70 Ruminal fermentation characteristics and lactational performance of Holstein dairy cows fed whole safflower seeds. C. M. Dschaak*[1], C. T. Noviandi[1], J.-S. Eun[1], V. Fellner[2], A. J. Young[1], D. R. ZoBell[1], and C. E. Israelsen[3], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Animal Science, North Carolina State University, Raleigh, [3]Cooperative Extension, Utah State University, Logan.*

A lactation trial was conducted to determine the effects of supplementing whole safflower seeds (SS) on ruminal fermentation and lactational performance. Nine multiparous Holstein cows (DIM = 110 ± 20) were used in a replicated 3 × 3 Latin square design. Each period lasted 21 d with 14 d of adaptation and 7 d of data collection. Within square, cows were randomly assigned to a sequence of 3 dietary treatments as follows: cottonseed TMR (CST), conventional SS (variety S-208) TMR (CSST), and Nutrasaff SS (Safflower Technologies International, Sidney, MT) TMR (NSST). Diets contained approximately 63% forage (36% alfalfa hay, 4% grass hay, and 23% corn silage) and 37% concentrate supplemented with 2% cottonseed to the CST and 3% conventional or Nutrasaff SS to the CSST or the NSST, respectively. Intake of DM averaged 21.8 kg/d and did not differ ($P > 0.10$) across diets. Digestibility of DM was similar ($P > 0.10$) between diets, whereas feeding the CSST decreased ($P < 0.05$) fiber digestibility compared with the CST and the NSST. Milk yield was greater ($P = 0.03$) with the NSST (31.4 kg/d) when compared with the CST (30.2 kg/d). Milk protein increased with the NSST compared with the CST ($P = 0.05$). Diets had no effect ($P > 0.10$) on total or molar proportions of ruminal VFA and ammonia-N. Ruminal C16:0 and C18:0 concentrations increased with the CST ($P < 0.02$). Feeding the CST also increased milk C16:0 concentration, whereas C18:0, C18:1 cis-9, C18:1 trans-9, and C18:1 cis-11 increased with the NSST ($P < 0.03$). Supplementing whole SS in dairy diets at 3% of dietary DM can be an effective strategy of fat supplementation to lactating dairy cows without negative impacts on lactational performance.

Key words: safflower seeds, ruminal fermentation, lactational performance

71 The effects of NPH insulin and insulin glargine on milk yield and composition by lactating dairy cows. L. A. Winkelman* and T. R. Overton, *Cornell University, Ithaca, NY.*

Our study investigated the effects of neutral protamine hagedorn insulin (H) and insulin glargine (L) on milk composition in 30 cows (88 ± 25 DIM). Cows were blocked into 2 groups, balanced for DIM and production, and randomly assigned to 1 of 3 treatments (Control (C), H, and L). Subcutaneous injections of 0.2 IU/kg BW for H and L were given 2x/d every 12 h for 10 d. Blood samples were taken 2x/d, immediately before the morning injection and 6 h postinjection. Mammary tissue was biopsied on d 11. Cows were milked 2x/d and milk composition was determined on d 2, 4, 6, 8, and 10. Treatment means herein are presented in the following order: C, H, and L. Milk yield ($P = 0.46$) and DMI ($P = 0.58$) did not differ by treatment. Treatment with H and L increased milk protein content (3.00, 3.20, and 3.29 (±0.05)%; $P = 0.001$) and milk protein yield was increased by L (1.46, 1.49, and 1.54 (±0.03) kg/d; $P = 0.08$). Fat content (3.17, 3.32, 3.50 (±0.11)%; contrast C vs. L: $P = 0.04$) and yield (1.50, 1.55, 1.65 (±0.05) kg/d; contrast C vs. L: $P = 0.05$) were increased by L. Milk lactose content was reduced (4.84, 4.76, 4.70 (±0.02)%; $P = 0.001$) by treatment. Lactose yield was reduced by L ($P = 0.02$) but not H ($P = 0.13$) and averaged 2.34, 2.26, and 2.21 (±0.04) kg/d. Casein content ($P = 0.02$) and yield ($P = 0.09$) were increased by treatment with H and L, but casein as a percent of true protein did not differ ($P = 0.70$). Plasma glucose was reduced by treatment with H and L (56.8, 52.0, and 48.1 (±0.99) mg/dl; $P < 0.001$). Plasma urea nitrogen was reduced by L ($P = 0.004$) but not H ($P = 0.57$). Plasma NEFA was higher for cows treated with H (166, 197, and 181 (±9) μEq/L; $P = 0.013$). Western blot of mammary protein lysates indicated that the ratio of phosphorylated Akt:total Akt differed by treatment and was greatest for H (1.16, 1.72, 0.96 (±0.62) arbitrary units; $P = 0.05$) but the ratio of phosphorylated rpS6:total rpS6 did not differ by treatment ($P = 0.60$). Overall, H and L improved milk component production, but more research needs to be conducted to further elucidate the mechanism underpinning the effects of insulin on milk composition.

Key words: insulin, milk protein

72 The effects of degradable nitrogen level and degradation rate on nitrogen balance and urea kinetics in Holstein steers. V. B. Holder*[1], J. Tricarico[2], D. H. Kim[1], N. B. Kristensen[3], and D. L. Harmon[1], *[1]University of Kentucky, Lexington, [2]Alltech, Brookings, SD, [3]Aarhus University, Tjele, Denmark.*

The objective of this study was to compare nitrogen metabolism and urea kinetics between diets containing either rapidly degrading or slow degrading non protein nitrogen (NPN) at varying levels of degradable intake protein (DIP). Treatments were slow release urea (Optigen II, OPT) fed at 101 and 114% and feed grade urea (Urea) fed at 89 and 100% of calculated DIP requirements. Eight Holstein steers (209 ± 15 kg) implanted with Synovex Plus were used in a replicated 4 × 4 Latin square. Periods were 27 d, with 19 d adaptation followed by 7 d of urine and fecal collection and 1 d of blood sampling. Continuous (78h) intravenous infusion of $^{15}N^{15}N$-urea allowed estimation of urea kinetics. Dry matter intake was not different between treatments (7.2 kg/d). Increasing DIP had a tendency to increase dry matter digestibility (DMD) for both Urea and OPT. Urea had higher DMD than OPT. Increasing DIP increased urinary N output, and increased N-retention with OPT but not Urea. Increasing DIP increased urea–N entry rate (UER) and urinary urea-N excretion (UUE) for both OPT and Urea. Gastrointestinal entry of urea-N, urea-N lost to feces and urea-N apparently used for anabolism were not different between treatments. Plasma urea concentration was greater in higher DIP diets and higher for Urea than OPT at 100% DIP. Therefore increasing DIP level will increase N-excretion related to higher urea production and excretion in urine but may also increase diet digestibility. Most changes in N metabolism were driven by N intake; however, providing a slow release DIP source may allow for greater N retention when DIP is not limiting.

Table 1. Experiment results

	Treatment					Contrasts		
Item	114% DIP OPT	101% DIP OPT	100% DIP Urea	89 % DIP Urea	SEM	114% vs. 101%, OPT	100% vs. 89 %, Urea	100% Urea vs. 101% OPT
DMD, %	59.8	58.2	60.7	58.8	1.6	0.09	0.06	0.01
Urine N, g/d	62.2	53.6	54.3	41.7	7.4	<0.001	<0.001	0.75
N Retention, g/d	39.6	31.3	34.8	34.1	4.0	0.001	0.73	0.10
UER	70.1	57.8	56.7	45.4	8.1	0.002	0.004	0.75
UUE	36.3	26.5	26.6	15.5	2.5	<0.001	<0.001	0.96
Plasma Urea, mM[1]	2.8	2.3	2.5	1.8	0.1	<0.001	<0.001	0.02

[1]Data were transformed for statistical analysis. SE of original data reported.

Key words: urea recycling, nitrogen metabolism, cattle

73 Effects of monensin on metabolic parameters, feeding behavior, and productivity of transition dairy cows. C. R. Mullins*[1], L. K. Mamedova[1], M. J. Brouk[1], C. E. Moore[2], H. B. Green[2], K. L. Perfield[2], J. F. Smith[1], J. P. Harner[1], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Elanco Animal Health, Greenfield, IN.*

The effects of monensin on transition cow metabolism may be dependent on modulation of feeding behavior, ruminal pH, and/or expression of metabolic genes. Multiparous Holstein cows (n = 16 per treatment) were alternately assigned, based on calving date, to control or monensin (400 mg/d) treatments 21 d before expected calving date, and cows remained on treatments through 21 d postpartum. Feeding behavior and water intake data were collected daily. Liver biopsies were obtained, after assessing BCS and BW, on d −21, −7, 1, 7, and 21 relative to calving (RTC), for analysis of triglyceride (TG) content and mRNA abundance of phosphoenolpyruvate carboxykinase 1(PCK1) and carnitine palmitoyltransferase 1a (CPT1a). Blood samples were collected on d −21, −7, −4, 1, 4, 7, 14, and 21 RTC for plasma NEFA, β-hydroxybutyrate (BHBA), glucose, insulin, and haptoglobin analyses. Ruminal pH was collected every 5 min on d 1 to 7 RTC by a wireless indwelling probe. On d 7 RTC, a caffeine clearance test was performed to assess liver function. Data were analyzed using mixed models with repeated measures over time. Monensin decreased mean plasma BHBA (734 vs. 616 ± 40 μM; $P < 0.05$) and peak concentrations (1076 vs. 777 ± 70 μM on d 4 RTC; $P < 0.01$). Monensin also decreased time between meals prepartum (143 vs. 126 ± 5.0 min; $P < 0.03$) and postpartum (88.8 vs. 81.4 ± 2.9 min; $P < 0.08$), which was likely related to a smaller ruminal pH variance in the first day after cows changed to a lactation ration (SD = 0.31 vs. 0.26 ± 0.015 units; $P < 0.02$). Monensin increased liver mRNA abundance of CPT1a (0.10 vs. 0.15 ± 0.002 arbitrary units; $P < 0.04$), which corresponded with a slower rate of liver TG accumulation from d −7 to +7 RTC (412 vs. 128 ± 83 mg TG/g protein per 2 wk, $P = 0.03$). There were no significant effects of monensin supplementation on milk production, liver PCK1, plasma NEFA, glucose, insulin, or haptoglobin. No effects on disease incidence were detected, but sample size was small for detecting such effects. Overall, results confirm that the effects of monensin on transition cows extend beyond altered propionate flux.

Key words: monensin, transition cow, feeding behavior

74 The effect of ketoprofen following left displaced abomasum surgery on lying behaviour and ketosis. N. C. Newby*[1], S. J. LeBlanc[1], K. E. Leslie[1], D. L. Pearl[1], M. A. G. von Keyserlingk[2], and T. F. Duffield[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]University of British Columbia, Vancouver, British Columbia, Canada.*

Surgical correction of left displaced abomasum (LDA) is common in lactating dairy cattle, but it is not common practice to administer analgesia following LDA surgery although surgery is normally associated with pain. The objectives of this research were to examine the effect of administering a label dose of the non-steroidal anti-inflammatory drug ketoprofen on lying behavior and ketosis (blood β-hydroxybutyrate (BHB)), as well as on farmer's perception of recovery following LDA surgery. A total of 148 Holstein cows were enrolled in a field study following LDA surgery (standing right flank (RF) or paramedian (P) approaches). Using a double-blind randomized method, each animal was assigned to receive either 3 mg ketoprofen/kg body weight or saline by intramuscular injection, immediately following surgery and 24 h post-operatively. A subset of cows (n = 37) were fitted with a 3-axis accelerometer on the hind leg to access lying activity. Farmers were asked to provide information on the cow's appetite in the days following surgery. Lying time data were analyzed using multivariable linear models with a random effect for cow and binary outcomes were analyzed using a mixed logistic model. Cows subjected to P surgery lay down less (β = −3.8 h; 95% C.I.: −2.3, −5.4 h; $P < 0.01$) in the first 3 d, and had higher heart rate (β = 9.4 beats/min; 95% C.I.: 6.9 – 12 beats/min; $P < 0.05$) 2–4 d after surgery, compared with animals that underwent RF surgery. In all cows, regardless of surgical procedure or ketoprofen treatment, BHB significantly decreased from surgery to d 2–4 (β = −1.9; 95% C.I.: −2.1, −1.7; $P < 0.001$) and d 8–10 (β = −2.0; 95% C.I.: −0.2.2, −1.8; $P < 0.001$). Based on observations by producers (who were blinded to treatment status), animals that received ketoprofen were more likely to begin eating when provided fresh feed on the first 3 d following surgery compared with those that received saline (OR = 4.2; 95% C.I.: 1.4, 12.5; $P = 0.01$). These results suggest that that P surgery of LDA may result in more pain than the RF approach. Further investigation of assessment and management of post-surgical pain is warranted.

Key words: displaced abomasum surgery, post-surgical pain, dairy cattle behaviour

75 Ruminal fermentation and nutrient digestion by dairy cows fed different concentrations of forage and dried distillers grains with solubles. S. D. Ranathunga*, K. F. Kalscheur, A. R. Hippen, and D. J. Schingoethe, *South Dakota State University, Brookings, South Dakota, USA.*

The study objective was to investigate the effects of concentrations of forages and dried distillers grains with solubles (DG) on ruminal fermentation and nutrient digestion in lactating dairy cows. Four Holstein cows with ruminal fistula were assigned to a 4 × 4 Latin square in a 2 × 2 factorial arrangement of treatments. Diets were formulated containing low forage (LF; 41% of diet DM) or high forage (HF; 60% of diet DM) and DG at 0 or 18% of diet DM. Ground corn and soybean feeds were partially replaced by DG from 0% DG diets to formulate 18% DG diets. Average DMI was not affected by diets (23.8 kg/d). Rumen evacuation at 4h post-feeding showed that rumen digesta DM were greater for cows fed HF regardless of the addition of DG. There was a tendency for digesta NDF (7.00 vs. 7.49 kg) to be less for cows fed LF compared with HF, whereas digesta starch (0.53 vs. 0.33 kg) were greater for cows fed LF compared with HF. Lower ruminal pH

(6.10 vs. 6.34) was observed in cows fed LF whereas there was no DG effect on ruminal pH. Cows fed LF had greater total VFA concentration compared with cows fed HF (122 vs. 116 mM). Acetate concentrations were lesser for LF (57.5 vs 62.6 mol/100 mol) and 18% DG (61.3 vs 58.7 mol/100 mol) diets whereas propionate concentration were greater for LF (26.0 vs 20.1 mol/100 mol) and 18% DG (21.9 vs 24.2 mol/100 mol) diets. Greater acetate:propionate ratio was observed in HF and 0% DG diets. Total tract digestibility for DM, NDF, CP, and starch was not affected by diets. Results suggest that forage and DG concentration in diets affect ruminal degradability of nutrients.

Table 1.

	LF	LF	HF	HF		
Item	0DG	18DG	0DG	18DG	SEM	P-value a
Digesta DM, kg	11.2	13.2	13.9	12.9	1.84	F
Digesta NDF, kg	6.52	7.48	7.56	7.42	1.02	FT, F×D
Digesta starch, kg	0.62	0.44	0.32	0.35	0.05	F
Rumen pH	6.17	6.02	6.32	6.36	0.09	F
Total VFA, mM	119	124	117	114	3.59	F
VFA, mol/100 mol						
Acetate	58.9	56.0	63.8	61.3	0.72	F, D
Propionate	24.2	27.7	19.5	20.6	0.88	F, D, F×D
A:P ratio	2.53	2.05	3.32	3.00	0.12	F, D

[a]F or D= Forage or DG effect; F×D=Forage and DG interaction ($P < 0.05$); FT= Forage effect (tendency) ($P < 0.10$).

Key words: distillers grains, forage, rumen

76 On-farm validation of two rapid methods to estimate IgG in bovine colostrum. K. M. Morrill*[1], E. Conrad[1], A. Lago[2], J. D. Quigley[2], and H. D. Tyler[1], *[1]Iowa State University, Ames, [2]APC Inc., Ankeny, IA.*

Our objective was to validate a rapid, cow-side method to estimate IgG in bovine maternal colostrum (MC) based on caprylic acid (CA) fraction of MC followed by refractometry of the IgG-rich supernatant. Samples of MC (n = 827) were collected from 67 farms in 12 states. Samples were fresh (not stored; n = 196), previously frozen (n = 490) or refrigerated (n = 152). One ml of MC was added a tube containing 75 µL CA and 1 mL 0.06 M acetic acid and refractive index (nD) of the IgG-rich supernatant was determined. We also measured nD of whole (non-fractionated) MC and IgG of whole MC by radial immunodiffusion. Correlation of nD of CA supernatant to IgG (r = 0.53) was low, whereas the correlation between nD of whole MC and IgG was greater (r = 0.73). Correlations of nD of CA supernatant and IgG (r = 0.93) and nD of whole MC and IgG (r = 0.89) of MC samples that and were not stored before analysis (n = 146) were much greater, suggesting that storage of MC impaired our ability to measure nD or IgG. Correlations of whole nD of MC and IgG were similar for Holsteins (r = 0.77) and Jerseys (r = 0.80). Regression equations were used to estimate the IgG concentration of samples based on the nD of CA supernatant or whole MC. The equation created from nD of CA supernatant resulted in 34.3% of samples accurately estimated within 10 mg/ml, 23.7% of samples estimated within 10–20 mg/ml, 14.5% of samples estimated within 20–30 mg/ml and 27.5% of samples estimated to greater than 30 mg/ml of actual IgG concentration. Equation created from the nD of whole MC resulted in 43.8% of samples estimated within 10 mg/ml, 28.0% of samples within 10–20 mg/ml, 14.4% of samples within 20–30 mg/ml and 13.8% of samples greater than 30 mg/ml compared with actual IgG concentration. These results suggest that the nD of whole MC provides a more accurate estimation of colostral IgG concentration than the nD of CA supernatant and both tests are most accurate on fresh colostrum samples.

Key words: colostrum, refractometer, IgG

77 Physiological and transcriptional adaptations in adipose tissue of dairy cows in response to prepartal plane of dietary energy. P. Ji*, J. S. Osorio, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Our objective was to determine the effect of prepartal energy overfeeding during the close-up period on physiological and transcriptional responses of adipose tissue (AT) of dairy cows during the transition period. Multiparous Holstein cows (n = 14) were randomly assigned to either a controlled-energy diet (CON; NE_L = 1.30 Mcal/kg DM) for the entire dry period or CON during the far-off period (d −50 to −21 relative to expected parturition) followed by a moderate-energy diet (Overfed; NE_L = 1.49 Mcal/kg DM) during the close-up period (d −21 to calving). Both groups were fed the same lactation diet postpartum (NE_L = 1.67 Mcal/kg DM). Blood samples were collected before morning feeding twice weekly. Subcutaneous AT was biopsied from tail-head regions at d −10, 7, and 21 for total RNA extraction. Quantitative RT-PCR was utilized to analyze mRNA expression of 50 genes. Overfeeding energy increased DMI ($P = 0.05$) and serum insulin concentration ($P < 0.01$) during the close-up period, but tended to increase serum BHBA concentration postpartum ($P = 0.06$). Overfed cows experienced more marked increases in serum NEFA and BHBA postpartum ($P < 0.05$). Milk yield did not differ ($P = 0.89$) between diets. Compared with CON, close-up overfeeding led to greater expression of genes ($P < 0.05$) associated with fatty acid (FA) biosynthesis (ACLY, ACACA, and FASN), FA import, FA activation and desaturation (LPL, ACSS2, ACSL1, and SCD), NADPH production (G6PD and IDH1), triglyceride synthesis (GPAM and DGAT2), transcriptional regulation of lipogenesis (PPARG, CEBPA, and THRSP) and basal lipolysis (PNPLA2 and ABHD5) at d −10. Abundance of mRNA for these genes decreased between d −10 and d 7. The expression of IRS1, AKT2, GLUT4, and INSIG1 was downregulated in both groups at d 7 compared with d −10 ($P < 0.05$). Overall, overfeeding energy during the close-up period may increase both lipid accumulation and basal lipolysis in AT through transcriptional regulation. Decreased circulating insulin and lower expression of IRS1, AKT2, and GLUT4 in the early postpartum period may contribute to the downregulation of lipogenic genes.

Key words: adipose tissue, energy overfeeding, transition period

78 Expression of novel, putative stem cell markers in prepubertal and lactating bovine mammary glands. R. K. Choudhary*[1], C. M. Evock-Clover[2], and A. V. Capuco[2,1], *[1]Department of Animal Sciences, University of Maryland, College Park, [2]Bovine Functional Genomics Lab, USDA-ARS, Beltsville, MD.*

Mammary stem cells (MaSC) are essential for growth and maintenance of the mammary epithelium. Two main phases of mammary growth include ductal elongation before puberty and lobulo-alveolar growth during pregnancy. Some studies utilized morphological characteristics and retention of bromodeoxyuridine (BrdU) label to identify MaSC. However, these approaches may not be feasible or require considerable expertise. An alternative approach to identify resident MaSC is based on detection of appropriate protein markers by immunohisto-

chemistry. The focus of this study was to evaluate staining patterns (in prepubertal and lactating mammary tissue) of 3 novel, candidate markers for bovine MaSC. These proteins were identified as candidate MaSC markers because their transcripts were highly expressed in laser microdissected-MaSC, which were identified by BrdU label retention and basal location within the mammary epithelium. The 3 novel candidate markers for MaSC were: nuclear receptor subfamily 5 group A member 2 (NR5A2), nucleoporin 153 (NUP153) and fibronectin type III domain containing 3B (FNDC3B). We also evaluated presumptive MaSC markers [aldehyde dehydrogenase 1 (ALDH1) and Musashi 1 (Msi1)] and differentiation factors [Notch 3 receptor (Notch3) and cytokeratins (CK) 14 and19] that have been used in other species. We found that NR5A2 and NUP153-positive nuclei were more abundant in prepubertal than lactating mammary glands and their distributions were consistent with expectations for a MaSC marker. FNDC3B was localized mainly in the nucleus prepubertally and in the cytoplasm during lactation. Preliminary results showed colocalization of the novel markers with label retaining MaSC. Abundant expression of ALDH1 precludes its use as a marker for bovine MaSC, whereas Msi1 staining was distributed in a fashion consistent with MaSC localization. Additionally we noted that onset of lumen formation in terminal ducts of prepubertal glands were coincident with Notch3 expression in luminal cells. This study demonstrates that nuclear expression of NR5A2, NUP153 and FNDC3B are potential markers for bovine MaSC.

Key words: mammary stem cell, novel biomarker

79 Effect of dietary protein level and rumen-protected methionine supplementation on performance of lactating dairy cows. C. Lee*[1], A. N. Hristov[1], T. Cassidy[1], H. Heyler[1], H. Lapierre[2], G. A. Varga[1], and C. Parys[3], *[1]Pennsylvania State University, University Park, [2]Agriculture and Agri–Food Canada, Sherbrooke, QC, Canada, [3]Evonik Degussa GmbH, Hanau, Germany.*

The objective of this experiment was to investigate the effect of rumen–protected Met (RPMet) supplementation of a low-CP diet on dairy cow performance. The experiment was conducted for 12 wks with 36 Holstein cows (95 ± 6.2 DIM). Following a 2-wk covariate period, cows were assigned to one of the following treatments: 15.6% CP diet [HighCP; metabolizable protein (MP) balance: +26 g/d], 14.0% CP diet (LowCP; MP balance: –313 g/d) supplemented with 100 g/cow/d of rumen-protected Lys (AminoShure-L, 24 g/d estimated digestible Lys supply), and 14.0% CP diet supplemented with rumen-protected Lys plus 24 g/cow/d RPMet (Mepron, 15 g/d estimated digestible Met supply; LowCPMet). DMI and milk yield were not affected by treatment (24.8 ± 0.40 kg/d and 38.4 ± 0.80 kg/d, respectively). Compared with HighCP, LowCP decreased milk protein content ($P = 0.02$); with LowCPMet the effect was not significant ($P = 0.07$). Milk protein yield was not different ($P = 0.22$) among diets. Milk urea–N concentration was decreased (by 15%; $P = 0.05$) by LowCP and LowCP-Met compared with HighCP. Plasma Lys and Met concentrations were not affected by treatment. His and Val concentrations were 48 and 22% lower ($P = 0.001$ and 0.016) and Thr, Arg, Phe, and Gln tended to be lower ($P = 0.08$ to 0.05) for the LowCP diets compared with HighCP. The LowCP diets decreased ($P = 0.01$) blood urea–N concentrations and NDF and ADF apparent digestibilities compared with HighCP. Urinary excretion of purine derivatives was lower (by 13%; $P = 0.03$) for LowCP compared with HighCP. Compared with HighCP, the LowCP diets resulted in lower ($P < 0.001$) urinary total (by 31%) and urea-N (by 51%) excretions. Ammonia emission from LowCP manure was 37% lower ($P < 0.001$) compared with HighCP manure. In conclusion, the LowCP diets, supplemented with rumen–protected amino acids maintained milk production similar to the HighCP diet, except that protein concentration was significantly decreased without RPMet supplementation. Nitrogen losses and ammonia emissions from manure were decreased with the LowCP diets.

Key words: dietary protein, rumen-protected methionine, dairy cow

80 Summer assessment and validation of metabolic profile reference values for transition Holstein dairy cattle. K. J. Lager*[1,2], E. R. Jordan[1], and D. R. Topliff[2], *[1]Texas AgriLife Extension Service, Texas A&M System, College Station, [2]West Texas A&M University, Canyon.*

Dairy cattle genetics and management continue to evolve over time, but it is not known whether the available diagnostic tools have kept pace with the ever changing industry. The objective of this project was to assess the validity of current metabolic profile reference values in relation to current dairy cattle genetics and management strategies. Blood samples (n = 1787) were collected between late August and mid-September, 2010 from cows within the transition period via coccygeal vessel venipuncture into nonheparinized vacuum blood tubes at morning feeding on 8 commercial dairies ranging in approximate size from 1800 to over 5000 head of lactating cows. One day per dairy was utilized to collect blood samples for cows within the transition period. Samples were placed on ice immediately following collection until processing. Following centrifugation, samples were stored frozen (−20°C) in duplicate before laboratory analysis for calcium, phosphorus, magnesium, albumin, urea, glucose, cholesterol, sodium, potassium, chloride, and nonesterified fatty acids. Data points were excluded for cows experiencing dystocia, retained placenta, displaced abomasum, twin births, and stillbirths, as well as for cows being dry <40 d or >80 d. Mean lactation number and days dry were 3.0 ± 1.2 and 57.8 ± 7.5, respectively. Serum phosphorus values (mg/dl) for wk −3, −2, −1, 1, 2, and 3 relative to calving were 5.23 ± 0.83, 5.43 ± 0.74, 5.48 ± 0.95, 5.39 ± 1.2, 4.90 ± 0.88, 5.31 ± 0.80, respectively; while calcium values (mg/dl) were at 8.94 ± 0.43, 8.87 ± 0.54, 8.87 ± 0.54, 8.26 ± 0.86, 8.76 ± 0.74, 9.08 ± 0.53, respectively. Nonesterified fatty acids were numerically greatest in wk 1 (0.67 mEq/l ± 0.36), while sodium and chloride were reacted similarly (143.65 mEq/l ± 2.4 and 108.89 mEq/l ± 2.6, respectively) at wk −1 relative to calving. Serum cholesterol concentrations were numerically lowest in wk 1 (74.54 mg/dl ± 17.8), displaying a non-static trend similar to that of other metabolic profile analytes for the duration of the transition period.

Key words: dairy cow, metabolic profile, transition cow

81 Effect of follicular wave and progesterone (P4) concentration during follicle growth on fertility of dairy cows. R. S. Bisinotto*[1], H. Ayres[1], M. R. Carvalho[1], E. S. Ribeiro[1], R. L. A. Cerri[2], L. F. Greco[1], F. S. Lima[1], M. G. Favoreto[1], A. P. Monteiro[1], M. C. Perdomo[1], W. W. Thatcher[1], and J. E. P. Santos[1], *[1]University of Florida, Gainesville, [2]University of British Columbia, Vancouver, BC, Canada.*

Effects of wave of the ovulatory follicle and P4 concentration during follicle growth on corpora lutea (CL) function and conceptus development were evaluated in dairy cows. Nonlactating Holstein cows had their estrous cycles synchronized with GnRH and a controlled internal drug release (CIDR) device containing P4, followed 7 d later by CIDR removal and 2 injections of $PGF_{2\alpha}$ 24 h apart. All cows received GnRH 1 d after the 2nd $PGF_{2\alpha}$ which, for cows induced to ovulate a first wave follicle (FW, n = 13) or a FW follicle supplemented with P4 (FWP4, n = 8), was the 1st GnRH of the timed artificial insemination (AI)

protocol (d-9 GnRH, d-2 and d-1 $PGF_{2\alpha}$, d0 GnRH and AI, d1 AI). Cows induced to ovulate a second wave follicle (SW, n = 12) received the timed AI protocol beginning 6 d after the previous GnRH. Cows in FWP4 received 3 CIDR, one at 12, 24 and 48 h after the GnRH (d-9), that were removed at the $PGF_{2\alpha}$ (d-2). Blood was sampled from d-9 to 17 for P4 and estradiol (E2) analyses. Cows were slaughtered on d17 and uteri flushed. Interferon-tau (INF-τ) on uterine flush was quantified. Concepti IFN-τ mRNA expression was accessed by RT-PCR. Orthogonal comparisons were performed to determine the effects of P4 (FW vs. FWP4+SW) and follicle wave (SW vs. FWP4). Ovulation of a FW follicle reduced pregnancy and this effect was mediated by low P4 concentration during their development. Luteal function during early gestation, concepti elongation and their ability to produce IFN-τ were not compromised by ovulation of follicles developing under low concentrations of progesterone.

Table 1.

	Treatment			*P*-value	
	FW	FWP4	SW	Wave	P4
P4, ng/mL					
d-9 to −2	1.4±0.2	3.8±0.3	5.4±0.3	<0.01	<0.01
d4 to 16	6.3±0.2	5.0±0.3	5.0±0.3	0.84	<0.01
Ovulatory follicle (d0), mm	17.9±0.6	15.3±0.7	14.7±0.6	0.47	<0.01
E2 peak before AI (d-1), %	58.3	12.5	0.0	0.77	0.01
E2 at peak, pg/mL	8.0±0.6	7.0±0.7	5.9±0.6	0.25	0.05
CL on d7, mm^3	5.2±0.5	3.6±0.6	4.2±0.5	0.39	0.03
Pregnant, %	50.0	87.5	72.7	0.45	0.10
Conceptus length, cm	17.5±2.8	13.7±2.6	11.2±2.6	0.52	0.15
INF-τ on uterine flush, ng/mL	300±92	211±86	60±92	0.06	0.22
INF-τ mRNA, dCt ratio	1.5±0.2	1.6±0.2	1.2±0.2	0.13	0.78

Key words: dairy cow, follicle, progesterone