from 12E to 19E with the lowest level of 60pg/ml at 15E. The molar ratios of insulin to glucagon (I/G) from 14E to 17E ranged from 1.8 to 2.2 which were significantly greater than normal I/G ratio in the post-absorptive state in avian species (1.2-1.7). The results indicate that insulin is an important promoter of chick embryo growth by anabolic drive to promote protein deposition especially during the embryonic rapid growth period. There also was a significant increase in plasma glucose from 13E to 18E suggesting glucose is an important regulator of protein anabolism in the chick embryo via suppression of amino acid oxidation. Plasma IGF-1 and IGF-II levels increased from 10E to 14E and then IGF-1 slowly decreased until hatch, while IGF-II remained constant. IGF-II levels were about 10 fold greater than IGF-1 suggesting IGF-II is an important functionary for chick embryonic development. Plasma T3 and T4 levels showed a significant increase during the third week of incubation and reached a peak at 19-20 E. The findings are consistent with previous research showing a sharp rise in T3 and T4 activities when the embryo switches to lung respiration.

Key Words: Chick Embryo, Hormones, Developmental Change

T120 Developmental changes of hepatic enzyme activities involved in methionine metabolism for chick embryo. J. Lu* and C. N. Coon, *University of Arkansas*.

Developmental changes in hepatic methionine adenosyltransferase (EC 2.5.1.6, MAT), cystathionine β-synthase (EC 4.2.1.22, CBS), cystathionase (EC 4.4.1.1, C-ase) , 5-methyltetrahydrofolate-homocysteine S-methyltransferase (EC.2.1.1.13, MFM) and glycine N-methyltransferase (E.C.2.1.1.20 , GNMT) were determined in 11, 14, 17 and 19 day-old chick embryos and hatched chicks. Enzyme activities were expressed as nmole of product formed /min/mg of protein. The methionine-activating enzyme (MAT) activity was present at low level at day 11 of incubation but increased 8-fold to a maximum at day 19 and remained 6-fold at hatch. The MAT enzyme developmental pattern resembles the pattern observed in the rat fetus suggesting additional SAM (S-adenosyl-Methionine, sole product of MAT enzyme) is needed for rapid growth in the development of the chick embryo. Hepatic CBS activities did not change much during embryogenesis except the activity decreased to a low at day 19. High levels of hepatic C-ase were detected from day 11 through hatch. The developmental pattern of C-ase resembles the pattern observed in the rat fetus, although C-ase activity is absent from human fetal liver. Cystine can not be produced in premature human infants but chick embryos do not have this limitation. Hepatic MFMT activity was higher during embryogenesis than that at hatch suggesting remethylation of homocysteine through MFMT may be a priority for the chick embryo. Previous studies indicate MFMT activity in rat liver decreases with age. MFMT is one of two methionine-conserving enzymes in broilers and layers. Chick embryos have a higher GNMT activity at day 14 than that at day 17, 19 and hatch suggesting the enzyme is more important for regulating the intrahepatic ratio of SAM to SAH (S-adenosyl-homocystine) during the middle of the incubation period. GNMT is considered the main enzyme for maintaining methyl group availability for more than 200 methylation reactions in mammals and birds.

Key Words: Chick Embryo, Enzyme Activities, Methionine Metabolism

Physiology and Endocrinology: Nutrition, Growth and Stress

T121 Effects of injecting transition cows with low doses of bovine somatotropin (bST) on milk yield, IGF-1, glucose and hepatic gene expression of gluconeogenic enzymes. M. Liboni*, M. S. Gulay, L. Badinga, M. J. Hayen, T. I. Belloso, C. J. Wilcox, and H. H. Head, *Department of Animal Sciences, University of Florida, Gainesville*.

Objectives were to evaluate effects of supplemental bST (0.4 mL, 10.2 mg/d, POSILAC®) during the prepartum and/or early postpartum periods on milk yield (MY), plasma concentrations of IGF-1 and glucose, and on steady state mRNA concentrations of hepatic gluconeogenic enzymes pyruvate carboxylase (PC) and phosphoenolpyruvate carboxykinase (PEPCK). Multiparous Holstein cows were assigned randomly to a 2x2 factorial arrangement of treatments (TRT) to give four groups (I=no bST, n=26; II=bST postpartum, n=25; III=bST prepartum, n=27; IV= bST prepartum and postpartum, n=25). Biweekly injections of bST were in left or right ischiorectal fossa beginning -21 d from expected calving through 70 DIM. Blood samples were collected from all cows thrice weekly throughout experiment, and liver biopsies were taken from 9 cows per TRT at -21, +2, +14 and +28 d from calving. Supplemental bST increased daily MY in all bST groups through 28 DIM ($P<0.019$) compared to TRT I; increases were 13.9, 12.7, and 26.6% for TRT II, III and IV, respectively. From 28 through 70 DIM, only TRT IV cows had greater daily milk yield than controls (18.7%, $P<0.019$). For IGF-1, significant increases were detected only during the postpartum period for cows on TRT II and IV (0-70 DIM, $P<0.045$); TRT group means were 107.0, 120.0, 102.8, and 132.6 ng/mL, respectively. No differences were detected in glucose concentrations ($P=0.52$). Hepatic levels of PC mRNA did not differ among TRT ($P=0.47$); PEPCK mRNA differed ($P<0.01$); mean levels were 165.9, 168.2, 162.7 and 161.2 arbitrary units, respectively. Results indicated that supplemental bST caused increased MY and postpartum plasma IGF-1 concentrations, but did not affect plasma glucose, or hepatic PC mRNA. Despite a small, but significant down-regulation of PEPCK mRNA for cows in TRT III and IV, these cows produced more milk than controls, and maintained similar plasma glucose concentrations.

Key Words: bST, Transition Period, Liver Gluconeogenesis

T122 Effect of insulin and growth hormone administration to mature miniature Brahman cattle on circulating concentrations of metabolic hormones and metabolites. C. C. Chase, Jr.*[1], D. G. Riley[1], T. H. Elsasser[2], L. J. Spicer[3], M. C. Lucy[4], S. W. Coleman[1], and T. A. Olson[5], [1]*USDA, ARS, Brooksville, FL,* [2]*USDA, ARS, Beltsville, MD,* [3]*Oklahoma State University, Stillwater,* [4]*University of Missouri, Columbia,* [5]*University of Florida, Gainesville*.

The objective of this study was to determine the effect of administration of GH, insulin (INS), and GH plus INS to mature miniature Brahman cows (n = 6; 9.7 ± 2.06 yr; 391 ± 48.6 kg) and bulls (n = 8; 9.4 ± 2.00 yr; 441 ± 54.0 kg) on plasma concentrations of metabolic hormones (GH, INS, IGF-I) and metabolites (glucose, urea nitrogen [PUN]). We hypothesized that IGF-I secretion could be enhanced by concomitant administration of exogenous GH and INS, but not by either hormone alone. Animals were allotted to a modified crossover design that included four treatments: control (CON), GH, insulin (INS), and GH+INS. At the start of the study, one-half of the animals were administered GH (POSILAC; 14-d slow release) and the other one-half served as controls (CON) for 7 d. Beginning on day 8 and for 7 d, insulin (Novolin L) was administered (0.125 IU/kg BW) twice daily (0700 and 1900) to all animals; hence the INS and GH+INS treatments. Animals were rested for 14 d and then were switched to the other treatment combination. Blood samples were collected at 12-h intervals during the study. Sex affected ($P < 0.05$) plasma concentrations of metabolic hormones but not ($P > 0.15$) blood metabolites. Compared to CON, GH treatment increased ($P < 0.01$) mean plasma concentrations of GH (11.1 vs 15.7 ± 0.94 ng/mL), INS (0.48 vs 1.00 ± 0.081 ng/mL), IGF-I (191.3 vs 319.3 ± 29.59 ng/mL), and glucose (73.9 vs 83.4 ± 2.12 mg/dL), but decreased ($P < 0.05$) PUN (14.2 vs 11.5 ± 0.75 mg/dL). Compared to INS, GH+INS treatment increased ($P < 0.05$) mean plasma concentrations of INS (0.71 vs 0.96 ± 0.081 ng/mL), IGF-I (228.7 vs 392.3 ± 29.74 ng/mL) and glucose (48.1 vs 66.70 ± 2.12 mg/dL), decreased ($P < 0.01$) PUN (13.6 vs 10.4 ± 0.76 mg/dL), and did not affect GH (13.5 vs 12.7 ± 0.95 ng/mL). In the miniature Brahman model, using mature animals, both GH and GH+INS treatments dramatically increased circulating concentrations of IGF-I.

Key Words: Miniature Cattle, GH, IGF-I

T123 Influence of low doses of bovine somatotropin (bST) on plasma NEFA, and β-Hydroxybutyrate, hepatic lipid metabolism and gene expression of Holstein transition cows. M. Liboni*, M. J. Hayen, M. S. Gulay, L. Badinga, T. I. Belloso, and H. H. Head, *Department of Animal Sciences, University of Florida, Gainesville*.

Multiparous Holstein transition cows (n=103) were assigned randomly to a 2x2 arrangement of treatments (TRT) based upon biweekly injections of bST (0.4 mL, 10.2 mg/d, POSILAC®), which began 21 d before expected calving and continued through 70 DIM. The TRT were I=no bST, n=26; II=bST postpartum, n=25; III=bST prepartum, n=27; IV= bST prepartum and postpartum, n=25. During the transition period (-21 d through 28 DIM), blood samples were collected thrice weekly from all cows for quantification of non-esterified fatty acids (NEFA) and β-hydroxybutyrate (β-HBA) concentrations in plasma. Liver biopsies (9 cows per TRT) were conducted on d -21, +2, +14 and +28 from calving for the determination of total fat (FAT) and triglyceride (TG) accumulation, and the steady state expression of microsomal triglyceride transfer protein I (MTP-I) mRNA. No TRT effects were detected on NEFA (p=0.91); means ranged from 794.3 to 840.1 μeq/L. For β-HBA, a trend for TRT effect was detected, but only during the postpartum period (P<0.07); means were 8.3, 12.6, 10.7 and 8.3 mg/dL, respectively. No TRT effects were detected on liver FAT (p=0.45) or TG (p=0.39). However, liver fat content of TRT II cows was greater than for cows on TRT II and IV (P<0.042), and also, TRT II cows had greater TG concentrations (P<0.038) than TRT I, III and IV cows on d 28; FAT and TG means were 8.45, 13.04, 8.04 and 8.31%; 1.89, 4.49, 2.32 and 1.90%, respectively. For MTP-I, significant TRT effects were detected (P<0.045); mean values were 178.6, 179.1, 174.2, 171.4 arbitrary units. As for FAT and TG, on d 28, TRT II cows had greater expression of MTP-I than TRT III (P<0.089) and IV (P<0.01) cows. In conclusion, when bST was injected only during the postpartum period (TRT II), β-HBA was increased. Despite the small but significant up-regulation of MTP-I of TRT II cows, FAT clearance from the liver was not greater than for cows on TRT I, III and IV after calving.

Key Words: bST, Transition Period, Liver Lipids

T124 Muscle and liver IGF-I mRNA expression and plasma IGF-I levels in channel catfish administered rbGH over time. B. Peterson*, G. Waldbieser, and L. Bilodeau, *USDA/ARS Catfish Genetics Research Unit Thad Cochran National Warmwater Aquaculture Center, Stoneville, MS*.

We have reported previously increased growth rates of 48% in as little as 6 wk in channel catfish administered recombinant bovine growth hormone (rbGH). Identifying genes involved in regulating growth may prove important to selecting fish for efficient lean growth. Research was conducted to examine plasma IGF-I and IGF-I mRNA expression in the muscle and liver of catfish administered rbGH. Ninety-six fish (41.1 ± 1.5 g) were assigned randomly to one of two treatments with four replicates each. The treatments were: 1) Sham-injected control (needle puncture/week) and 2) rbGH (30 μg/g BW/week, Posilac). Eight fish per treatment (2 fish/tank) were sampled on d 0, 1, 2, 7, 14, and 21. The fish were bled and muscle and liver samples were excised on each of the 6 sampling d. Relative expression of IGF-I mRNA was determined by real time RT-PCR. Circulating levels of IGF-I increased (55.5 ± 2.5 ng/ml vs 22.2 ± 1.7 ng/ml; P = 0.03) in rbGH-injected fish compared to sham-injected controls only at d 14. Expression of muscle IGF-I mRNA was not different in rbGH-injected fish compared to controls throughout the 21-d study. Liver IGF-I mRNA was increased 6-fold by d 1 in rbGH-injected fish compared to controls (P = 0.05). However, expression of liver IGF-I mRNA was not different from controls on d 2, 7, 14, and 21. Results of this study show that the growth promoting effects of rbGH were not mediated by the expression of IGF-I in the muscle. Instead, the results suggest that rbGH promotes growth by stimulating plasma IGF-I release, probably through its direct effect on the liver to synthesize IGF-I. The changes in expression and protein levels of IGF-I support IGF-Is role in growth regulation of channel catfish.

Key Words: IGF-I, Real Time PCR, Channel Catfish

T125 Cloning, expression and functional analysis of the porcine prolactin receptor. J. F. Trott, N. R. Farley, and R. C. Hovey*, *University of Vermont, Burlington*.

Prolactin (PRL) is an important reproductive hormone in pigs that functions through the prolactin receptor (PRLR) protein that is present in tissues such as the mammary gland, ovary and uterus. PRL may be of particular significance for reproduction in pigs due to their lack of placental lactogens that can bind the PRLR. Our objective was to clone the full length pPRLR cDNA and study its function. Using 5′ RACE we have cloned the full-length pPRLR that encodes a mature protein of 601 amino acids. As anticipated, the pPRLR transduced a differentiation signal to the β-casein milk protein gene promoter *in vitro* following PRL treatment. Analysis of different ligands in this assay revealed that human growth hormone (hGH) and pPRL effected a greater transcriptional response (P#8804.0005) compared to oPRL. Transfection of CHO-K1 cells with the pPRLR revealed binding of hGH at high affinity (Kd=1.75 nM), similar to characteristics for the hPRLR (Kd=3.6 nM). The pPRLR also displayed higher affinity (P#8804.01) for pPRL compared to oPRL. Under normalized transfection conditions, the number of active receptor sites per cell was higher for the pPRLR than the hPRLR (P#8804.001), consistent with results from western blotting experiments. While both the pPRLR and hPRLR showed perinuclear intracellular distribution in transfected CHO cells as determined by immunocytochemistry, the pPRLR primarily localized to the cytoplasm whereas the hPRLR was more concentrated in vesicles (P#8804.05). Expression of pPRLR mRNA in miniature pig tissues as determined by quantitative RT-PCR was lowest in the ovary and highest in the mammary gland (P#8804.05). Our data indicate that the pPRLR demonstrates several unique characteristics at the post-transcriptional, post-translational and functional level.

Key Words: Prolactin, Pig, Prolactin Receptor

T126 Fluctuation of plasma ghrelin and growth hormone in fed and fasted cattle. A. E. Wertz*[1], T. J. Knight[2], A. Kreuder[2], M. Bohan[2], D.C. Beitz[2], and A. Trenkle[2], [1]*South Dakota State University, Brookings*, [2]*Iowa State University, Ames*.

Four steers (450±28.5 kg) were used in a crossover design to determine fluctuation of plasma ghrelin and growth hormone (GH) concentrations in fed and fasted beef cattle. Cattle were adapted to a once daily feeding schedule over an 11-d period. Feed, sufficient to result in 10% weigh-back, was offered at 0800 h and removed at 2000 h. After adaptation, two steers continued the once daily feeding schedule (FED) whereas; feed was withheld from the other two steers (FAST). Steers were fitted with indwelling jugular catheters 24 h before sampling. Serial blood samples were collected at 10-min intervals from 1800 to 2000 h (22 to 24 h fasting) and from 0600 to 0800 h (34 to 36 h fasting). From 0815 to 2000 h (36 to 48 h fasting), steers were sampled at 15-min intervals. A 5-d crossover period was used between sampling periods to re-establish the once daily feeding schedule. Treatment groups then were switched, and the sampling period was repeated. Plasma ghrelin and growth hormone concentrations were quantified using radioimmunoassays. Data were analyzed statistically as repeated measures using the mixed procedure of SAS. Peak concentrations were defined as concentrations that were two standard deviations greater than the baseline using PEAK software. Average plasma ghrelin concentrations were elevated (P<0.001) in FAST (648±10.4 pg/mL) compared with FED (115±3.5 pg/mL) steers. Plasma ghrelin concentration for FED steers reached a maximum just prior to feeding and then returned to baseline post-feeding, whereas ghrelin concentrations for FAST steers did not exhibit this pattern during the time period. Episodic ghrelin peaks, however, were detected for FAST steers beyond 40 h fasting. Plasma GH peaks tended to be more frequent (P=0.06) just prior to feeding, from 0600 to 0800, for FED compared with FAST steers. In contrast, FAST steers had more frequent (P#88040.02) GH peaks beyond 40 h of fasting. Plasma ghrelin concentrations fluctuated when feed intake was restricted, and differences in ghrelin concentrations correspond to difference in GH peak frequency.

Key Words: Ghrelin, Growth Hormone, Beef Cattle

T127 Plasma hormones and expression of growth hormone receptor (GHR) 1A and IGF-I mRNA in hepatic tissue of feed-restricted peri-parturient dairy cows. R. P. Radcliff*[1], B. L. McCormack[1], B. A. Crooker[2], and M. C. Lucy[1], [1]*University of Missouri, Columbia,* [2]*University of Minnesota, St. Paul.*

The primary GHR mRNA transcript in liver (GHR 1A) is decreased at parturition and then gradually increases. We hypothesized that decreased food intake after parturition inhibits normal postpartum upregulation of GHR 1A mRNA expression. Liver was biopsied from Holstein cows (n = 11) on d 10 ± 1, 1, 7, 14 and 21 postpartum. Blood samples were collected during the biopsy period. Cows were offered feed ad libitum prepartum. After parturition, six cows were fed 70% of their expected feed intake (feed-restricted; FR) for 14 d and five cows were fed ad libitum (Control). Both groups had ad libitum feed after d 14. Total cellular RNA was isolated from liver samples and GHR 1A and IGF-I mRNA were measured using quantitative real-time polymerase chain reaction. Dry matter intake (7 vs. 11 ± 1 kg/d; $P < 0.03$), milk yield (29 vs. 34 ± 2 kg/d; $P = 0.1$), and energy balance (-18.5 ± 0.7 vs. -15.4 ± 0.8 Mcal/d; $P < 0.02$) were less for FR compared to control cows (d 1 to 14). Plasma NEFA concentrations were greater (1190 ± 105 vs. 715 ± 115 μEq/L; $P < 0.02$) and plasma glucose concentrations tended to be less (50.2 ± 3.4 vs. 59.1 ± 3.7 mg/dL; $P = 0.1$) for FR vs. control cows (d 1 to 14). Amounts of GHR 1A mRNA decreased after parturition ($P < 0.001$). A treatment by day interaction for GHR 1A was detected because GHR 1A mRNA was less for FR cows on d 21 (7 days after FR ended; 986 ± 107 vs. 421 ± 97 fg/25 ng RT; $P < 0.001$). Amounts of IGF-I mRNA and plasma IGF-I concentrations decreased after parturition. Postpartum plasma IGF-I concentrations tended to be lower (51 vs. 65 ± 5 ng/ml; $P = 0.09$) but postpartum liver IGF-I mRNA concentrations were similar for FR vs. control. Feed-restriction decreased GHR 1A mRNA. The decrease in GHR 1A mRNA was present 7 days after the end of FR. We conclude that feed intake partially controls GHR 1A mRNA expression in early postpartum dairy cows and that the effect of FR may persist for at least one week.

Key Words: Growth Hormone Receptor, Feed Intake, Parturition

T128 Effect of naloxone, an opioid antagonist, on serum calcium concentrations immediately after parturition in multiparous Holstein cows. F. Frago[1], A. Ahmadzadeh*[1], R. Manzo[1], M. A. McGurie[1], and J. C. Dalton[2], [1]*University of Idaho, Moscow,* [2]*Research and Extension Center, University of Idaho, Caldwell.*

This experiment was conducted to investigate the effect of naloxone, an opioid receptor antagonist, on serum calcium (Ca) homeostasis and pH, within the first 24 hours post-partum, in Holstein cows. Prior to parturition cows received a close up ration that met the NRC requirements for dry cows. Shortly after parturition and the first milking, cows were weighed and assigned randomly to receive either saline (n = 6), or 0.01 mg/kg of BW of naloxone (n = 6). Blood samples were collected at 10-minute intervals for 20 min before and 50 min after treatments. Mean serum Ca was not different between groups before treatments (8.6 vs. 10.4 mg/dL; SEM = 1.0). Naloxone caused a transient increase ($P < 0.05$) in serum Ca concentrations within 20 min after injection (from 10.4 to 14.8 mg/dL; SEM = 1.0). Mean serum Ca was not altered in saline-treated cows. There was no change in the mean serum pH in naloxone- or saline-treated groups. These results suggest that endogenous opioid peptides (EOP) play a role in Ca homesostasis in lactating Holstein cows and its inhibitory action is immediated through opioid receptors. Therefore, EOP may play a part in milk fever.

Key Words: Opioid Antagonist, Early Postpartum, Calcium

T129 Effects of short-term fasting on channel catfish growth and nychthemeral concentrations of plasma GH, IGF-I, and cortisol. B. C. Small*, *USDA/ARS Catfish Genetics Research Unit, Thad Cochran National Warmwater Aquaculture Center, Stoneville, MS.*

Short-term fasting is a common management tool for controlling enteric septicemia of catfish; however, little is known concerning the physiological ramifications of short-term fasting. In many animals, long-term starvation affects the somatotropic and the corticotropic axes, often resulting in increased plasma concentrations of growth hormone (GH) and cortisol, and decreased concentrations of circulating IGF-I. This study was conducted in order to characterize the effect of short-term fasting on plasma concentrations of GH, IGF-I, and cortisol over a 24-h period. Channel catfish fingerlings (mean=14.8 g) were stocked into forty-eight 76-L aquaria and acclimated for two wk. A photoperiod of 12L:12D was maintained throughout the study, with lights coming on at 0600 h daily. Treatments were assigned randomly such that fish in 24 aquaria were fed twice daily to satiety and fish in the remaining aquaria were fasted. The study was conducted for 21 d. On d 21, fish in the fed treatment were fed at 0650 h. Beginning at 0700 h and continuing every 2 h for 24 h, fish from two tanks per treatment were bled and plasma collected. After 3 wk, weight of fed fish increased an average of 65.7%, while fasted fish lost 21.3% on average. Nychthemeral concentrations of plasma GH were not significantly ($P>0.05$) different between fed (24.7 ng/mL) and fasted (26.8 ng/mL) fish. Paradoxically, nychthermeral IGF-I concentrations were different ($P<0.05$) between fed (23.4 ng/mL) and fasted (17.8 ng/mL) fish, and not different for times within treatments. Nychthemeral plasma cortisol concentrations were also different ($P<0.05$) between fed (14.5 ng/mL) and fasted fish (11.0 ng/mL), and different ($P<0.05$) for times within treatments. The present study indicates little or no effect of short-term fasting on plasma GH levels, but does demonstrate fasting-induced suppression of plasma IGF-I levels, and a correlation between feeding and cortisol secretion in channel catfish.

Key Words: Channel Catfish, Fasting, Hormone Profiles

T130 Microarray analysis of gene expression in ovarian dominant follicles (DF) following heat stress (HS). S. J. Kolath*[1], P. M. Coussens[2], S. S. Sipkovsky[2], S. J. Wilson[1], D. E. Spiers[1], J. N. Spain[1], and M. C. Lucy[1], [1]*University of Missouri, Columbia,* [2]*Michigan State University, East Lansing.*

Heat stress decreases follicular growth and causes infertility in cattle. Our objective was to compare gene expression in DF from heifers exposed to HS or thermoneutral (TN) environments. Estrous cycles were synchronized (estrus = d 0) in Holstein heifers assigned randomly to HS (n=3) or TN (n=3) treatment. On d 5, heifers were moved into the Brody Environmental Chambers (19°C). Ambient temperature for HS heifers was increased on d 10, 3°C per day to 33°C on d 14. Ambient temperature for TN heifers remained at 19°C. The second wave DF was collected after ovariectomy on d 15. Total RNA was isolated, amplified using MessageAmp aRNA Kit (Ambion Inc., Austin, TX), reverse transcribed, labeled, and hybridized to the NBFGC microarray (18,263 unique ESTs) from the Center for Animal Functional Genomics (http://gowhite.ans.msu.edu). Follicular cDNA was labeled with Cy5 and a reference sample cDNA (comprised of mRNA from 29 bovine tissues) was labeled with Cy3 (n=10 microarrays). Fluorescence was measured using the GenePix 4000B scanner (Axon Instruments Inc., Union City, CA) and data were analyzed using GeneSpring™ software (Silicon Genetics, Redwood City, CA). A Students t-test was performed using a Benjamini and Hochberg False Discovery Rate. Genes whose mRNA was enriched in DF had a florescent signal greater ($P<.05$) than the reference sample. There were 1,354 candidate genes whose mRNA was enriched in DF; 179 of which were increased greater than two-fold above the reference. Genes with greater than two-fold up-regulation encoded cell structural components (FMOD, ACTA2, GNB2L1), were involved in cell growth (VSGP/F-spondin, SPARC) and hormone transport (SHBG), and were transcription factors (ATF1, HIF-1, TFIID). Some of the discovered genes had not been reported previously in ovary. Heat stress increased body temperature ($P<.01$) but had no effect on follicle-specific mRNA. We conclude that microarray analysis with a reference design can be used to identify novel mRNA in ovary.

Key Words: Microarray, Ovary, Heat Stress

T131 Effects of conjugated linoleic acid on culture of adipose tissue explants of growing pigs. A. A. F. B. V. José, M. A. S. Gama, and D. P. D. Lanna*, *LNCA-ESALQ-USP, Brazil.*

The objective of this study was to evaluate the effects of conjugated linoleic acid (CLA; 94.5% of t10,c12 CLA) on lipogenesis (measured as rates of 14C labeled glucose incorporation over a subsequent 2 h incubation), lipolysis (release over a subsequent 2 h incubation of non-esterified fatty acid - NEFA), and activities of lipogenic enzymes in explants of adipose tissue collected from growing pigs. Adipose tissue explants from nine pigs (78±3 kg) were cultured in medium 199 with insulin, dexamethasone and antibiotics for 4, 12, 24 and 48 hours. Treatments were: Control: 100 μM of PVA (polyvinyl alcohol); CLA

200: 200 μM of CLA; CLA50: 50 μM of CLA; LA: 200 μM of linoleic acid and pGH: 100 ng/mL (porcine growth hormone - Reporcin, Southern Cross Biotech). Free fatty acids were complexed to PVA (2:1) as a carrier. After each culture period explants were collected and assayed for lipogenesis. After 48 h in medium 199 samples were analyzed for NEFA release (Krebs-ringer buffer, for 2 h) and explants taken for measurement of fatty acid synthase (FAS), glucose 6-phosphate dehydrogenase (G6PDH), 6-phosphogluconate dehydrogenase (6PGDH) and NADP-malate dehydrogenase activities. Glucose incorporation was significantly decreased (P<0.05) in response to pGH treatment. The activity of FAS was consistently decreased by pGH (P=0.07). Linoleic acid had no effect on any parameter evaluated. Lipid synthesis was decreased after culture; Control = 5390 and 2333 nmoles/2h.g; and CLA200 = 4296 and 1900 nmoles/2h.g, respectively. However, the effect of CLA was not statistically significant. Despite the lack of a significant effect of CLA on lipogenesis, FAS activity was decreased in response to CLA at 200 μM (P<0.05). The NADPH generating enzymes were not affected by any of the treatments. The pGH treatment increased basal lipolysis (P<0.05), but CLA treatment had no effect (P>0.05) on NEFA release after 48 h of culture. These data suggest CLA decreases FAS activity in cultures of pig adipose tissue explants.

Key Words: Adipose Tissue Explants, Lipid Metabolism, Swine

T132 Somatotropic axis components following administration of exogenous bovine somatotropin to neonatal beef calves having an IGF-I promoter polymorphism. E. F. Jones*, K. E. Govoni, T. A. Hoagland, G. W. Kazmer, and S. A. Zinn, *University of Connecticut, Storrs*.

In cattle, serum concentrations of components of the somatotropic axis and its response to bovine somatotropin (bST) are age dependent. In addition, changes in serum concentrations of insulin-like growth factor (IGF)-I are associated with a polymorphism in the promoter region of IGF-I. To determine the response of components of the somatotropic axis and the association of the polymorphism with concentrations of IGF-I in neonatal calves, 44 newborn beef calves (22 males, 22 females) were utilized. Within 24 hr of birth, blood samples (n=3, 10mL, 30 min apart) were collected via venipuncture of a jugular vein. Following collection of the third blood sample, half of the males and half of the females were administered bST (500 mg; d 0). Blood samples (n=3, 10 mL, 30 min apart) were collected from each animal on d 1, 3, 5 and 7. Concentrations of ST and IGF-1, and IGF binding protein (BP) -2 and -3 were determined by RIA and ligand blot, respectively. Calves were genotyped using single stranded conformational polymorphism techniques. Concentrations of ST, IGF-I, IGFBP-2 and IGFBP-3 averaged 14 $\pm$ 4 ng/mL, 104 $\pm$ 16 ng/mL, 20 $\pm$ 1 AU (arbitrary units) and 25 $\pm$ 2 AU, respectively. Concentrations of ST (18 $\pm$ 6 vs 94 $\pm$ 6 ng/mL) and IGF-I (114 $\pm$ 24 vs 142 $\pm$ 22) were increased (P< 0.01) on d 1 and 3 by bST treatment, after which increased concentrations of ST and IGF-I were maintained. Neither serum IGFBP-2 (17 $\pm$ 1 vs 17 $\pm$ 1 AU) nor IGFBP-3 (23 $\pm$ 1 vs 23$\pm$ 1) were altered (P>0.10) by bST treatment. Response to bST was greater in males than females (91 $\pm$ 7 vs 53 $\pm$ 7 ng/mL), but no gender differences (P> 0.10) in IGF-1 or IGFBP-2 and -3 were found. Frequencies were 24%, 52% and 24% for AA, AB and BB genotypes, respectively. Concentrations of IGF-1 in AA (179 $\pm$ 17 ng/mL), AB (201$\pm$ 12 ng/mL) and BB (211$\pm$ 17 ng/mL) calves were not different (P > 0.37). As early as 1 d of age IGF-I concentrations in calves increased in response to bST, but no association between IGF-I concentrations at this age and IGF-I promoter polymorphism was found.

Key Words: Somatotropic Axis, Beef Cattle, IGF-I Polymorphism

T133 Microarray analysis of hepatic gene expression from dry-off through early lactation in dairy cows fed at two intakes during the dry period. J. J. Loor*, N. A. Janovick, H. M. Dann, R. E. Everts, S. L. Rodriguez-Zas, H. A. Lewin, and J. K. Drackley, *University of Illinois, Urbana*.

A bovine cDNA microarray was used to study gene expression during the periparturient period in response to restricted or ad libitum DMI during the dry period. Liver from four Holstein cows with ad libitum (ca. 150% of NRC requirements; AA) or restricted (80% of requirements; RR) DMI of far-off and close-up diets was biopsied at -65, -30, -14, 1, 14, 28, and 49 d relative to parturition. All cows had ad libitum access to the same lactation diet. A microarray consisting of 7,872 cDNA inserts was used for transcript profiling. Annotation was based on similarity searches using BLASTN and TBLASTX against human and mouse UniGene databases and the human genome. Cy3- and Cy5-labelled cDNA from liver and a reference standard (derived from a mixture of cattle tissues) were used for hybridizations (106 microarrays). Loess-normalized log-transformed ratios (liver/standard) were used to detect differential gene expression. Using Benjamini and Hochberg's False Discovery Rate ($P = 0.10$) to determine effects of prepartum DMI, day, or their interaction on differential gene expression resulted in 2,537, or 29 significant genes, respectively. Among those with significant interactions were genes associated with lipid metabolism, signal transduction, and insulin action. Genes differentially expressed by day relative to parturition included some involved in cell proliferation, carbohydrate metabolism, and protein catabolism. Hierarchical clustering showed that expression patterns on d -14, 1, and 14 were grouped in two clusters according to prepartum DMI. RR resulted in greater number of genes being upregulated 1.5 fold or greater ($P = 0.05$) on d 1 vs. d -14 (AA, 21; RR, 286). A similar trend was observed when comparing d 14 (AA, 31; RR, 139), d 28 (AA, 334; RR, 910), and d 49 (AA, 398; RR, 1,036) vs. d 1. Our data indicate that prepartum plane of nutrition alters hepatic gene expression during the peripartum period. (Supported by award 2001-35206-10946 from NRI Competitive Grants Program/CSREES/USDA).

Key Words: Liver, Microarray, Gene Expression

T134 Mammary and hepatic gene expression analysis in peripartal dairy cows using a bovine cDNA microarray. J. J. Loor*, H. M. Dann, R. E. Everts, S. L. Rodriguez-Zas, H. A. Lewin, and J. K. Drackley, *University of Illinois, Urbana*.

Simultaneous analysis of mammary and hepatic gene expression in peripartal dairy cows was studied using cDNA microarray technology. Mammary and liver tissue were collected at -14, 1, and 14 d relative to parturition from two multiparous Holstein cows fed according to current NRC recommendations. A microarray consisting of 7,872 cDNA inserts was used for transcript profiling. Annotation was based on similarity searches using BLASTN and TBLASTX against human and mouse UniGene databases and the human genome. Cy3- and Cy5-labelled cDNA from liver and a reference standard (derived from a mixture of cattle tissues) were used for hybridization (24 microarrays). Loess-normalized log-transformed ratios (tissue/standard) were used to detect differential gene expression. Benjamini and Hochberg's False Discovery Rate ($P = 0.05$) and a global gene error model, to account for the dependence of variation on signal intensities, were used to determine differential gene expression for the effect of tissue (1,040), day (20), and tissue by day (392) interactions. Among genes with a significant tissue by day interaction, expression ratios greater than 5-fold in liver compared with mammary were found for 15, 12, and 13 genes on d -14, 1, and 14, respectively. Among those showing tissue-specific expression, there were 26 genes with >5-fold expression in mammary compared with liver, and 44 genes with >5-fold expression in liver compared with mammary. Expression patterns in liver clustered together on d -14 and 14, and in mammary on d 1 and 14. Differences in expression patterns within these clusters ranged from 11% (liver) to 30% (mammary). Results show the power of microarrays to dissect gene expression patterns in tissues during the peripartum period. (Supported by award 2001-35206-10946 from NRI Competitive Grants Program/CSREES/USDA).

Key Words: Liver, Mammary, Microarray

T135 Adipose, mammary, and hepatic gene expression profiling in lactating dairy cows using a bovine cDNA microarray. J. J. Loor*, N. A. Janovick, R. E. Everts, S. L. Rodriguez-Zas, H. A. Lewin, and J. K. Drackley, *University of Illinois, Urbana*.

Simultaneous analysis of gene expression in four adipose depots [mesenteric (MS), omental (OM), subcutaneous (SQ), perirenal (PR)], mammary (MG), and liver (LV) of lactating cows was performed using cDNA microarray technology. Tissues were collected at slaughter from multiparous cows around peak (50 DIM), mid (95 DIM), and late (245 DIM) lactation. A microarray consisting of 7,872 cDNA inserts was used for transcript profiling. Annotation was based on similarity searches using BLASTN and TBLASTX against human and mouse UniGene databases and the human genome. Cy3- and Cy5-labelled cDNA from liver and a standard reference (derived from a mixture of cattle tissues) were

used for hybridizations. Loess-normalized log-transformed ratios (tissue/standard) were used to detect differential gene expression. Clustering analysis of gene expression around peak lactation (12 microarrays) showed that SQ had expression patterns that differed by 57% from other tissues. LV gene expression differed from MG and adipose by 50%; whereas expression in MG differed from adipose by 44%. Among adipose depots, gene expression in PR differed from MS and OM by 17%. Using Benjamini and Hochberg's False Discovery Rate ($P = 0.05$) and a global gene error model, to account for the dependence of variation on signal intensities, we detected differential expression of 355 genes across tissues. The same 24 genes were >5-fold ($P = 0.05$) in SQ than LV or MG. Some of these genes were associated with intracellular signaling, inflammatory responses, and apoptosis. One gene involved in the regulation of glucose oxidation was 3-, 5-, and 20-fold greater ($P = 0.05$) in MS, OM, and PR, respectively, than SQ. Thirteen genes were >5-fold in LV than MG, and 10 were >5-fold ($P = 0.05$) in MG than LV. Genes with >5-fold ($P = 0.05$) expression in LV than other tissues included one of the mitochondrial lipid oxidation pathway and one of unknown function. Our results reveal previously unknown tissue-specific gene expression patterns during established lactation.

Key Words: Tissue, Gene Expression, Lactation

T136 Gene expression profiles in liver of dairy cows in response to feed restriction using a bovine cDNA microarray. J. J. Loor*, D. B. Carlson, R. E. Everts, S. L. Rodriguez-Zas, H. A. Lewin, and J. K. Drackley, *University of Illinois, Urbana*.

Dairy cows decrease DMI around parturition but little is known about associated changes in tissue gene expression. We studied the effects of acute feed restriction on hepatic gene expression using cDNA microarray technology. During a 14-d period, six Holstein cows in mid-lactation (132 ± 38 DIM) had ad libitum access to a TMR (NR) or were restricted to 50% of previous 5-d DMI (FR) from d 10 through 14. Liver was biopsied on d 14. A microarray consisting of 7,872 cDNA inserts was used for transcript profiling. Annotation was based on similarity searches using BLASTN and TBLASTX against human and mouse UniGene databases and the human genome. Cy3- and Cy5-labelled cDNA from liver and a reference standard (derived from a mixture of cattle tissues) were used for hybridizations (24 microarrays). Loess-normalized log-transformed ratios (liver/standard) were used to detect differential gene expression. Ninety-nine differentially expressed genes were found using Benjamini and Hochberg's False Discovery Rate ($P = 0.10$) and a global gene error model (to account for the dependence of variation on signal intensities). Forty-six were 0.9- to 0.5-fold lower and 53 were 1- to 5-fold greater with FR. Genes associated with intracellular acyl-CoA ester transport, stress responses, and the tricarboxylic acid cycle were among those downregulated by FR. In contrast, FR increased hepatic expression of genes with links to immune responses, antioxidant activities, signal transduction, and apoptosis. Our results demonstrate that hepatic gene expression is altered in response to plane of nutrition. (Supported by award 2001-35206-10946 from NRI Competitive Grants Program/CSREES/USDA).

Key Words: Feed Restriction, Liver, Microarray

T137 Accuracy and precision of commercially available glucometers for use in dairy cattle. C. C. Williams*, A. M. Ponson, C. C. Stanley, H. G. Bateman, II, P. T. Richardel, and D. T. Gantt, *LSU AgCenter, Baton Rouge, LA*.

An experiment was conducted to validate two commercially available glucometers for use in dairy cattle. Six female Holstein calves approximately one mo of age, six Holstein steers approximately 4 mo of age, and six lactating Holstein cows were subjected to intravenous glucose tolerance tests (IVGTT) and insulin tolerance tests (ITT). These tests induced glucose concentrations ranging from very high (IVGTT) to very low (ITT) to test the sensitivity of the glucometers. In both tests, conducted on consecutive d, animals were fitted with indwelling jugular catheters 1 h prior to testing. In the IVGTT, glucose (0.5 g/kg BW) was infused at once, while in the ITT bovine insulin (0.03 units/kg BW) was infused at once. Relative to the glucose or insulin bolus, blood samples were collected at -10, 0, 5, 15, 25, 35, 45, and 60 min. Blood glucose concentrations were immediately measured in duplicate using the Accu-Chek® Glucometer (Roche, Inc.) and the Glucometer Elite® (Bayer Corp.). At each time point a blood sample was collected and plasma was frozen for glucose analysis using commercial spectrophotometric kits. Correlation coefficients were calculated to determine the degree of linear association between glucometer readings and plasma glucose concentrations. Both glucometers were strongly correlated with plasma glucose concentrations in calves (r = 0.975 and 0.979), steers (r = 0.992 and 0.989), and cows (r = 0.993 and 0.996) for Accu-Chek® and Elite®, respectively. Glucometers were strongly correlated with plasma glucose in the IVGTT (r = 0.980 and 0.985 for Accu-Chek® and Elite®, respectively). However, in the ITT the correlations decreased (r = 0.873 and 0.754 for Accu-Chek® and Elite®, respectively) as plasma glucose concentrations were reduced. Coefficients of variation were 3.60% and 3.51% for the Accu-Chek® and Elite®, respectively, in the IVGTT, and 1.85% and 1.79% for the Accu-Chek® and Elite®, respectively, in the ITT. These data indicate that commercially available glucometers are valid for measuring blood glucose concentrations in dairy cattle.

Key Words: Glucometers, Blood Glucose, Dairy Cattle

T138 Effects of bovine somatotropin (bST), pregnancy and a diet enriched in omega-3 fatty acids on the uterine GH/IGF system in lactating dairy cows. T. R. Bilby*[1], F. Michel[1], T. Jenkins[2], C. R. Staples[1], and W. W. Thatcher[1], [1]*University of Florida, Gainesville,* [2]*Clemson University, Clemson, SC*.

The objective was to examine the effects of bST, pregnancy and dietary fatty acids on the GH/IGF system in lactating dairy cows. Two diets were fed, starting 18 days postpartum (PP), in which the oil of whole cottonseed (15% of dietary DM; control diet; n=19) was compared to calcium salts of fatty acids containing fish oil (FO), high in eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA;1.9% of dietary DM; n=8). All cows started an Ovsynch protocol between d 5 and 12 of an estrous cycle and were assigned randomly to be time inseminated (d 0; ∼ 77 d PP) or not, and to receive either a bST (500 mg) injection on d 0 and 11 d later or not. On d 17, cows were slaughtered and uterine luminal flushings (ULF), endometriums and conceptuses were recovered. The number of cows in each group was as follows: control diet had 5 bST-treated cyclic (bST-C), 5 non bST-treated cyclic (C), 4 bST-treated pregnant (bST-P), and 5 non bST-treated pregnant (P) cows; FO diet had 4 bST-treated (bST-CFO) and 5 non bST-treated cyclic (CFO) cows. GH receptor mRNA was undetectable in the endometrium of all cows. Endometrial IGF-I mRNA was reduced in pregnant cows (P#88040.01) and tended to decrease in FO fed (+/- bST) versus C (+/- bST) cows (P#88040.06). IGF-II mRNA was increased in the endometrium of P and bST treated cows on the control diet (P#88040.01). Cows fed FO had increased concentrations of IGF-II mRNA, regardless of bST treatment (P#88040.05). IGFBP-2 mRNA was increased in bST-P cows (P#88040.05), whereas bST decreased the IGFBP-2 mRNA in all cyclic cows (P#88040.05). Treatments did not differ in endometrial IGFBP-3 mRNA or for ULF content of IGFBP-3, IGFBP-4, GH and IGF-I. EPA and DHA were increased in the endometrium and liver (P#88040.01), and DHA was increased in the milk of FO fed cows vs. control cyclic cows (P#88040.01). In conclusion, bST, pregnancy, and FO can have differential effects on the GH/IGF system.

Key Words: Pregnancy, Somatotropin, Fish Oil

T139 Unique effects of ovarian steroid hormones on parenchymal morphology in the mammary glands of swine. J. M. Scudder*, A. S. Barndollar, J. F. Trott, and R. C. Hovey, *University of Vermont, Burlington*.

Sufficient milk production by sows is a major limitation for piglet growth. The main structural component in the mammary glands of gilts is a lobular structure referred to as the terminal duct lobular unit (TDLU) that arises from mammary ducts. These can be classified as a TDLU-1, -2, or -3, depending on the number of ductules present. Separately, end buds (club-like structures) are also present in the mammary gland to direct ductal elongation. We hypothesized that the proportion of different structures in the mammary glands of gilts is regulated by ovarian steroid hormones. Ovary intact, sexually-mature Yucatan miniature swine were treated with estrogen (E2), progesterone (P4), or saline for 5 days. Mammary gland tissues were prepared as semi-thick sections and mounted on slides before staining to identify the various structures. Other sections were prepared at 4μm and stained with hematoxylin and eosin. We used a histomorphometric approach to quantify the number of different structures in the mammary glands of each animal. Across treatments we found that TDLU-1, -2 and -3 structures in

the mammary glands of gilts contained an average of 11, 35 and 81 ductules, respectively. In saline treated animals, 37.4%±10%, 59.2%±8% and 3.4%±2.5% of the structures were present as TDLU-1, -2 and 3, respectively (TDLU-1 vs TDLU-2, P#8804.16; TDLU-1 vs TDLU-3, P#8804.02). These proportions were not altered by hormone treatment (P#8805.05). We did however find hormone-induced changes in the number of end buds within the mammary gland. The number of end buds per gland following treatment with saline, E2 or P4 was 4.75±2.8, 16.5±5 and .5±.5 (SAL vs E2, P#8804.03; SAL vs P4, P#8804.09). Separately, histological examination revealed increased secretory activity with E2 treatment. Taken together, our results show that ovarian steroid hormones have pronounced effects on parenchymal morphology and cell proliferation in the mammary glands of gilts that may influence a sows milk production potential.

Key Words: Mammary Gland, Morphology, Ovarian Hormones

T140 Effects of bovine somatotropin (bST), pregnancy and a diet enriched in omega-3 fatty acids on reproduction in lactating dairy cows. T. R. Bilby*[1], A. Sozzi[1], M. Lopez[1], F. Silvestre[1], A. Ealy[2], C. R. Staples[1], and W. W. Thatcher[1], [1]*University of Florida, Gainesville,* [2]*The Pennsylvania State University, University Park.*

The objective was to examine effects of bST, pregnancy and dietary fatty acids on reproductive responses in lactating dairy cows. Two diets were fed, starting 18 d postpartum (PP), in which oil of whole cottonseed was compared to calcium salts of fatty acids containing fish oil (FO). The Ovsynch protocol was administered between d 5 and 12 of the estrous cycle, and cows were assigned randomly to be time inseminated (d 0; $\sim$ 77 d PP) or not, and to receive a bST (500 mg) injection on d 0 and 11 or not. Daily blood samples were taken from d 0 d 17, and ovarian responses were measured by ultrasound on d 7, 9, 11, 13, and 15-17. Cows were slaughtered on d 17, and uterine luminal flushings (ULF), conceptuses and CL were recovered. Number of cows in each group was as follows: control diet had 5 bST-treated cyclic (bST-C), 5 non bST-treated cyclic (C), 4 bST-treated pregnant (bST-P), and 5 non bST-treated pregnant (P) cows; FO diet had 4 bST-treated (bST-CFO) and 5 non bST-treated cyclic (CFO) cows. The bST increased pregnancy rate (83% [5/6]>40% [4/10]; P#88040.10), conceptus length (45>34 cm; P#88040.10) and INF-τ in the ULF (9.4>5.3 μg; P#88040.05) with no effect on INF-τ mRNA concentration in the conceptus. The CL tissue volumes tended to be higher in P cows versus C cows (P#88040.10) and was higher at slaughter (P#88040.05). Pregnancy altered (P$*$d; P#88040.05) size of the second wave dominant follicle and number of Class 2 follicles indicative of a less active dominant follicle in P cows. Treatment with bST increased plasma GH and IGF-I (P#88040.01); among control fed cows (cyclic and pregnant) bST decreased P4 (P#88040.05). The FO (+/-bST) cows had lower plasma insulin than C cows (+/-bST; P#88040.05), and FO altered (FO$*$d) the GH (bST-CFO>bST-C; P#88040.01) and IGF-1 (bST-C>bST-CFO; P#88040.05) responses to bST injections. In summary, bST and FO appear to modulate reproductive responses that may be beneficial to the developing conceptus.

Key Words: Pregnancy, Somatotropin, Fish Oil

T141 Effects of ambient temperature and solar radiation on skin evaporative water loss in dairy cattle. B. C. Pollard*, M. E Dwyer, A. C. Fitzgerald, P. C. Gentry, D. A. Henderson, and R. J. Collier, *University of Arizona, Tucson.*

To determine effects of ambient temperature and solar radiation on total evaporative water loss (TEWL) in cattle, non-lactating, Holstein cows (n=6) and heifers (n=6) were randomly assigned to one of two treatments in a climate control facility and given ad libitum access to feed and water. Both treatments were provided a dry bulb temperature at 0500 h of 27.8°C and a maximum temperature of 39.4°C at 1500 h to mimic the average for Summer Solstice (SS) in Tucson, AZ. The two treatments differed by either the addition of SS levels of solar radiation (S) or high ambient temperature alone (NS). Sunrise began at 0600 h, sunset at 1950 h, with maximum irradiation (1,061 Wh/m^2) at 1200 h. At two hour intervals, rectal temperature (RT), respiration rate (RR), and skin temperature (ST) were estimated by infrared reflection and TEWL were determined at five points (rump, loin, udder, rib and neck). Closed-chamber TEWL was determined with a Vapometer® (Delfin Technologies, Finland) calibrated and validated according to the manufacturers instructions. Solar radiation S increased (P<0.05) RR and ST at all locations. Average TEWL rose as ambient heat load increased and was greater in S (94.3 vs. 77.1 g/m^2; P $<$ 0.01) compared to NS. Correlations between skin temperature and TEWL were highly significant for the loin (r = 0.55, P $<$ 0.001), rib (r = 0.62, P $<$ 0.001) and neck (r = 0.42, P $<$ 0.001) while a tendency was noted for the rump (r = 0.23, P = 0.0807). There was no detectable relationship between udder ST and TEWL (P $>$ 0.10). This study begins to address the solar radiation component contributing to individual parameters of heat stress. Further, closed-chamber TEWL provides a novel method to determine sweating rate in dairy cattle.

Key Words: Heat Stress, Dairy Cattle, Solar Radiation

T142 Effect of growth hormone on the expression of liver-enriched transcription factors in the bovine liver. S. Eleswarapu* and H. Jiang, *Virginia Tech, Blacksburg.*

Growth hormone (GH) plays an important role in a variety of physiological processes. A major target organ of GH is the liver, where GH regulates the expression of many genes involved in metabolism, detoxification and other functions of the liver. A possible mechanism by which GH affects gene expression in the liver is that GH alters the expression of liver-enriched transcription factors (LETFs), which in turn change the expression of other genes in the liver. As part of the long-term goal to investigate this possibility, we determined the effect of GH on the expression of nine LETFs, including hepatocyte nuclear factor (HNF)-1α, HNF-1β, HNF-3α, HNF-3β, HNF-3γ, HNF-6, CCAAT/enhancer-binding protein (C/EBP)-α, C/EBP-β, and albumin D-element binding protein (DBP) in the bovine liver. Eighteen non-lactating and non-pregnant Angus cows were assigned randomly to three groups (n = 6 per group) and each cow received a single intramuscular injection of 500 mg of recombinant bovine GH. Liver biopsy samples were taken from group 1 cows 6 h after GH administration, group 2 cows 24 h after GH administration, and group 3 cows 1 wk after GH administration. Liver biopsy samples were also taken from group 3 cows 1 d before GH administration. Levels of the nine LETF mRNAs in these liver samples were quantified using ribonuclease protection assays. The levels of HNF-3γ and HNF-6 mRNAs were higher (P $<$ 0.05) in the liver samples taken from cows 24 h and 1 wk after GH administration than in the liver samples taken from cows 1 d before GH administration or 6 h after GH administration. The levels of other LETF mRNAs, including HNF-1α, HNF-1α, HNF-3α, HNF-3β, C/EBP-α, C/EBP-β and DBP mRNAs, were not different (P $>$ 0.05) between these liver samples. Thus, GH can increase the expression of HNF-3γ and HNF-6 mRNAs in the liver and these two LETFs may play a role in GH regulation of the expression of other genes in the liver.

Key Words: Growth Hormone, Liver, Transcription Factor

T143 Liver expression of growth hormone receptor 1A mRNA is decreased in dairy cows but not in beef cows at parturition. H. Jiang*[1], M. C. Lucy[2], B. A. Crooker[3], and W. E. Beal[1], [1]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg,* [2]*Department of Animal Sciences, University of Missouri, Columbia,* [3]*Department of Animal Sciences, University of Minnesota, St. Paul.*

Growth hormone receptor (GHR) mRNA in the liver of cattle is composed of variants that differ in the first exon. The expression of a major GHR mRNA variant, GHR 1A, is down-regulated in the liver of dairy cows at parturition. As part of the effort to understand the mechanism by which GHR 1A mRNA expression is decreased at parturition, we determined in this study if GHR 1A mRNA expression was also decreased in the liver of beef cows at parturition. Liver biopsy samples were taken from multiparous Angus (n = 6) and Holstein cows (n = 6) 7 to 23 d before parturition, within 24 h after parturition (i.e., at parturition), and 8 to 18 d after parturition, and the levels of GHR 1A and insulin-like growth factor-I (IGF-I) mRNA in these samples were measured by ribonuclease protection assays. As expected, the expression of GHR 1A mRNA in the liver of dairy cows was decreased at parturition (P $<$ 0.05). The expression of IGF-I mRNA in the liver of dairy cows was also decreased at parturition (P $<$ 0.05), perhaps as a result of decreased expression of GHR 1A mRNA. However, neither the expression of GHR 1A mRNA nor that of IGF-I mRNA was decreased in the liver of beef cows at parturition (P $>$ 0.1), when compared to that in the prepartum or postpartum periods. These results suggest that the decrease in GHR

1A mRNA expression in the liver of dairy cows at parturition is not caused by ending of pregnancy or by initiation of lactation *per se*.

Key Words: Growth Hormone Receptor, Cows, Liver

T144 A miniature condition in Brahman cattle is associated with a single nucleotide mutation within the growth hormone gene. B. L. McCormack[1], C. Agca[1], C. C. Chase, Jr.[2], T. A. Olson[3], T. H. Elsasser[4], A. C. Hammond[5], T. H. Welsh, Jr.*[6], and M. C. Lucy[1], [1]*University of Missouri, Columbia,* [2]*USDA, ARS, Brooksville, FL,* [3]*University of Florida, Gainesville,* [4]*USDA, ARS, Beltsville, MD,* [5]*USDA, ARS, Athens, GA,* [6]*Texas A&M University, College Station*.

Miniature Brahman cattle at the USDA, ARS in Brooksville, FL have normal proportioned growth but are approximately 70% of normal mature height and weight. Pedigree analyses suggest that the condition is inherited as a recessive gene. The objective was to clone the GH cDNA from miniature cattle and compare its sequence to normal cattle. Messenger RNA was isolated from pituitary and a cDNA for the protein coding region of the GH gene was amplified by reverse transcription PCR from each of two miniature cattle. The cDNA were cloned into plasmid vectors and the top and bottom strands were sequenced by automated DNA sequencing. Both cDNA clones contained a nucleotide polymorphism in which base number 641 of GenBank AF034386 (Bos indicus GH) was mutated from a cytosine (C) to a thymine (T). The C to T change encodes a mutation (threonine to methionine) at amino acid 200. The threonine is located in the fourth alpha helix of GH and is one of nine amino acids that participate directly in binding of GH to the GH receptor. Amino acid mutations at this location are associated with dwarfism in humans. Four miniature and four normal stature cattle from the Brooksville herd were tested for the polymorphism by using restriction fragment length polymorphism (RFLP) analysis of PCR-amplified GH gene with BsmBI restriction enzyme (specific for mutated nucleotide). The four miniature cattle were homozygous for the mutation (-/-). Two of the normal stature cattle were homozygous for the wild type allele (+/+) and two were heterozygous (+/-) ($P<.05$). Miniature Brahman cattle were homozygous for a single nucleotide polymorphism that encodes a mutation in an amino acid involved in binding of GH to the GH receptor. Normal stature cattle had at least one copy of the normal GH allele. We conclude that threonine 200 in bovine GH is required for normal growth in cattle.

Key Words: GH, Mutation, Growth

ASAS - Growth and Development

T145 Effect of gender and feeding program on productive performance and carcass quality of heavy pigs. J. Peinado*[1], M. Nieto[2], J. C. González[1], G. G. Mateos[3], and P. Medel[1], [1]*Imasde Agropecuaria Madrid, Spain,* [2]*Copese Segovia, Spain,* [3]*Universidad Politécnica de Madrid, Madrid, Spain*.

A total of 252 Duroc x Landrace*Large White pigs of 28.3 ± 2.1 kg of initial BW was used to study the influence of sex and a 10 % lysine restriction from 30 to 60 kg BW on productive performance and carcass quality. There were six treatments arranged factorially with two types of feed from 30 to 60 kg BW (LL, 0.89 % lys *vs* HL, 0.97 % lys) and three sexes (castrated females, CF; entire females, EF; castrated males, CM). Energy:lys ratio was maintained constant in all the diets, and each treatment was replicated three times (14 pigs housed together). Males were castrated at birth and females at 30 kg BW. From 60 kg BW to slaughter all pigs received a common diet *ad libitum* (2.4 Mcal NE/kg and 0.70 and 0.67 % lys from 60 to 90 and from 90 to 119 kg BW, respectively). From 30 to 60 kg BW pigs fed the LL diet had worse feed conversion than pigs fed the HL diet (2.12 *vs* 1.97 g/g; $P < 0.05$). However, from 60 to 90 kg BW pigs fed the LL diet ate more and grew faster than pigs fed the HL diet (1,982 *vs* 1,815 g/d; and 688 *vs* 619 g/d for LL and HL diet, respectively; $P < 0.05$). For the whole period, pigs fed the LL diet ate 5.5 % more feed than pigs fed HL diet (1,983 *vs* 1,879 g/d; $P < 0.05$) but gains and feed conversion were not affected. Gender did not influence productive performance. Backfat was higher for CF than for EF with CM in an intermediate position (28.3, 23.3, and 25.4 mm, respectively; $P < 0.05$). Fat thickness at *Gluteus medius* muscle (GM) was higher for CF than for EF or CM (20.2, 17.9, and 18.6 mm, respectively; $P < 0.05$). Feeding program did not affect backfat or GM fat. It is concluded that a reduction of 10 % of lysine from 30 to 60 kg BW increased feed intake in the global period without affecting growth or feed conversion. Also, castration of the females might improve some quality carcass parameters of pigs destined to the cured ham industry.

Key Words: Pig Performance, Castration, Lysine Level

T146 Effect of protein from placental bovine tissue on puberty and growth mice. F. A. Nunez[1], J. A. Garcia-Macias[1], J. A. Lopez[2], and F. G. Rios*[2], [1]*Facultad de Zootecnia - Universidad Autonoma de Chihuahua (Mexico) Periferico F. R. Almada, Mexico,* [2]*FMVZ - Universidad Autonoma de Sinaloa, Culiacan-Mazatlan, Mexico*.

Our aim was to evaluate activity of protein from placental bovine tissue partially purified by chromatographic column with Sephadex 50-40#8482. Sixty Balb/C pubertal mice, (thirty females and thirty males), were used in a randomized design experiment with 3 x 4 factorial arrangement to test two sex (females and males), two placental proteins (PI and PII) and four placental proteins (25, 50, 75 and 100 μg/mice/day of the placental protein). We compared this to a positive control (100μg/mice/day) of bovine serum albumin (BSA) and negative control group (100μL/mice/day) of ammonium bicarbonate (AB). Four groups (three males and three females) received four dose, 25, 50, 75 and 100 μg/mice/day of the placental protein PI (MW ranks 17 to 30 kDa), and four groups (three males and three females) received four dose, 25, 50, 75 and 100 μg/mice/day of the placental protein PII (MW ranks 31 to 97 kDa). Body weight and feed intake were measured daily for a ten day experimental period. The experiment was analysed as factorial design randomised with three factors; means comparison performed by contrast. Feed efficiency (FE) of female mice (0.095g:g) and male mice (0.091) were not affected (P#88050.05), by sex and treatments. The rate of growth (RG) observed a effect of sex; the male mice were heavier(P#88040.01) in 44.82% than female mice (2.61±0.23 vs. 1.17±0.23). RG in the mice group injected with AB was less (P#88040.05) than mice group injected with BSA (1.54±0.25 vs. 2.16±0.24), average daily gain (ADG) was different in male mice (P #88040.05) in 29.1% than female mice (0.51±0.01 vs. 0.36±0.09g/d). In the mice group injected with AB and the mice group injected with 50μg/mice/d of PII proteins, ADG was less than the other treatments in the same sex (P#88040.05). The female mice injected with 100 μg/mice/d were less ADG. The carcass composition was not affected (P#88050.05) by sex and treatments, 41.96±1.56 for male vs. 41.57±1.59, for female, however dreesing carcass percentage observed lineal tendency (P#88040.05) in PI and PII for male mice. It is concluded that proteins from placental bovine tissue partially purified, not improve growth in pubertal mice.

Key Words: Placental Protein, Mice, Growth

T147 Maternal undernutrition changes angiotensin type 1 and 2 receptors in ovine fetal heart. H.-C. Han*[1], K. J. Austin[1], S. P. Ford[1], P. W. Nathanielsz[2], and T. R. Hansen[1], [1]*University of Wyoming, Laramie,* [2]*New York University, New York*.

Nutrient restriction during early gestation causes compensatory growth of both the left and right ventricles of the ovine fetal heart by day 78 of gestation (Biol Reprod 69:133). Angiotensin II mediates cardiovascular pathologies through its effects on the type 1 (AT1) and type 2 (AT2) receptors. AT1 has been shown to mediate deleterious effects such as vasoconstriction, cellular growth, and endothelial cell damage in adult systems. Very little is known about fetal heart angiotensin receptors and the consequences of activation. Previously we reported that AT1 mRNA was down regulated in fetal left ventricle (LV) from nutrient restricted ewes when compared to control fed ewes. It was hypothesized that maternal undernutrition (energy and protein) would adversely affect AT1 and AT2 protein expression in the fetal LV. Pregnant ewes were randomly assigned to control (n = 8, 100% NRC requirements) or nutrient-restricted groups (n = 8, 50% NRC requirements). Ewes were maintained on diets from day 28-78 of gestation. Fetal LV was