ANIMAL HEALTH III: **PERIPARTURIENT AND LACTATION HEALTH**

0091 Milk quality and milk components in lactating dairy goats fed OmniGen-AF from dry-off through the entire lactation. A. D. Rowson*, T. J. Boyle, D. J. McLean, S. A. Armstrong, and S. B. Puntenney, *Prince Agri Products, Inc., Quincy, IL.*

In the United States, the legal somatic cell count (SCC) limit for dairy goat milk is 1500,000 mL^{-1}. However, it is common for SCC to be much higher than this. Production of milk with a SCC higher than the legal limit results in farms being unable to ship their milk and lost income. The objective of this study was to evaluate the supplementation of OmniGen-AF to dry and lactating dairy goats on milk quality and milk components over an entire lactation. Thirty-five, 2-yr-old does housed on a commercial goat dairy located in south central Wisconsin were randomly assigned to 1 of 2 groups: 1) Control-fed (n = 18) and 2) OmniGen-AF-fed (n = 17). Animals in Group 1 were fed a complete feed pellet twice a day and ad libitum alfalfa hay. Animals in Group 2 were fed the same diet but with 6 g/h/d of OmniGen-AF added to the pellet. The project started at dry-off (~40 to 60 d before kidding) and continued for the full lactation. Breeds of does were Alpine, Saanen, Nubian, and La Mancha, and all breeds were equally represented in both groups. Monthly Dairy Herd Improvement Association (DHIA) milk testing was performed on all animals for 9 mo. The SCC, percent milk fat, percent milk protein, and milk production data were collected at each test. The mean SCC for OmniGen-AF-supplemented does was 585,000 mL^{-1}, which was significantly lower ($P < 0.05$) than the mean SCC for control-fed does, which was 894,600 mL^{-1}. These differences were more pronounced as does approached the end of lactation where the mean SCC was 1669,000 mL^{-1} less in OmniGen-AF-fed does compared with controls (2094,000 mL^{-1} vs. 3763,000 mL^{-1}, respectively). Milk percent fat ($P < 0.01$) and percent protein ($P < 0.05$) were different between the OmniGen-AF-fed and control-fed does. Specifically, mean milk percent fat was 3.21% from control-fed does and 3.45% from OmniGen-AF-fed does. Mean milk percent protein was 2.93 and 3.08% from control and OmniGen-AF-fed does, respectively. There was no difference in milk production between groups. Data from this trial demonstrate that OmniGen-AF fed goats experienced benefits in milk components and attenuation of the dramatic increase in SCC that normally occurs late in lactation, both of which are indicative of improved mammary gland health.

Key Words: goats, OmniGen-AF, SCC

0092 Modulation of innate immune function and phenotype in bred dairy heifers during the periparturient period induced by feeding an immunostimulant 60 d before delivery. E. L. Nace, S. C. Nickerson*, F. M. Kautz, S. Breidling, D. Wochele, L. O. Ely, and D. J. Hurley, *University of Georgia, Athens.*

The purpose of this study was to evaluate the effect of an immunostimulating feed additive on innate immunity and health events during the periparturient period in dairy heifers when mammary immunity is suppressed. From 60 d prepartum through day of calving, supplemented heifers (n = 20) received OmniGen-AF daily and were compared with unsupplemented controls (n = 20). Blood leukocyte innate immune activity [phenotypic markers, phagocytic activity, and reactive oxygen species (ROS) production] was measured before feeding (60 d prepartum), 30 d later, and on d 1, 7, 14, and 30 postpartum. Health parameters and milk production were measured at calving and early lactation. Expression of CD62L among leukocytes from supplemented heifers was greater during the periparturient period than controls. Specifically, on d 1 postpartum, mean percentage of neutrophils exhibiting CD62L surface markers was 95.3% for OmniGen-AF treated heifers vs. 91.4% for controls ($P < 0.10$), and the percentage decreased from 98.3% 30 d prepartum to 91.4% on d 1 postpartum among controls ($P < 0.05$); values for supplemented heifers did not decrease. Likewise, leukocyte phagocytic activity against *Escherichia coli* and *Staphylococcus aureus* was greater in heifers supplemented with OmniGen-AF; e.g., on d 30 prepartum and d 7 postpartum, mean percentage of monocytes from supplemented heifers exhibiting phagocytic activity against *E. coli* were 11.7 and 11.3%, respectively, whereas values for controls were 7.3 and 7.4% ($P < 0.10$), respectively. In controls, phagocytosis decreased from 13.7% 60 d prepartum to 7.3 and 7.5% on d 30 prepartum and d 7 postpartum ($P < 0.05$), respectively, but values for supplemented heifers did not decrease over time. Conversely, ROS production in response to PMA and killed *S. aureus* stimulation was greater among control heifers compared with supplemented animals; e.g., the quantities of ROS generated in response to *S. aureus* lysate on d 1 and 7 postpartum were 68.8 vs. 51.9 and 56.1 vs. 41.3 units ($P < 0.05$), respectively. Supplemented heifers exhibited fewer deleterious health events (retained placenta, displaced abomasum, ketosis, udder edema, death) than controls (1.25 vs. 1.93/heifer) and a lower rate of new cases of mastitis (9.6% vs. 23.2%); however, no significant differences were observed in overall prevalence of mastitis, milk SCC, or milk production. Results demonstrated a positive role of OmniGen-AF in amplifying leukocyte antibacterial activity during the periparturient period and support the continued study of dietary supplementation to enhance mammary gland health in dairy cattle.

Key Words: dairy heifer, innate immunity, periparturient period

0093 Restriction in energy or protein affects differentially behavior of lactating dairy cows.

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Feed restriction adversely affects feeding and social behavior in cattle. However, data on the effects of nutrient composition on these characteristics are limited. The objective was to quantify the effects of dietary energy and protein restriction on feeding and behavior in lactating Holstein and Jersey cows. Twelve cows in mid-lactation balanced for breed and days in milking were used in a Latin square design: 3 cows × 3 periods. Each experimental period lasted 3 wk and consisted of: 1) adaptation, where all animals were fully fed according to their requirements, 2) restriction, where animals were fed to provide 50% of their daily energy (E) and protein (P) requirements, and 3) treatment, where animals were fed with 1 of the following diets: 100E + P, 50E + 100P, and 100E + 50P, to provide 100% of energy + protein requirement, 50% of energy requirement, 50% of protein requirements, respectively. On the last day of the treatment period, cows were visually observed from 0600 to 2100 h. The behavioral attributes were recorded as time spent in feeding behavior and number of social and adaptation events. Data were logarithmic transformed and submitted to analysis of variance, considering main effects of diet, cow, and period. Nutrient restriction did not change feeding and ruminating times or aggressive interactions. Energy restriction reduced time spent lying but increased tongue curling and licking events. Protein restriction reduced idling time, number of low intensity vocalizations, and tended to reduce standing time. The data are consistent with the concept that cows react differently to limitations in energy or protein in the diet.

Key Words: behavior, nutrient, restriction

Table 0093.

	Diet				
Attribute	100% E+P	50%E + 100%P	50%P + 100%E	$P > F_{diet}$	RSD (%)
Eating (min)	276.1	254.1	278.7	NS	2.2
Ruminating (min)	116.6	129.1	145.2	NS	6.7
Idling (min)	243.1[a]	243.7[a]	182.6[b]	0.0094	4.3
Lying (min)	203.7[ab]	176.6[b]	243.7[a]	0.0381	5.1
Standing (min)	169.8[d]	130.0[de]	87.7[e]	0.0615	12.6
Aggressing (n°)	0.9	1.6	2.9	NS	300.6
Being aggressed (n°)	1.9	1.2	1.6	NS	257.7
Vocalizing (n°)	0.5 a	0.3[ab]	0.1[b]	0.0440	93.5
Licking the floor (n°)	0.1 b	1.7[a]	0.5[ab]	0.0271	217.0
Curling the tongue (n°)	0.1 b	0.2[a]	0.1[b]	0.0279	15.6

[a,b] Means in the same row are different (least squares means, DMS test, $P < 0.05$).
[d,e] Means in the same row tend to be different (least squares means, DMS test, $P < 0.10$).
RSD = relative standard deviation; NS = not significant

0094 Dynamics of culling for Jersey, Holstein, and crossbred cows in large multi-breed dairy herds.

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The objective of this observational study was to describe and compare the dynamics of reason-specific culling risk for the genetic groups Jerseys (JE), Holsteins (HO), and Jersey × Holstein crossbreds (JH), considering parity, stage of lactation, and milk yield, among other variables, in large multi-breed dairy herds in Texas. The secondary objective was to analyze the association between survival and management factors, such as breeding and replacement policies, type of facilities, and use of cooling systems. After edits, available data included 202,384 lactations in 16 herds, ranging from 407 to 8773 cows calving per year during the study period from 2007 to 2011. The statistical analyses were performed through logistic regression (PROC GLIMMIX, SAS) and by estimation of hazard functions (PROC LIFETEST, SAS). The distribution of lactation records by genetic group was 58%, 36%, and 6% for HO, JE, and JH, respectively. Overall culling rates across breeds were 30.1%, 32.1%, and 35.0% for JH, JE, and HO, respectively. The dynamics of reason-specific culling were dependent on genetic group, parity, stage of lactation, milk yield, and herd characteristics. Early lactation was a critical period for "died" and "injury-sick" culling. The risk increased with days after calving for "breeding" and, in the case of HO, "low production" culling. Open cows had a 3.5 to 4.6 times greater risk for overall culling compared with pregnant cows ($P \leq 0.01$). The odds of culling with reason "died" within the first 60 d in milk (DIM) were not significantly associated with genetic group. However, both JE and JH had lower odds of live culling within the first 60 DIM compared with HO cows [OR = 0.72 ($P \leq 0.001$) and 0.82 ($P \leq 0.002$), respectively]. Other cow variables significantly associated with the risk of dying within the first 60 DIM were cow relative 305 mature equivalent (MEQ) milk yield, parity, and season of calving. Significant herd-related variables for death included herd size and origin of replacements. In addition to genetic group, the risk of live culling within 60 DIM was associated with cow relative 305 MEQ milk yield, parity, and season of calving. Significant herd-related variables for live culling included herd relative 305 MEQ milk yield, herd size, type of facility, origin of replacement, and type of maternity. Overall, reason-specific culling followed similar patterns across DIM in the 3 genetic groups.

Key Words: culling, death, Holstein, Jersey

0095 Effect of an organic-certified treatment (Optimum UterFlush) for toxic puerperal metritis on cure and reproductive performance of dairy cows. P. J. Pinedo[*1], J. S. Velez[2], H. Bothe[3], D. Merchan[3], J. M. Piñeiro[3], and C. A. Risco[4], *[1]Texas A&M AgriLife Research, Amarillo, [2]Aurora Organic Farms, Boulder, CO, [3]Aurora Organic Dairy, Boulder, CO, [4]College of Veterinary Medicine, University of Florida, Gainesville.*

The objective was to evaluate the efficacy of an organic-certified product (Optimum UterFlush, Van Beek Natural Science) on the treatment of toxic puerperal metritis (TPM) in cows in an organic dairy farm. Evaluation included clinical cure, survival, and reproductive performance. The TPM was defined as an abnormally enlarged uterus and fetid watery red-brown vaginal discharge, associated with systemic illness and fever (rectal temperature > 39.5°C), within 12 d postpartum. Cows diagnosed with TPM (n = 220) were randomly assigned to 2 intrauterine treatments (every other day for a total of 3 treatments): 1) Control (CON) = 200 mL of Povidone iodine diluted in 2 L of distilled water (n = 113) and 2) UterFlush (UF) = 15 mL diluted in 105 mL of distilled water (n = 107). All treated cows received hypertonic solution (500 mL of 25% calcium borogluconate IV) and oral aspirin (5 boluses/d). Outcome variables for treatment efficacy included fever and presence of fetid vaginal discharge at d 6 and 14 after diagnosis, survival at d 6, 14, and 30, and reproductive performance. Control variables were parity, BCS at enrollment, and calving season. Logistic regression and ANOVA were used for the analyses (PROC GLIMMIX and PROC GLM, SAS). The odds of surviving at d 6, 14, and 30 for cows in the UF treatment were 4.7 (95%, CI = 1.4 to 15.8), 2.8 (95%, CI = 1.3 to 6.1), and 3.6 (95%, CI = 1.7 to 7.7) times the odds of cows in the CON treatment. Occurrence of fever at d 6 and 14 was not different between the 2 treatments. Presence of a fetid vaginal discharge at d 6 and 14 was lower in cows treated with UF compared with cows in the CON group [11% vs. 28% (P < 0.001) and 1% vs. 8% (P = 0.017)]. The odds of breeding until 150 d in milk (DIM) and the time to first breeding were not different for the 2 treatments. The odds of pregnancy at the first breeding and at 300 DIM for cows treated with UF were 2.2 (95%, CI = 1.1 to 4.4) and 2.0 (95%, CI = 1.1 to 3.5) times the odds of cows in the CON group. Days to pregnancy were similar in both treatments. The number of breedings per pregnancy was 1.96 vs. 2.58 for cows in the UF and CON treatments (P = 0.01), respectively. Results indicated that cows with TPM treated with Optimum UterFlush had higher odds of recovering and improved reproductive performance, compared with cows treated with Povidone iodine.

Key Words: puerperal-metritis, organic, UterFlush

0096 Effects of yeast product supplementation on immunity and uterine inflammation in transition dairy cows. K. Yuan[*1], L. Mendonca[1], L. Hulbert[1], L. Mamedova[1], M. Muckey[1], Y. Shen[1], C. C. Elrod[2], and B. Bradford[1], *[1]Kansas State University, Manhattan, [2]Vi-COR, Inc., Mason City, IA.*

The objective of this study was to assess the effects of supplementing a yeast product derived from *Saccharomyces cerevisiae* on immunity and uterine inflammation in transition cows. Forty multiparous Holstein transition cows were blocked by expected calving date and randomly assigned within block to 1 of 4 treatments (n = 10) from 21 d before expected calving to 42 d postpartum. Rations were top dressed with yeast culture plus enzymatically hydrolyzed yeast (Celmanax, Vi-COR, Mason City, IA) at the rate of 0, 30, 60, or 90 g/d throughout the experiment. Blood samples collected on -21, −7, 1, 4, 7, 14, 21, and 35 d relative to calving were incubated with *E. coli* (# 51813) to assess the ability of blood to kill bacteria. Uterine samples were collected on d 7 and 42 postpartum by cytobrush technique to determine neutrophil populations and relative abundance of transcripts involved in inflammation. Fecal samples were collected on d 7 and 21 for analysis of immunoglobulin A (IgA) concentration. Data were analyzed using mixed models with repeated measures over time. The percentage of *E. coli* killed by whole blood was not affected by yeast treatments (P = 0.28). Uterine neutrophil populations were much greater in samples collected on d 7 compared with those on d 42 (32.0% vs. 7.6% ± 3.7 of cells, P < 0.01), indicating greater neutrophil infiltration immediately after calving, but no treatment (P = 0.53) effect was detected. There were significant ($P \leq 0.01$) day effects for IL-6, IL-8, neutrophil myeloperoxidase, and neutrophil elastase, reflecting greater abundance of these transcripts in uterine tissues collected on d 7 compared with d 42. Interestingly, there was a quadratic dose effect (P = 0.02) for IL-6, indicating that 30 and 60 g/d decreased uterine IL-6 mRNA. The mRNA abundance of neutrophil myeloperoxidase and elastase was increased (P < 0.05) by yeast product. Yeast product quadratically increased fecal IgA concentrations (P = 0.03), suggesting that 30 and 60 g/d doses enhanced mucosal immunity. Yeast product supplementation did not affect whole blood bacterial killing ability but modulated uterine inflammatory signals and mucosal immunity in transition dairy cows.

Key Words: immunity, transition cow, yeast

0097 Hyperketonemia in early lactation dairy cattle: Component and total cost per case.

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The purpose was to develop deterministic economic models to estimate the costs associated with: 1) the component cost per case of hyperketonemia (HYK) and 2) the total cost per case of HYK when accounting for costs related to HYK-attributed diseases in dairy cows. Data from current literature were used to model the incidence and risks of HYK, displaced abomasa (DA), and metritis, disease associations, and milk production, culling, and reproductive outcomes. The component cost of HYK was estimated based on 1000 calvings per year, incidence of HYK in primiparous and multiparous animals, percentage of animals receiving clinical treatment, costs associated with diagnostics, therapeutics, labor, and death loss, and costs of future milk production losses, future culling losses, and reproduction losses. Costs attributable to DA and metritis were estimated based on the incidence of each disease in the first 30 d in milk, number of cases of each disease attributable to HYK, costs associated with diagnostics, therapeutics, discarded milk during treatment and withdrawal period, veterinary service (DA only), death loss, and costs of future milk production loses, future culling losses, and reproduction losses. The component cost per case of HYK was estimated at $127 and $106 for primiparous and multiparous animals, respectively; the average component cost per case of HYK was estimated at $112. Thirty-one percent of the average component cost of HYK was due to future reproductive losses, 28% to death loss, 22% to future milk production losses, 13% to future culling losses, 3% to therapeutics, 2% to labor, and 1% to diagnostics. The total cost per case of HYK was estimated at $361 and $247 for primiparous and multiparous animals, respectively; the average total cost per case of HYK was $279. Forty percent of the average total cost of HYK was due to the component cost of HYK, 32% to the cost attributable to metritis, and 28% to the cost attributable to DA. The high total cost of HYK at reported incidences of 40 to 60% highlights the importance of appropriate transition cow nutrition and management to decrease the impact of HYK on both a disease and economic basis. In addition, these estimates can be used to model the cost benefit of various preventative and treatment interventions.

Key Words: component cost, dairy cow, hyperketonemia, total cost

0098 The effects of grain-induced subacute ruminal acidosis on interleukin-6 and acute phase response in dairy cows.

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Subacute ruminal acidosis (SARA) resulting from excessive grain feeding to dairy cows is accompanied by an acute phase response. Interleukin 6 (IL-6) has been proposed as a mediator of this response. We tested if the acute phase response associated with grain-induced SARA is mediated by IL-6. Six lactating Danish Holstein cows were used in an incomplete block design study that included 2 periods with 2 cows in a SARA-challenge treatment and 2 cows in a control treatment, and a third period with 2 cows in a SARA-challenge treatment. In the first 2 wk of each experimental period, all cows received a control diet (17.4% CP, 19.2% starch, 6.28 MJ NEL/kg DM). In the third week, the diet for control cows remained unchanged. For the SARA-challenge cows, 40% of the control diet was gradually substituted with grain pellets (50:50 wheat:barley) within 3 d to induce SARA. This SARA-challenge diet was fed for another 4 d. Jugular vein blood was sampled at 7 h post-feeding on Tuesday and Thursday of the second week and during the first 2 and last day of the SARA-challenge diet feeding. The ELISA kits were used for measurement of IL-6 and acute phase proteins haptoglobin (Hp), LPS binding protein (LBP), and serum amyloid A (SAA). For data analysis, a mixed model was used, in which cow was treated as a random factor, whereas treatment (SARA challenge vs. control), period, day within period, as well as the interaction between day within period and treatment, were treated as fixed factors. Compared with control cows, the SARA challenge tended to increase LBP (7.54 vs. 10.23 mg/L, $P = 0.10$) and increased SAA (4.24 vs. 11.60 mg/L, $P = 0.04$) and Hp (3.57 vs. 22.09 mg/L, $P = 0.04$) in blood, confirming that the SARA challenge caused an acute phase response. Concentrations of IL-6 were not affected by the SARA challenge and averaged 5.06 ng/mL across treatments. Our data do not confirm that IL-6 mediates the acute phase response during grain-induced SARA. This confirmation may require more frequent blood sampling around the time of the SARA challenge.

Key Words: acute phase proteins, dairy cow, IL-6

0099 Evaluation of propylene glycol and glycerol infusions as potential treatments for ketosis in dairy cows. P. Piantoni* and M. S. Allen, *Michigan State University, East Lansing.*

Our objective was to evaluate propylene glycol (PG) and glycerol (G) as treatments for ketosis. Two experiments lasting 4 d each were conducted in which cows received 1 bolus infusion per day. All data were analyzed by ANOVA. Experiment 1 used 6 ruminally cannulated cows [28 ± 7 d in milk (DIM)] randomly assigned to 300-mL infusions of PG or G (both ≥ 99.5% pure) in a crossover design experiment. Within each period, cows were randomly assigned to sequence in a crossover for site of infusion in the abomasum (A) or reticulorumen (*R*). Treatments were infused in the cranial reticulorumen (R-PG and R-G) to simulate drenching and abomasum (A-PG and A-G) to prevent metabolism by ruminal microbes. Treatment did not affect DMI or milk yield. Glycerol infused abomasally increased plasma glucose concentration the most (15.2 mg/dL; interaction $P < 0.05$), followed by R-PG (12.0 mg/dL), A-PG (9.7 mg/dL), and R-G (7.9 mg/dL). Glucose area under the curve (AUC) was also highest for A-G (1480 min × mg/dL; interaction $P < 0.10$), followed by A-PG (1167 min × mg/dL), R-PG (1009 min × mg/dL), and R-G (302 min × mg/dL). Abomasal infusions increased glucose AUC compared with ruminal infusions (1324 vs. 656 min × mg/dL; $P < 0.05$). Experiment 2 used 4 ruminally cannulated cows (23 ± 5 DIM) randomly assigned to treatment sequence in a Latin square design experiment balanced for carry-over effects. Treatments were: 300 mL PG, 300mL G, 600 mL G (2G), and 300 mL PG + 300 mL G (GPG), all infused into the cranial reticulorumen. Infusions did not affect DMI or milk yield, but affected time to reach plasma glucose baseline after maximum and glucose AUC (both $P < 0.05$). Treatment contrasts compared PG with G, 2G, and GPG. Propylene glycol increased plasma glucose concentration and glucose AUC compared with G (16.4 vs. 6.6 mg/dL and 1768 vs. 213 min × mg/dL; both $P < 0.05$), but not compared with 2G or GPG. Abomasal infusion of G elicited the best plasma glucose response followed by infusion of PG into the rumen or abomasum. Plasma glucose response to ruminal infusion of PG was better than G, likely because of greater ruminal metabolism of G, and no benefit was detected for doubling the dose of G or infusing G in combination with PG. A 300-mL dose of propylene glycol is as effective a treatment as twice the amount of glycerol when administered in the reticulorumen.

Key Words: fresh cows, glucose precursors, ketosis

0100 Integrating metabolomics and transcriptomics of liver to study susceptibility to ketosis in response to prepartal nutritional management. K. Shahzad*[1], J. S. Osorio[1], D. N. Luchini[2], and J. J. Loor[1], *[1]University of Illinois, Urbana-Champaign, Urbana, [2]Adisseo S.A.S., Alpharetta, GA.*

Postpartal ketosis is associated with body fat mobilization postpartum. Subclinical and clinical ketosis arise more frequently in cows that are overfed energy during the entire dry period or during the close-up period (i.e., last 21 d before parturition). Metabolomics (GC–MS, LC-MS; Metabolon Inc.) and transcriptomics (45K-whole-transcriptome microarray; Agilent) analyses were performed in liver tissue harvested at -10 d relative to parturition from cows that were healthy (H) on 7 d postpartum or diagnosed with clinical ketosis (Ke). Cows in Ke consumed a higher-energy diet (OVE) from -21 d to calving. Cows in H consumed OVE ($n = 8$) or a high-straw, lower-energy diet (CON; $n = 8$) from -21 d to calving. Out of 313 biochemical compounds identified, statistical analysis ($P \leq 0.10$) of metabolomics data for Ke vs. CON, OVE vs. CON, and Ke vs. OVE revealed 34, 33, and 25 affected compounds, respectively. The top-5 affected and up regulated biochemical compounds in Ke vs. CON were taurocholate, adenine, hypotaurine, γ-glutamylcysteine, and taurochenodeoxycholate. In OVE vs. CON cysteine, methylphosphate, cysteinylglycine, and taurocholate were up regulated and γ-glutamylthreonine was downregulated. In Ke vs. OVE, the top-5 affected compounds were all downregulated: xylitol, 1-palmitoylglycerophosphoglycerol, leucylaspartate, sphinganine, and glycylvaline. Bioinformatics analysis revealed that primary bile acid production through cysteine and taurine precursors, and oxidative stress-like activities were affected in both Ke and OVE vs. CON groups. In contrast, in Ke vs. OVE, ketone body production was up regulated and cell signaling pathways were inhibited. Bioinformatics analysis of 2908 differentially expressed genes (DEG; $P \leq 0.05$), using the Dynamic Impact Approach (DIA), revealed that the top-5 impacted pathways in Ke vs. OVE were "hedgehog signaling," "glycosphingolipid biosynthesis-globo series," "renin-angiotensin system," and "other glycan degradation," all of which were inhibited. The "circadian rhythm" pathway was among the most induced pathways. Furthermore, there was marked inhibition in Ke vs. OVE of pathways associated with cellular growth, communication, signal transduction, fatty acid biosynthesis, and immune-related responses. These results suggest that prepartal diet alters hepatic metabolome and transcriptome. Liver from cows developing ketosis postpartum appears to exhibit unique alterations in the transcriptome and metabolome.

Key Words: ketosis, metabolomics, systems biology, transition cows

0101 A competitive and unpredictable feeding environment pre-calving increases inflammation and endometritis in Holstein dairy cows.

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Pre-calving management may influence the risk of disease after calving. Our objective was to determine the effects of a competitive and unpredictable feeding environment on inflammation and uterine health in dairy cows. Sixty-four animals were randomly assigned to a treatment (n = 4 animals × 8 groups) or control group (n = 4 animals × 8 groups). Each group consisted of 3 multiparous cows and 1 primiparous heifer. During a 1-wk baseline period (5 wk before calving), all groups had free access to 4 electronic feed bins (Insentec, Marknesse, Holland). From 4 wk before calving until calving, control cows were given ad libitum access to 6 feed bins. For treatment groups, 4 non-experimental cows were added to the pen; after 2 wk, treatment groups were moved into a pen with 4 new cows. Throughout the treatment period, morning feeding times were delayed at random 0, 1, or 2 h on alternate days. Cows were excluded if they calved twins, aborted, or calved > 2 wk early. Blood samples were taken at baseline and weekly thereafter until 1 wk after calving. Serum was analyzed for TNF-a using ELISA. A uterine cytology smear was taken 3 to 5 wk post-calving. Smears were stained and examined under 400X magnification for presence of neutrophils and uterine epithelial cells; cows were considered to have endometritis if > 5% neutrophils were identified. Preliminary analysis revealed treatment × parity × week interactions so data were analyzed separately by parity. The percentage of endometritis cases per group was compared among treatments using a Mann–Whitney U test in SAS. Log-transformed TNF-a data were analyzed using a mixed model, including baseline data as a covariate, treatment as a main effect, week as a repeated measure (wk -2, -1, 0, 1 relative to calving), and group as a random effect. There was no difference in the number of cases of endometritis or differences in TNF-a between control and treatment first-calf heifers. For cows, treatment groups had a higher percentage of endometritis cases (64% vs. 17% cases/group; P = 0.02) and higher TNF-a (2.1 vs. 1.8 ± 0.06 log pg/ml; P = 0.02), compared with controls. These results indicate that management practices that create a competitive and unpredictable feeding environment, such as regrouping, overstocking, and variable feeding times, can disrupt immune function and increase disease risk in cows but not first-calf heifers.

Key Words: endometritis, parturition, stress