T176 Effects of mild heat stress on growth and carcass characteristics in broiler chickens. E. Sucu[1,2], M. V. Sanz-Fernandez[1], S. C. Pearce[1], A. Nayeri[1], G. P. Murugesan[1], R. R. Rhoads[3], M. E. Persia[1], and L. H. Baumgard*[1], *[1]Department of Animal Science, Iowa State University, Ames, [2]Department of Animal Science, Uludag University, Bursa, Turkey, [3]Department of Animal Science, Virginia Polytechnic Institute and State University, Blacksburg.*

Heat stress (HS) markedly alters bioenergetics in a variety of farm animals but how HS affects growth, carcass characteristics, and metabolic responses in broiler chickens has not been thoroughly evaluated. Thirty-six Ross male chickens, 28 d of age (1120 ± 20 g BW) were housed in climate chambers at the Iowa State University Zumwalt Station and exposed to one of 2 environmental conditions: 1) thermal neutral (TN) conditions (constant 25°C) with ad libitum water and feed intake (n = 15) or 2) mild HS conditions (constant 35°C) and ad libitum water and feed intake (n = 21). A blood sample was collected via cardiac puncture, and liver, abdominal fat pad and breast muscle were immediately weighed following sacrifice at 24 h, 3 d or 7 d of environmental exposure. All animals were feed restricted for 6 h before sacrifice. All data were analyzed using the PROC MIXED procedure of SAS (SAS Inst. Inc. Cary NC). The statistical analysis included the effects of environmental treatment, day of sacrifice and their interaction. Overall, HS birds had an increased rectal temperature compared with TN birds ($P < 0.05$, 41.7 ± 0.07 vs. 41.2 ± 0.08°C) and this temperature difference tended ($P = 0.13$) to become less pronounced with time. There was a treatment by time interaction ($P < 0.05$) on body weight gain as ADG was decreased by 77, 40 and 22% in HS compared with TN birds at d 1, 3 and 7, respectively. The temperature and ADG data indicate the birds were acclimating to the mild heat strain. Overall, compared with TN birds, actual liver weight and liver weight as a percentage of BW were decreased ($P < 0.05$) in HS birds (15 and 9%, respectively), but liver lipid content (4.22%) and liver dry matter (25.5%) did not differ between environmental treatments. The abdominal fat pad (22.6 g), breast muscle (137.5 g) and plasma insulin (1.3 ng/ml) levels did not differ between environments. Results of this study indicate that a mild but constant heat strain markedly reduces productivity and alters liver weight in broiler chickens. Reasons why HS affected liver weight are unknown but are of bioenergetic interest.

Key Words: heat stress, broiler chicken, metabolism

T177 Effect of season on copper concentration in blood serum from goats in different reproductive status. R. Rojo, B. Albarrán-Portillo, A. García-Martínez, J. Cedillo-Monroy, and J. F. Vázquez-Armijo,* *Centro Universitario UAEM Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, México, Mexico.*

The effect of season (rainy: RS, and dry: DS) on copper (Cu) concentration in blood serum of crossbred goats were studied. Blood samples from 40 crossbred goats were taken each season. The goats were clustered into 5 different groups considering their reproductive status, as follows: pubertal goats, anestrous adult goats, cyclic adult goats, pregnant goats, and kidded goats. Concentration of Cu in blood serum (mg/L) were assayed using atomic absorption. Data were analyzed for a completely randomized design with a factorial arrangement with 8 replicates. Blood serum concentration of Cu were 1.15, and were affected by reproductive status, season, and their interaction. Blood serum concentration of Cu were lower in RS (0.92) than DS (1.37) ($P < 0.05$). Overall, kidded goats had the highest ($P < 0.01$) Cu concentration (RS: 0.98 ± 0.07; DS: 1.95 ± 0.06) than other animals in both seasons. Adult goats showed a deficiency of Cu concentration in blood serum, especially during RS (0.88 ± 0.09). However, the lowest value obtained was to Pubertal goats in RS (0.69 ± 0.07). The results reflect the different requirements imposed by reproductive status and season interaction on goats.

Key Words: copper, blood serum, goats

T178 Effects of the beta-2 adrenergic agonist zilpaterol hydrochloride in castrated male goats: Plasma insulin, cortisol, thyroids, triglyceride, and glucose concentrations. A. Hatefi*[1], A. Towhidi[1], A. Zail[1], M. Ganjkhanlou[1], and A. Plascencia[2], *[1]Department of Animal Science, University of Tehran, Karaj, Alborz, Islamic Republic of Iran, [2]Instituto de Investigaciones en Ciencias Veterinarias, Universidad Autónoma de Baja, California Mexicali, Baja California, México.*

To evaluate the influence of zilpaterol hydrochloride (Zilmax, Intervet, South Africa) supplementation on blood insulin, cortisol, T3 and T4 (as thyroid hormones) and the metabolites glucose and triglyceride, 16 Mahabadi castrated male goats were individually fed a dry-rolled barley-based finishing diet with or without zilpaterol hydrochloride supplementation dosed at 0.20 mg/kg BW/d for finishing 30 d of 90 d feedlot period. Blood samples were taken at first and end of supplementing period and plasma was stored at –20°C until analysis. These samples were quantified by spectrophotometry procedure for glucose and triglyceride, by RIA for insulin and cortisol and triiodothyronine (T3) and thyroxin (T4) were determined according to standard ELISA methods. Obtained data were analyzed MIXED procedure of SAS software according to a completely randomized design. A P-value < 0.05 was considered statistically significant. Results showed that ZH supplementing has significant effect on metabolic hormones at d 90; as caused to increase insulin (108.02 vs. 100.56 ng/mL and $P < 0.01$), T3 (0.75 vs. 0.65 ng/mL and $P < 0.01$), T4 (25.41 vs. 21.99 ng/mL and $P < 0.01$) and decrease cortisol (20.78 vs. 28.55 ng/mL and $P < 0.01$) concentrations compare with control and d 60. Following to expressed hormonal changes at d 90, this β-agonist significantly influenced on blood metabolites as caused to decrease glucose (104.55 vs. 119.43 mg/dL and $P < 0.01$) and triglyceride (43.25 vs. 49.42 43mg/dL and $P = 0.02$) than control and d 60. Our study indicated zilpaterol hydrochloride supplementation of 0.20 mg/kg BW/d on castrated male goats at end of feedlot period has significant effects on blood metabolic hormones and metabolites at end of supplementing period.

Key Words: zilpaterol hydrochloride, metabolic hormones, castrated male goat

T179 Effect of water deprivation on the thermoregulatory system of desert goats (*Capra hircus*). A. Al-Haidary* and E. Samara, *King Saud University, Riyadh, Saudi Arabia.*

This study was conducted during summer season to investigate the effect of water deprivation under heat stress conditions on the thermophysiology of desert goat. The experiment was conducted on 4 stages (euhydration, dehydration, rehydration, d 10 of rehydration). The first 3 stages were lasted for 72 h each, while the last stage lasted for 24 h. A telemetry system was used for continuous measurement of goat's

core body temperature. Results revealed that desert goat had showed a distinguished circadian rhythm of core body temperature during euhydration. The rhythm minimum and maximum were attained early in the morning and at the end of the day, respectively with 0.79°C oscillation range. Water deprivation that coincided with high ambient temperature of summer season has affected goat's core body temperature. The range of oscillation of core body temperature increased during dehydration stage to 1.78°C, then decreased to 88°C during rehydration stage, and further decreased to 0.72°C at d 10 of rehydration. The observed increase in core body temperature due to water deprivation indicates thermo-labile characteristics of desert goat. Goat's body heat storage was significantly ($P < 0.05$) increased during dehydration stage. Furthermore, dehydration had significantly ($P < 0.05$) increased daily averages of respiration rate, heart rate, skin, coat, and rectal temperatures of desert goat. Dehydration had also significantly ($P < 0.05$) decreased overall means of daily feed intake, dry matter intake, feces water content, and body weight. Ten days of rehydration has been approved sufficient for all measured thermo-physiological parameters to recover from the effect of water deprivation. These results demonstrate the capability of desert goat to ameliorate the stressful effects of water deprivation under heat stress conditions.

Key Words: core body temperature, gaot, dehydration

T180 Comparison of the morphological characters of ovulated follicular waves during synchronized and normal estrous cycle in dairy cattle. M. Poorhamdollah*[1], H. Kohram[1,2], A. Z. Shahneh[1], and A. Sadeghi-Sefidmazgi[3], *[1]University of Tehran, Karaj, Tehran, Iran, [2]Shahid Chamran University, Ahvaz, Iran, [3]Isfahan University of Technology, Isfahan, Iran.*

The objective of this study was to compare the morphological characteristics of follicular waves during a synchronized estrous cycle to those of a normal estrous cycle in dairy cattle. A total of 10 Holstein dairy cows were selected and divided into 2 groups (n1 = n2 = 5). In group 1, the estrous cycles were synchronized by 2 successive injections of $PGF_{2\alpha}$ (Vetglan, cloprostenol, Aburaihan, Iran), 14 d apart; and the characteristics of ovulated follicular waves were evaluated. In group 2, the ovulated waves during a natural estrous cycle for each cow were served as controls. Ovaries of all cows were examined daily by transrectal ultrasound (B mode; Pie medical, Falco 100, 8 MHz). *t*-test was used to assess the significance of difference between morphological characteristics of follicular waves in synchronized and normal estrous cycles. The results showed that there were no significant differences ($P > 0.05$) between morphological characteristics in terms of the maximum size of the largest follicle (F1); (15.60 ± 1.12 vs 13.60 ± 0.42; mm), maximum size of the second largest follicle (F2); (10.20 ± 1.01 vs 8.72 ± 0.59; mm), mean large size of subordinate follicles (6.04 ± 1.06 vs 6.03 ± 0.34; mm), mean size of F1 at deviation (8.80 ± 1.15 vs 7.64 ± 0.46; mm), mean days of emergence to deviation of F1 (4.00 ± 0.70 vs 3.48 ± 0.32), mean number of emergent follicles (11.00 ± 1.57 vs 7.44 ± 0.46) and mean size of F1 at growth and static phase (3.85 ± 0.63 vs 4.16 ± 0.67 and 2.72 ± 0.40 vs 2.44 ± 0.50; mm, respectively) as well as daily growth rates of F1 (1.04 ± 0.15 vs 1.38 ± 0.04) of follicular waves in synchronized estrous cycle versus normal estrous cycle in dairy cattle, respectively. In conclusion, there were no significant differences between morphological characters of follicular waves in synchronized estrous cycle and normal estrous cycle in dairy cattle.

Key Words: cattle, follicular wave, $PGF_{2\alpha}$

T181 Effect of methionine supplementation during postpartum period in dairy cows. II: Embryo quality. A. H. Souza*[1], P. D. Carvalho[1], A. R. Dresch[1], L. M. Vieira[1,2], K. S. Hackbart[1], D. Luchini[3], S. Bertics[1], N. Betzold[4], M. C. Wiltbank[1], and R. D. Shaver[1], *[1]University of Wisconsin-Madison, Madsion, [2]University of Sao Paulo-VRA, Brazil, [3]Adisseo, Alpharetta, GA, [4]U.S. Dairy Forage Research Farm, Prairie du Sac, WI.*

Objectives of this study were to evaluate the effects of supplementing methionine in the postpartum period on embryo quality in dairy cows. Holstein cows (n = 72), receiving same basic TMR (NRC 2001), were milked twice a day and were kept in tie-stalls. Animals were blocked by parity and calving date and randomly assigned to 2 treatments differing in level of dietary methionine: 1) Methionine (MET); diet composed of (%DM) corn silage (39.7), alfalfa silage (21.8), HMSC (17.2), roasted soybeans (8.6), grass hay (4.6), canola meal (4.0), mineral-vitamin mix (2.7) and ProVAAl Ultra (w/Smartamine, 1.4), formulated to deliver 2875 g MP with 6.8 Lys %MP and 2.43 Met %MP; 2) Control (CON); cows fed the same basal diet but replacing ProVAAl Ultra by ProVAAL Advantage (no added Smartamine), formulated to deliver 2875 gr MP with 6.8 Lys %MP and 1.89 Met %MP. Data was analyzed with the proc GLIMMIX of SAS and cows treated as a random experimental unit. Cows were superovulated with a modified 5d-Double Ovsynch with 4 d of decreasing FSH (Folltropin, 400mg/cow) doses and flushed 6 d after synchronized ovulations. A single batch of FSH and frozen semen (single ejaculates 15x106 sptz/straw) of 2 sires were used. In addition, a single treatment-blinded technician graded all embryos. There were no differences between groups in CL number, fertilization, or embryo quality. Surprisingly, % of structures recovered/CL was greater for MET than CON. Thus, most ova/embryo properties did not differ between groups; however, potential effects of MET on embryo development after the first week of pregnancy need to be investigated. Supported by Adisseo, Accelerated Genetics, USDA Grant 2010–85122–20612.

Table 1.

	MET	CON	
n	35	37	*P*-value
CL number	17.0±1.3	17.7±1.5	0.90
Total ova/embryos recovered	9.1±1.4	6.8±1.0	0.18
% Ova/embryos recovered per CL	49.5±4.9	35.8±4.4	0.05
Number of fertilized ova	6.5±1.1	5.5±0.9	0.56
% Fertilized ova	74.7±5.6	82.2±3.8	0.27
Number of transferable embryos	5.0±0.9	4.3±0.1	0.57
% Transferable embryos of fertilized	59.7±6.5	62.4±6.0	0.55
Number of degenerate embryos	1.5±0.4	1.3±0.4	0.75
% Degenerate of fertilized	25.1±5.8	27.5±6.0	0.74

Key Words: methionine, embryo quality, dairy cow

T182 Lactation and physiological performance in Holstein dairy cows managed under summer heat stress conditions in northwest Mexico. P. Luna-Nevarez*[1], C. Leyva-Corona[1], F. Rivera-Acuña[1], J. F. Medrano[2], G. Rincon[2], G. A. Silver[3], D. M. Hallford[3], R. L. Ashley[3], and M. G. Thomas[4], *[1]Instituto Tecnologico de Sonora, Ciudad Obregon, Sonora, Mexico, [2]University of California, Davis, [3]New Mexico State University, Las Cruces, [4]Colorado State University, Fort Collins.*

Milk production is challenging for Holstein dairy cows managed under severe high temperature and humidity weather conditions common to

northwest Mexico during summer, such that a cooling system is recommended to alleviate heat stress. Thus, the objective of this study was to evaluate the effect of a low-pressure cooling system on milk production and physiological responses indicative of heat stress during summer in dairy cows milked in Sonora. Twenty-eight multiparous Holstein cows with ~150 d in milk, that received bovine somatropin every 14 d during lactation, were randomly assigned in 2 groups, cooling (CL, n = 14) and heat stress (HS, n = 14), from May 7 to July 23, 2011. All cows were maintained in shaded holding pens. Cows in the CL group received a cooling program in the waiting parlor, which included 4 series of shower (5 min) alternated with forced ventilation (10 min) 6 times per day (0700, 0900, 1100, 1300, 1500 and 1700). Heat-stressed cows were cooled only before milking (0700 and 1700). Milk production was recorded daily using an electronic system. Blood samples were collected once per week to measure serum levels of prolactin and IGF1. Rectal temperature and respiratory frequency were measured twice the day before bleeding. Ambient temperature and humidity values were collected from a nearby climatic station. Data were analyzed in SAS (2009) using a mixed model procedure with repeated measures. Cows in the CL group had higher ($P < 0.05$) milk production (22.6 vs. 21.6 ± 0.5 kg/day) and serum concentrations of prolactin (35.1 vs. 29.4 ± 1.2 ng/mL) and IGF1 (295.8 vs. 269.6 ± 15.7 ng/mL) relative to HS cows. Conversely, relative to CL cows, HS cows had a higher ($P < 0.05$) rectal temperature (38.4 vs. 38.2 ± 0.1°C) and respiratory frequency (70.5 vs. 66.6 ± 1.2 breath/min). We conclude that reduced serum levels of prolactin and IGF1 in dairy cows during summer are a consequence of heat stress, which is remedied by cooling to maintain an acceptable level of lactional performance in Holstein dairy cows.

Key Words: cooling, heat stress, prolactin

T183 Relative quantification of mRNA abundance for LH receptor, angiogenin and p450scc, and determination of hormone levels in dominant follicles and follicular cysts from dairy cows. R. M. Villaseñor-González, J. A. Grado-Ahuir,* E. Burrola-Barraza, P. Hernández-Briano, L. E. Escobedo-Morales, and S. A. Quintana-Quintana, *Facultad de Zootecnia y Ecología, Universidad Autónoma de Chihuahua, Chihuahua, Chihuahua, México.*

Follicular cysts are nonovulatory structures that contribute to prolong the calving interval in dairy cattle. The objective was to compare the expression of mRNA encoding LH receptor (LHCGR), angiogenin (Ang) and cytochrome P450 side-chain cleavage enzyme (CYP11A1) in granulose cells and the hormonal level in dominant follicles (DF) and follicular cysts (FC). We obtained follicular structures (DF, n = 16; and FC, n = 16) from dairy cows slaughtered at a local abattoir. The follicular fluid was subjected to ELISA to determine estradiol 17β (E2), progesterone (P4) and IGF-1 (intraassay coefficient of variation was 5.58, 7.02, and 10.30% for E2, P4, and IGF-1, respectively). Abundance of target genes mRNA relative to GAPDH was quantified by real-time PCR. The experiment was conducted using a completely randomized design, with the fixed effect of type (DF or FC). Correlation among gene expression and hormones levels were also calculated. There were no difference ($P > 0.05$) between DF and FC for the expression (fold change) of LHCGR (8.18 ± 0.54 vs 7.16 ± 0.28), Ang (1.79 ± 0.20 vs 1.78 ± 0.21), CYP11A1 (3.50 ± 0.24 vs 3.42 ± 0.24) and the concentrations of E2 and P4 (1384.64 ± 1.82 vs 1142.11 ± 1.82, and 13.10 ± 1.41 vs 18.63 ± 1.41 ng/ml, respectively). The concentrations of IGF-1 in FC was higher ($P < 0.05$) than in DF (132.78 ± 1.18 and 78.21 ± 1.18 ng/ml, respectively). Positive correlations ($P < 0.05$) between LHCGR with CYP11A1 (r = 0.74), LHCGR with E2 (r = 0.95), and CYP11A1 with E2 (r = 0.69) were detected in DF. In FC there was a positive correlation ($P < 0.05$) between LHCGR with E2 (r = 0.82), and a negative correlation between CYP11A1 with IGF-1 (r = −0.70) and follicular diameter (r = −0.59). The results provide evidence for IGF-1 to be involved in the growth and extended lifespan of follicular cysts

Key Words: follicular cysts, gene expression, IGF-1

T184 Hormonal regulation of the hedgehog system in ovarian granulosa and theca cells of cattle. L. J. Spicer,* P. Y. Aad, and N. B. Schreiber, *Oklahoma State University, Stillwater.*

Although expression of Indian and Desert hedgehog (Hh) proteins, as well as their receptor Patched 1, dramatically decrease during follicular atresia in rodents, little is known about the hormonal regulation of these Hh system proteins in cattle. Therefore, in vitro experiments were conducted to study the effects of gonadotropins, steroids, transforming growth factor-β superfamily proteins, wingless-type MMTV integration site family member 3A (WNT3A), and IGF1 on components of the Hh system. Gene expression of Indian hedgehog (*IHH*), Desert hedgehog (*DHH*) and its type 1 receptor, Patched 1 (*PTCH1*), were quantified by real-time RT-PCR in cultured bovine granulosa (GC) of small (1–5 mm) follicles or theca (TC) cells of large (5–20 mm) follicles collected from bovine ovaries. In cultured GC, 24-h treatment with 300 ng/mL of E2 increased ($P < 0.05$) *IHH* mRNA abundance in the presence of FSH as well as in the presence of 30 ng/mL of IGF1 ($P < 0.05$). Alone IGF1 suppressed GC IHH mRNA abundance by 78% ($P < 0.05$). In IGF1-treated GC, cortisol (300 ng/mL) and WNT3A (300 ng/mL) increased ($P < 0.05$) GC *IHH* mRNA by 1.9- and 5.5-fold, respectively, whereas 300 ng/mL of prostaglandin E2 (PGE2) or angiogenin had no effect ($P > 0.10$). Relative expression of *DHH* mRNA was 20-fold less than that of *IHH* mRNA in small follicle GC treated with WNT3A. In cultured TC, 24-h treatment with 30 ng/mL of IGF1 and LH decreased ($P < 0.05$) *PTCH1* mRNA expression by 50% and 40%, respectively. The combined treatment of IGF1 and LH was less inhibitory (i.e., 20% suppression) on *PTCH1* expression than either treatment alone. Treatment of TC with bone morphogenetic protein 4 (BMP4; 30 ng/mL) reduced ($P < 0.05$) *PTCH1* mRNA abundance by 50%, whereas treatment with growth differentiation factor 9 (GDF9; 250 ng/mL) or activin (25 ng/mL) was without effect ($P > 0.10$). We conclude that the ovarian Hh system in cattle is controlled by several hormones including IGF1 and FSH, and that these effects are regulated by estradiol and other intra-ovarian factors such as WNT3A and BMP4. We hypothesize that as follicles grow and develop, increased free IGF1 may suppress production of IHH by GC and PTCH1 by TC.

Key Words: hedgehog proteins, granulosa, theca

T185 Pregnancy per AI of conventional versus sex sorted semen in dairy heifers subjected to a modified CIDR-PGF2α-GnRH timed-AI protocol. J. Howard*[1,2], C. Autran[1], J. Branen[2], K. Carnahan[1], R. Kasimanickam[3], G. Sasser[2], and A. Ahmadzadeh[1], *[1]University of Idaho, Moscow, [2]BioTracking LLC, Moscow, ID, [3]Washington State University, Pullman.*

The 5-d CIDR-CoSynch is an effective timed-AI protocol in heifers. Sexed sSorted (SS) yields lower fertility than conventional semen (CS), and thus, there is less room for technical error when SS semen is used in timed-AI protocols. The objectives of this study were to evaluate the effect of GnRH at CIDR insertion on pregnancy per AI (P/AI) in a 5-d CIDR-CoSynch protocol and to compare the P/AI of CS versus SS in dairy heifers subjected to timed-AI. In a 2 × 2 factorial design, 477 Holstein replacement heifers, received a CIDR insert on d 0 (start

of treatment). Subsequently, heifers were paired by age and assigned randomly to receive either 100 µg of GnRH (GnRH-CIDR, n = 241) or no GnRH treatment (CIDR5, n = 236). On d 5, the CIDR was removed and all heifers received 25 mg PGF2α. Seventy-two hours after CIDR removal all heifers received GnRH (100 µg, i.m.) and were randomly assigned to be inseminated with CS (n = 234) or SS semen (n = 243). Estrus activity was monitored using tail chalk methods from d 5 to d 8. Pregnancy status was determined via ultrasound and by PSPB analysis (bioPRYN) on d 32 and 45 after AI. P/AI data were analyzed by logistical regression. P/AI was marginally ($P = 0.06$) different between treatments (GnRH-CIDR 45.8% vs. CIDR5 50.2%). P/AI was greater ($P < 0.01$) for CS compared with SS semen (59.5% vs. 37.0%), however there was no treatment by semen effect. Regardless of semen type and across both treatments, P/AI was greater ($P < 0.01$) in heifers detected in heat then not observed in heat (54.5% vs. 32.1%). Pregnancy detection did not differ between ultrasound and bioPRYN. The results of this experiment indicate that GnRH administration at CIDR insertion does not improve P/AI in heifers subjected to 5-d CIDR-CoSynch protocol, and the use of sex-sorted semen should be limited to use in heifers detected in estrus.

Key Words: dairy heifers, timed AI, sex-sorted semen

T186 Insulin action on hepatic gene expression in dairy cows with different fat mobilization during early lactation. H. M. Hammon*[1], U. Kautzsch[1], C. Weber[1], B. Kuhla[1], M. Röntgen[1], and R. M. Bruckmaier[2], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Veterinary Physiology, Vetsuisse Faculty, Bern, Switzerland.*

Changes in insulin action around calving contribute to metabolic adaptation in dairy cows during the transition from pregnancy to lactation. Insulin action may be affected by the physiological status and body fat mobilization. The objective of this study was to investigate insulin effects on hepatic gene expression of factors involved in energy metabolism in cows with variable liver fat concentration (LFC) after calving. German Holstein cows (>10,000 kg milk/305 d; ≥ 2nd lactation) were classified by LFC postpartum (pp) in low (L; < 240 mg fat/g DM; n = 9) and high (H; > 240 mg fat/g DM; n = 10). Euglycemic-hyperinsulinemic clamps (6 mU/kg BW × min insulin for 6 h) were performed in wk 5 ante partum (ap) and wk 3 pp and liver biopsies were taken before and at the end of the clamp to measure LFC and mRNA concentrations of pyruvate carboxylase (PC), cytosolic and mitochondrial phosphoenolpyruvate carboxykinase (PEPCKc, PEPCKm), propionyl-CoA-carboxylase (PCCA), carnitine palmitoyl-transferase 1A (CPT1A), glucose transporter GLUT2 and GLUT4, IGF-I, and glucocorticoid, growth hormone, and insulin receptors (GR, GHR1A, InsR). Phosphoglycerate kinase 1 was usesd as reference gene and data were analyzed by Mixed Model of SAS with LFC, time, and insulin as fixed effects. LFC differed between cows ($P < 0.01$) (H: 306 ± 0.2 mg/g; L: 195 ± 0.1 mg/g). PC mRNA concentrations increased ($P < 0.05$), but mRNA of GLUT2, GLUT4, IGF1, GHR1A and GR decreased ($P < 0.05$) from ap to pp. Insulin decreased ($P < 0.05$) mRNA concentrations of PC, PEPCKc, PEPCKm, PCCA, CPT1, and InsR, but increased mRNA of IGF-I and GLUT4 ap and pp. Insulin increased GHR1A mRNA only pp and PEPCKc mRNA decreased from ap to pp only without insulin (time × insulin: $P < 0.05$, respectively). PEPCKc mRNA tended to be lower ($P = 0.1$), but expression of GLUT4 and GR were higher ($P < 0.05$) in L than in H. Hepatic gene expression depended partly on time, but was less affected by LFC. Insulin strongly inhibited enzymes involved in hepatic glucose production and fat oxidation, but stimulated parameters of the somatotropic axis and GLUT4. Supported by DFG, Germany.

Key Words: dairy cow, insulin action, hepatic gene expression

T187 Modulation of the metabolic response to an endotoxin challenge in Brahman heifers through OmniGen-AF supplementation. N. C. Burdick*[1], J. A. Carroll[1], J. D. Chapman[2], T. H. Welsh Jr.[3], R. C. Vann[4], and R. D. Randel[5], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]Prince Agri Products Inc., Quincy, IL, [3]Texas AgriLife Research, Texas A&M System, College Station, [4]MAFES, Mississippi State University, Raymond, [5]Texas AgriLife Research, Texas A&M System, Overton.*

This study examined the effect of feeding OmniGen-AF (OG; Prince Agri Products) on the metabolic response of newly-weaned heifers to an endotoxin (lipopolysaccharide; LPS) challenge. Brahman heifers (n = 24; 183 ± 5 kg) from the Texas AgriLife Research Center in Overton, TX were separated into 2 treatment groups at weaning: 1) Control (C; n = 12) and 2) OG (n = 12; fed at 4 g per 45.4 kg BW) and fed for 69 d. On d 39, heifers were transported from Overton to New Deal, TX. On d 40, heifers were fitted with indwelling jugular catheters and moved into a barn with individual stalls. On d 41 heifers were challenged with LPS (0.25 µg/kg BW i.v.) and blood samples were collected at 0.5 h intervals from −2 to 8 h and again at 24 h relative to LPS challenge (0 h). Serum was isolated and stored at −80°C until analyzed for glucose, insulin, nonesterified fatty acids (NEFA), and blood urea nitrogen (BUN). Heifer weight was also recorded at various intervals throughout the study. Heifer BW increased throughout the study ($P < 0.01$) and was not affected by treatment ($P > 0.21$). Pre-LPS glucose concentration was greater in OG (255.7 ± 6.6 mg/dL) than C heifers (227.8 ± 6.6 mg/dL; $P < 0.01$). Glucose concentration increased post LPS ($P < 0.01$), but was not affected by treatment with OG ($P = 0.36$). Insulin concentration pre- and post-LPS was not affected by treatment with OG ($P = 0.84$ and 0.89). Post-LPS insulin concentration increased ($P < 0.01$) and peaked at 2 h post LPS. Pre- and post-LPS NEFA concentration was greater in C (0.19 ± 0.01 and 0.39 ± 0.01 mmol/L) than OG heifers (0.16 ± 0.01 and 0.31 ± 0.01 mmol/L; $P < 0.05$), with NEFA concentration increasing post LPS ($P < 0.01$). Pre- and post-LPS BUN concentration was also greater in C (10.2 ± 0.2 and 10.5 ± 0.1 mg/dL) than OG heifers (8.5 ± 0.3 and 9.3 ± 0.1 mg/dL; $P < 0.03$), with BUN concentration increasing post LPS ($P < 0.01$). These data suggest that supplementing heifers with OG altered their metabolic response by increasing available glucose before the LPS challenge and reducing the need for OG heifers to mobilize energy through lipolysis and proteolysis, which may have allowed for a more acute response to the challenge.

Key Words: cattle, metabolism, OmniGen-AF

T188 Ultrasound body composition traits response to an endotoxin challenge in Brahman heifers supplemented with OmniGen-AF. R. C. Vann*[1], N. C. Burdick[2], J. A. Carroll[2], J. D. Chapman[3], T. H. Welsh Jr.[4], and R. D. Randel[5], *[1]MAFES-Brown Loam Experiment Station, Raymond, MS, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Prince Agri Products Inc., Quincy, IL, [4]Texas AgriLife Research, Texas A&M University, College Station, [5]Texas AgriLife Research, Texas A&M University, Overton.*

This study examined the effect of feeding OmniGen-AF (OG; Prince Agri Products) on body composition response of newly weaned heifers to an endotoxin (lipopolysaccharide; LPS) challenge. OmniGen-AF is a yeast-based product and our hypothesis was that this yeast based product would provide a level of stress/immunological protection that would allow for nutrient sparing during times of stress. Brahman heifers (n = 24; 183 ± 5 kg) from the Texas AgriLife Research Center in Overton, TX were separated into 2 treatment groups at weaning: 1) Control (C; n = 12) and 2) OG (n = 12; fed at 4 g per 45.4 kg BW) and fed for 69 d. On d 39, heifers were transported from Overton to New Deal, Texas.

On d 40, heifers were fitted with indwelling jugular catheters and moved into a barn with individual stalls. On d 41, heifers were challenged with LPS (0.25 µg/kg BW i.v.) and blood samples were collected at 0.5 h intervals from −2 to 8 h and again at 24 h relative to LPS challenge (0 h). Ultrasound body composition traits for longissimus muscle area, rib fat, percent intramuscular fat and rump fat were collected at weaning (d 0), d 39, 44 and 69. Data were analyzed using the PROC Mixed procedure of SAS specific for repeated measures. Heifer BW increased throughout the study ($P < 0.001$) and was not affected by treatment ($P > 0.68$). Ultrasound body composition traits for longissimus muscle area, percent intramuscular fat, rib fat and rump fat increased ($P < 0.0001$) throughout the study. However, there were no effects ($P > 0.20$) of feeding treatment on ultrasound body composition traits throughout the study. There were tendencies ($P < 0.09$) for the OG group to have more stable rib fat and percent intramuscular fat measurements after transport and an endotoxin challenge. While no significant differences between treatments were observed in this study, the data suggest that OG supplementation before transport and LPS challenge may have preserved energy stores in Brahman heifers.

Key Words: cattle, ultrasound, OmniGen-AF

T189 Hepatic expression of mitochondrial respiratory complex genes of pure and crossbred beef cows grazing different herbage allowances of native pastures. M. Veyga, A. L. Astessiano, A. Kaitazoff, V. Bassaizteguy, A. I. Trujillo, and M. Carriquiry,* *School of Agronomy, UdelaR, Montevideo, Uruguay.*

Hepatic expression of genes encoding proteins of the mitochondrial respiratory complexes has been related to mitochondrial function and feed efficiency, which in turn may depend on nutritional plane and animal genotype. Adult cows (n = 24) in a factorial arrangement of herbage allowances throughout the year (2.5 vs. 4 kgDM/kgBW; LO vs. HI) and cow genotype (purebred: Angus and Hereford vs. F1 crossbred; PB vs. CB) were used in a complete randomized block design to evaluate hepatic expression of 9 genes encoding proteins of the mitochondrial respiratory complexes. Cows were maintained in the herbage allowance treatment since May 2007 and gestated and lactated one calf every year from 2007 to 2009. At the end of the third year, cows were slaughter at 190 ± 15 d postpartum and liver mass was recorded and samples were collected to measure gene expression by SYBR-Green real time PCR using HPRT and β-actin as endogenous control genes (which expression did not differ among cow groups by microarray analysis). Data were analyzed using a mixed model and means were considered to differ when $P < 0.05$. Liver mass did not differ between HI than LO cows but was less in PB than CB cows (45.9 vs. 49.6 ± 1.26 g/kgPV0.75). Expression of SDHA and SDHD (complex II), UQCRC1 (complex III) mRNA did not differ due to herbage allowances or cow genotype. However, hepatic expression of NDFUS4 (complex I, 0.90 vs. 1.51 ± 0.24), CYC1 (complex III, 0.68 vs. 1.05 ± 0.13), and ATP5B and ATP5O (complex V, 0.72 vs. 1.08 ± 0.16 and 0.56 vs. 1.02 ± 0.16, respectively) mRNA tended ($P \leq 0.094$) to be less in HI than LO cows. Hepatic expression of ATP5B and ATP5O and CYC1 and COX5B (complex IV) mRNA were greater in PB than CB cows (1.10 vs. 0.7 ± 0.17; 1.08 vs. 0.5 ± 0.16; 1.04 vs. 0.69 ± 0.13 and 1.28 vs. 0.97 ± 0.13, respectively). However, ATP50 mRNA tended ($P = 0.066$) to be affected by the interaction between herbage allowance and cow genotype as its expression was greater in LO-PB cows than the other groups. Results suggest that increased mitochondrial gene expression may compensate reduced liver size in PB than CB cows and could indicate a higher feed efficiency of cows grazing low vs. high herbage allowance of native pastures.

Key Words: liver, respiratory chain, mRNA

T190 Expression of adipokines and their receptors in adipose tissue of pure and crossbred beef cows grazing different herbage allowances of native pastures. A. Kaitazoff,* A. Casal, A. L. Astessiano, M. Veyga, A. I. Trujillo, and M. Carriquiry, *Facultad de Agronomía, UdelaR, Montevideo, Uruguay.*

Adipose tissue metabolism plays an important role during periods of negative energy balance or feed restriction and adipokines secreted by adipose tissue participated in regulating energy homeostasis. Pure and crossbred adult beef cows (n = 10) were used in a complete randomized block design to evaluate the effects of herbage allowances throughout the year (2.5 vs. 4 kgDM/kgBW; LO vs. HI) on adipokines and their receptors mRNA expression in mesenteric adipose tissue. Cows were maintained in the same herbage allowance treatment since May 2007 and gestated and lactated one calf every year from 2007 to 2009. At the end of the third year, cows were slaughter at 190 ± 15 d postpartum, mesenteric adipose tissue was dissected and weighed and samples were collected to measure gene expression by SYBR-Green real time PCR using HPRT and $\hat{I}^2$-actin as endogenous control genes. Data were analyzed using a mixed model and means were considered to differ when $P \leq 0.05$. Cow BW at slaughter did not differ between HI and LO cows (436 ± 16 kg). However, mesenteric adipose tissue mass was less for HI than LO cows (25.1 vs. 28.3 ± 2.6 g/kgPM). Adipose adiponectin (ADIPO) and its receptor-1 (ADIPOR1) mRNA expression were not affected by herbage allowance but ADIPOR2 mRNA tended ($P = 0.13$) to be greater for HI than LO cows (1.04 vs.0.57 ± 0.23). Expression of leptin and its receptor-b (LEPRb) mRNA, as well as insulin receptor (INSR) mRNA in adipose tissue did not differ between herbage allowances but LEPR-a was less in HI than LO cows (0.90 vs. 2.23 ± 0.69). Adipose angiopoietin-like protein 4 (ANGLP4) mRNA was greater in HI than LO cows (1.19 vs. 0.09 ± 0.65). Expression of adipokine receptors (ADIPOR2 and LEPR-a) as well as ANGPL4 mRNA in mesenteric adipose tissue could be mediating differences in energy metabolism in rangeland beef cows grazing different herbage allowances.

Key Words: beef cattle, grazing, adipokines

T191 Hepatokines in periparturient dairy cows with different extent of body fat mobilization. C. Schäff, T. Laeger, H. M. Hammon, M. Röntgen, and B. Kuhla,* *Nutritional Physiology "Oskar Kellner," Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Adropin and the fibroblast growth factor-21 (FGF21) are 2 hepatokines linking feed intake with energy homeostasis and lipid metabolism. While adropin acts to reduce feed intake and hepatic fat synthesis, FGF21 increases hepatic ketogenesis and feed intake/kg BW in rodents. Thus we investigated whether adropin and FGF21 are regulated during the periparturient period of dairy cows and if their expression/secretion is associated with the postpartum (pp) liver fat content (LFC). German Holstein cows (>10,000 kg milk/305 d; >2nd lactation) were grouped retrospectively according to the mean LFC pp in low (L; <24% total fat/DM; n = 9) and high (H; LFC > 24.4% total fat /DM; n = 10). Cows were fed TMR ad libitum and frequent blood samples were withdrawn to analyze the concentration of FGF21, nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHBA). Liver biopsies were taken at d −34, −17, 3, 18, 30 relative to parturition and at slaughter (d 40 pp) to measure LFC and mRNA concentrations of the hepatokines and the non-regulated house-keeping gene phosphoglycerate kinase 1 (PGK1) via real-time RT-PCR. Data were evaluated by Mixed Model of SAS with LFC and time as fixed effects and pairwise comparisons (multiple *t*-test). Daily dry matter intake (DMI) varied with time ($P < 0.001$) with a continuous rise after calving in both groups. The DMI/kg BW increased also with time

($P < 0.001$) and was lower in H than in L cows ($P < 0.01$). LFC peaked at d 18 pp and was higher in H than in L cows (H: 41.3%; L: 24.5%; $P < 0.001$). Pairwise comparison revealed that at d 30 pp, mRNA expression of adropin was higher in H than in L cows ($P < 0.05$). Expression of FGF21 was not different between groups. Plasma concentrations of FGF21 decreased from ante partum by d 3 pp and re-increased thereafter ($P < 0.01$) whereas NEFA and BHBA (each $P < 0.001$) were higher in H than in L cows pp. Higher expression of adropin in H cows after the LFC peak pp may contribute to the depletion of liver fat but also to the lower feed intake pp in H as compared with L cows. Hepatic FGF21 mRNA expression is not paralleled by FGF21 plasma concentration. Supported by DFG, Germany.

Key Words: dairy cow, adropin, FGF21

T192 Glucose and epinephrine tolerance tests in steers categorized as residual feed intake efficient versus inefficient. M. H. Ramos*[1], D. H. Keisler[2], and M. S. Kerley[2], *[1]Research Instituto Flavio Guarani - Rehagro, Belo Horizonte, Minas Gerais, Brazil, [2]University of Missouri, Columbia.*

Two experiments were performed to examine peripheral glucose and insulin dynamics in feedlot steers classified as residual feed intake efficient (–RFI) vs. inefficient (+RFI). Crossbred Angus steers were used in experiment one (n = 72; initial weight 333 ± 8.5 kg) and 2 (n = 60; initial weight 355 ± 7.3 kg). All steers were fed for a total of 70 d and had access to the same diet (87% corn, 8% corn distiller's grains, 1% blood meal, 1.6% feather meal, and 2.5% mineral and vitamins). Residual feed intake was calculated based on the regression of dry matter intake (DMI) onto metabolic body weight (BW0.75) and average daily gain (ADG). In experiment one, 2 –RFI and 2 +RFI steers were selected for a glucose tolerance test (GTT1) and in experiment 2, 4 –RFI and 4 +RFI steers were selected for a glucose tolerance test (GTT2) and an epinephrine tolerance test (ETT). Therefore, as planned, body weight and ADG did not differ ($P > 0.05$) between treatments for all tolerance tests, yet DMI and RFI differed ($P < 0.05$) between treatments for all tolerance tests, which allowed us to have 2 distinct groups of animals to perform our experiments. For GTT1, each steer was injected with 150 mg/kg BW of glucose via jugular catheter and 20 min later given 30 mU/kg BW of insulin. For GTT2, each steer was injected with 150 mg/kg BW of glucose via jugular catheter, but no insulin followed. For ETT, each steer was injected with 1 ug/kg BW of epinephrine via jugular catheter. Frequent blood samples were collected before and after injection of glucose for all tests. Serum was assayed for glucose and insulin. Basal, peak, area under the curve, clearance rate (%/min) and half-life's of glucose and insulin did not differ between treatments for GTT1 and GTT2. In addition, results for ETT did not show any difference ($P > 0,05$) for basal, peak, area under the curve, clearance rate (%/min) and half-life's of glucose and insulin. We conclude that peripheral glucose and insulin dynamics do not differ according to RFI classification of feedlot steers.

Key Words: RFI, glucose, epinephrine

T193 Insertion of used CIDRs on day 3 to 5 post-insemination in heifers to improve pregnancy rate. C. E. Ferguson*[1], B. Pousson[1], H. Nordberg[1], J. Veillon[1], W. Storer[1], and D. J. Kesler[2], *[1]McNeese State University, Lake Charles, LA, [2]University of Illinois, Champaign-Urbana.*

Increasing progesterone (P_4) concentrations from d 3 to 5 of the estrous cycle improves pregnancy rates in repeat-breeder beef cattle. This study was designed to determine if increasing P_4 on d 3 to 5 post-insemination improves pregnancy rates in beef heifers. A total of 92 beef heifers were used in 2 replicates during this experiment. All heifers were synchronized using the Co-Synch + CIDR protocol and were timed AI (TAI) at 56 h following $PGF_{2\alpha}$ administration and CIDR removal. They were administered 100 µg of GnRH at TAI and on d 3 to 5 post-GnRH all treated heifers received a used CIDR from the prior synchronization and control heifers received insertion of the empty CIDR gun. Jugular blood samples were collected from all heifers in replicate 2 (n = 60). Plasma P_4 concentrations were determined via radioimmunoassay, and ~30 post-TAI heifers were tested for pregnancy using ultrasonography. Statistical analysis was performed in SAS using a proc glm with a tukey's chi-squared and proc glimmix with lsmeans post-hoc tests. In replicate one, significantly more ($P < 0.05$) treated heifers were pregnant (12/16, 75%) compared with control heifers (5/16, 31%). In replicate 2, there was no difference in pregnancy rates for treated (12/30, 40%) and control (12/30, 40%) heifers. The mean pregnancy rates between replicates were different ($P < 0.05$); therefore, they were not combined. In replicate 2, all heifers in the control group with plasma P_4 below 1 ng/ml (on consecutive blood samples from d 3 to 5) were removed from further P_4 analysis. Plasma P_4 was significantly higher in pregnant vs. control heifers on d 4 (1.25 ± 0.09 ng/ml vs. 0.85 ± 0.21) and d 5 (1.89 ± 0.18 ng/ml vs. 1.40 ± 0.11). The pregnancy rate among the heifers, with >1ng/ml of P_4, was 12/21 (57%). Use of used CIDRs on d 3 to 5 produced variable pregnancy rates due possibly to differences in P_4 remaining within the CIDR. However, supplementing P_4 at this time may improve pregnancy rates as pregnant heifers had significantly higher P_4 concentrations during this time compared with open heifers.

Key Words: progesterone, heifer, supplementation

T194 Effect of phase of estrous cycle and fixed-timed insemination on fertility of Criollo cows after a norgestomet or progesterone based treatment. A. Quezada-Casasola*[1,2], L. Avendaño-Reyes[1], J. A. Ramírez-Godínez[3], J. R. Núñez-Cuesta[2], F. J. Carlos-Pérez[2], G. Mena-Ortíz[2], and K. Siqueiros[2], *[1]Instituto de Ciencias Agrícolas, Universidad Autónoma de Baja California, Mexicali, B. C., México, [2]Universidad Autónoma de Ciudad Juárez, Cd. Juárez, Chihuahua, México, [3]Universidad Autónoma de Chihuahua, Chihuahua, Chihuahua, México.*

Phase of estrous cycle and time of insemination were examined for their influence on fertility of 86 cycling mature Criollo (Corriente) cows after a 9-d norgestomet (Crestar; n = 28) or a 7-d progesterone (CIDR; n = 58) synchronization. Cyclicity was assumed if serum progesterone (P4) concentrations were ≥ 1 ng/mL in either one of 2 samples taken 8 d apart, being the second sample taken the same day of onset of synchronization treatment for phase of estrous cycle determination as well (follicular = P4 ≥ 1 ng / mL in first sample and < 1 ng/mL in second sample, and luteal P4 <1 ng/mL in first sample and ≥1 ng/mL in second sample). Cows were randomly inseminated at 48 or 60 h after the progestin or progesterone device withdrawal along with an injection of 100 µg of GnRH analog. Fertility (pregnancy rate as dependent variable and norgestomet or progesterone, phase of cycle and time of insemination as well as their interactions as independent variables) was analyzed using Proc Logistic of SAS. Synchronization method (Crestar and CIDR) had no effect on pregnancy rate (39.2% and 34.4%, respectively; $P > 0.1$). Also, cows with ovaries in follicular phase had similar pregnancy rate to those with ovaries in luteal phase (34.1% and 37.7%, respectively: $P > 0.1$). Pregnancy rate was higher in cows inseminated at 60 h than those at 48 h after progestin or progesterone removal (53.1% and 15.3%, respectively; $P < 0.01$). Follicular or luteal phase of estrous cycle at

start of treatment did not have an effect on pregnancy of Criollo cows after insemination. Furthermore, the higher pregnancy rate of cows inseminated 60 h after the end of progestin or progesterone treatment might indicate that, in Criollo cows, ovulation may occur at a longer time interval after synchronization treatment than other cattle breeds and/or that the dominant follicle and its oocyte present after synchronization require specific conditions that may include a longer period of time to be successfully ovulated.

Key Words: Criollo cattle, ovulation, artificial insemination

T195 Injection site does not alter effectiveness of beef cattle synchronization. C. L. Pickworth*[1,2], D. H. Poole[2], and W. Greene[1], *[1]The Ohio State University, Wooster, [2]North Carolina State University, Raleigh.*

Quality assurance programs are valuable assets to the beef cattle industry for improving meat product quality and consumer acceptance. A key area in beef quality assurance programs is to reduce injection site blemishes in valuable meat cuts by administering all intramuscular injections in the neck. A common belief among cattle producers utilizing estrus synchronization is that the drugs are more effective when administered in the rump compared with the neck. The objective of this study was to compare the effectiveness of injection site of prostaglandin (PGF2α) on first service conception rates following estrus synchronization. One hundred and 5 beef cows and heifers were blocked by breed and stratified by parity before being randomly assigned to 1 of 2 treatments. The 2 treatments were: intramuscular PGF2α administration in the neck or in the rump. Cows and heifers were synchronized using a combination of a 7 d intravaginal progesterone implant (CIDR) and PGF2α injection followed by estrus detection and breeding either on observed heats or timed insemination. Days pregnant was determined by a veterinarian using ultrasonography approximately 70 d post-insemination. Data were analyzed as a randomized complete block design in Proc Mixed with animal as the experimental unit. Differences are declared significant at $P < 0.05$ and means are reported as LS means. Site of PGF2α injection did not affect ($P > 0.05$) overall conception rates in response to artificial insemination at 57.5 and 55.6% conception after first service for cattle receiving injections in the neck and rump, respectively. Nor did injection site affect ($P > 0.05$) whether cattle were bred based on estrus detection or timed insemination. Parity and breed of cattle did not affect ($P > 0.05$) pregnancy rates, nor were there any interactions ($P > 0.05$) with site of injection. Overall conception rate at the end of the breeding season was 86.6%. Administering PGF2α intramuscularly in the neck does not alter conception rates or effectiveness of the synchronization protocols as is misconceived by producers. Therefore, all producers should follow beef quality assurance protocols when administering intramuscular injections during estrus synchronization.

Key Words: beef production, estrus synchronization, quality assurance

T196 Presynchronizing $PGF_{2\alpha}$ injection before a fixed time artificial insemination (TAI) CO-Synch + CIDR program. S. L. Hill*[1], S. L. Pulley[1], H. I. Mellieon Jr.[1], K. C. Olson[1], J. R. Jaeger[1], R. M. Breiner[1], G. A. Perry[2], G. C. Lamb[3], and J. S. Stevenson[1], *[1]Kansas State University, Manhattan, [2]South Dakota State University, Brookings, [3]University of Florida, Marianna.*

We hypothesized that follicular wave synchronization may be improved by inducing luteal regression before initiating a TAI program. The objective of the current study was to determine if injecting $PGF_{2\alpha}$ (PG) 3 d before initiating CO-Synch + CIDR program would: 1) increase uniformity of follicles; and 2) improve pregnancy outcomes. Suckled beef cows at 9 locations (n = 1,537) were assigned randomly to 2 treatments after stratification of cows based on breed, parity, and days postpartum: 1) PG-CO-Synch + CIDR: PG (25 mg i.m.) on d −-13, GnRH-1 (100 µg i.m.) and insertion of a CIDR insert on d −10, PG (25 mg i.m.) and CIDR insert removal on d −-3; or 2) control: same as PG-CO-Synch + CIDR without the initial PG injection. All cows were inseminated at 72 h after CIDR removal and GnRH-2 (100 µg i.m.) was administered after TAI. Blood was collected on d −23, −13, −10, −3, and 0 for later progesterone analyses. Cows treated with PG on d −13 were more likely ($P < 0.05$) to have luteolysis after d −13 than control cows (83 vs. 29%) and reduced ($P < 0.05$) serum progesterone (0.55 vs. 1.40 ng/mL) on d −10. PG-CO-Synch + CIDR cows had larger ($P < 0.05$) follicles (12.5 vs. 10.8 ± 0.4 mm) on d −10 and more ($P < 0.05$) ovulated after GnRH-1 than controls (60.6 vs. 36.5%); however, follicle diameters on d 0 were not more uniform in PG-CO-Synch + CIDR cows. Multiparous cows treated with PG on d −13 had a greater ($P < 0.05$) incidence of estrus between d −13 and −10 than multiparous controls and all treated and control primiparous cows (32.3 vs. 15.4, 16.8 and 16.2%, respectively). Incidence of estrus between d −3 and 0 after PG on d −3 was likewise greater ($P < 0.05$) for treated multiparous cows vs. other treatment-parity groups (74.1 vs. 64.3, 58.6, and 59.1%, respectively). Pregnancy rates at d 35 did not differ between treatments but were greater ($P < 0.001$) at d 35 (60.0 vs. 47.7%) and at the end of the breeding season (96.2 vs. 92.3%) for multiparous vs. primiparous cows, respectively. In summary, more multiparous cows in the PG-CO-Synch + CIDR treatment exhibited estrus and had greater pregnancy outcomes than primiparous cows, but no overall treatment advantage was detected compared with the control.

Key Words: timed AI, luteolysis, follicle diameter

T197 Effects of pregnancy on endometrial gene expression related to amino acid, fatty acid and glucose metabolism in dairy cattle. R. L. A. Cerri*[1,2], I. M. Thompson[1], I. H. Kim[3], A. D. Ealy[1], P. J. Hansen[1], C. R. Staples[1], J. L. Li[1], and W. W. Thatcher[1], *[1]University of Florida, Gainesville, [2]University of British Columbia, Vancouver, BC, Canada, [3]Chungbuk National University, South Korea.*

Objectives were to determine effects of pregnancy on endometrial gene expression related to amino acid, fatty acid and glucose metabolism on d 17 of the estrous cycle and pregnancy. Heifers (n = 33) were assigned randomly after parturition to lactating (L, n = 17) or nonlactating (NL, n = 16) groups. Cows were subjected to an ovulation synchronization program for a timed artificial insemination (TAI); 10 cows in L and 12 in NL were inseminated. Slaughter occurred 17 d after the day equivalent to TAI, and conceptus and intercaruncular endometrial tissues collected. Only pregnant (L, n = 8; NL, n = 6) and non-inseminated cyclic (L, n = 7; NL, n = 4) cows were analyzed. Microarray analysis used the bovine Affymetrix platform. Data were analyzed using Bioconductor GCRMA and Limma methods. Differentially expressed genes were selected with P-value <0.01 and fold differences >1.5. Analyses detected 697 genes differentially expressed for pregnancy (406 downregulated and 291 upregulated). Gene ontology (GO) analyses of downregulated genes during pregnancy revealed several terms related to amino acid, fatty acid or glucose metabolism. Genes upregulated in pregnant cows were associated with 89 GO terms, among them terms related to amino acid metabolism (amino acid and derivative metabolic processes, GO:0006519; translation, GO:0006412), fatty acid metabolism (monocarboxylic acid metabolic processes, GO:0032787), and glucose metabolism (carboxylic acid metabolic process, GO:0019752). Several genes such as ASL, ARG2, SLC27A5, CRAT, FBP1, PCK2, SLC2A1

were upregulated in pregnancy and are candidate targets for interventions aiming for improvement in fertility of dairy cows. New insights into changes that occur in the endometrium during the period of corpus luteum maintenance identify several upregulated metabolic genes that may contribute to countering sub-fertility observed in lactating dairy cows.

Key Words: endometrium, gene expression, pregnancy

T198 Use of bovine pregnancy-associated glycoproteins (bPAGs) to diagnose pregnancy in postpartum Nelore beef cows. K. G. Pohler*[1], M. F. Smith[1], T. Martins[2], R. F. G. Peres[3], and J. L. M. Vasconcelos[2], *[1]Division of Animal Sciences, University of Missouri, Columbia, [2]FMVZ – UNESP, Botucatu, SP, Brazil, [3]Agropecuária Fazenda Brasil, Barra do Garças, MT, Brazil.*

Although accurate pregnancy diagnosis is a critical factor affecting reproductive management success, relatively few beef operations utilize the technology. Binucleate trophoblast cells constitute 15 to 20% of the ruminant placenta trophoblast population, appear around d 19 to 20 of gestation in cattle and secrete bPAG. Bovine PAG are commonly used to diagnose pregnancy success in *Bos taurus* breeds and are a marker of placental function; however, much less is known about the efficacy of bPAG for pregnancy diagnosis in *Bos indicus* breeds. The objective was to measure serum concentrations of bPAG to detect the presence of an embryo/fetus on d 30 after artificial insemination (AI; d 0) in *Bos indicus* (Nelore) beef cows. In experiment 1, postpartum Nelore beef cows (n = 56) were AIed at a fixed time following synchronization of ovulation. Serum samples were collected on d 0, d 21, d 24, d 27, and d 30. Real-time ultrasonography for diagnosis of pregnancy was performed on d 30 with 39% confirmed pregnant (n = 22). The first increase ($P < 0.0001$) in serum bPAG occurred on d 24 and there was no relationship ($P = 0.44$) between ovulatory follicle diameter and bPAG concentrations at d 30; which is similar to *Bos taurus* breeds. In experiment 2, ovulation was synchronized in postpartum Nelore beef cows (n = 720). Pregnancy diagnosis and blood sample collection occurred between d 29 and 33 post insemination. Pregnancy rate at d 30 was 54% (n = 386) and average serum concentration of bPAG was 15.11 ± 9.92 ng/mL (mean ± SD). Serum concentrations of bPAG accurately detected pregnancy in 97% of all cows compared with real-time ultrasonography and none of the nonpregnant cows had a serum bPAG concentration that exceeded the threshold level for pregnancy detection. Serum concentrations of bPAG were higher ($P < 0.03$) in primiparous cows (n = 55; 20.45 ng/mL ± 1.80 ng/mL; mean ± SEM) compared with multiparous cows (n = 331; 14.23 ng/mL ± 0.49 ng/mL; mean ± SEM). In summary, bPAG first increased in Nelore beef cows on d 24 following insemination and a single serum sample on d 29–33 post-insemination was 97% accurate in diagnosing pregnancy.

Key Words: cattle, pregnancy, placenta

T199 Fetal to maternal transplacental DNA transfer in female beef cattle. D. R. Eborn,* T. G. McDaneld, R. M. Thallman, and S. E. Echternkamp, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Exchange of DNA between mother and fetus has been well documented in humans but only limited reports exist for beef cattle. Our objective was to determine if we could detect male fetal DNA in the maternal blood after parturition. Whole blood was collected within 48 h after parturition from multiparous (n = 48) and primiparous (n = 54) bovine females having single (n = 75) or twin (n = 27) births. Real-time PCR analysis was performed on genomic DNA, extracted from the blood sample, using male-specific primers that target the Y chromosome. Male genomic DNA isolated from whole blood was also included in each assay as a positive control. No dams (n = 30) giving birth to only female offspring were positive for the Y PCR test. However, of the dams that gave birth to a male calf (n = 72), a total of 9 were positive for the Y PCR test. Common characteristics of those 9 females included 8 primiparous and 1 multiparous (second parturition) dams that birthed either a single male calf (n = 4) or twins (n = 5) that included at least 1 male. In addition, 3 of the 4 single male births experienced dystocia requiring assistance with a calf jack, and the positive multiparous dam gave birth to a set of twins (1 male, 1 female) that were dead at birth due to dystocia. Samples that were positive for the Y PCR test were reassayed with the same primers as well as with additional Y-specific primers obtained from a bovine SNP beadchip assay to confirm results. Six of the 9 females that were positive for the original Y-PCR test were also positive for the additional Y SNP PCR tests. Results indicate that DNA can be transferred from the fetus to the dam and that it may be more likely to occur in younger females experiencing trauma at calving such as dystocia or birth of twins. USDA is an equal opportunity provider and employer.

Key Words: Y chromosome, parturition, transplacental DNA transfer

T200 Nutrient restriction during early pregnancy alters cotyledon arterial vascular reactivity in response to bradykinin in beef cows. A. Reyaz*[1], F. Yao[2], M. S. Sane[2], L. E. Camacho[1], C. O. Lemley[1], K. C. Swanson[1], S. T. O'Rourke[2], and K. A. Vonnahme[1], *[1]Center for Nutrition and Pregnancy, Department of Animal Sciences, Fargo, [2]Department of Pharmaceutical Sciences, North Dakota State University, Fargo.*

It is hypothesized that altered uterine or umbilical blood flows in nutrient restricted cows would be due to changes in placental arterial sensitivity to bradykinin (BK). To examine the effects of maternal nutrient restriction on cotyledonary (COT) artery vasoactivity during early gestation, multiparous beef cows were randomly assigned to either 100% (CON; n = 6) or 60% NRC requirements (RES; n = 4) on d 30 of gestation. At d 85 of gestation cows were slaughtered and arteries that terminated into the fetal portion of the placentome (COT artery) were dissected to be used for in vitro vasoreactivity assays using wire myography. Arterial rings were placed into organ chambers of a wire myograph filled with 5 mL of physiological saline aerated with a mixture of 95% O_2 and 5% CO_2. The arterial rings were normalized by progressive stretching. The presence or absence of endothelium in the arterial rings was verified by testing the ability of BK (10–7 M) to produce endothelium-dependent relaxation in arteries pre-contracted with U46619 (10–6 M). Endothelium-intact rings were contracted with U46619 (10–6 M) and the dose response curve (DRC) to BK was obtained. In addition, a BK DRC was obtained for rings which were incubated for 30 min with inhibitors to: 1) BK2 receptor, HOE 140 (10–6); 2) Ca^{2+}-activated K+ channels, iberiotoxin (IBTx;10–7 M); and 3) endogenous nitric oxide synthase; N(omega)-L-arginine (NLA 10–5). Cotyledonary arteries from RES cows were more sensitive ($P < 0.01$) to a BK induced relaxation compared with CON cows. There was a treatment by dose interaction ($P = 0.02$) when arteries were incubated with HOE140, with COT arteries from CON cows contracting, and no change in vasoactivity observed in COT arteries from RES cows. CON cows were more sensitive ($P < 0.01$) to BK induced relaxation in the presence of IBTx compared with RES cows. There was no effect ($P = 0.56$) of maternal diet in the response to BK when COT arteries were in the presence of NLA, which blocked relaxation.

Alterations in placental vasoactivity may affect uterine-umbilical blood flows and nutrient availability to the developing calf.

Key Words: bradykinin, cow, placenta

T201 Assessment of serum IGF-1 and β-hydroxybutyrate concentrations on reproductive performance prior to calving and breeding in young beef cows grazing native range. J. T. Mulliniks*[1], A. J. Roberts[2], R. C. Waterman[2], T. W. Geary[2], E. J. Scholljegerdes[1], and M. K. Petersen[2], *[1]New Mexico State University, Las Cruces, [2]USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.*

Metabolites involved in the metabolic adaptation to negative energy balance may potentially contribute to regulation of reproductive success. Therefore, the objective of this 4-yr study was to determine the association of serum metabolites, cow BW, BCS, and calf performance on conception date in spring calving 2- and 3-yr-old beef cows (n = 381) grazing native range at the Fort Keogh Livestock and Range Research Laboratory. Cows were classified by subsequent calving date in a 55 ± 2 d breeding season as either conceiving early (EC; conceived in first 15 d of breeding) or late (LC; conceived during the remaining breeding season). Blood samples were collected in 2 periods 30 ± 1 d before calving and 14 ± 1 d before breeding to determine circulating concentrations of IGF-1 and β-hydroxybutyrate (BHB). Assignment to conception group resulted in a mean conception date that was 33 d earlier ($P < 0.01$) in EC than LC cows. Cow age × sample period × conception date interaction ($P < 0.01$) occurred for serum BHB concentrations. Serum BHB concentrations were similar ($P > 0.10$) for 2-yr-old cows regardless of their conception date classification and sampling period. However, pre-calving serum BHB concentrations were greater ($P < 0.01$) for LC than EC in 3-yr-old cows with no difference ($P = 0.86$) at pre-breeding. Serum IGF-1 concentrations were greater ($P < 0.01$) for EC cows relative to LC cows at pre-calving and pre-breeding sampling periods. Cow BW and BCS were not different ($P \geq 0.43$) at pre-calving or pre-breeding between EC and LC cows. Calf BW at birth was not different ($P = 0.25$) between EC and LC cows, but EC cows weaned lighter (205-d BW; $P < 0.01$) calves, suggesting more energy may have been diverted from milk production toward reproduction in EC cows. This study indicates that pre-calving serum concentrations of BHB and IGF-1 may be indicative of their capacity for subsequent rebreeding. Chute-side measurements of these factors may provide producers opportunity to manage cows differently to improve overall reproductive efficiency.

Key Words: beef cows, conception date, serum metabolites

T202 Sex comparison of white Fulani cattle blood profile in southwestern Nigeria. A. O. Ladokun*[1], O. A. Oyebode[1], and T. O. Ososanya[2], *[1]University of Agriculture, Abeokuta, Ogun, Nigeria, [2]University of Ibadan, Ibadan, Oyo, Nigeria.*

Sexual dimorphism has been established in the brain regions of farm animals and poultry, but for their blood, reports do not agree as to differences at the same age. While some reports show no differences except for pregnant and lactating females, others indicate otherwise. This study was carried out to investigate the blood of white fulani breed of cattle in southwestern Nigeria if there would differences at same matured age (4 yr). A total of 100 cattle was used consisting of 50 bulls and 50 cows. Full hematology was investigated using the Vet Auto hemoanalyser machine. Some serum metabolites were also investigated including Total Protein, Albumin and total cholesterol. Data obtained were subjected to one-way ANOVA (ANOVA). The results show that white blood cell count (WBC) was significantly ($P \leq 0.05$) higher in females (17.23 ± 1.08) than in males (12.25 ± 0.77). Mean corpuscular hemoglobin concentration (MCHC) also showed sex differences with females having higher and significant ($P \leq 0.05$) average value (33.8 ± 0.19) than males (32.6 ± 0.24). The results from Serum analysis show that bulls (with 37.8 ± 0.54) have higher and significant ($P \leq 0.05$) Albumin values than cows (34.9 ± 0.29). Though the results obtained in this study fall within normal ranges for this species, it however does not indicate any specific sex effect for this breed.

Key Words: cattle, blood, sex

T203 Maternal diet restriction effects on fetal organ weights in beef cows during early pregnancy. L. E. Camacho,* C. O. Lemley, T. J. Swanson, K. C. Swanson, and K. A. Vonnahme, *Department of Animal Sciences, North Dakota State University, Fargo.*

The objectives were to examine the effects of maternal nutrient restriction on fetal organ weights during early gestation. On d 30 of pregnancy, multiparous beef cows were randomly assigned to either 100% (CON; n = 6) or 60% NRC requirements (RES; n = 6). Cows were individually fed once daily in a Calan gate system at 1000 h. At d 85 of gestation cows were slaughtered and fetal organ tissues were collected and weighed. Fetal eviscerated weight (g) was greater ($P = 0.05$) in RES vs. CON. Absolute fetal organ or tissue weights (g) and fetal organ or tissue weights relative to fetal weight (g/kg) were not different ($P \geq 0.09$) between dietary treatmens for adrenals, kidneys, perirenal fat, spleen, or stomach complex. Fetal brain weight was not different ($P = 0.5$) between treatments, while brain weight relative to fetal weight was decreased ($P = 0.02$) in RES vs. CON. Fetal lung weight was not different ($P = 0.67$) between treatments, while lung weight relative to fetal weight was decreased ($P = 0.04$) in RES vs. CON. Heart weight was increased ($P = 0.001$) in RES vs. CON fetuses, while heart weight relative to fetal weight was not different ($P = 0.33$) between treatments. Fetal pancreas weight was increased ($P = 0.06$) in RES vs. CON, while pancreas weight relative to fetal weight was not different ($P = 0.17$) between treatments. Fetal omental and mesenteric fat weight and omental and mesenteric fat relative to fetal weight were increased ($P \leq 0.06$) in RES vs. CON. Maternal diet restriction during early pregnancy alters fetal organ weights. Interestingly, compensatory fetal intra-abdominal visceral fat deposition appears to occur when beef cows are nutrient restricted during early gestation.

Key Words: beef cows, fetal organs, nutrient restriction

T204 Maternal feed efficiency during gestation is correlated with offspring birth weight and girth in nutrient restricted and control-fed ewes. A. M. Meyer*[1], K. A. Vonnahme[2], D. A. Redmer[2], L. P. Reynolds[2], and J. S. Caton[2], *[1]Department of Animal Science, University of Wyoming, Laramie, [2]Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University, Fargo.*

We hypothesized that some of the variation in offspring fetal and neonatal growth observed within a given gestational nutritional treatment (e.g., nutrient restriction) in developmental programming studies is related to differences in maternal metabolic efficiency and nutrient utilization. Thus, our objective was to investigate the relationship of maternal feed efficiency (G:F) during gestation with offspring birth and neonatal responses. Data from 2 studies with similar designs and dietary treatments were utilized. In both studies, primiparous ewes with singleton pregnancies received a pelleted diet providing either 100% (control; n = 24) or 60% (nutrient restricted; n = 24) of NRC recommendations for

gestation. Nutritional plane treatments began on d 40 to 50 of gestation and lasted until parturition. Ewes were fed individually, and G:F was calculated as ADG (g/d) divided by DMI (g/d). At birth, lambs were immediately removed from their dams for artificial rearing. Data were analyzed using the CORR procedure of SAS to determine the relationship of ewe G:F during gestation with lamb measures within each nutritional plane. For nutrient restricted ewes, gestational G:F (range: −0.12 to 0.10) was positively correlated with birth weight (r = 0.50; P = 0.01), curved crown rump length (CCR; r = 0.46; P = 0.02), and heart girth (r = 0.60; P = 0.002), as well as BW at 7 d (r = 0.46; P = 0.03) and 21 d (r = 0.42; P = 0.04). Despite this, G:F of nutrient restricted ewes was not correlated (P = 0.59) with lamb ADG from birth to 21 d. For control ewes, gestational G:F (range: 0.08 to 0.21) also was positively correlated with birth weight (r = 0.39; P = 0.06) and heart girth (r = 0.54; P = 0.006), but was not correlated (P > 0.16) with CCR, 7- or 21-d BW, or ADG to 21 d. These data indicate that ewe metabolic efficiency and nutrient utilization, as measured by G:F, are related to lamb weight and size at birth. This relationship is stronger in a nutrient restriction model, suggesting that more efficient dams are able to partition more nutrients for fetal growth when nutrients are limiting.

Key Words: developmental programming, feed efficiency, fetal growth

T205 Nutrient intake during lactation affects performance of beef cows and calf growth. K. J. McLean,* B. H. Boehmer, L. J. Spicer, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Fall calving cows grazing native grass pasture were used during 3 consecutive years (n = 44, n = 51 and n = 58, respectively) to evaluate the effects of nutritional supplementation during breeding and the first trimester of gestation on cow performance, plasma IGF-1, and subsequent postnatal growth of calves. Cows calved in Sept-Oct and were assigned to control (C, 1.82 kg/d of 38% CP supplement, approximately 100% of NRC requirements) or low (L, 0.2 kg/d of 8% CP supplement) from November 17 to March 20; supplement was individually fed in a stall barn. Cows were maintained on the same pasture and exposed to bulls for 60 d commencing Dec. 1. During lactation half of the cows on the C and L prenatal treatments were assigned to the C treatment the other half was assigned to the L treatment. The GLM procedure (SAS) was used to analyze BW, BCS and plasma IGF-1 of cows, and calf BW, as a 2X2 factorial ANOVA. Control cows lost less BW from Nov. to Jan. compared with L cows (37.8 ± 3.1 and 59.2 ± 3.1 kg, respectively, P < 0.001). Control cows were also heavier in May compared with L cows (566 ± 10 and 538 ± 10 kg, respectively, P = 0.05). However, BCS was not influenced (P > 0.11) by treatments. At breeding in Dec., C cows tended (P = 0.06) to have greater plasma concentrations of IGF-1 compared with L cows (26 ± 3 and 17 ± 3 ng/mL, respectively). Birth weight and postnatal growth of calves was not influenced (P = 0.63) by prenatal treatment. Calves on postnatal C cows had greater ADG from birth to Jan. compared with L calves (0.81 ± 0.03 and 0.74 ± 0.02 kg/d, P = 0.05). Weaning weight (205 d) was greater for calves on postnatal C versus L cows (188 ± 5 and 173 ± 4 kg, respectively, P = 0.02). Protein supplementation of beef cows during early gestation that caused greater BW loss, less BW gain of suckling calves, and reduced plasma concentrations of IGF-1, did not alter birth weight or postnatal growth of prenatally exposed calves.

Key Words: beef cows, gestation, nutrition

T206 Mineral supplementation associated with Megalac E and/or citrus pulp during timed AI synchronization programs in postpartum Nellore cows. **M. V. Biehl*[1], A. V. Pires[2,1], I. Susin[2], D. D. Nepomuceno[2], J. R. S. Goncalves[3], R. Sartori[2], F. M. da Rocha[1], L. H. Cruppe[4], J. L. M. Vasconcelos[5], and M. L. Day[4],** *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, PR, Brazil, [4]The Ohio State University, Columbus, [5]Sao Paulo State University, Botucatu, SP, Brazil.*

The objective of this study was to compare reproductive performance of Nellore cows (n = 215), synchronized with a 7 or 9-d CIDR + estradiol benzoate (EB) and 3 supplementation programs. Cows were blocked according to BW (428 ± 3.43), BCS (2.77 ± 0.03, scale 1–5) and DPP (81.9 ± 1.16) in a 2 × 3 factorial arrangement. The supplements were: mineral mixture (MM); MM + MegalacE + citrus pulp (CP) (MEG); MM + Kaolim + CP (KAO). Supplementation began 30 d before CIDR insertion and were terminated 30 d after timed AI. Blood samples for P4 analysis were collected 10 d before and at CIDR insertion to determine reproductive status. The CIDR was inserted with 2 mg of EB and it was removed either 7 or 9 d later. All cows received 25 mg PGF (Lutalyse) 48 h before CIDR removal, 300 IU eCG (Novormon) and 0.6 mg estradiol cipionate (ECP) at CIDR removal. Treatments were: 7dMM (n = 35; e.g., 7d CIDR and MM supplementation), 7dKAO (n = 34), 7dMEG (n = 36), 9dMM (n = 36), 9dKAO (n = 36), and 9dMEG (n = 38). Estrus was detected for 48 h and timed AI performed 50 h after CIDR withdrawal. Rebreeding with bulls 10 d after AI for period of 30 d. Pregnancy diagnosis was performed 30 and 60 d after AI. At CIDR insertion, 73.8% (158/215) of cows were anestrus. Estrus was detected in 77.7% (167/215) of the cows and time to estrus (41.2 ± 0.5 h) did not differ among CIDR and supplementation treatments. Timed AI pregnancy rates neither differed between the length of CIDR treatments nor among the supplementation programs (7dMM, 51.4%; 7dKAO, 50%; 7dMEG, 27.8%; 9dMM, 36.1%; 9dKAO, 38.9% and 9dMEG, 36.8%). Natural mating rebreeding pregnancy rate also did not differ between the length of CIDR treatments and among the supplementation programs. Final pregnancy rate was greater (P < 0.05) for the supplement KAO compared with the MEG (84.3 and 67.6%, respectively), and the MM group did not differ from any of the treatments. In conclusion, supplementation with Kaolim + CP or Megalac E + CP did not improve reproductive performance. In addition, timed AI pregnancy rates did not differ between 7-d and 9-d CIDR+EB programs.

Key Words: Megalac E, beef cows, timed AI

T207 Different luteolytic doses of $PGF_{2\alpha}$ in Nellore cows on days 5 and 7 of the estrous cycle. M. V. C. Ferraz Junior[1], A. V. Pires[2], R. Sartori[2], M. V. Biehl*[1], D. D. Nepomuceno[2], I. Susin[2], E. M. Ferreira[2], F. M. Rocha[1], J. R. S. Goncalves[3], L. H. Cruppe[4], and M. L. Day[4], *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, PR, Brazil, [4]The Ohio State University, Columbus.*

The aim of this study was to evaluate the luteolytic competence of different PGF2α (PGF) doses on d 5 and 7 of the estrous cycle. Nonlactating Nellore cows in random stages of the estrous cycle were treated with 25 mg PGF (Lutalyse) for synchronization purpose. Three hundred and 39 cows detected in estrus after PGF injection were divided into 2 groups to be treated on d 5 or d 7 of the subsequent estrous cycle. Treatments consisted of 3 different PGF doses (12.5, 25 and 50 mg) within target d of the cycle (d 5 and d 7). Treatments were defined as follow: 5d12.5PGF (n = 57); 5d25PGF (n = 58); 5d50PGF (n = 58); 7d12.5PGF (n = 56); 7d25PGF (n = 55) and 7d50PGF (n = 55). Blood samples for progesterone (P4) analysis were collected at 0, 24 and 48

h after PGF treatments to assess the incidence of luteal regression. The presence of a CL was defined as P4 concentration ≥1 ng/ml at the time of PGF and its regression defined as attainment of concentrations of P4 ≤ 1 ng/ml by 48 h after PGF. Detection of estrus was performed twice daily with the aid of teaser bull for 5 d after PGF. Serum P4 concentrations were quantified using a chemiluminescent immunoassay (Immulite 1000, Siemens Healthcare Diagnostics, Deerfield, IL, USA). Data were analyzed using the GLIMMIX and MIXED procedures of SAS. Estrus detection rate was greater ($P < 0.05$) in animals treated on d 7 compared with d 5 of the estrous cycle (48.8% and 32.4%, respectively). Furthermore, as dosage of PGF increased, the estrus detection rate increased ($P < 0.05$; 24.8%, 41.6% and 54.9% for the 12.5, 25 and 50 mg doses, respectively). Interactions of d of the estrous cycle and PGF dose were not detected for estrus detection rate. Incidence of luteolysis was greater ($P < 0.05$) on d 7 compared with d 5 of the estrous cycle (75.9% and 40.5%, respectively) and increased with dose of PGF (41.6%, 56.6% and 75.2% for 12.5, 25 and 50mg, respectively), with no day x dose interaction. In conclusion, in Nellore cows, the capacity of PGF to induce luteal regression increases between d 5 and 7 of the estrous cycle and as dose of PGF increases from 12.5 to 50 mg/dose.

Key Words: luteolysis, estrous cycle, beef cows

T208 Relationship of body condition with serum prolactin, antral follicle count, and calving rate of beef cows. M. L. Looper*[1], J. D. Patterson[1], B. C. Williamson[1], D. M. Hallford[2], and C. F. Rosenkrans Jr.[1], *[1]University of Arkansas, Fayetteville, [2]New Mexico State University, Las Cruces.*

Multiparous (mean age = 7.6 ± 2.1 yr; range 4 to 11 yr), Brahman-influenced beef cows were managed to achieve thin (BCS = 4.3 ± 0.6; BW = 462 ± 51 kg; n = 43) or good (BCS = 6.4 ± 0.8; BW = 582 ± 81 kg; n = 54) body condition (BC) beginning 164 d before breeding to determine the relationship of BC on serum prolactin, total antral follicle count, and calving rate. Cows grazed replicated (n = 4) common bermudagrass during a 60-d breeding season. Blood samples were collected at d 0, 30, and 60 of the breeding season, and serum concentrations of prolactin (PRL) were quantified; serum progesterone was determined on d −10 and 0 of the breeding season to determine luteal status at the beginning of breeding. Antral follicle count (AFC; total number of follicles >3 mm in diameter on both ovaries) was determined via ultrasonography at d 0 and 60 of the breeding season. Ovarian pairs were classified as low (<16 antral follicles), intermediate (16 to 24 antral follicles), or high (>24 antral follicles) AFC. Body weight and BCS were recorded during the breeding season (d 0, 30, and 60). Data were analyzed with ANOVA (model included BC, luteal status, and their interaction; pasture was used as a random effect), and CORR and chi-squared analyses of SAS. Seventy percent of cows were cyclic at the start of breeding. Thin cows gained more ($P < 0.001$) BW (76 ± 4 kg) and BC (1.0 ± 0.1 BCS units) than good-BC cows (51 ± 5 kg; 0.2 ± 0.1 BCS units) during the breeding season. Concentrations of serum PRL tended ($P < 0.12$) to be greater in cyclic cows (n = 68) than anestrous cows (n = 29) on d 30 and 60 of the breeding season. Cyclic cows had a decreased ($P < 0.02$) actual AFC on d 0 of the breeding season compared with anestrous cows (15.8 ± 1.4 vs. 21.7 ± 2.2 antral follicles, respectively). A luteal status × BC interaction tended ($P < 0.10$) to influence actual AFC on d 60 of the breeding season; anestrous, thin cows (21.3 ± 1.8 antral follicles) had increased actual AFC compared with all other groups (mean = 14.6 ± 2.1 antral follicles). More ($P < 0.05$) cyclic cows were classified as low AFC on d 0 than anestrous cows. Similarly, a greater ($P < 0.05$) number of cyclic cows than anestrous cows were classified as low or intermediate AFC on d 60. Body condition score on d 0 ($r = -0.29$; $P < 0.005$) and 60 ($r = -0.31$; $P < 0.003$) of the breeding season was inversely correlated with actual AFC on d 0. Calving rate was reduced ($P < 0.0001$) in thin cows (46%) compared with good-BC cows (87%). Calving rate of cows was similar ($P > 0.10$) among classifications of AFC at d 0 and 60 and averaged 76%. Luteal status tended to affect serum PRL during the breeding season. Further, presence of serum progesterone indicative of luteal activity as well as good BC appeared to negatively influence AFC in Brahman-influenced cows.

Key Words: antral follicle count, beef cow, prolactin

T209 Serum progesterone concentrations in Holstein and Nelore cows after the insertion of two different progesterone devices. A. B. Nascimento*[1], P. L. J. Monteiro Jr.[1], F. L. M. Silva[1], M. M. Guardieiro[1], A. B. Prata[1], G. P. Nogueira[2], G. B. Mourão[1], M. C. Wiltbank[3], A. V. Pires[1], and R. Sartori[1], *[1]University of São Paulo, Piracicaba, SP, Brazil, [2]São Paulo State University, Araçatuba, SP, Brazil, [3]University of Wisconsin-Madison, Madison.*

The objective of this study was to compare the circulating progesterone (P4) profile for 2 different commercial devices for delivery of P4, CIDR (1.9 g, Pfizer) and Sincrogest (1.0 g, Ourofino) in Holstein and in Nelore cows. We hypothesized that independent of the P4 device inserted, the P4 concentrations would be lower in Holstein than in Nelore cows, possibly due to greater P4 metabolism in dairy than in beef cattle. Also, we hypothesized the lower content of P4 present in Sincrogest (1.0 g) would produce lower circulating P4 than CIDR (1.9g) in either Holstein or Nelore cows. Nonlactating, non-pregnant cows (n = 10 Holstein and n = 10 Nelore) were randomly assigned to 1 of 2 groups: CIDR or Sincrogest devices. Blood samples were taken from all cows at hour 0, 1, 6, 12, 24, and 48 after insertion of the devices to analyze P4 concentration by radioimmunoassay. Cows were fed a maintenance diet 14 h before device insertion and at 12, 24, and 48 h after device insertion (following blood sampling). Data were analyzed using generalized linear models, considering the heterogeneous first-order autoregressive covariance matrix, due to repeated measures on the same cow at different times. There was a significant effect of breed (1.18 vs. 2.24 ng/mL, Holstein vs. Nelore, $P = 0.0004$), type of P4 device (1.99 vs. 1.43, CIDR vs. Sincrogest, $P = 0.03$), time ($P < 0.05$), and an interaction of breed by time ($P = 0.0004$). Progesterone concentrations were different ($P < 0.01$) among Holstein and Nelore at hour 0, 1, 6, 12, 24, and 48. Circulating P4 differed or tended to differ for CIDR vs. Sincrogest at hour 1 ($P = 0.09$), 6 ($P = 0.07$), 12 ($P = 0.09$), 24 ($P = 0.05$), and 48 ($P = 0.01$) but not at hour 0 ($P = 0.83$). Thus, independent of the brand of P4 device utilized, P4 concentrations were about 90% greater in Nelore than in Holstein cows, probably due the higher P4 metabolism in Holsteins. Interestingly, the Sincrogest device with 47% less P4 than the CIDR device, produced circulating P4 that was only 28% lower than CIDR. Supported by FAPESP, CAPES and CNPq of Brazil.

Key Words: intravaginal progesterone device, *Bos taurus*, *Bos indicus*