corn-soybean meal diet with 5% DDGS and 4) corn- soybean meal diet with 5% DDGS + 0.05% enzyme complex. The pigs were allotted randomly into four pigs per pen with six replicate pens per treatment in a completely randomized design. Pigs were slaughtered at the end of experiment and the loin muscle was obtained for meat quality. Meat pH ($p<0.01$), firmness ($p<0.01$) and redness ($p<0.05$) were higher in DDGS treatment than corn-soybean meal treatment. However, color, marbling, lightness, yellowness, TBARS, water holding capacity, drip loss, cooking loss and loin muscle area were not significantly different among treatments ($p>0.05$). The pigs fed the diet containing DDGS had higher total UFA concentration and total UFA/SFA ratio of loin and backfat. In conclusion, DDGS can change pH, firmness, redness and total UFA concentration and total UFA/SFA ratio of meat and backfat, however, enzyme addition has no affect on meat quality.

Key Words: DDGS, fatty acid composition, finishing pigs

M213 Supplementation with phytase and xylanase can increase energy availability in swine diets containing corn distillers dried grains with solubles (DDGS). M. D. Lindemann*[1], G. A. Apgar[2], G. L. Cromwell[1], P. H. Simmins[3], and A. Owusu-Asiedu[3], [1]*University of Kentucky, Lexington*, [2]*Southern Illinois University, Carbondale*, [3]*Danisco Animal Nutrition, Marlborough, UK*.

One way of enhancing dietary energy at times of high feed prices is to use exogenous enzymes to improve diet digestibility and utilize more of the nutrients already present in a diet containing byproducts such as DDGS. To examine the potential for enzymes to enhance nutrient release, a study was conducted with 96 crossbred pigs (mean initial and final BW of 64 and 123 kg) allotted to pens of 4 pigs (2 barrows and 2 gilts). Treatments were: 1) a positive control [PC] corn-soybean meal diet with 20% DDGS and 3% choice white grease [CWG], and 2) a negative control [NC] similar to the PC but with 1% CWG and no inorganic P source. The NC was lower in ME [90 kcal/kg] and available P [about 0.02%]. The enzymes added were phytase (Phyzyme® 6-phytase, EC 3.1.3.26; PHY; 250 or 500 U/kg diet) and xylanase (Porzyme® 9300, endo 1,4-beta-xylanase; XYL; 2000 or 4000 U/kg diet). Diets 3-8 were the NC plus: 3) 250 PHY and 0 XYL, 4) 250 PHY and 2000 XYL, 5) 250 PHY and 4000 XYL, 6) 500 PHY and 0 XYL, 7) 500 PHY and 2000 XYL, and 8) 500 PHY and 4000 XYL. The ADG for the PC and NC (1.04 vs 1.05 kg), ADF (2.78 vs 2.93 kg), and F/G (2.68 vs 2.78) were as anticipated with higher F/G in the NC diet. Fecal digestibility for DM (77.1 vs 73.7%, P=0.02), energy (75.5 vs 71.4%, P=.006), and N (72.7 vs 68.8%, P=0.007) was consistently higher for PC compared to NC. For Trt 3-8 the ADG (1.04, 1.07, 1.03, 1.00, 0.95, and 1.01 kg) and F/G (2.77, 2.73, 2.66, 2.75, 2.75, and 2.68) illustrated an apparent release of energy with incremental PHY and XYL additions. For Trt 3-8 the DM (76.1, 76.7, 74.6, 76.2, 74.4, and 74.6%), energy (73.8, 74.4, 71.2, 73.7, 72.0, and 71.6%), and N (70.9, 71.7, 70.3, 71.1, 69.5, and 71.3%) digestibility confirmed an improved digestibility. The inclusion of PHY improved digestibility ($P<0.05$) of all 3 components. Further improvements in fecal digestibility were not observed with XYL but the recovery of F/G was observed only when the high level of XYL was included with the PHY. These data demonstrate that appropriate exogenous enzymes are a means of nutrient release in diets containing byproducts.

Key Words: phytase, pigs, xylanase

Physiology and Endocrinology: Endocrinology and Metabolism

M214 Methionine requirements for the preimplantation bovine embryo. L. Bonilla*[1], D. Luchini[2], E. Devillard[3], and P. J. Hansen[1], [1]*University of Florida, Gainesville*, [2]*Adisseo USA, Inc., Alpharetta, GA*, [3]*Adisseo France, SAS, Commentry, France*.

The objective was to determine the requirement of in vitro produced embryos for the essential amino acid methionine. Oocytes were matured for 20-22 h and fertilized for 6-8 h. Embryos were cultured in groups of 15 in 25 µL microdrops of potassium simplex optimized medium - bovine embryo modification 2 (KSOM-BE2) at 38.5°C in 5% (v/v) oxygen. In Experiment 1 (n=963 putative zygotes in 4 replicates), embryos were cultured with 0, 35, 50, 100, 200 or 400 µmol/L L-methionine for 8 d. The percent of oocytes that cleaved was observed at Day 3 after insemination and blastocyst development at Day 7 and 8. At Day 7, a group of blastocysts was stained with Hoescht 33258 to determine total cell number. There was no effect of methionine concentration on cleavage rate. The percent of oocytes that developed to blastocyst was lower for embryos without methionine at Day 7 ($P<0.05$) and 8 ($P<0.01$) than other groups but was similar for embryos cultured with 35-400 µmol/L. Least-squares means were 4.2, 23.2, 18.2, 21.5, 16.3, and 21.3 for 0, 35, 50, 100, 200, or 400 µmol/L for Day 7 (SEM=3.4%) and 13.5, 36.1, 30.9, 33.6, 29.8 and 33.0 for Day 8 (SEM=3.4%). Total cell number was not affected by methionine concentration. In Experiment 2 (n=1,204 putative zygotes in 4 replicates), embryos were cultured with 0, 7, 14, 21, 28 or 35 µmol/L methionine. There was no effect of methionine concentration on cleavage rate. The percent of oocytes that developed to blastocyst was lower for embryos without methionine at Day 7 ($P<0.005$) and 8 ($P=0.01$). At Day 7, least-squares means were 8.2, 20.3, 27.2, 27.7, 24.3, and 21.2 for 0, 7, 14, 21, 28, or 35 µmol/L (SEM=2.5%). There was a tendency for 7 µmol/L to be lower than 14 ($P=0.07$) and 21 µmol/L ($P=0.06$). At Day 8, least-squares means were 17.8, 35.2, 37.8, 43.0, 37.9, and 33.6 for 0, 7, 14, 21, 28, or 35 µmol/L (SEM=3.5%). Means were similar for 7-35 µmol/L. In conclusion, methionine requirements for optimal blastocyst yield are between 7 and 21 µmol/L. Further studies to further define optimal concentration and to examine competence of embryos for development after transfer are warranted. *Support: Adisseo.*

Key Words: methionine, embryos, development

M215 Effect of exogenous insulin and fasting on estradiol production and growth hormone receptor (GHR) and insulin-like growth factor I (IGF-I) genes expression by the pre-ovulatory follicle of ewes. A. Schneider[1], L. F. M. Pfeifer[1], E. Schmitt[1], J. W. Silva Neto[1], L. T. Hax[1], M. M. Antunes[1], F. A. B. Del Pino[1], G. R. Paludo[2], and M. N. Corrêa*[1], [1]*Federal University of Pelotas, Brazil*, [2]*University of Brasilia, Brazil*.

The aim of this study was to investigate the effect of fasting and insulin injections for 96 hours on estradiol concentrations and expression of GHR and IGF-I mRNA in the pre-ovulatory follicle of ewes. In the eleventh day of the estrous cycle 15 ewes received an injection of $PGF_2\alpha$, 36 hours after a GnRH injection and 24 hours after a CIDR® was inserted and removed 6 days later together with an injection of $PGF_2\alpha$ (Day 0). In Day -2 the ewes were divided in: 1) control group (CG, n = 5) that received a maintenance diet; 2) insulin group (IG, n = 5) that received insulin injections (s.c., 0.25 IU/kg) every 12 hours

from Day -2 to 2 and 3) fasting group (FG, n = 5), that was submitted to fasting from Day -2 to 2. Estradiol concentrations were evaluated on Day 2, when ovaries were also collected for evaluation of the follicular population and dissection of theca (TC) and granulosa (GC) cells of the pre-ovulatory follicle (> 4 mm). Expression of GHR and IGF-I mRNA was evaluated through real time RT-PCR. Data were compared among groups by one-way ANOVA using the Tukey-Kramer adjustment. The diameter of the pre-ovulatory follicle on Day 2 was not different among groups (7.60 ± 0.38 mm) neither the number of small (< 2 mm, 10.73 ± 2.19), medium (< 4 mm, 0.8 ± 0.2) and pre-ovulatory (1.13 ± 0.09) follicles per ewe was different. IG had higher (P<0.05) estradiol concentrations on Day 2 (53.70 ± 1.82 pg/mL) than FG (29.97 ± 6.96 pg/mL), but was not different from CG (35.92 ± 5.72 pg/mL). Although GHR or IGF-I mRNA expression was detected in GC and TC, no difference among groups was detected. For IG estradiol was positively correlated to follicular diameter (r=0.93, P<0.05), GC GHR (r=0.87, P<0.01) and IGF-I mRNA (r=0.79, P<0.1). In conclusion, insulin injection increased estradiol production without any change in the expression of GHR and IGF-I mRNA in the pre-ovulatory follicle.

Key Words: GHR, IGF, insulin

M216 TNFα and adipocyte-hepatic metabolism at drying off and during early lactation in dairy cows. H. A. van Dorland[1], H. Sadri[2], and R. M. Bruckmaier*[1], [1]*University of Bern, Vetsuisse Faculty, Veterinary Physiology, Bern, Switzerland*, [2]*Isfahan University of Technology, Department of Animal Science, Isfahan, Iran*.

Adipose tissue excretes components, such as TNFα, that play a role in the multifaceted regulation of lipolysis. This study investigated TNFα and other metabolic modulators in adipose tissue over time, and if TNFα is involved in interactions between adipose tissue and liver metabolism. Blood was sampled from 28 cows from week 10 ante partum (wk-10) up to week 4 post partum (wk4), and analyzed for concentrations of NEFA, glucose, insulin, and TNFα. Liver and adipose tissue biopsies were obtained in wk-10, on d1 post partum (d1), and in wk4. Adipose tissue was analyzed for mRNA levels by real-time RT-PCR of genes encoding for TNFα, peroxisome proliferator activated receptor γ (PPARγ), hormone-sensitive lipase (HSL), and fatty acid synthase (FASN). Liver was analyzed for mRNA levels of genes encoding enzymes of fatty acid β-oxidation (CPT1A CPT2, ACADVL), and of PPARγ. Data were evaluated by the Mixed procedure of SAS including biopsy time-point and parity as fixed effects with cow as repeated subject. Spearman Rank correlation coefficients were also calculated. Concentrations of NEFA were highest in wk-10, followed by d1, compared to wk4, suggesting adaptation to the reduction of nutrients at the start of the dry period. Plasma TNFα concentrations were very low (0.11±0.01 ng/ml) with no significant differences over time, suggesting that TNFα had a local effect. TNFα mRNA levels in adipose tissue were lowest (P<0.05) on d1 compared to the other time-points. HSL mRNA was highest (P<0.05) in wk-10, followed by d1, compared to wk4, which correspond to the high NEFA concentrations in wk-10. PPARγ mRNA levels were lowest in wk4 compared to the other time points. Levels of mRNA of FASN and liver parameters did not significantly change over time. Most significant correlations between adipose and liver tissue-related parameters were observed in wk4 compared to the other time-points. TNFα was not involved. In conclusion, TNFα is not a signaling factor that links adipose tissue and liver metabolism in healthy dairy cows. Other factors are responsible for the orchestrated regulation of adipose tissue and liver metabolism in wk4.

Key Words: dairy cow, adipose tissue, TNFα

M217 Early-weaning up-regulates the expression of sucrase-isomaltase in the jejunum of the piglet. D. Lackeyram*, T. Archbold, K. C. Swanson, and M. Z. Fan, *University of Guelph, Guelph, ON, Canada*.

Sucrase-isomaltase (SIM) is a small intestinal apical membrane disaccharidase that hydrolyses both sucrose and maltose. The objectives of this study were to examine the responses of SIM activity and protein abundances associated with the mucosal homogenate (H), intracellular soluble (S), and the apical membrane (M) fractions as well as SIM mRNA abundance and its regulation during early-weaning in comparison with suckling pigs. A total of 20 Yorkshire piglets, 10 suckling (SU) and 10 early-weaning (WN) with an average BW of 3 kg at the age of 10 d, were used in this study. Weanling piglets were fed a corn and SBM-based diet for 12 d. Proximal jejunal samples from both SU and WN groups were collected. Sucrose (0-25 mM) and maltose (0-60mM) were used in the enzymatic kinetic experiments. Abundances of SIM protein and mRNA were analyzed by Western blot and the real time RT-PCR using β-actin as the housekeeping gene. The jejunal SIM maximal specific activity (μmol/mg protein.min) for sucrose was increased (P<0.05) in weaning piglets (H: WN, 159.02±3.25 vs. SU, 76.72±2.89; S: WN, 16.42±1.28 vs. SU, 5.85±1.01; and M: WN, 141.39±3.84 vs. SU, 69.47±4.73). Similar increases (P<0.05) were observed for maltose (H: WN, 55.11±0.29 vs. SU, 40.79±0.81; S: WN, 17.81±0.24 vs. SU, 12.70±0.61; and M: WN, 516.51±1.05 vs. SU, 389.92±1.18). Corresponding increases (P<0.05) in the SIM protein abundance for the WN group was also observed in all of the jejunal fractions, H, 34%; S, 84%; M, 61%, respectively. Furthermore, early weaning increased (P<0.05) the relative abundance of SIM mRNA by 1.9 fold (WN, 0.306±0.03 vs. SU, 0.105±0.01). The increase in SIM mRNA could be accounted for by an increase (P<0.05) in the abundance (arbitrary units) of a key intestinal homeodomain transcription factor Cdx2 (WN, 2.365±0.01 vs. SU, 1.073±0.03). In conclusion, early-weaning increases small intestinal SIM activity at transcriptional, translational and post-translational levels.

Key Words: gene expression, sucrase-isomaltase, weanling pigs

M218 Effect of propionate infusion on hepatic PEPCK and glucose-6-phosphatase expression in neonatal Holstein calves. S. S. Donkin*, E. Cedeño, and S. L. Koser, *Purdue University, West Lafayette, IN*.

Cytosolic phosphoenolpyruvate carboxykinase (PEPCK), a rate-limiting enzyme for gluconeogenesis in liver, is sensitive to nutritional and hormonal cues. The objective of this experiment was to determine the effects of in vivo propionate supply on hepatic PEPCK mRNA expression. Sixteen male Holstein calves were blocked by birth date, and assigned to either: saline infusion (4 ml/min), propionate infusion (2 mmol/h/kg $BW^{.75}$), acetate infusion (3.5 mmol/h/kg $BW^{.75}$), or pre-treatment with phlorizin (100 mg at 8 h intervals for 24h) followed by propionate infusion. Blood samples were collected immediately prior to the initiation of infusion via indwelling jugular vein catheters and at hourly intervals during the 8 h infusion period. Liver biopsy samples were obtained immediately after the end of the 8 h infusion period and analyzed by real time PCR for pyruvate carboxylase (PC), PEPCK, glucose-6-phosphatase (G–6–Pase) and 18S mRNA. Abundance of PEPCK mRNA, relative to 18S was increased (P < 0.05) in response to propionate and acetate infusion (0.34 vs. 1.89 ± 0.24, arbitrary units). Propionate with phlorizin pretreatment did not alter PEPCK mRNA (0.34 vs. 0.69 ± 0.24, arbitrary units). Expression of PC mRNA was similar among all treatments. Abundance of G–6–Pase followed a pattern similar to PEPCK mRNA and was elevated (P < 0.05) for calves given acetate and propionate relative to saline control (0.82 vs. 2.70

and 2.32 ± 0.45, arbitrary units for control, acetate, and propionate, respectively). The data indicate that propionate modulates expression of PEPCK and G–6–Pase in vivo and extends our previous observations that propionate induces bovine PEPCK expression by direct activation of the PEPCK promoter. The action of propionate to induce PEPCK gene expression identifies a novel feed-forward response for gluconeogenesis in bovine that is modulated by substrate sensing to activate PEPCK and G-6-Pase expression and consequently enhance the capacity for hepatic gluconeogenesis and hepatic glucose release. *Supported by NRI Grant no. 2006–35206–16646 from the USDA CSREES.*

Key Words: propionate, liver, gene

M219 The Effects of supplemented diet with fish oil and canola oil during transition period to early lactation on follicular dynamics of Iranian Holstein dairy cows. T. S. Vafa, A. Heravi Mousavi*, A. Naserian, M. Danesh Mesgaran, R. Valizadeh, and A. Parand, *Excellent Center for Animal Science, Ferdowsi University of Mashhad*, *Iran*.

Increasing ration nutrient density is one of the strategies to improve nutrient intake in early lactation cows. For studying the effects of combination of fish oil and canola oil on follicular dynamics in early lactation, Holstein cows were randomly assigned in 1 of 2 treatments: 1) 0% oil (Control, n=9) and 2) 2% oil (FoCo, 1% fish oil plus 1% canola oil, n=9). Holstein cows were blocked in pairs based on their previous 305 d milk production, parity and expected calving. To monitor follicular parameters, ultrasound measurements of follicular activity were made on alternate days from days 10 – 45 postpartum (PP) to ascertain the characteristics and fate of the first follicular wave utilizing a 7.5-MHz rectal transducer. Dominant follicle development was characterized by follicular mapping of recorded ultrasound images. A dominant follicle was defined as a follicle that was >10 mm in diameter in the absence of other large (>9 mm) growing follicles. The data were analyzed using the General Linear Model procedure of SAS for a completely randomised design. Diameter of follicles (≥3.5 mm) on d 10 PP (p=0.007; 3.9 and 7.9 ± 0.88 mm, respectively) was significantly increased in the supplemented diet. Number of follicles (≥3.5 mm) on d 10 PP and 14 PP, diameter of follicles on d 14 PP, number of days until detection of a follicle ≥10 mm in diameter (p=0.13; 17.37 ± 2.27 and 12.44 ± 2.14 d, respectively), and diameter of first ovulatory follicle (p=0.13; 12.50 ± 0.13 and 14.37 ± 0.78 mm, respectively) were all similar between diets. Number of days to first ovulation (p=0.07; 28.83 ± 2.63 and 21.85 ± 2.44 d, respectively) was not affected by the dietary groups. Results of this study showed that the combination of fish oil and canola oil had no apparent effect on most follicular parameters and days postpartum to first ovulation.

Key Words: dairy cows, follicular dynamic, fish and canola oils

M220 The effects of supplemented diet with fish oil and canola oil during transition period to early lactation on complete blood count of Iranian Holstein dairy cows. T. S. Vafa, A. Heravi Mousavi*, A. Naserian, M. Danesh Mesgaran, and R. Valizadeh, *Excellent Center for Animal Science, Ferdowsi University of Mashhad*, *Iran*.

The study was designed to test the effect of including fish oil and canola oil from transition period to early lactation on immunology responses in Holstein dairy cows. Holstein cows were randomly assigned in 1 of 2 treatments: 1) 0% oil (control, n=9) and 2) 2% oil (supplemented, 1% fish oil-1% canola oil, n=9). Cows were blocked by parity, previous 305-2x milk production and expected calving time. Using vacutainer tubes, blood samples were collected weekly from -2 to 7 week relative to calving via venipuncture of coccygeal vessels before the morning feeding to monitor Complete Blood Count (CBC). The blood samples for CBC were kept in room temperature until analyzing for CBC. Complete blood counts were automatically determined with a hematology analyzer. The data repeated in time were analyzed by using a mixed model for a completely randomized design with repeated measures. The number of red blood cells (p=0.99; 5496900±133000 and 5495200 ± 132300 / µl, respectively), number of white blood cells (p=0.45; 6602±376.91 and 7008.68±373.07 /µl, respectively), hemoglobin (p=0.56; 8.15±0.20 and 7.98±0.20 g/dl, respectively), platelet (p=0.67; 349100±26010 and 333220±25720 /µl, respectively), hematocrit (p=0.65; 25.11±0.58 and 24.73±0.58%, respectively), number of lymphocyte (p=0.28; 3993±284 and 4448±302, respectively), number of monocytes (p=0.64; 1865±213 and 1718±130, respectively), number of neutrophil (p=0.067; 3944±180 and 3413±201, respectively), and number of eosinophil (p=0.32; 190±29 and 145±32, respectively) were similar between control and supplemented diets. The results of this study demonstrate that feeding a combination of fish oil and canola oil pre- and postpartum had no apparent effects on immunological parameter measured as total cell count.

Key Words: dairy cow, complete blood count, fish oil-canola oil

M221 Serum metabolomics of multiparous Holstein cows during the transition period. C. Chen, W. J. Weber, M. Carriquiry, S. C. Fahrenkrug, and B. A. Crooker*, *Department of Animal Science, University of Minnesota*, *St Paul*.

Transition from pregnancy to lactation is associated with dramatic alterations in metabolism that can significantly impact health, milk yield and reproductive performance. Advances in metabolomic techniques have improved the ability to monitor metabolic profiles and flux of small molecules in serum to define changes in metabolism on a global scale. Cows from control (stable milk yield since 1964; CL; n = 5) and select (contemporary; SL; n = 6) lines that differed in milk yield (6,200 and 11,100 kg milk/305 d) were fed ad libitum quantities of the same diets, milked 2X/d, and exposed to the same environment. Diets were fed as TMR composed primarily of legume-grass hay, corn silage, ground corn, and soybean meal, and were formulated to meet or exceed requirements. A dry cow diet (15.5% CP, 1.60 Mcal NEL/kg DM) was fed until calving and an early lactation diet (18.2% CP, 1.67 Mcal NEL/kg DM) was fed thereafter. Production results were analyzed by repeated measures analysis and means differed if $P < 0.05$. Deproteinized serum samples collected at -14, -7, 3, 14, 28 and 38 DIM were separated by ultra-performance liquid chromatography and ionized chemical components detected by a time-of-flight mass spectrometer. Mass, retention time, and intensity of serum ions was extracted from chromatograms and spectra and used to construct a multivariate model by principal components analysis. Chemical structures of serum ions were determined by accurate mass measurement and MS/MS fragmentation. The SL cows produced more FCM (29.5 vs. 45.6 ± 2.1 kg/d) during the first 42 DIM. Differences between pre- and postpartum serum samples were due mainly to dramatic postpartum increases in several lipid species, especially lysophosphatidylcholines. Differences between CL and SL cows were less striking. Overall, this study demonstrated that serum metabolomics can serve as a useful tool to investigate the underlying mechanisms of lactation-induced metabolic changes.

Key Words: metabolomics, serum

M222 Effects of heat stress on ghrelin secretion in lactating dairy cattle. S. E. Cossel*, M. E. Field, M. V. Skrzypek, S. R. Sanders, S. L. Marion, J. B. Wheelock, S. R. Hartman, Y. Yuxi, P. B. Hoyer, R. J. Collier, R. P. Rhoads, L. H. Baumgard, and M. L. Rhoads, *University of Arizona*, *Tucson*.

The effects of heat stress on ghrelin, a potent regulator of feed intake and whole-body metabolism, was evaluated in two studies using lactating dairy cattle. In experiment 1, eight lactating Holstein dairy cows (90.0 ± 1.7 DIM; 566.48 ± 19.55 kg BW) were housed in environmentally controlled chambers and subjected to a thermal neutral (TN; 20.22 °C and 51.23% humidity) period for 2 days followed by a heat stress (HS; 35.34°C and 21.99% humidity) period for 3 days. On the final day of each period, blood samples were taken peri-prandially every 20 minutes beginning 2 hours prior to the morning feeding and ending 4 hours after the morning feeding. Plasma was harvested and stored at -20°C for assay of ghrelin concentrations. Vaginal temperatures, taken by intra-vaginal thermal dataloggers, increased during the HS period (38.61 ± 0.17 vs. 37.81 ± 0.17°C; $P<0.05$) while feed intake was lower on the HS sampling date (35.1 ± 1.7 vs. 39.6 ± 1.7 kg; $P<0.01$). Plasma ghrelin concentrations were affected by treatment ($P<0.05$) and time ($P<0.01$). Compared to TN, HS increased plasma ghrelin concentrations (234.97 ± 26.31 vs. 259.05 ± 26.32 pg/ml, respectively) and plasma ghrelin concentrations were greater during the pre-prandial period than the post-prandial period. In experiment 2, three lactating Holstein dairy cows were housed in environmentally controlled chambers and subjected to a TN period for 11 days followed by a HS period for 9 days. Plasma ghrelin concentrations were measured on day 8 of each period beginning 5 hours prior to the afternoon feeding and ending 1.5 hours prior to the afternoon feeding. Plasma ghrelin concentrations did not differ between treatments and were not affected by time. These results indicate that heat stress increases plasma ghrelin concentrations, but that measurable changes in ghrelin secretion are limited to the peri-prandial period.

Key Words: ghrelin, heat stress, dairy

M223 Plant oil supplementation in dietary concentrate improves milk yield, ovarian function and uterine health of postpartum dairy cows in a tropical environment. C. Navanukraw*, A. Boonsom, S. Guntaprom, S. Uriyapongson, and C. Wachirapakorn, *Khon Kaen University*, *Khon Kaen, Thailand*.

Thirty, Holstein Friesian, prepartum multiparous cows were randomly allocated to one of 3 treatments according to RCBD as follows; control (no supplement), 4% palm oil supplement, and 4% sunflower oil supplement. All cows were fed ad libitum of roughage and dietary concentrate 4 wk prior to parturition and 4 wk postpartum to meet requirements for lactating cows. Following parturition, milk yields, ovarian follicular dynamics and uterine health were monitored along with plasma concentrations of progesterone. Milk yields of cows fed palm and sunflower oil supplements were greater than that of control cows (23.8, 22.8 and 18.1 kg/d respectively, $P<0.05$). Numbers of small (3-5 mm) and large (≥10 mm) follicles of cows fed oil supplements were greater than those of control cows ($P<0.05$). Cows supplemented with sunflower oil had a lesser uterine score than control and cows supplemented with palm oil (1.4, 2.0 and 2.0; $P<0.05$). Uterine involution time and the first estrus postpartum of cows fed oil supplements occurred sooner ($P<0.01$) than control cows (42.0 and 56.4 days for cows fed palm oil; 32.2 and 50.2 days for cows fed sunflower oil; and 50.4 and 91.8 days for control cows). Cows fed oil supplements also had increased ($P<0.05$) progesterone concentrations since 3 wk after parturition. This study highlights the strategy of nutritional management of reproduction in pre- and postpartum dairy cows. *Supported by NRCT-50 to CN.*

Key Words: plant oil, ovarian follicular dynamics, uterine health

M224 Hematological profile of confined ewes fed corn silage. J. P. F. Silveira[1], J. L. C. B. Reis*[2], M. A. Factori[1], D. H. Vieira[3], V. L. Tierzo[1], L. F. D. Medeiros[1], and C. Costa[4], [1]*São Paulo State University*, *Botucatu, SP, Brazil*, [2]*University of Agrarian Sciences - University of Marília*, *Marília, SP, Brazil*, [3]*Center of Creation of Animals of Laboratory*, *Rio de Janeiro, RJ, Brazil*, [4]*Rural Federal university of Rio de Janeiro*, *Seropedica, RJ, Brazil*.

Hematological evaluation is considered an important tool for animal health analysis. This work was carried out to determine the hematological profile of animals confined in metabolic chambers. Twenty-four Santa Inês lambs having an average age of three months and an average initial weight of 25 kg were used. The experimental design was completely randomized, in a 2 x 2 factorial scheme (two corn hybrid, dent and flint; and two corn mass ensilage processing, present and absentee). Blood samples were collected after 27 days of confinement. Data were analysed by a two-way analysis of variance. Tukey's multiple test was used to determine differences due to corn hybrid and process. Differences were considered significant at the 0.05 probability level. Erythrocyte number (ERIT), hematocrit percentage (HTC) and hemoglobin rate (HB) were determined. Mean corpuscular volume (MCV) and mean corpuscular hemoglobin concentration (MCHC) were calculated. ERIT and MCV were significantly different among treatments. The highest ERIT and the lowest MCV were determined for animals fed flint no process diet. The lowest ERIT number and the highest MCV were determined for animals fed process dent diet. The animals fed process dent diet showed also the highest EPG. HTC, HB and MCHC did not differ among treatments. Confinement may have determined ERIT statistics difference since diets were formulated to reach the species nutritional requirement. The 27-day confinement determined alterations on sheep hematological profile.

Key Words: hematology, nutrition, physiological evaluation

M225 Effects of lactation and pregnancy on metabolic and hormonal responses of Holstein dairy cattle. I. M. Thompson*[1], R. L. Cerri[1], I. H. Kim[2], A. D. Ealy[1], P. J. Hansen[1], C. R. Staples[1], and W. W. Thatcher[1], [1]*University of Florida*, *Gainesville*, [2]*Chungbuk National University*, *South Korea*.

Objectives were to develop and characterize an experimental platform to evaluate lactation and pregnancy effects for subsequent analyses of the endometrial trancriptome in dairy cattle. Pregnant heifers (n=34) were assigned randomly after calving to a lactating group (LG, n=17) and a non-lactating group (NLG, n=17). The LG was fed a TMR (1.65Mcal NEL/kg, 16.5% CP) ad libitum. The NLG was fed a maintenance ration (1.45 Mcal NEL/kg, 12.2% CP) once per day. Rectal temperatures and blood, for analyses of progesterone and metabolites, were collected thrice weekly. Ovarian ultrasonography and BW measurements were performed weekly. BCS was measured every 14 d. All cows were pre-synchronized and enrolled in a timed(T)-AI protocol (Presynch/5 d CIDRSynch), but only 10 in the LG and 12 in the NLG were TAI. On d 17 after GnRH/TAI, all cows were slaughtered and endometrial, conceptus, oviductal and ovarian tissues collected. Temporal changes in BCS, BW, and rectal temperature did not differ between LG and NLG.

NLG cycled earlier than LG (26.3<34.7d postpartum; P<0.04) Mean plasma concentrations of NEFA postpartum did not differ between NLG and LG (236 vs 204 mEq/L); although NLG>LG in week one (573>276 mEq/L; P<0.01). Cows in LG had greater (P<0.01) plasma concentrations of BHBA (4.98>2.94 μg/mL) and BUN (11.65>6.5 mg/dL) than NLG. Glucose in plasma was lower (P < 0.01) for LG (74<80 mg/dL). Plasma progesterone from GnRH or TAI (d 0) until d 17 was lower for LG due to a lower progesterone concentration in pregnant than cyclic cows versus no difference between cyclic and pregnant of NLG (LactationxPregnantxDay; P<0.05). In conclusion, lactation\diet altered metabolic status even though BW and BCS were the same between LG and NLG. Lactation delayed initiation of cyclicity and tended to lower concentrations of progesterone in pregnant cows during a programmed period following an induced ovulation.

Key Words: lactation, metabolites, progesterone

M226 Does a low feeding level enhance estradiol synthesis in preovulatory follicles of Holstein × Normande dairy cows? E. Cutullic*[1], A. Benhaim[2], S. Barbey[3], H. Mitre[2], S. Carreau[2], and C. Disenhaus[1], [1]*UMR1080 INRA Dairy Production, Rennes, France*, [2]*INRA USC2006, Estrogen and Reproduction, Caen, France*, [3]*INRA UE326 Le Pin-au-Haras, Exmes, France*.

Enhanced estrus expression has been reported for feeding strategies which limit milk yield. The objective of this study was to evaluate 17β-estradiol (E2) in preovulatory follicles of cows submitted to 2 feeding levels. Holstein x Normande crossbred dairy cows were fed a total mixed ration composed either of 55% maize silage, 15% alfalfa hay and 30% concentrate (Control: C-group, N=7) or of 60% grass silage and 40% hay (L-group, N=8). Milk progesterone profiles were used to follow cyclic activity from calving to slaughter (85±6 days postpartum). Cows were synchronized by two prostaglandin-F2α analogue injections and slaughtered 40 hours after the 2nd one. Ovaries were collected. Follicular fluid (FF) from dominant follicles (DF, diameter>12 mm) was separated from granulosa cells (GC) by centrifugation. E2 concentration was measured in FF by RIA. In GC, aromatase activity (AA) was determined by the tritiated-water method and aromatase mRNAs (A-mRNA) were quantified by RT-PCR. L-group cows produced less 11-week average daily milk yield (MY) even though they lost more body condition (BC) from calving to slaughter than C-group (20.5 vs. 34.5kg/day; -0.66 vs. -0.20 unit; P<0.001). Seven cows were well synchronized. E2 concentration in FF was highly correlated to ln(AA) (r=0.98; P<0.001) and A-mRNA (r=0.92; P<0.05). L-group tended to have higher FF E2 concentration and AA than C-group (5699 vs. 960 ng/mL, 3106 vs. 295 fmol/h/mg protein, N=4 and 3, P<0.10). In regard to the literature and to some preliminary results (N=8, 33.4 kg/day MY, -0.33 unit BC loss, 524 ng/mL FF E2), FF E2 of the L-group appeared very high. More investigations are needed both to confirm this feeding level effect and to determine if it could be due to production or to nutritional restrictions.

Key Words: estradiol, aromatase, dairy cows

M227 Serum and anterior pituitary gland (AP) concentrations of IGF-I during an estradiol induced LH surge in gilts. N. M. Rasmussen*, C. E. Hostetler, and J. A. Clapper, *South Dakota State University*, *Brookings*.

Increasing serum concentrations of estradiol are known to trigger the LH surge in gilts. Administration of estradiol has been shown to increase serum and anterior pituitary gland (AP) concentrations of IGF-I in barrows. However, whether this occurs in gilts during the preovulatory LH surge has not been determined. Therefore, the objective of this experiment was to determine if serum and AP concentrations of IGF-I increase in response to an estradiol induced LH surge in ovariectomized gilts. Twelve crossbred gilts of similar weight (123 kg) were ovariectomized and assigned to either control (C; n=6) or estradiol (E; n=6) groups. E pigs received 2.5 mg estradiol in corn oil i.m. while C pigs received an equal volume of corn oil i.m. on d 0. Blood samples were obtained by jugular venipuncture on d 0, 1, and 2. Pigs were slaughtered on d 3 when blood and AP were collected. Serum and AP concentrations of LH and IGF-I were determined in duplicate by RIA. Differences in serum and AP concentrations of LH and IGF-I were determined using the Proc Mixed procedure of SAS. Serum concentrations of LH were not different (P>.05) in C and E pigs on d 0. Serum concentrations of LH decreased (P<.05) in E pigs compared to C pigs on d 1, but were not different (P>.05) than C pigs on d 2 and 3. Serum concentrations of LH in C pigs were not different (P>.05) from d 0 through d 3. Serum concentrations of IGF-I were not different (P>.05) between C and E pigs on d 0, but by d 3 serum concentrations of IGF-I were greater (P<.05) in E pigs than C pigs. AP concentrations of LH did not differ (P>.05) between C and E pigs, however, AP concentrations of IGF-I tended (P=.09) to be greater in E pigs than C pigs. These preliminary data suggest that serum and AP concentrations of IGF-I may increase during the preovulatory LH surge in gilts.

Key Words: pigs, IGF-I, LH

M228 Influence of heifer development method on post-AI blood metabolites. B. L. Perry*, J. A. Walker, C. L. Wright, K. C. Olson, and G. A. Perry, *Dept. Anim. and Range Sci., South Dakota State University*, *Brookings*.

Method of heifer development has been reported to have influenced pregnancy success. Therefore, the objective of the current study was to evaluate differences in plasma glucose and urea nitrogen (PUN) concentrations following AI between heifers developed in a feedlot or on grass and turned to grass immediately following AI. Weaned heifers were developed from weaning to breeding either in a feedlot (n=52; LOT) or on grass (n=53; GRASS). Immediately following fixed-time AI all heifers were moved to the same pasture. Blood samples were collected from all heifers on d -23, -9, the day of AI (d 0), and d 11. Pregnancy success was determined 42 d following AI. There tended (*P*=0.10) to be more LOT heifers cycling prior to the breeding season (94% vs 84%), but no difference (*P*=0.20) between GRASS and LOT in pregnancy success (57% vs. 44%). There were effects of development (*P*<0.01), time (*P*<0.01), and development by time (*P*=0.02) on glucose concentrations. Glucose concentrations decreased from d 0 to d 11 in both groups. Glucose was greater (*P*<0.01) in GRASS compared to LOT heifers (*P*<0.01; 87.3 ± 1.24 and 80.2 ± 1.25 mg/dL) on d 0 but similar (*P*=0.43; 76.29 ± 1.24 and 74.9 ± 1.24 mg/dL) on d 11. Pregnant heifers had greater glucose than open heifers on d 11 (*P*= 0.04; 77.4 ± 1.24 and 73.8 ± 1.24 mg/dL) but not on d 0 (*P*=0.88). Concentrations of PUN were influenced by development (*P*<0.01) and time (*P*<0.01). Concentrations increased from d 0 to 11, and were greater in GRASS (12.9 ± 0.22 and 15.1 ± 0.22 mg/dL) compared to LOT (11.8 ± 0.22 and 13.6 ± 0.22 mg/dL) heifers. There tended (*P*=0.07) to be a development by pregnancy interaction with similar (*P*=0.54) PUN concentrations between LOT pregnant and open heifers, but greater (*P*=0.04) concentrations in GRASS open compared to GRASS pregnant heifers. Method of heifer development (LOT or GRASS) influenced both glucose and

PUN concentrations with GRASS heifer having greater glucose and PUN concentrations compared to LOT heifers, and pregnant heifers tended to have greater glucose than open heifers.

Key Words: glucose, PUN, heifer development

M229 Relationships between dry matter intake (DMI), plasma progesterone (P4), and liver catabolic enzymes in lactating dairy cows. O. G. Sa Filho*[1,3], C. O. Lemley[2], M. E. Wilson[2], J. Hillegass[3], J. L. M. Vasconcelos[1], and W. R. Butler[3], [1]*FMVZ/UNESP, Botucatu, SP, Brazil*, [2]*West Virginia University, Morgantown*, [3]*Cornell University, Ithaca, NY*.

Increased liver blood flow in response to high DMI has been reported to increase steroid metabolism in lactating dairy cows, but little information exists on the regulation of steroid catabolic enzymes. The aim of this study was to evaluate the relationships between DMI, milk production, P4, ovarian structures, and hepatic catabolic enzymes. Day of ovulation was synchronized in lactating Holstein cows with the Ovsynch protocol and only cows that ovulated in response to GnRH treatment (d 0) were used (n=18). We evaluated the relationships between DMI (range 16-31 Kg/d), milk production (MP), follicle diameter (FD) on d 0, corpus luteum volume (CLV) and P4 on d 7, and progesterone catabolic enzymes cytochrome P450 2C (CYP2C) and 3A (CYP3A) activity (measured as the isoform specific substrate dependant oxidation of NADPH) from liver biopsy samples collected on d 7. Total enzyme activity (TEA) was calculated as sum of the activities of CYP2C and CYP3A. The ratio P4/CLV was used as a relative measure of P4 production and liver catabolic activity. Data were analyzed by PROC GLM of SAS. The DMI positively affected (P<0.05) MP (MP=2.6+1.9•DMI; r2=0.47), FD (FD=3.1+0.4•DMI; r2=0.34), and CLV (CLV=913.7+366.5•DMI; r2=0.33). Despite the positive effect on CLV, DMI had negative effects (P<0.05) on P4 (P4=7.2-0.1•DMI; r2=0.27) and on the ratio P4/CLV (P4/CLV=0.0015-0.000042•DMI; r2=0.5). Plasma P4 was negatively affected by CYP2C (P4=2.7-0.3•CYP2C; r2=0.4; P<0.05) and tended to be negatively affected by CYP3A (P4=2.0-0.04•CYP3A; r2=0.24; P=0.1) and TEA (P4=2.0-0.02•TEA; r2=0.29; P<0.1). The P4/CLV ratio was negatively affected by CYP2C (P4/CLV=0.0008-0.00043•CYP2C; r2=0.36; P<0.05) and tended to be negatively affected by TEA (P4/CLV=0.00059-0.000012•TEA; r2=0.29; P<0.1), whereas no effects of CYP3A or mRNA for the enzymes were found. In conclusion, higher DMI and liver catabolic enzymes in lactating dairy cows were related to decreased plasma P4 concentration.

Key Words: DMI, progesterone, catabolic enzymes

M230 Method development and preliminary evaluation of the potential for using erythrocyte membranes in the assessment of long-chain polyunsaturated fatty acid status in dairy cows. C. L. Preseault*[1,2], J. Kraft[1], H. M. Dann[2], and A. L. Lock[1], [1]*University of Vermont, Burlington, VT*, [2]*William H. Miner Agricultural Research Institute, Chazy, NY*.

Due to the limited availability of long-chain polyunsaturated fatty acids (LCPUFA) leaving the rumen, recent observations suggest that the modern high producing dairy cow may, under certain situations, be deficient in these fatty acids (FA). Erythrocyte membrane (EM) FA profile has been used previously in human studies to assess long term FA intakes, and can therefore possibly be used as a marker for LCPUFA status. The objectives of this work were to develop methods and undertake a preliminary examination of the potential for using EM-FA profile in the evaluation of LCPUFA status of dairy cows. Whole blood was collected from 53 Holstein cows at 5 stages of the lactation cycle (far-off dry, close-up dry, early lactation, mid lactation, and late lactation). After isolation and purification of the EM, total lipids were extracted and FA methyl esters prepared and purified by thin-layer chromatography. FA composition was determined by gas-liquid chromatography. Significant differences in the concentration (g/100g FA) of all reported FA was observed across the 5 stages. Late lactation cows were highest in C18:2 n-6 (31.29; *P*<0.01) whereas far-off dry cows were highest in C18:3 n-3 (0.81; *P*<0.01). C20:4 n-6 and C20:5 n-3 were highest in the close-up group (4.17 and 0.21; *P*<0.001 and P<0.05, respectively). Both dry cow groups had higher levels of C22:5 n-3 (*P*<0.001) than lactating cows. This preliminary evaluation highlights potential differences in LCPUFA status of cows at different stages of the lactation cycle and may help determine the efficacy of nutritional strategies aimed at improving LCPUFA status.

Table 1. Selected LCPUFA of EM in dairy cows at defined stages of the lactation cycle.

FA (g/100g)	Far-Off Dry Cows (n=10)	Close-Up Dry Cows (n=6)	Early Lactation Cows (n=12)	Mid Lactation Cows (n=12)	Late Lactation Cows (n=13)	SEM	*P*-value
C18:2 n-6	27.03^{b}	27.88^{ab}	24.80^{b}	27.88^{b}	31.29^{a}	1.73	<0.01
C20:4 n-6	3.86^{a}	4.17^{a}	2.52^{bc}	2.24^{c}	3.00^{b}	0.37	<0.001
C18:3 n-3	0.81^{a}	0.74^{ab}	0.58^{bc}	0.56^{c}	0.57^{bc}	0.07	<0.01
C20:5 n-3	0.10^{b}	0.21^{a}	0.13^{b}	0.09^{b}	0.11^{b}	0.03	<0.05
C22:5 n-3	0.36^{a}	0.46^{a}	0.09^{b}	0.09^{b}	0.18^{b}	0.06	<0.001

^{a,b,c} *P*<0.05.

Key Words: dairy cows, long-chain polyunsaturated fatty acids, erythrocyte membrane

M231 Effects of BCS and level of concentrate feeding during early lactation on plasma concentrations of blood metabolites in pasture–fed dairy cows. F. Y. Obese*[1,2], T. E. Stirling[3], C. R. Stockdale[4], K. L. Macmillan[3], A. R. Egan[2], and S. Humphrys[5], [1]*CSIR-Animal Research Institute, Accra, Ghana*, [2]*School of Agriculture and Food Systems, the University of Melbourne, Melbourne, Victoria, Australia*, [3]*School of Veterinary Science, the University of Melbourne, Werribee, Victoria, Australia*, [4]*Department of Primary Industries, Kyabram, Victoria, Australia*, [5]*Primegro Pty Ltd, Thebarton, South Australia, Australia*.

The objective of this research was to assess the effects of body condition score (BCS) at calving and level of supplementation on insulin-like growth factor-I (IGF–I), betahydroxybutyrate (BHB), non-esterified fatty acids (NEFA) and urea concentrations in Holstein cows in a pasture-based system. Concentrations of IGF-I in cows that had commenced estrous cycle were compared with that of cows that were anestrus at the start of the breeding program. Cows (n=72) were managed over a period of 5 months to calve in BCS of 4, 5 or 6 using a scale from 1 (thin) to 8 (obese). They grazed pasture and were supplemented in early lactation with either 1 or 6 kg of grain per day. Calving BCS affected NEFA and BHB concentrations at Week 0 (calving). The concentrations were higher in cows with BCS 6 than BCS 4 with respect to NEFA (1.23 ± 0.11 vs 0.84 ± 0.11 mmol/L; P=0.022) and BHB (0.61 ± 0.04 vs 0.38 ± 0.04 mmol/L; P<0.001). These effects had diminished by Week 10 postcalving. Plasma concentrations of IGF-I at Week 10 were increased with the higher level (6 kg) of grain feeding (87.8 ±

4.7 vs 72.1 ± 4.7 ng/mL; P = 0.022) whereas urea concentrations were decreased (5.16 ± 0.21 vs 4.11 ± 0.21 mmol/L; P = 0.001). Cows that had commenced estrous cycles by the start of the AI program had higher plasma concentrations of IGF-I than anestrous cows at Week 0 (56.5 ± 3.8 vs 39.8 ± 4.1 ng/mL; P=0.009) and Week 10 (87.3 ± 4.2 vs 64.5 ± 4.3 ng/ml; P=0.001). These results suggest an association between plasma concentrations of IGF–I and resumption of ovarian function in pasture-fed Holstein-Friesian cows.

Key Words: anestrus, blood metabolite, body condition

M232 Metabolic profile of the hypocalcemic dairy cows in an intensive grazing system in south of Brazil. E. Schmitt*[1,2], D. A. C. Hoffmann[1], M. E. Lima[1], T. dos S. Farofa[1], M. A. Goulart[1], M. S. Lopes[1], P. Montagner[1], R. T. França[1], F. A. B Del Pino[1], J. J. Loor[2], and M. N. Corrêa[1], [1]*Federal University of Pelotas, Pelotas, RS, Brazil*, [2]*University of Illinois, Urbana*.

Some dairy farms in the south of Brazil rely on intensive grazing due to low cost of this practice. This nutritional management system without supplementation of grain could increase the risk of periparturient clinical and subclinical problems. We used 13 crossbred Jersey cows grazing tropical pastures to research blood metabolic profiles during the transition period emphasizing subclinical hypocalcemia. During -22 and 22 DIM, every 2 d blood was collected from the coccygeal vein to measure concentrations of calcium, magnesium, phosphorus, chlorides, glucose, insulin, glucagon, NEFA, aspartate aminotransferase (AST), and gamma-glutamyl-transferase. Cows were retrospectively divided into a hypocalcemic (HYP, n = 5) and normocalcemic (NOR, n = 8) group (total calcium < 8 mg/dL >) prior to statistical analysis. Average milk yield for the first 3-wk postpartum was higher (P <0.01) for HYP cows (14.4 vs. 10.7 L/d). These cows had higher (interaction P <0.05) calcium at -12 and lower calcium at 4 DIM. Glucose concentration also was higher (interaction P < 0.05) prepartum (-14 DIM) and lower postpartum (16 DIM) than NOR cows. The HYP cows had higher levels (interaction P < 0.05) of AST (6 DMI), NEFA (0, 4 and 10 DIM), glucagon (6, 10, 18, 20 and 22 DIM) and glucagon:insulin (6 and 20 DIM). Other variables were not different between groups. Results indicate that high milk production potential, in particular, is related to the incidence of subclinical hypocalcemia in cows grazing tropical pastures. These animals might be at higher risk of development other disorders in the transition period due to the more sever negative energy balance.

Key Words: hypocalcemia, energy balance, transition period

M233 A comparison of physiological and endocrine parameters during the periestrual period in lactating dairy cows that did and did not conceive. A. K. Sanders*[1], D. Ray[1], C. H. Hamilton[1], C. Tritsch[1], M. E. Risley[2], M. F. Smith[2], and W. J. Silvia[1], [1]*University of Kentucky, Lexington*, [2]*University of Missouri, Columbia*.

Reproductive physiological and endocrine parameters during the first periestrual period postpartum were compared in lactating dairy cows that conceived versus those that did not. Holstein (n=48) and Holstein X Jersey crossbred (n=7) cows were used in the experiment. A modified Ovsynch protocol was initiated 52 to 94 days postpartum (100 ug GnRH, i.m., Factrel, Fort Dodge Animal Health). Seven days later (day 0), two injections of prostaglandin (PG) F2a (25 mg, i.m., Lutalyse, Pfizer Animal Health) were administered, 12 h apart, to induce luteolysis. The ovaries were examined ultrasonographically 2x daily beginning on day 0. Blood samples were collected at 6-h intervals for quantification of estradiol-17b. On day 2, the frequency of sample collection was increased to every 2 h for quantification of LH. Beginning on day 2, cows were observed for estrus behavior at 4-h intervals. For each cow, 27 variables were calculated from the data collected. These included the timing and magnitude of estradiol-17b and LH secretion, time of onset, intensity and duration of estrus, maximum follicle diameter, time of ovulation and intervals from onset of estrus to peak of LH and ovulation. Preovulatory surges of LH and ovulation were observed in 31 cows. Differences between cows that conceived (n=13) and those that did not (n=18) for each variable were examined by t-test. Estrus began at 74.4 h after PGF2a and lasted for 12.6 h. Peak LH occurred at 77.3 h. Ovulation occurred at 104.1 h, 25.7 h after peak LH. Peak concentration of estradiol-17b occurred at 75.8 h and averaged 2.6 pg/ml. The diameter of the preovulatory follicle was 15.4 mm. None of these variables were different between cows that conceived and those that did not (p > 0.2). The interval from onset of estrus to peak LH tended to be different between groups (p = 0.08) (4.7 h in cows that conceived, 1.6 h in cows that did not). The impact of this asynchrony in time of estrus relative to peak LH on fertility remains to be determined. *Supported by the KY Agr Expt Stn and USDA NRI-CGP 2006-35203-17133.*

Key Words: dairy cow, conception, estrus

M234 Plant-based diets enriched with linseed oil or marine algae and organic selenium alter reproductive performances of broiler breeder hens over the reproductive season. C. Brèque*[1,2], C. Coss[1,2], C. Lessard[1,2], R. Gervais[2], D. Venne[3], M. R. Lefrançois[2], P. Y. Chouinard[2], G. Vandenberg[2], and J. L. Bailey[1,2], [1]*Centre de recherche en biologie de la reproduction, Québec, QC, Canada*, [2]*Département des Sciences Animales, Québec, QC, Canada*, [3]*Couvoir Scott Ltée, Scott Jonction, QC, Canada*.

There are indications that plant-based diets and organic (org) Se alter fertility in broiler breeders. We hypothesised that supplementing plant-based diets with n-3 fatty acids and org Se may improve female reproductive parameters. Individually caged, 23-week (wk) old female broiler breeders were fed 8 diets (n=50/diet). The control diet contained meat meal + 50 IU/kg vit E (MM50), while the others were plant-based: 2.3% soya oil + 50 IU/kg vit E (SO50), 2.3% soya oil + 100 IU/kg vit E (SO100), 2.3% soya oil + 100 IU/kg vit E + 0.3 ppm org Se (SO100Se), 2.3% linseed oil + 100 IU/kg vit E (LO100), 2.3% linseed oil + 100 IU/kg vit E + 0.3 ppm org Se (LO100Se), 1% marine algae (42% oil) + 100 IU/kg vit E (MA100), and 1% marine algae + 100 IU/kg vit E + 0.3 ppm org Se (MA100Se). Hens were inseminated at 41-46 wk and 55-60 wk of age at 3 wk intervals. Insemination doses from pooled ejaculates from males fed the same diets were standardized to $100x10^6$ spz/hen and repeated on 2 consecutive days. Overall fertility rates (F), hatchability (H) and embryo mortality (early: EEM, intermediate: IEM and late: LEM) were estimated. Data were analysed as a completely randomized design. Regardless of the insemination period, LO diets had the best overall F (P<0.05). However, after the first inseminations, H was higher in SO50 and SO100, whereas F was highest after the second inseminations for SO100Se (P<0.05). Dietary MA increased EM and reduced F and H at both periods (P<0.05). Org Se as replacement for inorganic Se in plant-based diets decreased EEM (wk 41-46) and IEM (wk 55-60) but had adverse effects on LEM (both periods) (P<0.05). Supplementing plant-based diets with LO provides insight towards improving the reproductive performances of broiler breeder hens but research is needed to elucidate the role of org Se.

Key Words: broiler breeder, fertility, hatchability

M235 Temporal changes in hepatic gene expression during the periparturient period of spring-calving beef cows on grazing conditions. A. L. Astessiano*[1], R. Perez-Clariget[1], G. Quintans[2], P. Soca[1], B. A. Crooker[3], and M. Carriquiry[1], [1]*School of Agronomy, UDELAR, Uruguay*, [2]*INIA, Treinta y Tres, Uruguay*, [3]*Department of Animal Science, University of Minnesota, St. Paul*.

Primiparous crossbred (Hereford/Angus; n=10) were used in a randomized block design, to study effects of day postpartum (DPP) on hepatic gene expression during the periparturient period. Cows grazed together on a native pasture paddock (60 ha) with an average forage mass available of 453 kg DM/ha (13.2% CP and 24.4% ADF). Milk yield was measured at 14 and 35±4 DPP and liver biopsies obtained at -11, 7, 31, and 52 DPP. The amount of mRNA for growth hormone receptor (GHR), GHR-1A, insulin-like growth factor-I (IGF-I), IGF binding proteins-2 (BP2),-3 (BP3), and an endogenous control (hypoxanthine phosphori bosyltransferase;(HPRT) were measured by real time RT-PCR. Means from a repeated measures analysis differed when P<0.05. Cows lost 1.25 units of body condition score (BCS,scale 1-8) during the last 60 d of gestation, calved with a BCS of 3.7 ±0.08 units, and lost only 0.25 units during the first 60 DPP. Milk yield tended (*P=0.07*) to decrease from 6.3 to 5.5±0.4 kg/d from 14 to 35 DPP, but this decrease was evident only in cows that calved with BCS≤3.5. Abundance of HPRT mRNA was not affected by DPP or BCS at calving. Relative amounts of GHR mRNA reached nadir at 7 DPP, and increased thereafter until 52 DPP, but there was no effect of DPP on amounts GHR-1A pr IGF-I mRNA amounts. However, when BCS at calving was considered in the analysis, mRNA expression of GHR1A and IGF-I tended (*P<0.10*) to increase for cows with BCS≤3.5 but tended to decrease for cows with BCS>3.5 from -11 to 52 DPP. Although BP2 and BP3 mRNA relative amounts were not affected by DPP, BP2/BP3 mRNA ratio tended (*P=0.11*) to decrease from -11 to 52 DPP and BP2 mRNA was greater for cows with BCS≤3.5 at calving. Hepatic expression of genes associated with GH-IGF the axis were affected during the periparturient period in spring-calving beef cows under grazing conditions and tended to be modulated by BCS at calving.

Key Words: liver, somatotropic axis

M236 Effect of short-term prepartum supplementation on reproduction of multiparous beef cows on grazing conditions. G. Quintans*[1], G. Banchero[1], G. Roig[1], and M. Carriquiry[2], [1]*INIA, Treinta y Tres, Uruguay*, [2]*School of Agronomy, UDELAR, Uruguay*.

Multiparous Aberdeen Angus x Hereford crossbred cows were used to evaluate the effect of supplementation during the last month of gestation on reproductive performance. Cows were ranked by body weight (BW) and body condition score (BCS, scale 1-8) and assigned randomly to supplement (SUP; n=18) or control (CON; n=17) treatments. Supplemented cows were offered (1 kg/100 kg BW) a mix (67:33% as-fed basis; 16% CP, 11% ADF) of sorghum grain and protein concentrated from 33±1.4 d prepartum until calving. Before, during, and after the supplementation period, cows grazed together a native pasture paddock with an average forage mass available of 1345 kg DM/ha (10.4% CP, 45.2% ADF). The breeding season (BS) started at 60 d postpartum (DPP) and lasted 60 d. Means were considered to differed when *P*<0.05. Cow BCS at calving and at the onset of the BS were, respectively, 0.25 and 0.5 units greater for SUP than CON cows. Plasma NEFA concentrations during the last month of gestation were reduced for SUP cows (0.81 vs 0.66±0.05 mEq/L for CON and SUP cows, respectively) but there were no differences between treatments in plasma NEFA during the postpartum. The maximum follicle diameter at the beginning of the BS did not differ between treatments (10.8±0.7 mm); however, the probability of cows presenting follicles with diameter≥10 mm was greater for SUP than CON cows (77 vs 55%). Days to first ovulation did not differ between treatments and averaged 80±1.4 DPP. The incidence of anovulation at the beginning of the BS did not differ between treatments but the probability of cows cycling during the first 90 DPP tended (*P*=0.084) to be greater for SUP than CON cows (83 vs 65%). The interval beginning of BS-conception did not differ between treatments but final pregnancy rate tended (*P*=0.082) to be greater in SUP than CON cows (100 vs 88%). Supplementation during the last month of gestation could benefit reproductive performance of spring calving-beef cows on grazing conditions.

Key Words: prepartum supplementation, reproduction

M237 Endocrine and reproductive parameters of North American Holstein × New Zealand Holstein-Friesian crossbred cows on grazing conditions. A. Fernandez-Foren*[1], M. Carriquiry[2], V. Artegoitia[1], D. Laborde[3], and A. Meikle[1], [1]*Veterinary School, UDELAR, Uruguay*, [2]*School of Agronomy, UDELAR, Uruguay*, [3]*Private consultant, Uruguay*.

The aim of this work was to study endocrine and reproductive parameters in North American Holstein (NAH) and NAH x New Zealand Holstein-Friesian crossbred (NAxNZ) multiparous cows on grazing conditions. Cows (n=50) were blocked by calving date, body condition score (BCS) at calving, lactation number (3 or 4), and economic value of milk (New Zealand selection index). All cows grazed on the same implanted pasture (legume-grass mix; 14.5 kg DM/cow/d of assigned forage) and were supplemented with 5.1 kg DM/d of corn whole-plant silage, 3.8 kg DM/d of high moisture sorghum silage and 6.3 kg DM/d of concentrate (corn grain, wheat middling, barley grain and sunflower meal). Days to first ovulation were determined as days to plasma progesterone concentrations >1 ng/ml). Means from repeated measure analysis differed when *P*<0.05. Body weight (BW) for NAH was 33 ± 6 kg greater than for NAxNZ cows along the period evaluated (calving to 140 days postpartum, DPP). Cow BCS tended (*P*=0.10) to be greater for NAH cows, but this was due to a greater BCS at calving. Both groups lost 0.7 ± 0.06 units, reached BCS nadir at 35 DPP, and at 140 DPP had not returned to BCS at calving. Plasma insulin and insulin-like growth factor-I (IGF-I) concentrations along the period evaluated did not differ between genetic origins. The incidence of anovulation at 30 (62%) and at 60 DPP (28%) and days to first ovulation (42.1 and 42.8 ± 4 d for NAH and NAxNZ, respectively) were not different between genetic origins. The reproductive performance in terms of reinitiation of ovarian cyclicity was similar among NAH and NAxNZ origins and this is consistent with insulin and IGF-I profiles after calving in cows on grazing conditions.

Key Words: dairy, genetic origin, reproduction

M238 Effect of short-term prepartum supplementation on milk production and calf performance of multiparous beef cows on grazing conditions. M. Carriquiry*[1], G. Roig[2], G. Banchero[2], and G. Quintans[2], [1]*School of Agronomy, UDELAR, Uruguay*, [2]*INIA, Treinta y Tres, Uruguay*.

Multiparous Aberdeen Angus x Hereford crossbred cows were used to evaluate the effect of supplementation during the last month of gestation on milk production and composition, and calf performance. Two month

prior to calving, cows were ranked by body weight (BW) and body condition score and assigned randomly to supplement (SUP; n=18) or control (CON; n=17) treatments. Supplemented cows were offered (1 kg/100 kg BW/d) a mix (67:33% as-fed basis; 16% CP, 11% ADF) of sorghum grain and protein concentrate from 33±1.4 d prepartum until calving. Before, during, and after the supplementation period, cows were grazed together in a native pasture paddock with an average forage mass available of 1345 kg DM/ha (10.4% CP, 45.2% ADF). Means from a repeated measures analysis differed when $P<0.05$. Cow BW did not differ between treatments (470±3 kg) but there was an interaction of treatment by d postpartum (DPP). During the last month of gestation, BW decreased 3.2% for CON but was maintained for SUP cows. Milk production decreased from 6.9 to 3.9±0.42 kg/d from 30 to 180 d DPP. Although there was no difference in milk production between treatments (5.0 vs 4.8±0.22 for CON and SUP cows, respectively), milk yield tended ($P=0.11$) to be 1 kg/d greater at 30 DPP for CON than for SUP cows. No differences were detected for milk fat, protein, and lactose contents between treatments (2.0±0.13, 3.3±0.04, 4.9±0.05%, respectively). Milk energy output (4.9 Mcal EN/d) represented approximately 50% of energy requirements. Calf weight at birth did not differ between treatments (42.5 kg), but at weaning, calf weight was greater for CON than SUP cows (182 vs 172±4.2 kg). This was associated with greater average daily gain during the first 30 DPP in calves from CON cows (0.97 vs 0.83±0.04 kg/d for CON and SUP cows, respectively). Short-term supplementation during the last month of gestation could modify postpartum nutrient partitioning between body reserves and milk production in beef cows.

Key Words: prepartum supplementation, milk yield

M239 Effect of bovine somatotropin (bST), dietary fat, and day in milk (DIM) on hepatic mineral concentrations in Holstein cows. M. Carriquiry*[1], W. J. Weber[2], W. A. House[3], and B. A. Crooker[2], [1]*School of Agronomy, UDELAR, Uruguay*, [2]*Department Animal Science, University of Minnesota, St. Paul*, [3]*SDA-ARS, Ithaca, NY*.

Multiparous cows (n=59) were blocked by expected calving date and previous milk yield and assigned randomly to treatments to determine effects of bST, dietary fat, and DIM on hepatic minerals (Ca, P, Mg, Na, K, Fe, Mn, Zn, Cu, Cd, Mo). Dietary n-6 or n-3 fatty acids were provided from calving as whole, high-oil sunflower seeds (SS; 10% of diet DM) or as a mixture of Alifet-High Energy® and Alifet-Repro® (AF; 3.4 and 1.5% of diet DM). Cows received 0 (N) or 500 (Y) mg bST (POSILAC®) every 10 d from 12 to 70 DIM and at 14-d intervals thereafter. Treatments from the factorial combination were designated SSN, SSY, AFN, and AFY. Biopsies were collected at -12, 10, 24, and 136 DIM and mineral content (μg/g DM) determined by inductively coupled plasma atomic emission spectrometry. Means from a repeated measures analysis differed when $P< 0.05$. Liver DM decreased from -12 to 136 DIM (27.6 ± 1.1% vs. 23.9 ± 1.3%) and was not affected by bST or diet. Hepatic P, K, Zn, Cu, Mo, and Cd decreased and Ca tended ($P < 0.09$) to decrease after calving, reached nadir at 10 or 24 DIM, and returned to or exceeded prepartum values by 136 DIM. The Mg values at -14 DIM were intermediate and values at 10 and 24 DIM less than at 136 DIM. Hepatic Fe increased from -12 to 10 DIM and decreased from 10 to 136 DIM. Hepatic Mn increased 50% from -12 to 136 DIM but Na was not affected by DIM. Hepatic Zn (100 vs. 90 ± 3.3 μ/g) and Fe (213 vs. 188 ± 7 μ/g) were reduced in bST treated cows. Hepatic Zn (101 vs. 89 ± 3.3 μ/g), Mn (7.6 vs. 6.7 ± 0.3 μ/g), and Fe (210 vs. 192 ± 7 μ/g) decreased in cows fed AF. There was an interaction of bST, diet, and DIM on K and Mo as their concentrations were less at 24 and 136 DIM in AFY cows than in SSN, SSY, and AFN cows. Hepatic concentration of several minerals decreased with initiation of lactation, bST and AF but no signs of deficiency were detected.

Key Words: minerals, liver, dairy

M240 Responses of physiological parameters in cattle to a short period of induced heat load. Y. Aharoni[1], A. Brosh*[2], E. Tahar[1], and A. Abud[1], [1]*VETERIX Ltd, Or Aqiva, Israel*, [2]*Agricultural Research Organization, Ramat Yishai, Israel*.

Changes in the physiological status of an animal are reflected in changes in the levels of some of its physiological parameters, such as temperature, heart rate, etc. Therefore, detection of events such as illness, parturition, estrus or stress conditions that affect the physiological status will be possible if these parameters are monitored continuously and interpreted in real time. The basic physiological parameters in cattle are now monitored continuously by a system that was developed by Veterix®, Israel. The system comprises capsules, which are inserted through the mouth to the reticulum of the cows and record at 5-min intervals the following physiological parameters: heart rate (HR), respiratory rate (RR), interval between rumen contractions and rumen temperature (Tr). These data are transmitted by RF communication to a central computer unit that stores and interprets the data to produce a set of alerts for the herd manager. According to this system, Tr was about 0.6°C greater than vaginal temperature. This higher level sharply dropped for a short while after the animal had drunk water. This higher level of Tr, was probably due in part to heat produced by rumen fermentation. The sequence of changes in parameter levels following exposure to a short period of heat load was compared to that during natural estrus: during estrus a simultaneous rise of HR, RR and Tr was evident, but when a cow was exposed to heat load, its first response was to increase its HR considerably; later the HR decreased to a level lower than the initial one, simultaneously with a sharp increase of RR and a moderate increase of Tr, which was interrupted by Tr drops due to more frequent drinking. We suggest that the first response of a cow to heat load is to increase blood flow to the skin in order to increase heat dissipation. When this cooling was not sufficient, HR was decreased as a result of the animals' effort to reduce intrinsic heat production, and RR is increased to enhance evaporative heat dissipation from the lungs.

Key Words: cow, heat load, heart rate

M241 Differential propionate effects on the mRNA expression of a putative beta-hydroxybutyrate sensitive receptor GPR109A in two adipose depots of goats. M. Mielenz* and H. Sauerwein, *University of Bonn, Bonn, Germany*.

The short chain fatty acid (SCFA) propionate is the main energy substrate in ruminants. We have demonstrated that propionate which is a ligand for the fatty acid binding receptors GPR41/43, increases the expression of a putative GPR41 mRNA in subcutaneous (SC) but not in perirenal (PR) adipose tissue (AT) of goats. The concentrations of beta-hydroxybutyrate (BHB) increase during negative energy balance. Stimulation of the BHB sensitive receptor GPR109A with nicotinic acid results in a reduction of lipolysis in monogastrics. We herein tested the effects of a propionate infusion on the mRNA expression of a putative GPR109A in SC and PR AT of goats in short-term. In addition, the mRNAs of PPARγ and PGC-1α were analyzed. Castrated male goats (Deutsche-Edelziege, 10 to 12 months old) were allocated to infusions

through jugular catheters after an over-night fast. They received propionate infusions (96 µmol/kg/min, pH 7.4; n=4) or NaCl-solution of the equivalent Na-concentration (n=5). Infusions were carried out for 260 minutes. The mRNAs were quantified by real-time RT-PCR after euthanasia in PR and SC AT and were evaluated using independent samples t-test. The abundance of putative GPR109A mRNA was decreased by propionate infusion in PR AT (P=0.037), but not in SC AT (P=0.782). In PR AT the mRNA for PPARγ and PGC-1α was numerically increased (P=0.142 and 0.117, respectively) but could only be considered as trend when using a relatively high P-value in defining a trend, e.g. P<0.15. This might be attributable to the limited number of animals. In conclusion, the responsiveness towards BHB which will increase in situations of lipid mobilization seems to be maintained in situations of energy surplus solely in the SC depot but will be decreased in PR AT. PPARγ / PGC-1α seem to be involved in down-regulating the putative GPR109A in short-term; however, it remains to be elucidated what changes might be induced during short and long term energy deficits.

Key Words: GPR109A, beta-hydroxybutyrate, goat

M242 Effect of maternal nutrition and selenium (Se) supply on growth and thyroxine (T4) and triiodothyronine (T3) concentrations in female lambs. L. A. Lekatz*, J. J. Reed, T. L. Neville, D. A. Redmer, L. P. Reynolds, J. S. Caton, and K. A. Vonnahme, *Department of Animal Sciences, North Dakota State University, Fargo*.

To examine the effects of maternal dietary Se and nutrient restriction or excess on postnatal growth and T4 and T3 concentration in female lambs, 82 pregnant ewe lambs (52.2 ± 0.8 kg) were allotted randomly to one of six treatments in a 2 x 3 factorial. Factors were dietary Se from Se enriched yeast [adequate Se (ASe, 9.5 µg/kg BW) vs. high Se (HSe, 81.8 µg/kg BW], initiated at breeding and maternal nutrition [control (CON, 100% of requirements) vs. restricted (RES, 60% of controls) vs. excess (EXC, 140% of controls], initiated at d 50 of gestation. At parturition lambs were removed from ewes and fed artificial colostrum for the first 20 h followed by milk replacer until weaning (d 57). Lambs were maintained on common diets until necropsy (d 180). The RES female lambs had a smaller ($P < 0.01$) girth at birth compared to the CON lambs (38.3 vs. 40.6 ± 0.53 cm) with EXC lambs being intermediate (39.6 cm). The RES female lambs were lighter ($P < 0.01$) at birth and d 7 compared to the CON and EXC lambs (birth: 3.77 vs. 4.46 and 4.35 ± 0.17 kg; d 7: 4.95 vs. 5.70 and 5.71 ± 0.19 kg); however, after this time all female lambs were similar ($P \geq 0.08$) in wt. Female lambs had similar ($P \geq 0.12$) ADG. Diet did not affect ($P \geq 0.08$) T4 or T3 concentration; however, there was a day effect ($P = 0.01$) for both T4 and T3. Concentrations of T4 were similar ($P = 0.54$) at birth and d 7 (106.2 and 109.4 ± 5.23 ng/ml), increasing on d 21 and 35 (126.9 and 122.2 ± 4.17 ng/ml), and falling sharply by weaning (79.5 ± 2.65 ng/ml). Concentration of T4 remained similar ($P = 0.73$) from post weaning (d 78) until d 180 (70.8 and 71.8 ± 2.43 ng/ml). Concentration of T3 was similar ($P = 0.56$) at birth and d 7 (3.38 and 3.49 ± 0.17 ng/ml) and significantly decreased ($P < 0.01$) until d 57 (2.99, 2.19, 1.79, and 1.22 ± 0.09 ng/ml for d 21, 35, 49, and 57, respectively). The T3 concentrations at d 57 and d 78 were similar ($P = 0.52$) and were greater ($P = 0.01$) than the T3 at d 180 (1.22 and 1.18 vs. 1.02 ± 0.06 ng/ml). Postpartum female lamb T3 and T4 concentrations are not affected by gestational maternal diet.

Key Words: thyroxine, triiodothyronine, sheep

M243 Stearoyl-CoA desaturase gene expression and its fatty acid products in bovine tissues. P. Rezamand, J. Watts, D. Pfeifer, K. M. Hunt*, S. Zaman, and M. A. McGuire, *University of Idaho, Moscow*.

Stearoyl-CoA desaturase (SCD) contributes greatly to the fatty acids present in milk and meat of cattle. The SCD enzyme introduces a double bond into some saturated fatty acyl-CoAs producing monounsaturated fatty acids (MUFA) as well as converts 18:1 t11 (vaccenic acid) to c9, t11 conjugated linoleic acid (CLA). The objective of this study was to determine any association between the gene expression of SCD and occurrence of its products (14:1 c9, 16:1 c9, 18:1 c9, and 18:2 c9 t11) in various bovine tissues. Tissue samples were obtained from lactating Holstein cows (n=28) at slaughter, frozen in liquid nitrogen and stored at -80°C. Total RNA was extracted and converted to cDNA for quantitative real time PCR analysis of the *SCD* gene. Extracted lipid was converted to fatty acid methyl esters and analyzed by gas chromatography. Tissues varied in expression of SCD gene with mammary ≈ intestinal adipose ≈ skeletal muscle > liver (384, 328, 284, and 21 copies/ng RNA, respectively). Across tissues, the desaturase indices for 18:1 c9 (r=0.45), all SCD products (r=0.36), and overall index (all products/(all substrates + all products); r=0.43) were positively correlated with SCD gene expression (P<0.001 for all) whereas a negative correlation was detected for the desaturase index of 14:1 c9 (r=- 0.26; P=0.05). Within each tissue, the relationship between *SCD* gene expression and the desaturase indices varied. No correlation was detected between *SCD* expression and desaturase indices in the liver or skeletal muscle. Positive correlations, however, were detected between *SCD* expression and all of the desaturase indices in intestinal adipose tissue (P<0.02 for all) whereas only 18:1 c9, CLA, and all SCD products desaturase indices were positively correlated with SCD expression in mammary tissue ($P \leq 0.03$). Overall, the relationship between *SCD* gene expression and occurrence of its products seems to be tissue specific. A greater understanding of the regulation of tissue fatty acids is necessary because the activity of SCD has clear benefits to human health.

Key Words: bovine tissue, fatty acid, stearoyl-CoA desaturase

M244 Effects of heat stress on glucose homeostasis and metabolic response to an endotoxin challenge in Holstein steers. R. P. Rhoads*[1], S. R. Sanders[1], L. Cole[1], M. V. Skrzypek[1], T. H. Elsasser[2], G. C. Duff[1], R. J. Collier[1], and L. H. Baumgard[1], [1]*University of Arizona, Tucson*, [2]*USDA-ARS, Beltsville, MD*.

Twelve steers (318 ± 49 kg BW) housed in climate chambers were subjected to either a thermoneutral (TN: constant 19°C) environment or heat stress (HS) conditions (cyclical temperatures; 32.2 to 40.0°C) for 9d. On d 4 and 7 steers received an endotoxin challenge (LPS, 0.2 µg/kg BW, i.v.) and blood samples collected at 0, 1, 2, 4, 7 and 24h relative to LPS administration. A 4-h hyperinsulinemic-euglycemic clamp (HEC) was preformed on 3 steers during TN conditions and again during HS. Insulin was infused at 10 µg/kg BW/h and euglycemia maintained by varying intrajugular glucose infusion rates. All body temperature indices were increased in HS steers. Rectal temperatures increased (0.78°C) at 1h post LPS and the maximum difference (1.19°C) occurred at 7h and there were no differences between the 1st and 2nd LPS challenge. During each LPS challenge, steers exhibited hyperglycemia within 1h but the glucose response was larger in HS (53%) compared to TN steers (10%). Both HS and TN steers were hypoglycemic (19%) at 4 and 7h post LPS and had normal glucose values 24h later. Plasma insulin levels increased (>10-fold) 2h but returned to basal levels by 4h post LPS in each challenge and was not affected by environment. NEFA levels decreased (26%) 2h then increased (42%) 7h post LPS and was similar between

challenges and environments. During the HEC, plasma insulin levels increased (>20-fold) and stabilized after 1h. The rate of glucose infusion was similar between TN and HS steers during the first 3 h of the HEC, but increased (152 vs 119 g/h) in HS steers during the 4th h of the HEC. Overall, these data indicate that glucose utilization appears to increase during HS. Moreover, combined environmental stresses (HS and LPS challenge) alter glucose homeostasis to a greater extent than LPS challenge alone. Taken together, this suggests the contribution of glucose in support of whole-body energetics increases when steers experience a thermal load alone or when coupled with an LPS challenge.

Key Words: heat stress, endotoxin, insulin

M245 Impact of unsaturated fatty acid supply on the regulation of CLA-induced milk fat depression in lactating cows. M. J. de Veth[1], J. M. Griinari[2], V. Toivonen[3], and K. J. Shingfield*[3], [1]*BASF-AG, Offenbach/Queich, Germany*, [2]*University of Helsinki*, *Helsinki, Finland*, [3]*MTT Agrifood Research Finland*, *Jokionen, Finland*.

Trans-10, *cis*-12 conjugated linoleic acid (CLA) reduces milk fat synthesis in a predictable and dose dependent manner in the lactating cow. In some situations the decrease in milk fat to CLA supplements is less than predicted, with evidence that the supply of fatty acids to the mammary gland may be an important determinant of the overall response. In this experiment, the impact of unsaturated fatty acid (oleic and linoleic acid) supply on milk fat responses to *trans*-10, *cis*-12 CLA was examined. Four rumen-fistulated cows in mid-lactation were used in a 4 x 4 Latin square design. Treatments were 1) control, 2) 3.65 g/d of *trans*-10, *cis*-12 CLA alone (CA), 3) 3.65 g/d of *trans*-10, *cis*-12 CLA and a mixture of methyl esters supplying 239 g/d of *cis*-9 18:1 (CO), and 4) 3.65 g/d of *trans*-10, *cis*-12 CLA and a mixture of ethyl esters supplying 247 g/d of 18:2n-6 (CL). All treatments were abomasally infused four-times/d over a 7 d period with a 7 d interval between infusions. All CLA treatments reduced ($P < 0.01$) milk fat yield compared to the control, with CA reducing milk fat yield by 26.4%. The decrease in milk fat yield was less with treatments CO and CL (13.5 and 13.3%, respectively). Reductions in the synthesis of fatty acids de novo were comparable across CLA treatments; whilst the incorporation of preformed fatty acids was lower ($P < 0.05$) for CA compared to CO and CL and accounted for the differences in the extent of the milk fat depression. Milk fatty acid content of *trans*-10, *cis*-12 CLA (g/100g fatty acids) increased ($P < 0.01$) from < 0.01 for the control to 0.11, 0.10, and 0.11 for CA, CO, and CL respectively. Results indicate that despite the comparable transfer and incorporation of *trans*-10, *cis*-12 CLA into milk fat, the extent of reductions in milk fat synthesis may, at least in part, be regulated by the availability of unsaturated fatty acids at the mammary gland. In conclusion, altering either oleic acid or linoleic acid supply available for absorption at the small intestine may alter the magnitude of decreases in milk fat synthesis to *trans*-10, *cis*-12 CLA in the lactating cow.

Key Words: conjugated linoleic acid, unsaturated fatty acids, mammary lipogenesis

Production, Management and the Environment: Beef and Dairy

M246 Sexed-biased semen for nulliparous heifers: Effects on reproductive and lactational performances. F. Guagnini[1], J. E. P. Santos[2], J. R. Lima[1], J. Fetrow[3], and R. C. Chebel*[1], [1]*Veterinary Medicine Cooperative Extension, University of California Davis*, *Tulare*, [2]*Department of Animal Science, University of Florida*, *Gainesville*, [3]*Department of Veterinary Population Medicine, University of Minnesota*, *Saint Paul*.

Objectives were to evaluate the effects of using sexed-biased semen for first AI of heifers on reproductive and economic performances during first lactation. Holstein heifers (herd A=227 and herd B=1,144) received first AI with sexed-biased semen (SS, n=343) or conventional semen (CS=1,028). Heifers that displayed estrus following first AI were re-inseminated with conventional semen. In herd AI, age at first AI were SS=13.1±0.1 and CS=13.8±0.1 mo ($P<0.01$), and, in herd B, 12.9±0.1 mo for both groups ($P=0.44$). Pregnancy per AI after first AI was greater for CS heifers (51.8 vs. 40.2%; $P<0.01$), but risk of pregnancy was not different. From heifers initially enrolled, 70.2% calved in herds A (n=188) and B (n=774) and first lactation data were collected. Interval from first AI to calving was not different in herd A (10.1±0.1 mo), but, in herd B, SS heifers had longer ($P < 0.01$) interval than CS heifers (10.3±0.1 vs. 9.8±0.1 mo). In herd A, SS heifers were younger ($P<0.01$) at calving (22.8±0.1 vs. 23.5±0.2 mo), but in herd B there was no difference (22.8±0.1 mo). Among heifers conceiving to first AI, SS heifers were ($P<0.01$) more likely to have a female calf (85.7 vs. 47.7%) and, overall, 64.6% of SS heifers and 51.0% of CS heifers had a female calf ($P<0.01$). More SS heifers conceiving to first AI had stillbirths (8.8 vs. 3.4%; $P<0.01$), but among heifers conceiving to later AI there was no difference. Among heifers conceiving to first AI, gestation length of SS heifers delivering female calves was ($P<0.01$) longer than those delivering males (277.3±0.8 vs. 267.8±1.7 d), but CS heifers delivering females had ($P=0.02$) shorter gestation than those delivering males (275.2±0.6 vs. 276.6±0.6 d). No differences in incidence of disease, risk of pregnancy, and risk of culling were observed. In herd A there was no difference in rearing cost from first AI to calving ($764.9±7.5), but, in herd B, rearing cost of SS heifers was ($P<0.01$) greater ($778.8±8.7 vs. 740.8±4.3). Calf revenue ($288.0±7.5), milk yield (9,245.5±84.7 Kg), income over feed cost ($832.1±7.6), and overall economic return ($78.1±34.1) did not differ between SS and CS heifers.

Key Words: sexed-biased semen, dairy heifer, economics

M247 Use of sex-sorted semen in superovulated Holstein cows and heifers: A case study. S. R. Potter[1], B. J. Paus[1], J. M. DeJarnette[2], and R. L. Nebel*[2], [1]*Spruce Haven Farm, LLC*, *Union Springs, NY*, [2]*Select Sires, Inc.*, *Plain City, OH*.

Data from use of commercially available, flow-cytometrically sex-sorted semen (SS) in superovulated (SO) Holstein cows (n=10) and heifers (n=34) were compared to SO results using conventional semen (CS) in cows (n=255) and heifers (n=104) in the same herd. Procedures for AI were identical for SS and CS with 1 straw administered at 36, 48, and 60 h after SO treatment. Preferential use of SS in females responding to SO resulted in more ($P<0.05$) total embryos/ova recovered per flush than CS (14.2±1.6 vs. 10.4±0.4). Across all ova, the percentage fertilized was lower ($P<0.05$) in cows (73%, n=2963) than in heifers (86%, n=1471) but was not influenced ($P>0.05$) by semen type. Across all flushes, the distribution of embryo quality was influence ($P<0.05$) by semen source in both cows and heifers. The embryo quality distribution of cows for SS (n=148) and CS (n=2815) was: Grade 1, 17 vs. 36%; Grade 2, 17 vs. 16%; Grade 3, 6 vs. 10%; fertile-dead (FD), 27 vs. 15%; and unfertilized ova (UFO), 33 vs. 23%, respectively. The embryo quality distribution within heifers for SS (n=464) and CS (n=1007) was: Grade 1, 33 vs. 42%; Grade 2, 22 vs. 24%; Grade 3, 10 vs. 9%; FD, 21