 (mean = 20.5 × 10^6 cells/mL); but SCC were highly correlated (R^2 = 0.970). Duplicate SCC measures produced a within-sample coefficient of variation of 15.8% and mean DCC SCC ranged from 0.926 to 16.0 × 10^6 cells/mL (mean = 6.16 × 10^6 cells/mL; SD = 3.09 × 10^6 cells/mL). When average DCC SCC were compared with counts produced by counter 1, counter 2, and their average using PROC CORR in SAS, respective Pearson correlation coefficients of 0.342, 0.321, and 0.334 resulted. Overall, a weak relationship existed between the microscopic SCC and those produced by the DCC which is not surprising because the DCC was designed and calibrated to quantify SCC in milk rather than secretions containing extremely high concentrations of cells. Modifications will be necessary for the DCC to better mirror values obtained by direct microscopic examination.

Key Words: mastitis, SCC, dry cow
M33  Bovine mammary epithelial cell (MAC-T) phenotype impacts TNFα-mediated MAPK signaling and inflammation. L. G. Silva*,1 B. S. Ferguson1, L. Hernandez2, and A. P. Faciola4, 1University of Nevada, Reno, NV, 2University of Wisconsin, Madison, WI.

The objective was to determine if MAC-T phenotype would impact inflammatory signaling and inflammatory gene expression. MAC-T cells were cultured under basal (DMEM 10% fetal bovine serum and 10 μg/mL of insulin) or lactogenic conditions (basal media + 1 μg/mL ovine prolactin, 0.5 μg/mL hydrocortisone, and 10 mM sodium acetate) and mitogen-activated protein kinase (MAPK; ERK, JNK, and p38) phosphorylation and pro-inflammatory gene expression examined in response to tumor necrosis factor α (TNFα). Statistical analysis was assessed via ANOVA and Tukey’s post-hoc analysis at P ≤ 0.05. MAC-T cells were co-stimulated with increasing concentrations of TNFα (0, 10, 30, 100, 300, 1000 pM). Cell lysates were harvested 15 min post-TNFα stimulation and assessed for MAPK phosphorylation via immunoblotting. JNK and p38 phosphorylation increased in a dose-dependent manner; yet the magnitude of JNK and p38 signaling was greater under basal compared with lactogenic conditions. Cells were next stimulated in parallel with TNFα (300 pM) and lysates harvested over time (0, 15, 30, 100, 180 min). JNK and p38 phosphorylation were robust and transient in MAC-T cells stimulated with TNFα over time. Similar to dose-response experiments, JNK and p38 signaling were significantly more robust in MAC-T cells under basal conditions. We next examined inflammatory gene expression in MAC-T cells cultured under basal or lactogenic conditions and co-stimulated in the presence or absence of TNFα (300 pM). RNA was isolated and PCR array performed to evaluate the expression of 83 inflammatory genes. Pro-inflammatory gene expression was increased in MAC-T cells in response to TNFα. Consistent with enhanced MAPK signaling; pro-inflammatory gene expression was significantly increased in MAC-T cells under basal compared with lactogenic conditions. Real-time qPCR was used to validate PCR array findings. Collectively, our data demonstrate that MAC-T cells cultured under basal conditions are more responsive to TNFα. These findings suggest that investigators consider the importance of MAC-T phenotype when designing future inflammation-related studies.

Key Words: gene expression, mammary, transition period

M34  Prediction algorithms for early detection of clinical mastitis caused by gram-positive and gram-negative pathogens. N. M. Steele1,2, A. Tholen3, A. De Vriese5, S. J. Lacy-Hulbert4, R. R. White6, and C. S. Petterson-Wolfe7, 1Department of Dairy Science, Virginia Tech, Blacksburg, VA, 2Department of Animal Sciences, University of Florida, Gainesville, FL, 3DairyNZ Ltd., Private Bag 3221, Hamilton, New Zealand, 4Department of Animal and Poultry Science, Blacksburg, VA.

Producers now have many technologies available for monitoring daily changes in milk composition and cow behavior to assist in disease detection. This study aimed to develop algorithms for identifying gram-negative (GN) and gram-positive (GP) mastitis using a combination of milk and activity measures. Milk yield, quality (electrical conductivity and SCC) and composition (lactose, protein, and fat percentage) were collected using an in-line milk analyzer (AfiLab, S.A.E. Afikim, Israel) at Virginia Tech (VT) and University of Florida (UF) Dairy for 14 d before and following a clinical mastitis (CM) event (n = 268). Activity measures included daily steps at UF (Afi Pedometer), as well as number of rest bouts, total resting time and rest bout duration at VT (Afi PedometerPlus). A quarter milk sample was collected for bacteriology upon detection of CM. Data were also retained for control animals matched to each clinical case (n = 268) based on breed, lactation number and DIM. Rather than using the absolute value of variables as the primary explanatory variable, slopes of each variable were estimated using linear regression over the days before CM detection. Slopes were calculated between d 7 and 5, 4, 3, 2 or 1 before infection to better understand how early these metrics could be used to detect CM. Infection was treated as a binomial response and backward stepwise elimination mixed-effect regression was used to relate infection to explanatory variable slopes. Farm was included as a random effect. Explanatory variable slopes ranging between 7 and 2 d before CM had the highest detection accuracy rate for both pathogen types. Instance of GN infections was correctly identified in the algorithm in 85% of cases. This detection algorithm included slopes of milk yield (P = 0.02), SCC (P = 0.01) and daily steps (P = 0.11). For GP infections, the most accurate model included slopes of conductivity (P = 0.07), protein percentage (P = 0.02) and SCC (P = 0.01), and correctly identified 75% of infections. The algorithms suggest activity and milk data may be potentially useful for early detection of CM.

Key Words: sensor data, milk component, activity


Most rumen bacteria are uncultured, making their niche hard to identify. Fluorescent substrates could potentially identify the substrate preferences and the niche of these uncultured bacteria, but uptake of these substrates has not been tested with mixed rumen bacteria. Our objective was to determine if a fluorescent analog of glucose (2-NBDG) would be taken up by mixed bacteria from the rumen. A second objective was to determine if we could separate cells taking up 2-NBDG by using fluorescence-activated cell sorting. We prepared mixed bacteria from rumen fluid by centrifugation, incubated them in 2-NBDG (0 to 100 μM) for up to 60 s, and monitored uptake of 2-NBDG with fluorimetry. We found mixed bacteria took up 2-NBDG, and they did so with a maximum velocity (Vmax) of 0.180 (0.05 SEM) nmol mg protein−1 min−1 and Michaelis constant (Km) of 6.37 (SEM 4.86) μM (n = 3). We confirmed that cells took up 2-NBDG by using flow cytometry, which revealed that up to 18.5% cells were positive after incubating them in 100 μM 2-NBDG for 5 min. Positive cells could be separated with fluorescence-activated cell sorting, and post-sort analysis revealed 94% of sorted positive cells were in fact positive. Work is ongoing to (1) optimize cell sorting, (2) sequence sorted cells for identification, and (3) synthesize and test uptake of other glucose analogs. Our work supports that 2-NBDG, in combination with other analogs, could be used to identify which bacteria consume which substrates, helping define what role uncultured bacteria play in the host.

Key Words: 2-NBDG, rumen bacteria, cell sorting

M36  Effects of replacing soybean meal with canola meals varying in rumen undegraded protein on ruminal fermentation in vitro. H. F. Monteiro*,1 E. M. Paula1, J. L. P. Daniel2, P. D. B. Benedetti3, R. Bittrner1, L. G. Silva1, T. Shenkoru1, and A. P. Faciola1, 1University of Nevada, Reno, NV, 2State University of Maringá, Maringá, PR, Brazil, 3Federal University of Viçosa, Viçosa, MG, Brazil.

This study aimed to evaluate the effects of replacing soybean meal (SBM) with canola meals (CM) differing in rumen-undegraded protein (RUP; % of CP) content (38% RUP, LCM or 50% RUP, HCM) on in
In vitro ruminal fermentation, including total gas and CH₄ production. Two in vitro experiments were conducted. Both experiments had 3 48 h incubations, totaling 18 observations per treatment. Experiment 1 tested 3 protein supplements as the sole ingredient (SBM, LCM, and HCM). Experiment 2 tested 3 TMR containing the protein supplements from experiment 1. Measurements were: pH, gas production (GP), degradation kinetics, metabolizable energy (ME), in vitro true organic matter digestibility (iv-tOMd), CH₄ and volatile fatty acids (VFA) production. Mixed linear models were used to analyze the data. Degradability kinetics were fitted using nonlinear regression. Means were compared by orthogonal contrasts: SBM vs. (LCM + HCM) and LCM vs. HCM. Partial data are presented in Table 1. The SBM ingredient had greater iv-tOMd, VFA production, ME, total GP₄₈ and CH₄ (mM) when compared with both CM. When comparing both CM ingredients, HCM had shorter lag phase and lower branched-chain VFA production. However, ingredients did not differ in CH₄ (g/kg dOM). In experiment 2, SBM diet had a trend to increase total CH₄ production (mM), but diets did not differ in CH₄ (g/kg dOM). The SBM diet also had a trend to increase valerate and iso-valerate concentration which may indicate more proline and leucine deamination. When comparing both CM diets, HCM increased final pH and had a trend to lower ME, while decreased total GP₄₈.

Key Words: degradability kinetics, metabolizable energy, methane

M37 Evaluation of the NRC predictions in response to changes in dietary rumen degradable and undegraded protein on dairy cows exposed to warm climates. J. D. Kaufman* and A. G. Rius, The University of Tennessee, Knoxville, TN.

A study was conducted to evaluate the prediction accuracy of the National Research Council (2001) model for metabolizable protein (MP) allowable for milk production. Thirty multiparous Holstein cows were used in a completely randomized design with a 2 × 2 factorial arrangement of treatments. Dietary treatments comprised 2 levels of rumen degradable protein (RDP; 10 and 8%) and 2 levels of rumen undegradable protein (RUP; 8 and 6%) as follows: 10RDP:8RUP, 10RDP:6RUP, and 8RDP:6RUP. The 10RDP:8RUP diet was fed from d 1 to 21 followed by respective treatments from d 22 to 42. Cows were exposed to the warm climates of July and August in Tennessee without supplemental cooling. Least squares means of dry matter intake, milk, and body weight from each treatment were input into the model, and tabular crude protein and fiber contents were adjusted to reflect chemically derived values. Treatments did not affect feed intake. The RDP treatment did not affect milk yield but, at 6% RUP, milk yield declined compared with the 10RDP:8RUP diet (RDP × RUP interaction; P < 0.01). The NRC model overpredicted a decline in milk yield (1.9 kg) in response to lowering RDP at 8% RUP (10RDP:8RUP vs. 8RDP:8RUP). At 6% RUP, the model predicted a decline in milk yield (2.0 kg) in response to lowering RDP (10RDP:6RUP vs. 8RDP:6RUP); however, milk yield increased by 2.3 kg. At 10% RDP, the model overpredicted a decline in milk yield (5.1 kg) in response to lowering RUP (10RDP:8RUP vs. 8RDP:6RUP). At 8% RDP, the model overpredicted a decline in milk yield (7.5 kg) in response to lowering RUP (8RDP:8RUP vs. 8RDP:6RUP). Reduction of dietary RDP decreased predicted RDP supply and increased RUP requirements. Reduction of dietary RUP decreased predicted RUP supply but did not affect RUP requirements. In summary, the NRC model underestimated RDP supply and overestimated RUP requirements in response to low dietary RDP. The model underestimated the RUP supply in response to low dietary RUP. An improvement in predictions of MP allowable for milk production should increase the accuracy of the NRC model.

Key Words: National Research Council, rumen degradable protein, rumen undegradable protein

M38 Relationship between ano-genital distance and fertility in Holstein cows. M. Gobikrushanth*1, T. C. Bruinjé1, M. G. Colazo2, and D. J. Ambrose1,2, 1Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, 2Livestock Research Section, Alberta Agriculture and Forestry, Edmonton, AB, Canada.

The ano-genital distance (AGD) has been studied as a marker for genital development and fertility in rodents and primates. An inverse relationship between AGD (distance from anus to clitoris) and fertility in dairy cows was first reported in a preliminary study. Current objectives were to determine associations between (1) AGD and height at hip, and (2) categories of AGD and reproductive outcomes [pregnancy at 1st AI (P/AI), cumulative pregnancy at 120 DIM (P120), times bred, days...
open) in a larger population. AGD and height were measured in 573 cows (1st, 2nd and 3rd lactation; n = 203, 155 and 215) at 165 ± 4.3 DIM from 3 herds. The overall mean (±SEM) AGD and height were 132.3 ± 0.5mm (range, 96.0–170.0) and 149.6 ± 0.2cm (range, 138.0–161.0). Mean AGD and height, respectively, were shorter (P < 0.05) for 1st (125.8 ± 0.7mm and 149.2 ± 0.2cm) than 2nd (128.4 ± 0.7mm and 150.5 ± 0.2cm) and 3rd+ lact (128.6 ± 0.6mm and 150.6 ± 0.2cm). The overall correlation between AGD and height was very weak (r² = 0.08; P < 0.01). The threshold AGD that predicted probability of P/AI (Receicer operating characteristic curve analysis) for 1st and 2nd lact cows were 126.0 (Sensitivity:61.9 and Specificity:66.4%), and 135.0 (Sensitivity:69.8 and Specificity:75.5%) mm, but AGD did not predict fertility in 3rd+ lact cows. Therefore, only 1st and 2nd lact cows were categorized into SHORT or LONG AGD (≤ or > threshold for each lact). First lact cows of SHORT AGD (119.2 ± 0.7mm) group had greater (P < 0.05) P/AI (56.7 vs. 28.8%) and P120 (60.7 vs. 51.5%), fewer times bred (1.6 ± 0.1 vs. 2.5 ± 0.1) and days open (95.4 ± 5.9 vs. 125.7 ± 5.5d) than those in LONG AGD (136.2 ± 0.7mm). Similarly, 2nd lact SHORT AGD (125.6 ± 0.8mm) cows had greater (P < 0.05) P/AI (41.6 vs. 24.2%) and P120 (60.7 vs. 51.5%), fewer times bred (2.2 ± 0.2 vs. 2.6 ± 0.2) and days open (116.9 ± 6.3 vs. 147.7 ± 7.8 d) than LONG AGD (144.9 ± 1.0mm). Height did not differ between SHORT and LONG AGD cows in 1st and 2nd lact. In summary, AGD was very weakly associated with height, highly variable even among cows of similar lactation, and cows with shorter AGD were more fertile than those with longer AGD. The factors determining AGD in dairy cows remain to be explored.

Key Words: ano-genital distance, height, fertility

M40 Fungal treatment of lower part of corn stem does not improve its nutritional value. Y. He¹, J. Dijkstra¹, A. S. M. Sonnenberg², T. M. B. Moultier³, M. A. Kabel³, W. H. Hendriks¹, and J. W. Cone¹, ¹Animal Nutrition Group, Wageningen University & Research, De Elst 1, Wageningen, the Netherlands, ²Plant Breeding, Wageningen University & Research, Droevendaalsesteenweg 1, Wageningen, the Netherlands, ³Food Chemistry, Wageningen University & Research, Borre Wellendael 9, Wageningen, the Netherlands.

The aim of this study was to evaluate the effects of fungal treatment on chemical composition, lignin composition and in vitro rumen degradability of lower parts of corn stem (LCS, internodes 6 and 7). Two lignin degrading fungal species (Lentinula edodes and Pleurotus eryngii) and 2 corn cultivars (LG30211 and MZF8057), which differed in lignin content and rumen degradability were used. Autoclaved LCS was inoculated at 24°C and a relative humidity of 70% in an air-conditioned chamber for 3, 6, and 9 wk and autoclaved LCS was used as control. All treatments were tested in triplicate. Neutral detergent fiber (NDF), acid detergent fiber (ADF) and acid detergent lignin (ADL) content were determined. Lignin composition was analyzed by pyrolysis GC-MS and S:G ratio (ratio of syringyl units to guaiacyl units being lignin building blocks) was determined. An in vitro gas production (IVGP) technique was used as a measure of rate and extent of organic matter degradability (OMD). Data on chemical composition, S:G ratio, and IVGP were analyzed using a generalized linear model in SAS (v9.3) as a measure of rate and extent of organic matter degradability (OMD). Increasing treatment period was stressful for high-producing Holstein cows. To meet her energy requirements leads to a state of negative energy balance, often accompanied by increased lipid mobilization from adipose tissue. Body condition scoring (BCS) provides a visual appraisal of lipid mobilization. Our aim was to investigate the association of body condition loss on hepatic and ovarian tissue function in dairy cows during the transition period until onset of breeding. Holstein cows were studied as of 4 weeks pre-calving until 8 weeks post-calving and retrospectively grouped by changes in BCS. Group 1 (n = 9) consisted of cows that lost <0.75 BCS and Group 2 (n = 8) cows that lost ≥0.75 BCS during the sampling period. Cows were subjected to blood collection and liver biopsies at ~3 weeks, approximate day of calving and +7 weeks. The last liver biopsy was accompanied by follicular aspiration of the dominant follicle and retrieval of granulosa cells (GC) and follicular fluid. We evaluated levels of circulating metabolic indicators, and hepatocyte and GC mRNA. Circulating levels of β-hydroxybutyric acid, glucose and haptoglobin used to assess liver and metabolic stress were unchanged between groups. The proportion of nonesterified fatty acids (NEFAs) were assessed by gas chromatography in both follicular fluid and blood samples collected at +7 wk, where linoleic acid was the predominant NEFA, representing 52% of all NEFAs, yet no differences were observed between fluids and groups. Reproductive competence was evaluated through mRNA abundance of genes required for follicular development (FSHR and LRP8) in granulosa cells, but remained constant between groups. In hepatocytes, CYP7A1 transcripts gradually increased (P < 0.05) in Group 2 from ~3 wk to +7 wk, but remained constant in Group 1. Other transcripts involved in lipid metabolism and inflammation (LDLR, ACAT1, and IL1B) remained unaltered between groups at all time points. Thus, cows experiencing elevated BCS loss lead to a gradual increase in hepatic CYP7A1, an enzyme involved in bile acid synthesis from cholesterol, suggesting that Group 2 experienced a greater need for cholesterol removal from the body.

Key Words: BCS, liver, ovary

M41 Evaluation of two adsorbents after an aflatoxin challenge in Holstein cows. M. E. Weatherly¹, R. T. Pate¹, G. E. Rottinghaus², F. de Oliveira Roberti Filho³, and F. C. Cardoso, ¹Department of Animal Sciences, University of Illinois, Urbana, IL, ²Veterinary Medical Diagnostic Lab, University of Missouri, Columbia, MO, ³Bioriginal, São Paulo, Brazil.

The objective of this study was to determine the effects of 2 different adsorbents composed of yeast fractions and bentonite in different proportions (AD1 and AD2) during an aflatoxin (AF) challenge. Lactating Holstein cows ([n = 76]; BW (mean ± SD) = 698 ± 72 kg; DIM = 153 ± 83 d) were assigned to 1 of 5 treatments in a randomized complete block design. Period was 28 d with measurement phase on d 22 to 28.
From d 22 to 24, cows received an AF challenge (100 μg of AFB1/kg of diet DM administered orally). The appearance and disappearance of AF excreted in milk was tested at each milking from d 22 to 28 using SNAP tests (SNP; IDEXX, Inc.). Blood was sampled on d 1, 22, and 26 (n = 3 per cow) of wk 1 and 4 for each period and analyzed for superoxide dismutase (SOD) content. Milk samples from d 22 to 26 were analyzed for AFM1 concentrations by HPLC. Treatments were: control (CON), no AD or AF; positive control (POS), no AD plus AF challenge; 30 g per cow per day of AD1 30 and AF challenge (AD30); 60 g per cow per day of AD1 60 and AF challenge (AD60); and 60 g per cow per day of AD2 and AF challenge. Statistical analysis was performed using the MIXED procedure of SAS. Cows in CON had no positive SNP tests, while cows in POS had 7.85 ± 0.27 positive SNP tests (P < 0.001). Plasma SOD concentrations were greater for POS than CON at 2.77 and 1.96 ± 0.05 U/mL, respectively (P < 0.001). A quadratic treatment effect was observed for plasma SOD concentrations at 2.77, 1.99, and 1.97 ± 0.05 U/mL for POS, AD30, and AD60 treatments, respectively. Aflatoxin M1 transfer (1.14 and 0.00 ± 0.16%), excretion (29.52 and 0.00 ± 4.58 µg/d), and concentrations in milk (0.76 and 0.00 ± 0.16 µg/kg) were greater for the POS treatment than the CON, respectively (P < 0.0001) but no differences were observed among other treatments. Oral supplementation of yeast and bentonite clay based AD during AF challenge resulted in quadratic changes in plasma SOD, and fecal AFB1 concentrations. In conclusion, yeast cell wall and bentonite based AD may be beneficial in reducing inflammation during AF challenge.

Key Words: aflatoxin, adsorbent, milk

M42 Producer perception of precision dairy monitoring technology health alerts. E. Eckelkamp* and J. Bewley, University of Kentucky, Lexington, KY.

The objective of this study was to assess how producers categorized alerts from a daily generated alert list designed to identify sick or injured animals. Data from 4 commercial farms in Kentucky were collected from October 2015 to 2016. Each cow was equipped with a CowWatch leg tag (Alta Genetics Inc., Watertown, WI) measuring steps (steps/d) and lying time (h/d), and a neck tag measuring eating time (h/d). Dairy producers evaluated a technology-generated daily herd health report where alerts were generated based on a cow level threshold of ≥30% decrease in steps, lying time, or eating time compared with each cow’s 10-d moving average. Producers evaluated alerts within overall categories: alert accepted to be true and cow checked (A), alert accepted to be true and cow not checked (B), and alert not accepted to be true (C). A total of 25,027 cow alerts occurred, with producers evaluating 15,644 cow alerts (62%). The FREQ procedure of SAS 9.4 (SAS Institute Inc., Cary, NC) with a Chi-squared analysis was used to assess category distribution. Overall, more alerts were categorized as A (5,129) and B (8,424) compared with C (2,091; P < 0.01). Producer categorization by farm (Table 1) indicated most of evaluated alerts were accepted to be true (75 to 99%, total A and B). However, 27 to 88% of alerts were categorized as B, indicating although behavior changes were real, the producer did not check the cow. Reasons for not checking cows included: changes from normal not enough for producer to worry, no time for producers to check alerts, changes in ambient temperature, and hoof trimming or veterinary checks. The frequency of A and B alerts indicated that producers believed the behaviors changes identified were real. The frequency of cows in category B indicated alert generation should be refined to identify only sick or injured cows.

Table 1 (abstract M42).

<table>
<thead>
<tr>
<th>Item</th>
<th>Farm 1</th>
<th>Farm 2</th>
<th>Farm 3</th>
<th>Farm 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Category A</td>
<td>105 (2)</td>
<td>429 (7)</td>
<td>1,599 (28)</td>
<td>2,996 (44)</td>
</tr>
<tr>
<td>Category B</td>
<td>2,802 (42)</td>
<td>2,708 (45)</td>
<td>1,778 (32)</td>
<td>1,136 (17)</td>
</tr>
<tr>
<td>Category C</td>
<td>292 (4)</td>
<td>609 (10)</td>
<td>1,151 (20)</td>
<td>39 (1)</td>
</tr>
<tr>
<td>Missing</td>
<td>3,427 (52)</td>
<td>2,282 (38)</td>
<td>1,100 (20)</td>
<td>2,574 (38)</td>
</tr>
</tbody>
</table>

Key Words: precision dairy technology, producer assessment, health monitoring