GROWTH & DEVELOPMENT II

1180 (W116) Effect of incubation temperature on the proliferation and differentiation of pig preadipocytes in primary culture. A. E. Bohan*, J. Bartosh, and T. D. Brandebourg, *Auburn University, Auburn.*

Better understanding molecular mechanisms governing the proliferation and differentiation of pig preadipocytes may provide insight into the regulation of adipose tissue development in vivo. Primary cultures of pig preadipocytes have served as a useful tool for investigating these mechanisms. However, to date, such cultures have generally been maintained at 37°C while normal body temperature in pigs is 39.2°C. This raises questions concerning the physiological relevance of culturing primary pig preadipocytes at 37°C. The objective of this study was to investigate the effect of culture temperature, 37 vs. 39°C, on the proliferation and differentiation of pig preadipocytes in primary culture. The effect of temperature on preadipocyte proliferation was determined using the MTT, resazurin, and cell count assays as markers for proliferation. Preadipocyte number was increased 30 to 50% when cultures were incubated at 39 vs. 37°C based upon cleavage of the tetrazolium salt, MTT ($P < 0.001$), reduction of resazurin ($P < 0.001$), and daily cell counts ($P < 0.001$). Differentiation was monitored on d 8 after induction morphologically, enzymatically, and by measuring the mRNA abundance of key adipogenic transcription factors via real-time PCR. Glycerol-3-phosphate dehydrogenase (GPDH) activity was higher in differentiating cultures maintained at 39°C than in cultures differentiated at 37°C ($P < 0.01$) in agreement with increased lipid accumulation observed in these cultures as measured by Oil Red O staining suggesting that cultures maintained at 39°C differentiated to a greater degree than those maintained at 37°C. Finally, the effect of temperature on gene expression was investigated. Expression of peroxisome proliferator-activated receptor gamma (*P*PARγ; $P < 0.01$), CCAAT/enhancer binding protein α (C/EBPα; $P < 0.01$), bone morphogenic protein 2 (BMP2; $P < 0.05$), bone morphogenic protein 4 (BMP4; $P < 0.05$), and adiponectin ($P < 0.001$) were higher while mRNA expression of CCAAT/enhancer binding protein beta (C/EBPβ; $P < 0.01$) was lower in cultures differentiated at 39°C versus those differentiated at 37°C. Collectively these data indicate that culturing primary preadipocytes at 37 rather than 39°C decreases their proliferation rates and suppresses their adipogenic potential. Furthermore the observation that incubation temperature influences gene expression in primary cultures of pig preadipocytes raises the possibility that studying porcine adipocyte hyperplasia at temperatures below physiological body temperatures may confound the ability to extrapolate observations concerning the underlying mechanisms regulating proliferation and differentiation of primary cultures of pig preadipocytes to the live animal.

Key Words: adipocyte, primary culture, pig

1181 (W117) Effects of maternal nutrient restriction on muscle satellite cell activity. J. S. Raja*, M. L. Hoffman, K. N. Peck, K. E. Govoni, S. A. Zinn, and S. A. Reed, *Dep. of Animal Science, University of Connecticut, Storrs.*

Postnatal muscle growth is altered by poor maternal nutrition during gestation. Satellite cells are myogenic precursor cells that contribute to postnatal muscle growth. Satellite cell activity can be evaluated by the expression of several transcription factors that are critical for proper myogenesis. Pax7 is expressed in quiescent and active satellite cells. Expression of MyoD is increased in active and proliferating satellite cells and terminal differentiation is marked by expression of myogenin. We hypothesized that poor maternal nutrition during gestation would alter the temporal expression of Pax7, MyoD and myogenin in satellite cells in vitro. Multiparous ewes ($n = 23$) were housed individually and fed 100% or 60% NRC requirements beginning at d 31 ± 1.3 of gestation. Lambs from control-fed (CON) or restricted-fed (RES) ewes were euthanized within 24 h of birth (d 1; $n = 12$) or were maintained on a control diet until 3 mo of age ($n = 11$). Satellite cells were isolated from the semitendinosus muscle at necropsy and cryopreserved until further use. Satellite cells were cultured in growth media for 24, 48 or 72 h before immunostaining for Pax7, MyoD and myogenin. Hoechst dye was used to visualize nuclei. The percent of immunopositive cells was calculated as the number of immunopositive cells divided by total nuclei. Data were analyzed by PROC PROC MIXED of SAS. After 24 h of culture, the percent of cells expressing MyoD was 5-fold greater in RES lambs at birth (58.40 ± 12.08%) than cells of CON lambs (11.68 ± 17.08%; $P = 0.03$). After 48 h of culture, there was a greater percentage of cells expressing myogenin in RES lambs at birth (63.25 ± 14.00%) compared with cells from CON lambs (17.57 ± 17.08%; $P = 0.04$). However, after 72 h of culture the percent of satellite cells expressing myogenin in RES lambs at birth (40.07 ± 14.00%) was approximately 50% less than cells from CON lambs (83.98 ± 17.08%; $P = 0.05$). There were no differences in the percent of Pax7 immunopostive cells at birth, or any factors in cells from lambs at 3 mo of age ($P > 0.05$). In conclusion, restricted nutrient availability during gestation alters the temporal expression of myogenic regulatory factors in the offspring and is suggestive of precocious differentiation.

Key Words: muscle, satellite cells, poor maternal nutrition

1182 (W118) Effects of milk replacer and multivitamin-mineral supplementation on performance of heat stressed dairy calves. S. Blair*[1], C. C. Williams[1], B. F. Jenny[1], M. Thomas[1], V. Morgan[1], and T. Earleywine[2], [1]*Louisiana State University AgCenter, Baton Rouge,* [2]*Land O'Lakes Animal Milk Products, Shoreview, MN.*

Seventy-one neonatal Holstein calves (40 female; 30 male) were used in a randomized block design with a 2x2 factorial arrangement of treatments to evaluate the effects of milk replacer (MR) alone or in combination with a multivitamin and electrolyte supplement on growth performance and mitigation of heat stress in southeast Louisiana. Milk replacer treatments consisted of Land O'Lakes Herdmaker Supreme (20% CP, 20% fat; CON) and Land O'Lakes Warm Front (27% CP, 10% fat; WF). Supplemented calves received either 0 or 20 ml Palamountains Calf Boost (CB) in MR once daily in the morning feeding. Calves were offered MR treatments beginning on day 2, and all milk replacer was mixed at 15% solids. Calves consuming CON were fed 2.28kg MR twice daily. Calves on WF were fed 2.72kg MR twice daily for the first three wk of life, and 3.86kg twice daily until weaning. Water and calf starter (20%CP) were offered ad libitum beginning on d 2. Beginning on d 42, MR feeding was reduced to 1 time per day for all treatment groups to decrease MR intake by 50%. On d 49 calves were weaned. Calves remained in their hutches until d 56 to determine immediate post weaning performance. Body weight, hip height, wither height, hip width, and body length were recorded weekly, and grain and water intakes were measured twice daily. Average rectal temperature, respiration rates, and fecal scores were recorded three times weekly at both 0800 h and 1600 h. All data were analyzed using the PROC MIXED of SAS. There was a main effect of MR, with calves fed WF showing greater body weights and increased hip height, wither height, and body length ($P < 0.05$). There was no significant effect of CB on growth or intake measurements. Calves fed WF consumed less grain than CON calves ($P < 0.05$) until the end of wk 7, but showed no difference at wk 8. Calves consuming WF also showed higher fecal scores ($P < 0.05$), but well within normal ranges for healthy calves. All calves consumed more water as age increased ($P < 0.05$), with no interactions of sex or treatment. There was no significant effect of MR or CB on temperature or respiration rates ($P > 0.05$). These data indicate that MR feeding management may improve growth performance in neonatal dairy calves, but multivitamin mineral supplements may not provide any additional benefit.

Key Words: calf milk replacer, multivitamin-mineral supplement, heat stress

1183 (W119) Effects of milk replacer feeding frequency on growth and performance of neonatal Holstein calves. M. Thomas*, C. C. Williams, B. F. Jenny, S. Blair, C. F. Hutchison, C. Burke, E. L. Chartier, M. Orellana, and A. H. Dolejsiova, *Louisiana State University AgCenter, Baton Rouge.*

Fifty-seven neonatal Holstein calves (40 female; 17 male) were assigned to one of three treatments at day 2 of age to study effects of milk replacer feeding frequency on growth, performance, and health. Treatments consisted of 1X, with total amount of reconstituted milk replacer fed at 0600 h; 2X, with total amount of reconstituted milk replacer divided into 2 equal amounts and fed at 0600 h and 1700 h; and 3X, with total amount of reconstituted milk replacer divided into three equal amounts and fed at 0600 h, 1200 h, and 1700 hp Calves were housed in individual hutches and fed milk replacer until abrupt weaning at 42 d of age. Total daily amount of milk replacer offered was equal to 1.5% of birth weight and reconstituted to a total volume of 10% birth weight. Water and an 18% crude protein calf starter were offered ad libitum beginning on d 3 throughout the duration of the trial. Calves remained in their hutches until day 56 to determine immediate post weaning performance. BW was determined at birth and weekly throughout the trial. Wither height (WH), hip height (HH) and hip width (HW) were measured on d 7, 14, 28, 42, and 56 of age. Feed intake, water intake, and fecal scores were recorded daily. Effects of treatment, week, and their interactions were analyzed using the PROC MIXED of SAS (Cary, NC). There was no effect ($P > 0.05$) of treatment on BW, HH, HW, or WH. There was a week effect ($P < 0.01$) for BW, HH, HW, and WH as well as grain and water intake, with all calves increasing intake and growth throughout the duration of the study. There was no effect ($P > 0.05$) of treatment on fecal scores, with scores being similar and within the normal ranges for healthy calves throughout the project. Overall, milk replacer feeding frequency did not show any significant effects on growth or performance of these Holstein dairy calves.

Key Words: dairy calves, milk replacer, feeding frequency

1184 (W120) High energy diet enhances intramuscular adipogenesis in Hanwoo steers distributed to breeding value for meat quality. K. Y. Chung*, S. W. Lee, U. H. Kim, S. C. Jang, Y. M. Cho, E. M. Lee, S. M. Lee, and H. S. Kang, *Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, South Korea.*

High energy diet has been used for enhancing intramuscular adipose tissue in high quality beef cattle. Estimated breeding value (EBV) was used as a selection method to determine high quality beef group. The aim of this experiment was to determine the effect of high energy diet on the high and low

beef group distributed by EBV for carcass quality grade. We hypothesized that adipogenic gene expressions and adipose carcass traits are increased in high EBV groups when fed a high energy diet. A 2 x 2 factorial arrangement (High EBV, Low EBV, and High energy diet, control diet) in a completely random design was used to feed 26 Hanwoo steers. Two steers were fed in same pen and 13 pens were used for treatment. Blood sample was drawn once a month at the beginning from 11 to 28 month. Longissimus Dorsi (LD) muscle was collected within 10 min of harvest for analysis of mRNA SCD, PPARγ, GLUT4, MHC1, MHC2X abundance. Overall ADG and DMI were not different between high energy diet and control diet ($P > 0.05$). Serum glucose and triglyceride concentrations were increased ($P < 0.05$) by high EBV group from 22 to 28 month old. Serum NEFA levels were greater ($P < 0.05$) in 24 mo old at high EBV group and steady decreased at 28 mo old. Marbling score and yield grade were not affected by high energy diet and EBV ($P > 0.05$). Real-time quantitative PCR revealed that the mRNA content of PPARγ and SCD of high EBV group increased ($P < 0.05$) as compared to low EBV group. The mRNA level of GLUT4 and MHC1 tend to increase ($P = 0.08$, 0.09) when control diet fed at high EBV group. These data indicate that high energy diets increased serum glucose and triglyceride concentrations of high EBV-steers at final fattening period. Although there are no interaction between diet and EBV levels, adipogenic gene expressions in high EBV-steers were greater than those in low EBV-steers. The selection of EBV for meat quality affected serum glucose level and adipogenic gene expression of feedlot Hanwoo steers.

Key Words: Hanwoo, EBV, adipogenesis

1185 (W121) Impact of the sires on puberty onset in Nellore heifers.
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In Brazil the main breed of beef cattle is Nellore, where it represents 70% of the national herd. Since the late onset of puberty one of the principal problems associated with this breed. The aim of this study was to evaluate the expected progeny differences (EPDs for scrotal circumference) of sires and its effect on puberty in Nellore heifers. The daughters of 12 sires (143 calf heifers) were used. After weaning at 210 days of age, the animals were mantained in cultivated pasture of Brachiaria ssp. with mineral supplement and water ad libitum. The heifers were weighed, and the puberty onset was assessed monthly from 12 to 30 mo (by ultrasonography - corpus luteum detection). The sires were classified in precocious and non-precocious groups according to the positive (PEPD, $n = 8$) or negative (NEPD, $n = 4$) EPD to scrotal circumference. Continuous variables were analyzed by PROC MIXED, and variables with binomial distribution were analyzed by GLIMMIX procedure, both through SAS 9.3. Heifers that were NEPD daughters had the puberty onset heavier ($P = 0.009$) and older ($P = 0.013$) than the PEPD daughters (weight: 317.0 ± 10.6 vs 294.8 ± 8.7 Kg; age: 644.7 ± 59.3 vs 593.5 ± 62.7 days; for NEPD and PEPD, respectively). The percentage of pubertal heifers at 14, 18, 26 and 30 months of age, not were different between NEPD and PEPD (14 months of age: 11.1 vs 8.2%; 18 months of age: 26.7 vs 30.6%; 26 months of age –66.7 vs 73.5%; 30 months of age: 93.3 vs 92.8%, for NEPD and PEPD, respectively). We can conclude that there is genetic heterogeneity to onset puberty in Nellore breed. Furthermore, the results reveal the importance of the use of proven sires for sexual precocity. Financial support: FAPESP.

Key Words: sexual precocity, Nellore, sire

1186 (W122) Microarray studies in high and low rfi cattle reveal a potential role for gonadotropin releasing hormone (GnRH) in regulating feed efficiency.
S. D. Perkins*[1], C. Foradori[1], A. K. McNeel[2], L. A. Kriese-Anderson[1], and T. D. Brandebourg[1], *[1]Auburn University, Auburn, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Residual feed intake (RFI) is a heritable feed efficiency measure. Mechanisms underlying variation in feed efficiency are currently poorly understood. To address this issue, two divergent cohorts consisting of High (H) and Low (L) RFI individuals were created by assessing RFI in forty-eight Angus-sired steers during a 70 d feeding trial to identify steers with divergent RFI. Microarray studies using the Affymetrix Bovine Genome Array were then conducted on hypothalamic tissue (HT) RNA samples harvested from H and L RFI steers. The test diet was 50% sorghum-sudan silage, 50% grain (2.9 Mcal ME/kg DM). While on test, feed intake was recorded daily with BW and hip heights recorded at 14 day intervals. Ultrasound measurements of rib eye area (REA) and backfat (BF) were recorded initially and prior to harvest. Carcass and growth data were analyzed using a mixed model with RFI level (L, H) as the independent variable. The lsmeans for RFI were -1.25 and 1.51 for the L and H cohorts ($P < .0001$). Dry matter intake was higher for the H individuals versus the L steers ($P < .0001$) while on test BW gain was not different between the two groups ($P < 0.73$). Of the 24,000+ probes included on the Affymetrix Bovine Genome Array, 891 were found to be significantly different ($P < 0.05$) with 149 of these being highly different ($P < 0.01$) between high and low RFI. Pathway analysis of the data set using Ingenuity Pathway Analysis software revealed that the pathways most heavily represented in the differentially expressed genes were consistent with the known functions of the central nervous

system, specifically; increased cellular movement (important for synapse formation and neuronal communication), cell-to-cell communication and cellular development ($P = 1.34x10^{-24}$, $9.54x10^{-20}$,$3.14x10^{-17}$, respectively). In terms of canonical pathways, dendritic cell maturation and interleukin signaling ($P = 3.56x10^{-6}$ and $5.24x10^{-6}$, respectively) were identified as differentially activated by RFI status of particular interest and warrant further investigation. Furthermore, GnRH signaling (including GnRH agonist and GnRH signaling) was predicted to be to be greater in H steers. These findings are consistent with targeted gene expression assays using real-time PCR where GnRH mRNA abundance was lower in the arcuate nucleus of L steers**.** These data support the hypothesis that differences in hypothalamic neuropeptide gene expression underlie variation in feed efficiency in steers while the gonadotropin axis may also influence feed efficiency.

Key Words: RFI, steer, feed efficiency

1187 (W123) Microbiota diversity is inversely related to adiposity in Mangalica pigs. J. W. Broady, L. Wang, A. G. Moss, T. D. Brandebourg, and E. Schwartz*, *Auburn University, Auburn.*

Alabama is at the epicenter of an obesity epidemic representing a critical threat to public health by precipitating increased risk to stakeholders for diabetes, heart disease, stroke, arthritis, and certain cancers. Several studies in humans and in mice have demonstrated a strong interaction between the composition and diversity of gut microbiota, inflammation, and obesity. To address the connection between these parameters, we used the Mangalica pig as a model organism given the extreme, early onset, hyperphagic obesity displayed by this breed. A growth trial was conducted where obese and lean groups were created by either allowing ad libitum access to feed or restricting energy intake to 65% of ad libitum levels. Throughout the trial longitudinal analyses of the bacterial composition of the fecal microbiota was performed using denaturing gradient gel electrophoresis (DGGE). Circulating glucose was measured in whole blood samples taken from pigs following fasting or administration of an oral glucose dose. Body composition was determined at regular intervals using ultrasound and subcutaneous adipose tissues (SC) harvested at the end of the trial to facilitate gene expression studies. As animals aged and increased in adiposity, a general reduction in the overall diversity in the gut bacteria was observed with several other changes in specific bacterial taxa as indicated by DGGE analysis. At mature weight, obese pigs exhibited 2.5-fold greater SC mass ($P < 0.001$) but no differences in muscle mass ($P < 0.39$) compared to lean counterparts. Obese pigs exhibited severe fasting hypoglycemia and impaired glucose tolerance following oral glucose challenge suggesting development of insulin resistance. The mRNA expression of interleukin-6 (IL6) and tumor necrosis factor-α (TNF-α) were 4.72- and 3.74-fold higher respectively in the SC of obese versus lean Mangalica as measured by real-time PCR ($P < 0.01$). These data provide evidence that obese Mangalica pigs indeed develop a metabolic phenotype consistent with insulin resistance and this is associated with a proinflammatory shift in gene expression in SC. Furthermore, these data suggest that obesity is inversely correlated with diversity in gut microbiota. These findings will inform the design of therapies aimed at manipulating gut microbiota and/or inflammation in the treatment of obesity.

Key Words: microbiota, obesity, mangalica

1188 (W124) Muscle hypertrophy induced by myostatin inhibition is suppressed by rapamycin administration. D. Choi*[1], J. Yang[1], S. K. Park[2], and Y. S. Kim[1], *[1]University of Hawaii, Honolulu, [2]National Institute of Animal Science, RDA, Suwon, South Korea.*

Recent studies have shown that myostatin (MSTN), a skeletal muscle specific negative growth factor, may regulate skeletal muscle mass through the mTOR pathway. The mTOR pathway is known to be blocked by rapamycin (RAP), thus it was hypothesized that muscle hypertrophy induced by MSTN inhibition would be blocked by RAP treatment. This study was designed to examine the effect of RAP administration on muscle growth in MSTN-propeptide transgenic mice, a hypermuscular phenotype by MSTN inhibition. 5 wk old male heterozygous MSTN-propeptide transgenic mice and wild-type littermates were administered with 0 or 3 mg/kg body weight of RAP intraperitoneally every other day for 4 wk. At the end of RAP treatment, animals were sacrificed, and gastrocnemius, plantaris, and soleus muscles were dissected, weighed, and snap-frozen for later analysis. Body weight gain of transgenic mice was greater ($P < 0.01$) than that of wild-type mice. RAP suppressed ($P < 0.05$) body weight gain about 40% in both genotypes. Soleus, plantaris, and gastrocnemius muscle weights of transgenic mice were greater ($P < 0.05$) than those of wild-type mice. RAP suppressed ($P < 0.05$) muscle growth in both genotypes, but the extent of suppression was greater in transgenic mice than in wild-type mice (6.6% vs. 18.6% in plantaris, and 20.7% vs. 24.8% in gastrocnemius). When the expressions of MyoD and myogenin were analyzed by real time PCR, expressions of these myogenic regulatory factors were not affected by either genotype or RAP administration. The current result of suppressing muscle growth by RAP in MSTN-propeptide transgenic mice supports that the mTOR pathway is involved in the regulation of muscle growth by MSTN.

Key Words: myostatin, rapamycin, mTOR pathway

1189 (W125) Poor maternal nutrition during gestation reduces mesenchymal stem cell (MSC) proliferation in offspring. S. M Pillai[*1], M. L. Hoffman[1], K. N. Peck[1], E. V. Valley[1], T. D. Crenshaw[2], S. A. Zinn[1], and K. E. Govoni[1], *[1]Dep. of Animal Science, University of Connecticut, Storrs, [2]University of Wisconsin, Madison.*

Poor maternal nutrition may alter bone and adipose development in offspring by diverting MSC from osteoblast to adipocyte lineage. To determine if poor maternal nutrition during gestation alters bone and adipose development and function of MSC in offspring, 36 ewes were fed 100%, 60%, or 140% of requirements (NRC, 1985) beginning at d 31 ± 1.3 of gestation. Lambs from ewes fed 100% (CON), 60% (RES) and 140% (OVER) were euthanized within 24 h of birth (d 1; n = 18) or at 3 mo of age (n = 15). At necropsy, the left tibia and femur were collected for MSC culture and mineral analysis, and backfat thickness and BW were measured. The MSC were isolated from bone marrow at d 1 and cultured (α- MEM + 10% fetal bovine serum + 0.5% penicillin streptomycin + 0.25% Amphotericin-B). Proliferation of MSC was determined by bromodeoxyuridine assay. Gene expression was quantified using real-time RT-PCR. Data were analyzed using PROC MIXED in SAS. As previously reported, BW were 13% greater in OVER than CON at 1 d and 3 mo ($P \leq 0.05$), but not different in RES ($P > 0.1$). Maternal diet did not affect ($P > 0.2$) bone length, area, mineral content and mineral density at d 1 or at 3 mo. Backfat thickness was reduced 50% in RES compared with CON at 3 mo ($P = 0.01$). Compared with CON, MSC proliferation was reduced 51% and 58% in RES ($P = 0.07$) and OVER ($P = 0.03$), respectively in the presence of serum and reduced 27% and 44% in RES ($P = 0.11$) and OVER ($P = 0.05$), respectively without serum. Expression of markers of MSC commitment to adipocyte and osteoblast cell lineages were evaluated. *P2Y purinoceptor 14* was reduced 1.7 ± 0.1-fold in OVER ($P = 0.09$) and *P2Y purinoceptor 1* was reduced 1.7 ± 0.1-fold in OVER ($P = 0.09$) vs. CON. Whereas *C/EBPβ, Msh homeobox 1, Protein delta homolog 1, P2Y purinoceptor 2* were not affected by maternal diet ($P >$ 0.3). Studies are in progress to determine if maternal diet alters differentiation of MSC into osteoblasts and adipocytes. In conclusion, poor maternal nutrition reduces the proliferation of MSC in offspring which may contribute to altered bone and adipose tissue development.

Key Words: mesenchymal stem cells, proliferation, sheep

1190 (W126) Regulation of key markers of lipid metabolism by short chain fatty acids in differentiated pig adipocytes. H. Yan[*1], and K. M. Ajuwon[2], *[1]Purdue University, West Lafayette, IN, [2]Dep. of Animal Sciences, Purdue University, West Lafayette, IN.*

Short chain fatty acids (SCFA), primarily acetate, propionate and butyrate, are the major carbohydrate fermentation end products of in the gut. Previously, we had demonstrated that inulin, a fermentable fiber, alleviated high fat diet induced fat mass accumulation, and that this was accompanied by increased expression of acyl CoA oxidase (ACO), a marker of peroxisomal fatty acid oxidation, decreased expression of fatty acid synthase (FAS) and alteration in the gut microbial community structure to favor increased level of butyrate-producing bacteria. Although gut microbial structure is highly associated with SCFAs production, direct effect of SCFAs on lipid metabolism is still unclear. Therefore, we examined, by RT-PCR, the effect of SCFAs administration on markers of lipid metabolism in differentiated pig adipocytes. Increasing concentrations of SCFAs (μM to low mM) led to an upregulation of expression of acyl CoA oxidase (ACO) and sterol regulatory element binding protein 1c (SREBP-1c), which play a key role in fatty acid synthesis. Furthermore, butyrate, but not propionate and acetate, significantly reduced ($P < 0.05$) the expression of fatty acids synthase (FAS) and carnitine palmitoyl transferase 1α (CPT1α). Butyrate, but not propionate and acetate, significantly increased ($P < 0.05$) adiponectin and glucose transporter type 4 (GLUT4) expression and led to decreased leptin expression. This study showed that SCFAs, especially butyrate, may exert direct influence on lipid metabolism and adipokine expression profile in adipocytes. Results are consistent with previously observed in vivo effects of fermentable fiber on metabolic markers in pig adipose tissue and suggest that in vivo fiber effects may be partly mediated by SCFA produced during fiber fermentation.

Key Words: SCFA, adipocyte, metabolism

1191 (W127) Relationship among efficiency measures, economic value and feedlot performance assessed in growing phase of Nellore cattle. A. M. Castilhos[1], C. L. Francisco[*1], A. M. Jorge[1], R. H. Branco[2], M. E. Z. Mercadante[2], S. F. M. Bonilha[2], C. M. Pariz[1], and D. C. Rivaroli[1], *[1]Universidade Estadual Paulista–FMVZ, Botucatu, Brazil, [2]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho-SP, Brazil*.

Data from 6 yr of studies (2007–2012) were compiled using 357 Nellore bulls (212 + 38 kg BW; 279 + 29 d of age) to evaluate the relationship among efficiency measures, current economic value and feedlot performance. Dry matter intake (DMI) was recorded for two different ways: using a GrowSafe automated feeding system (GrowSafe Systems Ltd., Air-

Table 1191.

	RFI		RIG		RG		
Variable	Low	High	Low	High	Low	High	SEM
Profit, $/steer·d^{-1}	0.72^{b}	0.56^{c}	0.48^{d}	0.77^{a}	0.38^{e}	0.77^{a}	0.03
ADG, kg/d	1.04^{bc}	1.05^{b}	1.00^{c}	1.08^{ab}	0.89^{d}	1.10^{a}	0.02
DMI, kg/d	6.40 ^{c}	7.46^{a}	7.49^{a}	6.46^{c}	7.00^{b}	6.75 ^{b}	0.12
Final BW, kg	330.39^{a}	333.88^{a}	335.63^{a}	329.91^{a}	334.66^{a}	328.39^{a}	59,39

^{ab} $P < 0.05$

drie, Alberta, Canada) or individual pens. Efficiency measures evaluated were: residual feed intake (RFI), residual intake and BW gain (RIG) and residual BW gain (RG). Residual feed intake was calculated as the residuals from the regression of total DMI on $BW^{0.75}$ and ADG. Residual gain was calculated as the residuals from the regression of total ADG on $BW^{0.75}$ and DMI. Residual intake and BW gain was determined from linear combination into RFI and RG. Animals were classified for each efficiency measure as Low (< 0.5 SD mean), Medium (within ± 0.5 SD), and High (> 0.5 SD mean) groups. Economic value included was profit ($/steer.d^{-1}), calculated from the economic data from 2006 to 2012. Feedlot performance variables were ADG (kg/d), DMI (kg/d), and final BW (kg). Profit for all groups differed ($P < 0.05$), with the exception between $High_{RIG}$ and $High_{RG}$ groups ($P = 0.98$) which had the highest profitability (Table 1191). When the groups were analyzed separately, within each of efficiency measures, the profit increased ($P < 0.0001$). Final BW was similar among all groups of efficiency measures ($P = 0.78$). Body weight gain was not different between groups $High_{RFI}$ and Low_{RFI} ($P = 0.64$), Residual feed intake groups had lower gain only compare to $High_{RG}$ group ($P = 0.01$). The $High_{RIG}$ and $High_{RG}$ increased approximately 8% and 23% ($P < 0.0001$) compared to Low_{RIG} and Low_{RG}, respectively. Among all the groups Low_{RFI} and $High_{RIG}$ had lower DMI ($P < 0.01$) and reduced by approximately 14% compared to $High_{RFI}$ and Low_{RIG}, respectively. Therefore, residual intake and body weight gain is a recommended measure to increase profitability and reduce dry matter intake of Nellore cattle.

Key Words: efficiency measures, Nellore cattle, profit

1192 (W128) Retinoic acid alters expression of key genes during differentiation of bovine intramuscular preadipocytes. J. Kim*[1], K. Chung[2], S. Chang[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, South Korea.*

Retinoic acid has been shown to be important in regulating mammalian tissue development, such as, proper bone formation, growth, energy metabolism, and cell differentiation. Retinoic acid has been reported to be a potent inhibitor of adipocyte differentiation by binding to the retinoic acid receptor (RAR) or retinoid X receptor (RXR). The objective was to determine the effect of RAR agonist (retinoic acid) and RAR antagonist (LE540) on gene expression during differentiation of bovine intramuscular preadipocytes. Intramuscular (IM) adipose tissue was collected between the 10th and 13th from longissimus muscle and cultured in growth media consisting of DMEM, 10% fetal bovine serum, and antibiotics at 37°C under a humidified atmosphere of 95% O_2 and 5% CO_2. Upon reaching confluence, the growth medium was replaced by a differentiation medium consisting of DMEM and 10 μg/mL insulin, 25 nM hydrocortisone, 10 μM oleic acid, 5 μM ciglitizone, and antibiotics with treatments The treatments were: 1)control, 2)10 μM all-trans retinoic acid (RA), and 3)10 μM LE540 (synthetic RA antagonist; Waco Co.). Real-Time RT-PCR was used to measure the quantity of C/EBPβ, PPARγ, SCD, and SMAD3 mRNA relative to the quantity of ribosomal protein subunit 9 (RPS9) mRNA in total RNA isolated from cultured bovine IM adipocyte cultures. Addition of RA reduced ($P < 0.05$) PPARγ and SCD mRNA levels compared to control IM adipocytes. However, addition of LE 540 increased expression of PPARγ and SCD mRNA ($P < 0.05$) levels in bovine IM adipocytes. Relative level of C/EBPβ mRNA was inhibited ($P < 0.05$) by LE540 during differentiation. Results of this study indicated that retinoic acid inhibits bovine IM preadipocyte differentiation by downregulation of PPARγ or SCD. However, treatment of RAR antagonist induces adiopogenic gene expressions during IM preadipocyte differentiation.

Key Words: bovine intramuscular adipose cell, marbling, retinoic acid

1193 (W129) Role of G protein-coupled estrogen receptor-1 and matrix metalloproteinases 2 and 9 in the effects of Estradiol-17β on proliferation, protein synthesis and protein degradation in bovine satellite cell cultures. E. Kamanga-Sollo, B. C. Reiter, K. J. Thornton*, M. E. White, and W. R. Dayton, *University of Minnesota, St. Paul.*

In feedlot steers, Estrogen (E2) and combined E2 and trenbolone acetate (TBA) (a testosterone analog) implants enhance rate and efficiency of muscle growth; and, consequently, these compounds are widely used as growth promoters. Although the positive effects of E2 are well established, the mechanism(s) involved is not well understood. Combined E2/TBA implants result in significantly increased muscle satellite cell number in feedlot steers. Additionally, E2 treatment stimulates proliferation of cultured bovine satellite cells (BSC). The ability of

E2 to stimulate satellite cell proliferation is significant because satellite cells provide nuclei needed to support postnatal muscle fiber hypertrophy and are crucial in determining the rate and extent of muscle growth. To identify the mechanism(s) involved in E2-stimulated muscle growth, we have focused on identifying the receptors involved in the effects of E2 on BSC proliferation, protein synthesis and protein degradation. Our previous studies have shown that silencing expression of estrogen receptor 1 (ESR1) or epidermal growth factor receptor (EGFR) suppresses E2-stimulated BSC proliferation. Studies in nonmuscle cells have shown that binding of E2 to G protein-coupled estrogen receptor (GPER)-1 results in activation of matrix metalloproteinases 2 and 9 (MMP2/9) resulting in proteolytic release of heparin binding epidermal growth factor-like growth factor (hbEGF) from the cell surface. Released hbEGF binds to and activates EGFR resulting in increased proliferation. To determine if GPER-1 and MMP2/9 are involved in the ability of E2 or IGF-1 to affect BSC, we have utilized specific inhibitors to inhibit the activity of GPER-1 and MMP2/9 and assessed the impact of this inhibition on the effects of E2 on proliferation, protein synthesis and protein degradation rates in BSC cultures. Treatment of BSC cultures with G36, a GPER-1 specific inhibitor, or with an inhibitor of MMP2/9 activity completely suppressed E2-stimulated proliferation and protein synthesis ($P < 0.05$) but had no effect on the ability of E2 to suppress protein degradation. Our results show that both GPER-1 and MMP2/9 are necessary for E2-stimulated proliferation and protein synthesis in BSC cultures.

Key Words: bovine, satellite cell, muscle, estradiol-17β

1194 (W130) The effect of pre-weaning feeding and housing strategy on calf growth performance and behavior following post-weaning housing transition.

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The objective was to compare the effects of pre-weaning housing and feeding strategy on post-weaning growth performance and behavior after housing transition. Forty-eight Holstein calves were fed 770 g DM/d from birth through 15 d of age and 900 g DM/d thereafter split into 2 feedings and housed in individual hutches ($n = 16$; FI), or fed ad libitum acidified milk replacer and housed in either individual hutches ($n = 16$; AI) or group hutches with 4 calves/hutch ($n = 16$; AG). Milk replacer was 24% CP and 20% fat, fed at 14% solids. Following weaning (wk 8), calves were moved to a separate housing area (wk 10) and housed in 3.05 × 3.66 m pens with 4 calves/pen. Calves were weighed before transit (FI = 79.2 ± 3.4 kg; AI = 89.7 ± 4.2 kg; AG = 88.1 ± 4.2 kg) and weekly thereafter. Behavior of individual calves ($n = 36$) for the first 5 h following transit and pen introduction was observed using 5-min scan sampling and averaged across pen. Calves were offered free choice chopped hay (16.1% CP; 58.7% NDF) and pelleted grain (25.7% CP; 29.8% NDF) daily. Dry matter intake was measured daily. Data were analyzed as a randomized block design using the PROC MIXED of SAS. Total DMI was greater ($P = 0.02$) for AI (mean ± SE; 5.85 ± 0.12 kg DM/d) compared to AG (5.29 ± 0.12 kg DM/d) and tended ($P = 0.06$) to be greater than FI (5.40 ± 0.12 kg DM/d). Average daily gain over the 2 wk period tended ($P = 0.08$) to be greater for FI (1.20 ± 0.08 kg BW/d) than AI (0.97 ± 0.08 kg BW/d) or AG (0.90 ± 0.08 kg BW/d). Feed efficiency was not altered ($P = 0.12$) by pre-weaning housing and feeding strategies averaging 6.16 ± 0.53 kg DMI/kg gain for AI, 5.67 ± 0.53 kg DMI/kg gain for AG, and 4.38 ± 0.53 kg DMI/kg gain for FI. Time spent in contact with another calf was greater ($P = 0.02$) for AG (85.4 ± 8.8 min) compared to AI (27.1 ± 8.8 min) and FI (40.0 ± 8.8 min). Housing and feeding strategy pre-weaning did not alter time spent standing ($P = 0.55$) or lying ($P = 0.55$) post-weaning. These data suggest post-weaning compensatory gain occurs with fixed intake feeding when compared to ad-libitum feeding.

Key Words: post-weaned calves, performance, behavior

1195 (W131) The effect of two sources of soy protein concentrate and hydrolyzed soy protein modified on growth and performance of calves fed milk replacer.

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Fifty-one (51) 3- 10 d old Holstein bull calves with an average initial BW of 50.1 kg (SD = 1.63 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility. Calves were randomly assigned according to BW and blood γ globulin to one of three 20% protein/20% fat non-medicated milk replacer (MR) diets offered in a 17.6% solution. The objective of this study was to evaluate calf performance and growth when fed MR containing one of two sources of soy protein concentrate or hydrolyzed soy protein modified as a protein source. Treatments were as follows: soy protein concentrate source 1 (SPC 1; Solae Profine F, Solae, Aarhus, Denmark); soy protein concentrate source 2 (SPC 2, Solae Danpro A, Solae, Aarhus, Denmark); hydrolyzed soy protein modified (HSPM). Calves were fed to provide 680 g DM/d during Days 1– 7, 907 g DM/d during Days 8– 14, 1134 g DM/d during Days 15– 21, and 1361 g DM/d during Days 22– 28, in 2 feedings at 0600 and 1515 h. Calf starter was not offered during this 28 d trial. Data were analyzed by PROC MIXEDs of SAS. Total weight gain, MR consumption, feed:gain, and scour scores did not differ ($P > 0.05$) among treatments. The three soy protein sources fed in this study can be interchangeably employed in calf milk replacers as all support calf growth and performance equally.

Key Words: calf, milk replacer, hydrolyzed soy protein modified

Table 1195.

Item[1]	MR Diet			
	SPC 1	SPC 2	HSPM	SE
BW Gain, kg, 4 wk total	8.69	8.58	9.36	0.710
MR Intake (DM), kg, 4 wk total	25.7	25.4	26.2	0.640
Scour Score*, 2 wk avg	1.51	1.47	1.60	0.070
Feed:Gain	3.47	3.28	3.06	0.330

* 1- 4 scale: 1 = normal, 2 = loose, 3 = water separation, 4 = 3 with severe dehydration.

1196 (W132) The effect of various fat levels and fat sources on growth and performance of calves fed milk replacer.

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Seventy-one (71) 3- to 10-d-old Holstein bull calves with average initial BW of 45.6 kg (SD = 1.95 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility. The objective of this study was to examine the growth and performance of calves fed milk replacer (MR) varying in fat level and fat source. Calves were randomly assigned according to BW and blood γ globulin to their respective MR diet offered in a 15.0% solids solution. Calves were assigned to 1 of 3 diets: 22% crude protein (CP), 20% fat with lard as the primary fat source; 22% CP, 15% fat with medium-chain triglycerides (MCT) as the primary fat source; 22% CP, 15% fat with lard as the primary fat source and supplemented with 8 g essential fatty acids per calf daily (EFA; Neotec4™, Provimi North America, Inc., Brookville, OH). Calves were fed to provide 680 g DM/d in 2 feedings at 0600 and 1515 h. Calves were offered 340 g DM/d in one feeding during the last week. Calf starter (20% CP, as fed basis) was fed ad libitum throughout this 42 d trial. Data were analyzed by PROC MIXEDs of SAS. There were no statistical differences ($P > 0.05$) in total BW gain, starter feed intake, or feed:gain among treatments. Calves fed a 22:20 MR with lard as the primary fat source consumed less ($P < 0.05$) MR compared to calves fed a 22:15 MR with lard as the primary fat source and supplemented with EFA. Milk replacers with MCT as the primary fat source may allow for a reduction in fat levels while supporting equal calf performance and growth.

Key Words: calf, milk replacer, medium-chain triglyceride

Table 1196.

Item[1]	MR Diet			
	22:20 w/Lard	22:15 w/MCT	22:15 w/lard, EFA	SE
BW Gain, kg	22.9	26.0	24.4	1.51
MR Intake (DM), kg	24.3[a]	24.8[ab]	25.3[b]	0.280
Starter Intake (DM), kg	20.2	23.2	20.8	1.56
Feed:Gain	1.98	1.89	1.97	0.070
Scour Score*, 2 wk avg	1.43	1.33	1.45	0.060

[1] Means in the same row not followed by a common letter differ ($P < 0.05$).
* 1- 4 scale: 1 = normal, 2 = loose, 3 = water separation, 4 = 3 with severe dehydration.

1197 (W133) Use of biometric measurements to predict age and body weight of bovine fetus.

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Fetal biometric measurements that can be achieved by ultrasonography were used to develop equations to predict fetal age and fetus body weight in *Bos indicus* cattle. Dataset from 32 purebred Nellore fetuses from 130 to 272 d of gestation, obtained from cows fed corn silage based diet at various feeding levels, was used. Cows were hand mated, with day of mating considered as day zero of pregnancy. Fetal weight and biometric measurements were taken at slaughter and biometrics measurements were (all in cm): body length (BL), thoracic circumference (TC), height at shoulder (HS), height at rump (HR), cranial eyes circumference (CEC) and cranial neck circumference (CNC). Nonlinear equations ($y = ax^b$) were fitted to the data and results are shown in Table 1197. Generated functions were evaluated regressing observed values in function of predicted. The joint hypothesis that $\beta_0 = 0$ and $\beta_1 = 1$ was tested and the results shown good fit for all functions generated ($P > 0.70$). However, these regressions do not predict fetal ages accurately in early gestation, thus should not be extrapolated beyond the scope of these data (130 to 272 d of gestation). The results suggest that the gestational age and fetal body weight can be estimated from biometric measurements of fetus using ultrasonography in live cows or directly in fetuses from cows that were slaughtered without specified gestational age. *Funded by INCT-CA, CNPq and FAPEMIG.*

Key Words: biometric measurements, fetal growth, gestation

Table 1197. Functions to predict fetus body weight and fetal age from biometric measures of fetus[1]

	Predicting fetal age (days)			Predicting fetus body weight		
Biometric predictor measure	Function	r^2_{xy}	*P*-value	Function	r^2_{xy}	*P*-value
Body length, cm	$y = 14.3 \times BL^{0.6516}$	0.960	0.998	$y = 0.000155 \times BL^{2.701}$	0.981	0.708
Thoracic circumference, cm	$y = 16.89 \times TC^{0.6588}$	0.964	0.999	$y = 0.000263 \times TC^{2.769}$	0.974	0.864
Height at shoulder, cm	$y = 24.21 \times HS^{0.5536}$	0.975	0.999	$y = 0.001 \times HS^{2.367}$	0.975	0.985
Height at rump, cm	$y = 26.42 \times HR^{0.5322}$	0.983	0.999	$y = 0.00192 \times HR^{2.209}$	0.958	0.944
Cranial eyes circumference, cm	$y = 10.45 \times CEC^{0.8215}$	0.953	0.999	$y = 0.000041 \times CEC^{3.412}$	0.946	0.884
Cranial neck circumference, cm	$y = 9.97 \times CNC^{0.8478}$	0.970	0.995	$y = 0.000073 \times CNC^{3.314}$	0.962	0.689

[1] The r^2_{xy} value is for observed values regressed in function of predicted. *P*-value is the significance value for testing the joint hypothesis that $\beta_0 = 0$ and $\beta_1 = 1$, wherein *P*-values greater than 0.05 means that the H_0hypothesis was accepted.