tolerance tests (GTT) were performed at d = 1, 21, and 49 relative to start of treatment. Tissue concentrations of sphingolipids were determined using liquid chromatography tandem mass spectrometry. Expression of ceramide synthesis genes was evaluated using real-time PCR. Data were analyzed under the generalized linear model. Pearson correlations were analyzed. The most abundant liver and muscle sphingolipids detected were C24:0-ceramide, C24:0-monohexosylceramide (GlcCer), and C16:0-lactosylceramide (LacCer). Relative to control, PALM increased C24:0-ceramide and total hepatic ceramide levels by 29 and 20%, respectively, at wk 7 (P <0.05); a response not observed in muscle. Similarly, PALM increased hepatic C22:0-, C22:1-, C24:1-, and C26:0-ceramide at wk 7. PALM increased C16:1- and C24:1-GlcCer in liver (P < 0.05). Plasma total ceramide and C24:0-ceramide were positively associated with hepatic total ceramide and C24:0-ceramide (r = 0.63 and r = 0.58, respectively, P < 0.05). Hepatic total ceramide and C24:0-ceramide were positively associated with plasma NEFA (r = 0.63 and r = 0.57, respectively, P <0.001) and negatively associated with NEFA disappearance during GTT (r = -0.57 and r = -0.65, respectively, P < 0.001). Ceramide synthase-6 (CerS6) was the predominant hepatic CerS isoform followed by CerS2 and CerS5. Surprisingly, PALM decreased CerS2 and CerS5 mRNA and sphingomyelinase mRNA by 35, 36, and 62%, respectively (P < 0.05). We conclude that feeding midlactation dairy cows C16:0 can increase hepatic ceramide accumulation and generate hepatic ceramide profiles that are similar to circulating ceramide. Our work also demonstrates a possible relationship between hepatic ceramide supply and adipose tissue insulin sensitivity.

Key Words: ceramide, insulin resistance, lactation

0740 Assessment of performance, oxidative stress status, and plasma amino acid profiles in peripartal dairy cows supplemented with rumenprotected methionine or choline and with different liver functionality indices. Z. Zhou^{*1}, M. Vailati Riboni¹, E. Trevisi², D. N. Luchini³, and J. J. Loor¹, ¹University of Illinois, Urbana, IL, ²UniversitaÂ Cattolica del Sacro Cuore, Piacenza, Italy, ³Adisseo S.A.S., Alpharetta, GA.

Objectives were to evaluate performance, oxidative stress status, and plasma AA profiles of peripartal dairy cows with different liver functionality indices (LFI). Forty multiparous Holstein cows were randomly assigned to control (CON), no methionine (MET) or choline (CHO), CON+MET, CON+CHO, and CON+MET+CHO treatments. Cows received the same diet (1.52 Mcal/kg DM) from -21 d (close-up) to calving. Cows were on the same diet (1.71 Mcal/kg DM) after calving and continued to receive the same treatments through 30 d. Blood samples were taken at -30, -10, 4, 14, and 28 d relative to calving. Liver samples were harvested at -10, 7, 20, and 30 d relative to calving. Methionine

supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow per day. Main effect of LFI was analyzed using PROC MIXED in SAS. The LFI is an index assessing transition cow metabolic health by measuring changes in plasma albumin, cholesterol, and bilirubin. A high LFI (better liver function) is characterized by lower bilirubin and higher cholesterol and albumin, and the opposite is true for low LFI. Cows were ranked retrospectively and assigned to low (L; LFI < 0), medium-low (ML; 0 < LFI < 1.5), medium-high (MH; 1.5 < LFI < 3), and high (H; LFI > 3) groups according to LFI regardless of MET or CHO supplementation. Most (13/20) of the MET cows fell into the MH and H groups, whereas CHO cows were evenly distributed across the 4 LFI groups. Close-up and lactation DMI, milk yield, and protein yield increased (P < 0.01) with higher LFI. Compared with L and ML, cows in MH tended (P = 0.08) to have greater total and reduced hepatic glutathione concentration. Similarly, compared with L, plasma paraoxonase was greater (P = 0.04) in MH and H, suggesting better oxidative stress status in cows with higher LFI. A main effect of LFI was detected for essential AA (P < 0.01) and branchedchain AA (P = 0.04) concentration due to increased (P < 0.05) concentration of methionine, lysine, histidine, arginine, tryptophan, valine, leucine, and isoleucine with higher LFI. Concentrations of serine, asparagine, proline, alanine, tyrosine, citrulline, and ornithine also increased (P < 0.05) with higher LFI and contributed to greater (P < 0.05) total AA concentration. Overall, results indicate that cows with higher LFI had improved production performance, a reduction in oxidative stress, and a better plasma AA profile.

Key Words: amino acid, liver functionality index, transition cow

ADSA PRODUCTION DIVISION GRADUATE STUDENT POSTER COMPETITION: MS

0741 Effect of intrammamary infusion of chitosan hydrogels on bovine mammary gland involution after drying-off. S. Lanctot^{*1}, X. Zhao¹, P. Fustier², A. Taherian², B. Bisakowski², and P. Lacasse³, ¹Department of Animal Science, McGill University, Montreal, QC, Canada, ²Food Research and Development Centre, St-Hyacinthe, QC, Canada, ³Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada.

The transition from lactation to the dry period in dairy cows is a period of high risk for acquiring new intramammary infections. This risk is reduced when the involution of the mammary gland is completed. Accordingly, approaches that accelerate the involution process after drying-off could reduce the incidence of mastitis. The current study aimed to develop a biological response modifier that could be injected into cow teats to promote immune cell migration and speed up involution. Chitosan is natural polysaccharide derived from chitin, which is able to trigger host innate immunity. We have developed two formulations, using crab or shrimp chitosan, which are liquid at room temperature but form a hydrogel at the body temperature. Each quarter of 7 Holstein cows in late lactation was randomly assigned at drying-off to an intramammary infusion of 2.5 or 5 mL of crab chitosan hydrogel (crab2.5 or crab5), 5 mL of shrimp chitosan (shp5), or 5 mL of saline (control). Milk (mammary secretion) samples of each quarter were collected on d -4, 0 (dry-off), 1, 3, 5, 7, and 10. Milk somatic cell counts (SCC) and concentrations of involution marker such as bovine serum albumin (BSA), lactate dehydrogenase (LDH), and lactoferrin gradually increased (P < 0.01) during the first 10 d following the last milking whereas the citrate concentration decreased (P < 0.01). Intramammary infusion of chitosan hydrogel (crab5, crab2.5, and shp5) hastened the increase in SCC, BSA, and LDH (P < 0.01). The SCC and BSA concentrations for chitosan-treated quarters were greater (P < 0.01) than those of milk from control guarters on Days 1, 3, and 5. The LDH concentration was greater (P < 0.01) in milk from chitosan-treated quarters than in that of control quarters on Days 1, 3, 5, and 7. Similarly, chitosan induced a faster rise in lactoferrin concentration, which was greater (P < 0.01) than that of the control quarters on Days 3 and 5. Milk citrate concentration was unaffected by treatments but the citrate:lactoferrin ratio was lower (P < 0.05) in chitosan treated quarters on Days 3 and 5 than that in control quarters. No major differences between source or volume of chitosan were noted for the measured parameters. These results suggest that chitosan hydrogel infusion hastened mammary gland involution, which may reduce the risk of acquiring new intramammary infection during the drying-off period.

Key Words: involution, mastitis, immunity

0742 Mitigation of variability in feeding patterns between competitively fed dairy cows through increased feed delivery frequency. R. E. Crossley*, A. Harlander, and T. J. DeVries, *Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to determine if increased frequency of feed delivery can mitigate the effects of feed bunk competition. We hypothesized that at a greater frequency of feed delivery, 1) there will be improved access to feed (i.e., greater feeding time and consumption of more meals per day) and 2) there will be greater consistency in feeding and meal patterns between cows. Sixteen lactating Holstein dairy cows, with an average DIM of 72 ± 35 d and production of $42 \pm$ 6 kg/d at the start of the trial, were categorized by parity as either young (\leq second lactation) or mature (\geq third lactation) and paired to maximize difference in parity. Pairs were housed 4 at a time and competitively fed at a ratio of 2 cows:1 feed bin. They were exposed, at a pair level, in a crossover design to each of 2 different treatments: 1) lower feed delivery frequency (2x/d) or 2) higher feed delivery frequency (6x/d). Treatments were applied for 10 d, with DMI and feeding behavior (feeding time, feeding rate, and meal patterns) for each cow recorded using an automated feed intake system on d 6 to 10 of each period. Data were summarized by pair and treatment period and analyzed using a general linear mixed model. Dry matter intake (27.1 kg/d), feeding time (180.2 min/d), and feeding rate (0.17 kg DM/min) were unaffected by increased feed delivery frequency ($P \ge 0.22$). There was a tendency for rumination time to increase with higher frequency of feed delivery (low = 520.5 min/d and high = 547 min/d; SE = 11.32, P = 0.06). No differences in meal patterns were found between feed delivery frequency treatments ($P \ge 0.20$). However, comparing the young and mature individuals within each treatment pair revealed differences in both feeding and meal patterns. Feeding rate (young = 0.16 kg DM/min and mature = 0.19 kg DM/min; SE = 0.032, P = 0.02) and DMI (young = 25.6 kg DM/min and mature = 28.6 kg DM/min; SE = 1.36, P = 0.04) were lower for the young cows on both treatments. Meal frequency was greater in young cows (young = 9meals/d and mature = 7 meals/d; SE = 0.7, P = 0.03) and meal size was greater in mature cows (young = 3.2 kg DM/mealand mature = 4.2 kg DM/meal; SE = 0.35, P < 0.001) across treatments. These results suggest that for cows fed at a high level of competition, increasing feed delivery frequency from 2x/d to 6x/d did not improve access to feed. However, under these conditions, the relative parity of competitively fed cows had a greater impact on feeding behavior and meal patterns than the frequency of feed delivery.

Key Words: dairy cow, competition, behavior, feed frequency, meal patterns

0743 Infusion of a serotonin precursor prepartum induces dynamic glucose and fat metabolism gene expression in the livers of multiparous dairy cows during peripartum. A. P. Prichard*¹, S. R. Weaver², E. L. Endres¹, M. S. Akins³, R. M. Bruckmaier⁴, and L. L. Hernandez², ¹University of Wisconsin-Madison, Madison, ²Department of Dairy Science, University of Wisconsin, Madison, ³University of Wisconsin, Platteville, ⁴Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland.

Nonneuronal serotonin receptors are dynamic in the liver of transition cows and serotonin is known to affect metabolism. Yet the extent to which glucose and fat homeostasis during the transition period are transcriptionally regulated in response to serotonin is unknown. To this end, we intravenously infused multiparous Holstein (n = 12) and Jersey (n = 12) cows daily with either 1 L of saline (CON; n = 6 for Holstein and Jersey)

or 1 mg/kg BW of 5-hydroxytryptophan (5-HTP; n = 6 for Holstein and Jersey). Holsteins were infused for 5.67 ± 0.78 d and Jersey cows for 8.67 ± 1.53 d prepartum, until parturition. A liver biopsy was performed before treatment, on the day following parturition (d 1), and on Day 7 (d 7) of lactation. Ribonucleic acid was extracted from all samples and real-time PCR was performed. Ribonucleic acid expression was analyzed using the delta-delta CT method and statistical analysis was conducted using a two-way ANOVA for time, treatment, and the interaction on gene expression of phosphoenolpyruvate carboxykinase 1 (PCK1), fructose 1-6 bisphosphatase (FBP1), acetyl co-A carboxylase (ACACA), and carnitine palmitoyltransferase 1 (CPT1A). On d 1, PCK1 and FBP1 expression was elevated in the liver of 5-HTP Holsteins relative to CON Holsteins, but not in Jerseys (P = 0.05 for both PCK1 and FBP1 in Holsteins). In Holsteins, FBP1 expression was greatest on d 1 and returned to baseline levels on d 7 (P < 0.0001). In Jerseys, time had a dynamic effect on FBP1 expression but without the dramatic decline to baseline expression seen in Holsteins (P = 0.04). Expression of ACACA was elevated on d 1 in 5-HTP Holsteins compared with CON (P < 0.05). ACACA expression in 5-HTP Jersevs compared with CON Jerseys was highest on d 7 compared with d 1 or baseline (P = 0.03). There was a treatment (P = 0.03) and time (P = 0.009) effect on CPT1A expression in the Holsteins, with 5-HTP Holsteins having higher expression than CON on d 1 and 7 of lactation. In Jerseys, CPT1A expression was higher on d 7 than on d 1 (P < 0.0001), but there was no treatment effect. Given the roles of PCK1 and FBP1 in promoting gluconeogenesis and the dynamic fatty acid metabolism roles of ACACA and CPT1A, serotonin appears to have an effect on regulating energy and fat homeostasis in a breed- and time-dependent manner during the transition period in dairy cattle.

Key Words: serotonin, liver, gene expression

744 Sire performance and reproductive breeding values are associated with feed efficiency and growth in dairy heifers. C. E. Owens*, Virginia Polytechnic Institute and State University, Blacksburg.

Feed costs represent upward of 60% of total inputs in the dairy industry; moreover, poor fertility is the primary factor influencing cow productive life (PL). To improve profitability, producers must begin selecting for metabolic and reproductive efficiency. To do this, the relationship between feed efficiency and growth must be assessed for milk production and fertility measures. Therefore, the objective of this study was to determine the relationship between sire performance predicted transmitting ability (PTA) with progeny feed efficiency (G:F) and ADG. Twelve dairy heifers (1 wk age and 40.41 \pm 4.34 kg BW) were randomly administered one of two diets, restricted (R; 20% CP and 20% fat) or enhanced (E; 28% CP and 25% fat), for 8 wks. Heifers were weighed weekly and daily feed intake measurements were collected

to determine G:F and ADG. Sire PTA (milk, fat, protein, PL, somatic cell score, daughter pregnancy rate, and heifer conception rate [HCR]) were collected via the Council on Dairy Cattle Breeding. Using PROC CORR in SAS, phenotypic correlations were determined between sire PTA with calf G:F and ADG, regardless of diet and within diet. There was a strong positive phenotypic correlation between heifer G:F and milk PTA ($r_p = 0.76, P = 0.007$), and ADG tended to have a moderate positive phenotypic correlation with milk PTA ($r_p = 0.57$, P = 0.068). A suggestive moderate positive phenotypic correlation ($r_p = 0.60, P \le 0.081$) was determined between G:F with HCR and PL ($r_p = 0.55$). Within treatment, R heifers had a strong positive phenotypic correlation between ADG with milk ($r_{p} = 0.94$, P = 0.005) and protein ($r_{p} = 0.90$, P = 0.016) PTA. There was also a strong positive phenotypic correlation between G:F with milk ($r_p = 0.93$, P = 0.008) and protein (r_p = 0.93, P = 0.007) PTA for R heifers. Results suggested that sires with more favorable predictors for milk and protein production compared with contemporaries produced heifers with increased feed efficiency and growth. Additionally, sires with increased HCR and PL PTA produced heifers with greater feed efficiency. Overall, favorable selection for sire PTA estimates for performance and reproduction may provide an opportunity to increase heifer feed efficiency and growth.

Key Words: feed efficiency, fertility, growth

0745 Dry matter intake, milk yield, and milk composition of dairy cows fed corn silage from corn treated with various application times of foliar fungicide. C. Kalebich*¹, M. Weatherly¹, G. M. Fellows², and P. Cardoso¹, ¹University of Illinois, Urbana, ²BASF Corporation, Research Triangle Park, NC.

Little is known about the ideal timing of foliar fungicide application on corn and its effects on corn silage when fed to dairy cattle. The objective of this study was to determine which timing of fungicide application on corn that was further ensiled as corn silage would have the most advantageous impact on DMI and milk yield and composition in dairy cattle. Holstein cows (n = 64) with parity 2.2 ± 0.8, 626 ± 77 kg BW, and 134 ± 37 DIM were blocked and randomly assigned to 1 of 4 treatments (45% of the DM as corn silage). Treatments were as follows: corn silage with no application of foliar fungicide (CON), corn silage from corn that received one application of pyraclostrobin and fluxapyroxad (PYR+FLUX) foliar fungicide (Priaxor; BASF Corp.) at corn stage V5 (V5), corn silage from corn that received one application of PYR+FLUX at corn stage V5 plus another application of PYR+FLUX at corn stage V8 (V5/V8), and corn silage from corn that received one application of PYR+FLUX at corn stage V5 and one application of PYR+FLUX at corn stage V8 plus a third application of pyraclostrobin and metconazole (PYR+MET) foliar fungicide (Headline AMP; BASF Corp) at corn stage R1 (V5/ V8/R1). Corn was harvested at 31.2% DM and three-fourths milk line kernel development, and ensiled for more than 200 d. Treatments were fed to cows for 5 wk with the last week being used for statistical inferences. Data was analyzed using the MIXED procedure in SAS (version 9.4), with cow as the experimental unit. No differences in DMI (19.5, 19.5, 20.8, and 20.4 kg for CON, V5, V5/V8, and V5/V8/R1, respectively; P = 0.48) or milk yield (30.55, 31.17, 29.06, and 29.33) kg/d, respectively; P = 0.55) were observed. However, corn silage in V5 compared with corn silage in V5/V8 fed to cows tended to increase 3.5% fat-corrected milk (FCM) (32.42 and 28.58 kg/d, respectively; P = 0.07) and energy corrected milk (ECM) (31.35 and 27.76 kg/d, respectively; P = 0.07). Percentage of milk lactose tended to be greater for cows fed corn silage treated with foliar fungicide when compared with CON (P = 0.09). In conclusion, cows receiving corn silage from corn treated with fungicide at V5 tended to have greater FCM and ECM than cows treated with corn silage from corn treated with fungicide at V5/V8.

Key Words: corn silage, foliar fungicide, fat-corrected milk

0746 Identification of loci associated with fertility in United States Holstein heifers. E. Keuter*1, C. M. Seabury², M. Neupane³, J. N. Kiser¹, J. Moraes⁴, G. Burns⁴, T. E. Spencer⁴, and H. L. Neibergs³, ¹Department of Animal Science, Washington State University, Pullman, ²Texas A&M University, College Station, ³Department of Animal Sciences, Washington State University, Pullman, ⁴Division of Animal Sciences, University of Missouri, Columbia.

Current conception rates in U.S. Holstein heifers are estimated to be between 55 and 60%. The objective here was to identify genomic loci associated with fertility in Holstein dairy heifers. Breeding and health records of Holstein heifers were analyzed from a commercial dairy heifer raising facility in southern Idaho. All heifers were bred by AI at observed estrus, and pregnancy was determined at Day 35 after AI via palpation. Records analysis identified 497 heifers that could be classified as highly fertile (HF) due to conceiving on first AI service and 429 subfertile (SF) that did not conceive until after fourth AI service or were culled due to failure to conceive. Deoxyribonucleic acid was extracted from blood samples and genotyped using the Illumina Bovine HD BeadChip. Quality control consisted of removing animals with <90% of genotypes and removing markers with <90% of genotypes or a minor allele frequency <1% or if they failed Hardy–Weinberg equilibrium testing. A total of 466 HF and 368 SF heifers and 590,904 SNP remained for the analysis. A genomewide associated analysis (GWAA) was conducted using an additive model of the efficient mixed-model association expedited statistical test with a genomic relationship matrix. Covariates used in the analysis accounted for relatedness (identity by descent ≥ 0.2) of heifers and the AI bull the heifer was bred to as conception rates differed between AI sires ($P < 6.9 \times 10^{-13}$). The GWAA identified 153 SNP representing 147 QTL ($P < 5.5 \times 10^{-5}$) that were moderately associated and 34 SNP representing 26 QTL ($P < 5.5 \times 10^{-7}$, proportion variance explained ranged from 0.032 to 0.115) that were strongly associated with heifer fertility. Pseudo-heritability was estimated to be 0.46 and I = 0.98. These results indicate that there is ample opportunity to make significant gains in fertility in Holstein heifers with genomic selection. This project was supported by Agriculture and Food Research Initiative Competitive Grant number 2013-68004-20365 from the USDA National Institute of Food and Agriculture.

Key Words: dairy, fertility, quantitative trait loci

0747 The effects of increased metabolizable protein and amino acid supplementation in fresh dairy cattle. E. G. Carder*, *The Ohio State University* – *OARDC, Wooster*.

The first few weeks after parturition in dairy cattle is a time marked by low but increasing feed intake and sharply increasing milk production. Because of low intake, nutrient density of the diet may need to be higher during this period to support increasing milk yields. We hypothesized that feeding higher levels of MP or feeding supplemental rumen protected methionine and lysine would increase milk yield and protein concentration. Fifty-six Holstein cows (21 primiparous and 35 multiparous), starting at 3 DIM, were used in a randomized-block design with three diets. The treatments were control (16.5% CP, 10.9% RDP, and 5.6% RUP, formulated for 25.1 kg/d MP allowable milk based on an NRC model), high protein (HP; 18.5% CP,11.6% RDP, 6.9% RUP, and 29.9 MP allowable milk), and AA treatment (AA; 17.5% CP, 10.5% RDP, 7.0% RUP, and 29.7 MP allowable milk). The AA diet included a proprietary spray-dried blood meal product (Perdue Agribusiness, Salisbury, MD) that provided 174 and 62 g/d of rumen-protected lysine and methionine, respectively, per the NRC model. The HP diet provided an estimated 156 g/d lysine and 45 g/d methionine and the control diet provided 149 g/d lysine and 41 g/d methionine. Milk production and DMI were measured daily and milk was sampled for components on Day 8, 15, and 20 after moving into tie stalls. Statistical model included parity, treatment, and week fixed effects, random effect of block, and cow as the experimental unit. Treatment and treatment by parity interaction did not affect milk yield (33.6, 34.5, and 33.1 kg for control, HP, and AA), DMI (17.8, 17.8, and 18.5 kg/d for control, HP, and AA), or milk protein yield (1.11 kg/d). Milk protein concentration was higher (3.30 vs. 3.16 and 3.17%; P < 0.05) for AA treatment compared with the HP and control, respectively. Energy corrected milk (ECM) was higher (35.1 and 35.1 vs. 32.0 kg; P <0.05) for HP and AA than for the control, respectively. MUN was higher (14.3 vs. 12.7 and 11.5 mg/dL; P < 0.05) for HP than for AA or control, respectively. Plasma BHBA and NEFA were unaffected by treatment or treatment × parity interaction but increased from Day 8 to Day 15 in both multiparous and primiparous cows. Overall, supplementing rumen-protected lysine and methionine with extra MP can increase ECM yield and milk protein concentration.

Key Words: rumen-protected lysine, rumen-protected methionine, metabolizable protein, fresh cow, dairy cow

0748 Effects of supplementing lactating dairy cow ration with sodium sesquicarbonate on reticulorumen pH, rumination, and dry matter intake. M. L. Jones^{*1}, J. D. Clark¹, N. A. Michael², and J. M. Bewley¹, ¹University of Kentucky, Lexington, ²Arm & Hammer Animal Nutrition, Princeton, NJ.

The objective of this study was to assess the effects of sodium sesquicarbonate (SQ-810), a reticulorumen buffer, on rumen pH, rumination time, and DMI. Sixteen early lactation multiparous, Holstein cows were housed in a tie-stall barn and milked twice daily at the University of Kentucky Coldstream Dairy from October 31, 2015, to January 1, 2016. Cows were balanced by parity and milk production and then split into 2 treatment groups for a crossover study with a low-buffer (LB; n = 8) group and a high-buffer (HB; n = 8) group. The base total mixed ration (TMR) contained 0.16 kg/d sodium bicarbonate. The LB group did not receive SQ-810 whereas the HB group received 0.30 kg of SQ-810 as fed. Eight cows proceeded through sequence 1: three 21-d periods receiving the LB diet in period 1, the HB diet in period 2, and the LB diet in period 3. The remaining 8 cows proceeded through sequence 2: three 21-d periods receiving the HB diet in period 1, the LB diet in period 2, and the HB diet in period 3. Each group was fed ad libitum and DMI was collected. All cows were administered an iNovotec Animal Care (iNovotec Animal Care, Austria) reticulorumen pH and temperature bolus. Daily rumination time was recorded using HR tags (SCR Engineers Ltd., Netanya, Israel) and CowManager SensOor (SENRUM) tags (Agis Automatisering, Harmenlen, Netherlands). Low pH was calculated as the total time pH was <5.60. The MIXED procedure of SAS was used to evaluate the effects of cow, sequence, treatment and period on each parameter measured. Rumen pH and low pH time (pH < 5.60) were influenced by treatment (P < 0.01). Rumen pH was 5.82 ± 0.07 for LB cows and 5.85 ± 0.07 for HB cows. Low pH time (pH < 5.60) was greater (P < 0.01) for LB days (64.17 ± 11.71 min/d) than for HB days $(56.31 \pm 11.71 \text{ min/d})$. Dry matter intake was 25.68 \pm 0.61 kg/d for LB cows and 26.53 \pm 0.61 kg/d for HB cows. Treatment affected SCR rumination times (P < 0.01) for LB cows (457.84 \pm 19.15 min/d) and HB cows (435.02 \pm 19.15 min/d). Rumination time measured using SENRUM was not significantly different between treatments. The addition of SQ-810 to the TMR significantly increased reticulorumen pH and DMI (P < 0.01). This research demonstrates the positive effects of SQ-810 rumen buffer in a lactating cow diet.

Key Words: rumen pH, sodium sesquicarbonate

0749 Feeding low crude protein diets in lactating dairy cows during summer months: 2. Improvements in energy metabolism. J. Kaufman*, K. Kassube, K. G. Pohler, and A. G. Rius, *The University of Tennessee, Knoxville.*

Lactating dairy cows experience changes in nutrient partitioning and decrease production during summer months. Dietary concentrations of RDP and RUP affect nutrient partitioning and utilization. A study was conducted to evaluate the effect of feeding low RDP and RUP levels on energy metabolism in cows during peak summer months. Forty-eight primiparous and multiparous midlactation Holstein cows were assigned to treatments using a complete randomized block design in a 2 \times 2 factorial arrangement of treatments (n = 12/treatment). Treatments included two levels of RDP (10 and 8%) and two levels of RUP (8 and 6%). A common diet (10% RDP and 8% RUP) was fed from d 1 to 21 followed by the respective treatment diets from d 22 to 42. Cows were housed in a freestall barn and exposed to the prevailing temperature and humidity of July and August with no supplemental cooling. Blood samples were collected from individual cows at d 42. Plasma was harvested for analysis of glucose, insulin, NEFA, and β-hydroxybutyrate (BHBA). Main effects and their interaction were tested using the Mixed procedure of SAS and reported as least squares means \pm SEM. Rectal temperatures and respiration rates were recorded before noon and after noon during the treatment period. Compared with before noon, after noon increased temperature and respiration rates $(38.9-39.7 \pm 0.07^{\circ}C)$ [P < 0.001] and 64.0–87.1 ± 1.4 breaths/min [P < 0.001]). The 10% RDP treatment decreased (P < 0.04) glucose concentrations compared with the 8% RDP treatment (3.0 vs. 3.1 ± 0.05 mmol/L). The 10% RDP treatment increased (P < 0.01) insulin concentrations compared with the 8% RDP treatment (20.9 vs. 15.8 \pm 1.1 μ U/mL). The 8% RUP treatment tended to increase (P < 0.08) insulin concentrations compared with the 6% RUP treatment (19.8 vs. $16.9 \pm 1.12 \,\mu\text{U/mL}$). The 8% RUP treatment decreased (P < 0.01) NEFA concentrations compared with the 6% RUP treatment (141 vs. 173 ± 16.5 µEq/L). Compared with 10% RDP, the 8% RDP treatment decreased BHBA concentrations in the 8% RUP treatment (251 vs. $407 \pm 26.5 \,\mu mol/L$) but increased BHBA concentrations in the 6% RUP treatment (190 vs. $173 \pm 26.5 \mu mol/L$; interaction, P < 0.01). In conclusion, these results indicate that lower RUP diets promoted lower concentrations of insulin and greater concentrations of NEFA. This may allow metabolic adaptations to mobilize lipids and sustain milk production.

Key Words: crude protein, energy utilization, heat stress