W9 Abundance of microbial virulence genes in rectal swabs from US dairy cows varies by stage of lactation. E. A. Galbraith1, A. M. Lange1, S. Son1, R. P. Arias2, C. M. Peter2, and M. R. King1.1Microbial Discovery Group, Franklin, WI, 2United Animal Health, Sheridan, IN.

Gastrointestinal disease can arise at any time during a dairy cow’s lactation cycle, yet periods of high feed intake and production or greater metabolic demand can increase susceptibility to opportunistic infection. *Clostridium*, *E. coli*, *Salmonella*, and mycotoxin-producing fungi are commonly found in the GI tract, however fluctuation in abundance of these microorganisms or their virulence genes at different stages of lactation remains unclear. The objective of this study was to quantify common microbial marker and virulence genes in rectal swabs from dairy cows during 3 stages of lactation. Rectal swabs were obtained from 370 dairy cows at 26 commercial farms across major US dairy-producing regions, and classified into 3 groups by days post-parturition at time of sampling: fresh (d1–21, n = 95), early lactation (d22–100, n = 146) and late lactation (>101d, n = 129). Genomic DNA was extracted from rectal swabs and genus- or species-specific marker or virulence genes from *E. coli*, *Salmonella*, *Clostridium*, and *Aspergillus* were quantified using a panel of qPCR assays. Data were log-transformed and the Kruskal-Wallis test, followed by Mann-Whitney pairwise comparisons were performed to detect differences in gene quantity between lactation stage groups. Cows in fresh and early lactation periods harbored higher quantities (H = 7.51, P = 0.02) of *EAST1*, a heat-stable enterotoxin gene in enteroaggregative *E. coli*, compared with cows in late lactation (2.06 and 2.13 vs. 1.82 log_{10} gene copies respectively). Similarly, quantities of *Aspergillus* 18S rRNA gene (H = 12.93, P < 0.01) and *C. difficile* toxin A gene tcdA (H = 7.52, P = 0.02) were elevated in fresh and early lactation groups. Fresh cows swabs also contained highest (H = 6.91, P = 0.03) quantities of the *C. perfringens* α toxin gene cpa compared with cows in early and late periods (0.76 vs. 0.35 and 0.41 log_{10} copies respectively). These results indicate that harborage of several opportunistic microorganisms and their virulence genes may be greater during the fresh and early lactation periods, providing insight into the increased vulnerability of cows during these stages.

Key Words: virulence gene, *Escherichia coli*, *Clostridium perfringens*

W11 Prevalence of five enteric pathogens on Ohio dairy farms. J. Barkley3, J. Pempek1, A. Bowman1, J. Nolting1, J. Lee2, S. Lee2, and G. Habing1.1Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, 2Division of Environmental Health Sciences, College of Public Health, The Ohio State University, Columbus, OH, 3Veterinary Public Health Program, The Ohio State University, Columbus, OH.

Calf diarrhea remains one of the main reasons for productivity and economic losses on US dairy operations. The majority of pre-weaned calf mortality (36.4%) is attributed to diarrhea or other digestive problems (USDA, 2014). Five enteric pathogens are commonly associated with diarrhea in dairy calves, including bovine rotavirus, bovine coronavirus, *Escherichia coli*, *Salmonella* spp., and *Cryptosporidium parvum*. However, pathogen-associated differences in health outcomes and case fatality rates have not been well characterized. The objective of this study was to estimate the prevalence of diarrheal pathogens on Ohio dairy farms, and longitudinally measure the health outcomes for diarrheal illnesses. For this study, fecal samples were collected from 277 clinically ill calves across 5 different farms on the first day of diarrheal diagnosis. Genomic techniques, including RT-PCR and ddPCR were used to test for the presence of the 5 enteric pathogens. A Poisson regression model was used to analyze the relative risk of mortality by pathogen and a survival analysis with a Cox regression model was used to analyze time to return to a healthy clinical status by pathogen. Rotavirus was the most prevalent at 75.5% (209/277), followed by K99+ *E. coli* at 42.8% (115/269), *C. parvum* at 28.0% (65/232), coronavirus at 10.1% (28/277), and *Salmonella* had the smallest prevalence at 3.7% (10/269). Risk of mortality was significantly higher for calves infected with *E. coli* and *Salmonella* with relative risks of 4.32 (95%CI: 1.08, 17.27) and 10.98 (95%CI: 2.39, 50.53) respectively (P = 0.038 P = 0.002). The pathogens did not, however, have any statistically significant effect on time to return to a healthy clinical status. Only farm was a significant predictor of time to return to health (P = 0.0139). The results suggest that rotaviral infections are prevalent and widely distributed across farms; however, mortality is more commonly associated with *Salmonella* and K99+ *E. coli* infections. Specific prevention and rapid
differentiation from other causes of calf diarrhea are important to reduce risk of mortality in pre-weaned calves with diarrhea.

Key Words: calf diarrhea, prevalence, enteric pathogen

W12 Advanced molecular spectroscopic techniques for screening mycotoxin concentrations in feed grains for dairy cows in western Canada. H. Shi1,2 and P. Yu*1, 1Ministry of Agriculture Strategic Feeds Research Chair Program, Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada 2College of Life Science and Engineering, Foshan University, Foshan, Guangdong.

The application of traditional methods to detect feed mycotoxin is time consuming and requires a high level of experience and expertise. The objective of this study was to test possibility of using advanced molecular spectroscopic techniques to screen mycotoxin concentrations in feed grains. barley and wheat grains are ranked as the most important feed crops for dairy cows in western Canada. However, they have been suffering from mycotoxins contamination for a long time. In this study, a total of 80 wheat and 42 barley samples were collected and detected for 6 major ergot alkaloids and 12 common mycotoxin concentrations by liquid chromatography- tandem mass spectrometry. The near-IR (NIR; 680–2500 nm) and mid-IR spectra (MIR; 4000–700 cm−1) of all samples were all collected with the grading NIR and FTIR. All spectra were averaged from 3 repeat NIR or FTIR measurements, each recorded from a new sub-sample. The final spectra data were imported into the UnscramblerX v10.3. Preliminary descriptive analyses were performed by both graphic tools and numerical results. To remove the spectral baseline shift, noise, and light scatter effects, 9 preprocessing methods were applied, including baseline offset, standard normal variate (SNV), detrending, SNV + detrending, multiplicative scatter correction, first derivative, second derivative, first derivative + SNV, and second derivative + SNV. The NIR and MIR spectra were calibrated with EAs reference values using PLS technique based on different spectral preprocessing methods and selected wavelength ranges. The possibility whether we could develop fast screening methods for wheat and barley major 6 ergot alkaloids and 12 common mycotoxins detecting by NIR and MIR were revealed in this study. In total ergot alkaloids, R2c for calibration was less than 0.55 and 0.96, R2 c/ n for cross validation was less than 0.14 and 0.96, R2 p for external prediction was NA, for barley and wheat, respectively. In general, the PLS models developed showed relatively weak cross-validation performance. More efforts are required to explore the direct detection limit of the NIR and ATR-FT/MIR techniques for the quantification in different sample matrix.

Key Words: feed, ergot alkaloids and mycotoxins, molecular spectroscopy

W13 Toxicity of deoxynivalenol and fumonisin B1 in primary bovine rumen epithelial cells and a calf intestinal epithelial cell line. N. Reisinger*1, D. Baranski2, S. Schürer-Waldheim1, D. Wend- ner1, G. Antonissen2, E. Mayer1, and V. Nagl1, 1BIOMIN Research Center, Tulln, Austria, 2Department of Pharmacology, Toxicology and Biochemistry, Department of Pathology, Bacteriology and Avian Diseases, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium.

The bovine rumen is capable to detoxify certain mycotoxins to less toxic metabolites. However, during rumen disturbance e.g., sub-acute ruminal acidosis, the ability of detoxification might decrease. There is only a limited number of studies available evaluating the effect of mycotoxins on rumen and intestinal epithelium of cattle. The aim of the study was therefore to access the toxicity of 2 common mycotoxins: deoxynivalenol (DON) or fumonisin B1 (FB1) in primary bovine rumen epithelial cells (REC) and in a calf intestinal epithelial cell line (CIEB). REC were isolated from rumen tissue of dairy cows by enzymatic dissociation with trypsin. CIEB is a spontaneously immortalized cell line derived from the small intestine of a calf. Both cells types were characterized via immunostaining for cytokeratin (epithelial cell marker). For toxicity studies, cells were seeded in 96 well plates (2 × 104 cells/well) for 24 h. Thereafter, cells were incubated with 0 to 25 µM DON and FB1 (n = 6). After 48 h of incubation, the water-soluble tetrazolium salt (WST-1; Mitochondrial metabolism) assay, the neutral red (NR; Lysosomal Activity) assay as well as the sulforhodamine B (SRB; Total protein synthesis rate) assay were performed. Statistical evaluation of data was performed with GraphPad Prism software (Version 7). Analysis of variance or Kruskal-Wallis test was used for data evaluation, depending if data were normally distributed or not. Data were considered as significant if P < 0.05. REC as well as CIEB were positively stained for cytokeratin, and therefore confirmed as epithelial cells. DON had the greatest effect on mitochondrial metabolism in REC starting at a concentration of 1 µM (P < 0.05) and in CIEB at a concentration of 0.39 µM (P < 0.05). FB1 had the greatest effect on lysosomal activity in REC starting at a concentration of 3.13 µM (P < 0.05) and in CIEB at a concentration of 6.25 µM (P < 0.05). Taken together, DON and FB1 had a toxic effect on bovine rumen as well as calf intestinal epithelial cells.

Key Words: in vitro, mycotoxin, digestive epithelium

W14 In vitro evaluation of anti-inflammatory activity of glycerol monolaurate, lauric acid, and methyl laurate. L. K. Mame- dova*1, G. Davis1, C. C. Elrod2, and B. J. Bradford1, 1Kansas State University, Manhattan, KS, 2Natural Biologics, Inc, Newfield, NY.

Glycerol monolaurate (GML) is a natural surfactant comprised of a monoester of glycerol and the medium-chain fatty acid lauric acid (LA). Both GML and LA have bacteriostatic properties, but less is known about the effects of these nutrients on immune or intestinal epithelial cells. The first objective of this study was to assess impacts of GML, LA, and methyl laurate (ML) on inflammatory signaling in RAW 264.7 murine macrophages transfected with a vector that drives expression of alkaline phosphatase (AP) upon activation of NFkB. RAW cells were challenged with 0.1 µg/mL LPS or not for 6 h. Medium was then replaced to provide varying doses of GML, LA and ML (0, 0.5, 2.5, 12.5, 62.5, and 312.5 µM) in 0.06% dimethyl sulfoxide (DMSO) for an additional 4 h (2 × 3 × 6 factorial, n = 6). In addition to AP activity, resazurin metabolism was used to assess cell viability. As expected, LPS treatment significantly increased AP activity and decreased cell viability, whereas DMSO mitigated the loss of viability from LPS. Therefore, the DMSO control served as the reference point for evaluating treatment effects. Increasing doses of GML, LA, and ML all decreased AP activity in a log-linear manner in the presence of LPS (P < 0.001), with significant effects detected at 62.5 and 312.5 µM for all 3 compounds (P < 0.05, Tukey test). No treatment effects were detected in the absence of LPS, and cell viability measures did not indicate toxic effects of these compounds. Second, we determined whether these compounds influence tight junction integrity in LPS-challenged intestinal cells. Caco-2 human colon cancer cells were cultured in transwell inserts for 10 d. Cells were treated with 312.5 µM GML, LA, or ML for 48 h, or with or without addition of 1 µg/mL LPS for the last 24 h (n = 3). Permeability was measured by the transepithelial flux of fluorescein-sulfonic acid. LPS increased monolayer permeability, whereas all 3 compounds significantly attenuated this response (P < 0.05), with LA and GML...
having a greater effect than ML. The results demonstrate that LA and 2 of its esters have anti-inflammatory impacts on macrophages and reduce permeability of colonocytes challenged with LPS.

Key Words: intestinal permeability, macrophage, bioactive

**W15 Effect of a Bacillus-based direct-fed microbial on production, health, and reproduction in lactating dairy cattle: A meta-analysis.** S. R. Fensterseifer¹, R. P. Arias¹, E. A. Galbraith², and C. M. Peter⁴*, ¹United Animal Health Inc., Sheridan, IN, ²Microbial Discovery Group, Franklin, WI.

This study investigated the effects of a Bacillus-based direct-fed microbial (DFM; Strateris ECL, United Animal Health Inc., Sheridan, IN) supplementation on production, health, and reproduction of lactating dairy cows. The DFM was fed at 15 g/hd/d (7.35 × 10⁹ cfu/cow/d) to supplementation on production, health, and reproduction of lactating cows. The DFM was fed at 15 g/hd/d (7.35 × 10⁹ cfu/cow/d) to a total of 18,724 dairy cows in 5 different farms located across major dairy-producing regions of the US (WI, OH, MN, MI and ID). A longitudinal design was used with monthly milk production, components, health, and reproductive metrics monitored via Dairy Comp 305 or PCDART. Reproductive metrics, when available, were evaluated during the same monthly time period over consecutive years. A meta-analysis was then performed on the entire data set comparing 3 mo pre- and post-DFM supplementation. Production, components and reproduction data were analyzed by the PROC MIXED of SAS, with fixed effects of treatment*farm and treatment. Health metrics were evaluated by the PROC GLIMMIX of SAS with the interaction of treatment*farm and treatment as fixed effects. DFM supplementation reduced (P < 0.05) the incidence of ketosis (18 ± 1.3% vs. 12.5 ± 1.4%), retained placenta (13.5 ± 1% vs. 9.7 ± 0.9%) and decreased (P = 0.0342) somatic cell counts (SCC, 438 ± 10.1 vs. 404 ± 10.7×10⁴ cells/mL). DFM increased (P < 0.05) both milk fat (4.05 ± 0.03 vs. 4.30 ± 0.03) and protein (3.2 ± 0.01 vs. 3.3 ± 0.01) percentages, resulting in 1.1 kg higher (P = 0.0387) energy corrected milk (ECM, 35.3 ± 0.4 vs. 36.4 ± 0.4 kg/hd/d). DFM supplementation resulted in increased (P < 0.05) overall heat detection (52.6% vs. 57.3%), conception rate (36% vs. 43.8%) and 21-d pregnancy rate (17.9% vs. 23.9%) and reduced (P < 0.05) services per conception (2.8 vs. 2.3) and abortions (4.1 ± 0.3% vs. 3.1 ± 0.2%). Feeding a Bacillus-based DFM to dairy cattle for 3 mo improved transition cow health, reduced SCC, increased milk fat and protein, ECM, and enhanced reproductive performance. The impact on health and production are probably the secondary and tertiary effects of improved gastrointestinal health.

Key Words: direct-fed microbial, health, performance

**W16 Feeding whey-based colostrum replacer for the first 14 days of life improves dairy calf performance.** A. J. Geiger*, C. Leonardi², and A. Lagó³, ¹Zinpro Corporation, Eden Prairie, MN, ²Dairy Experts, Tulare, CA.

While data surrounding the use of colostral immunoglobulins (IgG) to calves to achieve passive transfer of immunity is abundant, data supplementing calves with colostral immunoglobulins after 24 h of age is a seldom researched disease prevention strategy to reduce antibiotic use. The study objectives were to evaluate the effect of supplementing calves with a concentrated, whey-based IgG, from birth to d 14 on intake and performance. The IgG was from a commercially available colostrum replacer product (Premolac, Zinpro Corp., Eden Prairie, MN; PZ). Upon arrival at the facility, 1,037 newborn, Holstein calves were randomly assigned to 1 of 3 treatments of IgG: 1) 0 g (CON; negative control), 2) 10 g (CR10; 23 g PZ), or 3) 20 g (CR20; 46 g PZ)/d. Treatments were added to milk replacer and fed 2×/d to individually housed calves. Calf BW was recorded on d 0, 15, pre-weaning (d 53) and hutch exit (d 69). Grain intake was measured 1x/wk. All milk replacer refusals were recorded. Continuous outcomes were analyzed using the MIXED procedure of SAS (SAS Institute Inc., Cary, NC). Percentage of calves that refused milk and feeding refusal number were analyzed using the GLIMMIX procedure with a binary distribution or a Poisson distribution and log link, respectively. Supplementing IgG from PZ reduced the percentage of calves that had a milk refusal event in at least one meal during the first 3 weeks of age (38.8, 23.3 and 20.0% for CON, CR10, and CR20 respectively; P < 0.01). Among refusals, CR20 calves refused less feedings (1.5 vs. 2.1; P = 0.03) and less total milk (1.51 vs. 1.99 L; P = 0.04) compared with CON calves. Grain intake was similar among treatments (P = 0.29). Calves fed CR20 were heaviest at d 15 (43.5, 42.9 and 42.2 for CR20, CR10, and CON respectively; P < 0.01). Total gain and ADG from d 0 to 14 were greatest for CR20, intermediate for CR10, and lowest for CON calves (3.6, 3.0 and 2.2 kg and 0.24, 0.20 and 0.15 kg/d respectively; P < 0.01). Supplementing PZ, especially 20 g of IgG from PZ, d 0 to 14 improved growth and reduced milk refusals in Holstein calves.

Key Words: colostrum replacer, calf, immunoglobulin

**W17 Identification of biomarkers associated with mortality in grain-fed veal calves.** H. Goetz*, D. Kelton¹, J. Costa², C. Winder¹, and D. Renaud¹, ¹Department of Population Medicine, University of Guelph, Guelph, ON, Canada, ²Department of Animal and Food Sciences, University of Kentucky, Lexington, KY.

The objective of this prospective cohort study was to identify biomarkers associated with mortality in grain-fed veal calves. Upon arrival at a grain-fed veal facility in Ontario, blood was collected from the jugular vein of each calf into a 10-mL sterile blood collection tube without an anticoagulant. Blood was allowed to clot and then centrifuged at 1,500 × g for 15 min. Serum was separated and stored at −20°C until analysis at a commercial reference laboratory (Animal Health Laboratory, Guelph, Ontario, Canada). Several metabolites were measured including creatine kinase, cholesterol, haptoglobin, manganese, serum total protein, iron, cobalt, zinc, selenium, and molybdenum. Univariable mixed logistic regression models were created to evaluate metabolic biomarkers associated with mortality. A lowess smoother curve was generated to assess the linearity of each predictor variable to the outcome on a log odds scale. If a variable failed to meet the linearity assumption, the variable was categorized into quartiles. A total of 909 calves of unknown age had blood collected at arrival from January to December 2017. Of the calves examined, 67 calves (7.5%) died over the 11-week period under observation. The level of cholesterol, haptoglobin, and iron were associated with mortality. For every 1 mmol/L increase in cholesterol, the odds of mortality are reduced (Odds ratio (OR): 0.57; 95% CI: 0.37–0.91; P = 0.02). Compared with the referent category (less than 0.15 g/L), if the calf had a haptoglobin concentration between 0.15 and 0.16 g/L (OR: 2.24; 95% CI: 1.02–4.89; P = 0.04) or 0.19–3.3 g/L (OR: 2.38; 95% CI: 1.01–5.58; P = 0.047), calves had an increased odds of dying. Compared with the referent category (less than 2.1 mg/mL), calves with iron concentrations of 2.8–3.6 mg/mL (OR: 2.12; 95% CI: 1.03–4.37; P = 0.04) had a greater risk of mortality. These results demonstrate that cholesterol, haptoglobin, and iron could serve as biomarkers to identify calves at high-risk of mortality when measured at arrival to a veal facility.

Key Words: male dairy calf, mortality, biomarker
W18  **Transcriptional comparison between total RNA and mRNA isolated from same fecal samples of neonatal dairy calves.** F. Rosa* and J. S. Osorio, Dairy and Food Science Department, South Dakota State University, Brookings, SD.

Inflammatory-related genes are commonly expressed at a low abundance. However, these can still be detected in fecal RNA isolated from dairy calves, which contains a negligible amount of RNA from immune cells under non-diarrheic conditions. Additionally, genes related to common functions of the gastrointestinal (GI) tract were observed in total RNA from fecal samples. However, fecal RNA isolation remains a challenge, because of the potential enrichment of bacterial RNA, which can dilute the targeted eukaryotic RNA and consequently dampen the sensitivity of the fecal RNA method. Therefore, our objective in this study was to determine the differential eukaryotic RNA enrichment in total RNA vs mRNA from same fecal samples of healthy neonatal dairy calves. To test this, 200 mg of feces were used from 6 neonatal Holstein calves for total RNA isolation, using a Trizol based method along with calves. The internal control genes used in this experiment were GAPDH, ACTB, GAPDH, RPS9, and PPIA. Normalized gene expression data were log-transformed before statistical analysis using the Proc Mixed of SAS (SAS 9.4). Expression of genes specific for GI epithelial cells including log-transformed before statistical analysis using the Proc Mixed of SAS.

**Key Words:** calf, fecal RNA, gastrointestinal tract

W19  **Comparative transcriptomic analysis of epithelial cell markers across gastrointestinal tissues and fecal RNA isolated from dairy calves.** F. Rosa*, N. Carpinelli, R. Mohan, and J. S. Osorio, Dairy and Food Science Department, South Dakota State University, Brookings, SD.

Fecal RNA method can be used to evaluate biological adaptations of the gastrointestinal (GI) tract of dairy calves through gene expression analysis. A limitation with this method is the current lack of data indicating how the transcriptomic profile observed in fecal RNA mirrors that in specific sections of the GI tract. Therefore, our objective in this study was to compare the transcription of gene markers for GI epithelial cells, fatty acid binding protein 2 (FABP2) and cytokertatin 8 (KRT8) in fecal RNA against several GI tract sections in dairy calves. To test this, postmortem samples were collected from ruminal epithelium, cecum, large intestine, duodenum, jejunum, ileum, and feces from 6 healthy male Jersey calves (5 wk of age) for total RNA isolation. The standard curve was composite from all samples including cDNA from tissues and fecal. The internal control genes used in this experiment were B2M, ACTB, GAPDH, RPS9, RPS15A, and PPIA. Normalized gene expression data were log-transformed before statistical analysis using Proc Mixed of SAS. The expression of FABP2 was greater ($P < 0.01$) in the duodenum tissue than in GI section associated with fermentation (i.e., rumen, large intestine, and cecum). Within the small intestine the mRNA expression of FABP2 was greater ($P = 0.01$) in duodenum than in jejunum, but not different than ileum. In fecal RNA, the FABP2 expression was greater ($P ≤ 0.03$) than in GI section related to fermentation. However, FABP2 was similar ($P = 0.3$) between fecal RNA and ileum. The expression of KRT8 was greater ($P ≤ 0.02$) in cecum and large intestine than in rumen and jejunum. Among the small intestine sections KRT8 was greater ($P = 0.03$) expressed in duodenum than in jejunum. The fecal RNA had greater ($P ≤ 0.02$) expression of KRT8 than jejunum and ileum. In contrast, the KRT8 expression in fecal was not different than the transcripts observed in cecum and large intestine. Since the transcription of the genes specific for GI epithelial cells were significant observed in the RNA isolated from feces, these preliminary data further confirms that fecal RNA has a potential to be used as a tool to evaluate molecular adaptations in the GI tract of dairy calves.

**Key Words:** calf, fecal RNA, gastrointestinal tract

W20  **Milk metabolites as noninvasive indicators of nutritional status of mid-lactation Holstein and Montbéliarde cows.** P.-A. Billia*, Y. Faulconnier*, T. Larssen*, C. Leroux1,3, and J. Pires1, 1Université Clermont Auvergne, INRA, VetAgro Sup, UMR Herbivores, Saint-Genès-Champanelle, France, 2Department of Animal Science, Aarhus University, Tjele, Denmark, 3Department of Food Science and Technology, University of California Davis, Davis, CA.

The objective was to investigate the effects of feed restriction on concentrations of selected milk metabolites in mid-lactation Holstein and Montbéliarde cows, and explore their correlations with energy balance. Nine Holstein and 10 Montbéliarde cows (165 ± 21 DIM) underwent 6 d of feed restriction during which feed allowance was reduced to meet 50% of NEL requirements calculated before initiation of the challenge. The experiment was divided in 4 periods: Control (CONT; d −3 to −1), restriction (REST; d 1 to 6), WK1 (d 7 to 13) and WK2 (d 18). Milk concentrations of β-hydroxybutyrate (BHB), glucose, glucose-6-phosphate (Glucose6P), isocitrate and glutamate were measured and statistical analyses performed using mixed models of SAS with fixed effects of period and breed, and the random effect of cow. Relationships among variables were explored by Spearman correlations. Feed restriction induced a negative EB, increased Glucose6P and isocitrate (+38% and +39%, respectively) and decreased BHB, glucose and glutamate concentrations in milk (−20%, −57% and −65%, respectively) compared with pre-challenge values (Table 1). All milk metabolites were significantly correlated with EB (0.46, 0.62, −0.25, −0.41, 0.59 for BHB, glucose, Glucose6P, isocitrate and glutamate, respectively). Results suggest that milk metabolites may be used as noninvasive indicators of nutritional status of mid-lactation cows.

**Key Words:** milk metabolite, dairy cow, energy balance


Given the potential impacts of liver triglyceride (lTG) accumulation on hepatic metabolism, the ability to diagnose fatty liver without a liver biopsy could be advantageous in both the research and applied settings as accumulation of lTG can only be diagnosed by liver biopsy. Since fatty liver is related to the overall metabolic status of the cow, the
of feed restriction on energy balance and milk metabolite concentrations in mid-lactation cows

<table>
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<th>CONT</th>
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<th>WK2</th>
<th>SEM</th>
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^a^b Breed LSMEANS not sharing a common superscript differ (P ≤ 0.05).

W22 Antimicrobial usage for the treatment on respiratory diseases in calves: A systematic review. E. Gürdal* and N. Silva-del-Rio, Veterinary Medicine Teaching and Research Center, University of California Davis, Tulare, CA.

Our objective was to conduct a systematic review of the quality of previous publications that evaluated the efficacy of antimicrobials for the treatment of bovine respiratory disease (BRD) in calves. The literature search strategy, based on population, intervention, and outcome of studies written in English from CabDirect, PubMed, Web of Science and Scopus, was conducted on December 2018; a total of 2,058 publications were retrieved. Publications of interest were clinical trials and experimental challenges that used antimicrobials to treat BRD in calves ≤6 mo. Thirty-four manuscripts containing 37 trials were retained after screening the titles (n = 901), the abstracts (n = 308) and the full papers. The selected trials included clinical trials (n = 22) and challenge trials (n = 15) that dated back from 1979. The median number of animals enrolled was 49 and ranged from 11 to 696 calves. Seventeen manuscripts were either funded or had authors affiliated with pharmaceutical companies. A total of 29 trials were randomized but only 14 of those were blinded. Fifteen trials included a negative control treatment; but only 6 were randomized and blinded. Trials with negative control evaluated the efficacy of: one (n = 3) or more (n = 2) antimicrobials, anti-inflammatoriness combined with antimicrobials (n = 2), various dosages or timing of treatments (n = 7), or combination of antimicrobial treatments (n = 1). Macrolides were the most common antimicrobial class evaluated (n = 14). The length of the observational period for health outcomes ranged from 3 d to 8 wks. Fever was the most frequent clinical sign of BRD evaluated (n = 26). Only 8 trials evaluated clinical signs of respiratory disease using a scoring tool. In addition to clinical signs, 13 trials performed pathological examination of euthanized calves. Although considerable numbers of studies have been conducted on antimicrobial use for BRD in calves, very few studies were controlled and randomized. Future research on BRD should follow standardized methods for the evaluation of clinical outcomes. Funding provided by CDFA-AUS project.

Key Words: antimicrobial, calf, respiratory disease

W23 Effect of acupuncture therapy in dairy cows affected by pyometra: A randomized controlled clinical trial. P. Pinedo*1, L. Caixeta2,3, E. Barrell2,3, J. Herman2, J. Velez4, D. Manriquez1, and T. Holt2. 1Department of Animal Sciences, Colorado State University, Fort Collins, CO; 2Department of Clinical Sciences, Colorado State University, Fort Collins, CO; 3Department of Veterinary Population Medicine, University of Minnesota, St. Paul, MN, 4Aurora Organic Dairy, Platteville, CO.

Pyometra (PYO) is a uterine disease characterized by the accumulation of purulent or mucopurulent material within the uterine lumen in the presence of an active corpus luteum (CL). Due to prohibited use of artificial hormones in US certified organic dairies, conventional therapies for treatment of PYO are not applicable. The objective of this study was...
to evaluate the efficacy of 2 acupuncture procedures on the treatment of persistent CL in cows with PYO. We hypothesized that acupuncture would reduce CL diameter and serum progesterone (P4) concentrations resolving the PYO. Holstein cows with PYO, at a USDA certified organic dairy farm in Northern Colorado were enrolled in a randomized controlled clinical trial and assigned into 1 of 3 treatments: (1) control pyometra (CP; no treatment; n = 17); (2) electroacupuncture (EAP; n = 15); and (3) laser acupuncture (LAP; n = 15). Each cow received 3 20-min acupuncture sessions on alternate days. Cows had blood samples collected for determination of serum progesterone concentration at enrollment (−3 d) and at d 0, d 2, d 4, d 11, d 18, and d 25 after first treatment. CL diameter was determined by transrectal ultrasonography at −3 d, d 0, d 2, d 4, d 11, and d 18. Logistic regression was used for the analysis of binary outcome variables, whereas continuous variables were evaluated by ANOVA and by repeated measures analyses, accounting for baseline data (CL diameter and serum P4 concentration). Average ± SE for CL diameter change from d 0 to d 18 were 1.0 ± 1.0 mm, 0 ± 1.0 mm, and −0.33 ± 1.0 mm for CP, EAP, and LAP, respectively. None of the cows had serum P4 values <1 ng/mL by the end of the monitoring period and average ± SE P4 concentration change from d 0 to d 25 were −4.2 ± ng/mL, −0.7 ± ng/mL, and 4.5 ± ng/mL for CP, EAP, and LAP, respectively. The repeated measures analysis indicated no differences in time for CL diameter or serum P4 concentrations among groups. Two cows in EAP and 1 cow in LAP conceived 38 d, 68 d, and 38 d, after treatment completion. In conclusion, acupuncture was not an effective treatment for persistent CL in cows with PYO during the monitoring period.

Key Words: acupuncture, pyometra, corpus luteum

W24 Colostrum supplementation with omega-3 fatty acids and α-tocopherol decreases indicators of oxidative stress and alters plasma fatty acid profile in newborn calves during the first week of life. J. Oppegenorth*, L. M. Sordillo, and M. J. VandeHaar, Michigan State University, East Lansing, MI.

Oxidative stress (OS) occurs when antioxidants fail to neutralize an overabundant concentration of reactive oxygen species, resulting in damage to cellular components. This phenomenon is prevalent in neonatal calves, potentially causing disease vulnerability and immune dysfunction. Past studies have shown the benefits of fish and flax oil on calf health and growth due to their omega-3 fatty acids (n-3 FA); these metabolites may mediate inflammation and OS through anti-inflammatory and antioxidant properties. We hypothesized a 60 mL fish and flax oil colostrum supplement would improve indicators of calf health and plasma concentrations of n-3 FA during the first week of life. Sixteen Holstein calves were blocked by sex and birth date and randomly assigned to control (no supplement; Con), or fish and flax oil (FFtrt) supplemented in first colostrum (3 L within 6 h, > 22% on Brix). FFtrt was a 60 mL 1:1 blend of oils with 200 mg α-tocopherol. Blood was sampled on d 1, 2, 4, 7, 14, and 21 after birth for assessment of passive transfer, oxidant status, and FA profile. Health was scored daily. Hip height and body weight were recorded weekly. Data were analyzed with a mixed procedure in SAS 9.4 including treatment, sex, and day as fixed effects and calf and block as random effects. FFtrt did not alter concentration of total protein in blood serum, prevalence of diarrhea, or rate of growth (P > 0.10), but tended to improve nasal scores (P = 0.07). FFtrt increased plasma concentrations of n-3 FA as much as 90% by 1 d of age (P < 0.01). FFtrt decreased oxidant status index (OSi) by 55% by 2 d of age (Con: 73, FFtrt: 32 OSi; P < 0.01) and remained decreased overall in the first week of life (Con: 74, FFtrt: 50 OSi; P < 0.01). OSi and FA concentrations returned to control values by d 14. In conclusion, a colostrum supplement of n-3 FA and α-tocopherol decreased oxidant status and increased plasma n-3 FA concentrations in the first week of life and has the potential to improve health of neonatal calves.

Key Words: omega-3, colostrum, oxidative stress