0.96 ± 0.02 kg/d) but decreased DMI and milk protein yield in the 8% RUP treatment (19.4 vs. 20.1 ± 0.32 kg/d [interaction, $P < 0.01$] and 1.02 vs. 1.08 ± 0.02 kg/d [interaction, $P < 0.01$]). There was a trend ($P < 0.07$) for an interaction such that the 8% RDP treatment increased energy-corrected milk (ECM) yield compared with 10% RDP in the 6% RUP treatment (31.7 vs. 29.4 ± 0.76 kg/d) but reduced ECM yield in the 8% RUP treatment (32.5 vs. 33.0 ± 0.76 kg/d). The 10% RDP treatment increased ($P < 0.001$) milk-urea nitrogen compared with the 8% RDP treatment (10.2 vs. 6.9 ± 0.28 mg/dL). The 8% RUP treatment increased ($P < 0.001$) milk-urea nitrogen compared with the 6% RUP treatment (9.8 vs. 7.2 ± 0.28 mg/dL). The 8% RDP treatment increased ($P < 0.001$) NUE compared with 10% RDP (35.1 vs. 31.6 ± 0.76%). The 6% RUP treatment increased ($P < 0.001$) NUE compared with 8% RUP (35.1 vs. 31.6 ± 0.76%). Therefore, lower RDP diets can be fed with 6% RUP diets without compromising milk production, whereas the combination of low RDP with 8% RUP depressed productivity. Lower RDP and RUP diets increase NUE in heat-stressed cows.

Key Words: crude protein, nitrogen-use efficiency, heat stress

0763 Influence of a bovine respiratory disease complex vaccine with a modified live virus or KV infectious bovine rhinotracheitis component on estrous cycle parameters and anti-Müllerian hormone concentration in nulliparous heifers.

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The objective of this study was to examine the impact of a bovine respiratory disease complex (BRDC) vaccine with a modified live virus (MLV) infectious bovine rhinotracheitis (IBR) component on estrous cycle parameters and the follicular pool. Twenty-four Holstein heifers (mean 12.4 mo [SD 0.5]) in two replicates (spring, $n = 10$, and fall, $n = 14$) were synchronized for estrus using a 7-d CIDR protocol with 2 injections of PGF_{2a}, one at CIDR removal and a follow-up injection 16 h later. Heifers were calf-hood vaccinated with an IBR MLV. Heifers were observed for one complete estrous cycle to establish normal cyclicity. At Heat 2, heifers were vaccinated with either the calf-hood MLV (MLV; $n = 12$) or a BRDC vaccine with a killed (K; $n = 12$) IBR component. Heifers were blocked into treatment groups according to prevaccination bovine viral diarrhea virus (BVDV) serum neutralizing titers. Heifers were then tracked for two complete estrous cycles. Serum samples for estradiol (E2) and progesterone (P4) and ultrasound of ovarian structures were collected to track cyclicity every other day. Serum samples for anti-Müllerian hormone (AMH) were collected at estrus and mid cycle to evaluate the follicular pool. Data was normalized with ovulation as Day 0. Data were analyzed with the PROC MIXED procedure of SAS with cycle number, season, and vaccine as fixed effects. The model for P4 analysis added day of cycle as a fixed effect. There was no difference ($P > 0.05$) in postvaccination titers. Vaccination had no impact on P4 concentrations, luteal tissue area, peak E2 production, or estrous cycle lengths ($P > 0.05$). Overall variables that affected AMH concentrations were season (spring = 138.92 ± 43.1 pg/mL; $P = 0.0043$), vaccine type (MLV = −92.4 ± 42.9 pg/mL; $P = 0.0435$), and cycle number ($P < 0.0001$). Anti-Müllerian hormone concentration decreased between cycles 1 and 2 and cycles 1 and 3 for MLV vaccinated heifers ($P < 0.0003$). Anti-Müllerian hormone concentrations of cycle 2 were numerically lower between vaccine types (K = 308.22 ± 33.3 pg/mL and MLV = 181.13 ± 32.9 pg/mL; $P = 0.0953$), although not statistically different. This may be due to low animal numbers, the variability between animals, or the differences observed in the Fall killed vaccine (−70.93 ± 21.1 pg/mL; $P = 0.0145$) from cycle 1 to 2 but not in the Spring killed vaccine (3.40 ± 45.1 pg/mL; $P = 0.9969$). Anti-Müllerian hormone was weakly correlated with small follicle count ($r^2 = 0.15$, $P < 0.0001$). Although no differences were seen in overall cycle parameters, these differences in AMH concentrations may indicate a reduction of the follicular pool as a result of vaccination with an IBR MLV.

Key Words: infectious bovine rhinotracheitis modified live virus, cyclicity, anti-Müllerian hormone

GROWTH AND DEVELOPMENT

0764 Functional characterization of porcine SCD1 in stably transduced porcine SK6 cells.

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Fatty acid composition is an important component of foods derived from livestock species, as it contributes to both the healthfulness and the functionality of beef, lamb, pork, and dairy products. The most highly regulated and most abundant fatty acid in animal tissues and dairy products is oleic acid (18:1*n*-9). Oleic acid is synthesized by the Δ9 desaturase, stearoyl CoA desaturase (SCD1), which also is responsible for the synthesis of the putative cytokine palmitoleic acid (16:1*n*-7) and *cis*-9, *trans*-11 CLA. Owing to the importance of SCD1 in lipid metabolism, we generated a porcine SK6 transgenic cell lines for sustained overexpression or knockdown of pSCD1 in an inducible manner by using a novel All-in-One Tet-On Lentiviral expression system. We combined the inducible transcriptional activator (tetracycline-controlled transactivator protein) vector and the vector encoding the pSCD1 gene under the influence of a tetracycline-responsive promoter element into one to generate an inducible all-in-one lentiviral vector system. The cell culture models were validated for expression and functionality of pSCD1 by documenting that

the pSCD1 transformed cells overexpressed pSCD1 protein and mRNA over 1,000-fold ($P < 0.0001$). Similarly, an SCD1 shRNA designed to inhibit SCD1 gene expression decreased pSCD1 mRNA and pSCD1 protein expression levels by over 75% ($P < 0.001$). The pSCD1-transformed cells increased the synthesis of palmitoleic acid nearly 4-fold ($P < 0.05$), which was almost completely abolished when SK6 cells were transfected with the SCD1 shRNA. These results indicate that the lentiviral constructs used in this study can be further used to document the regulation of lipid metabolism by SCD1 in pigs.

Key Words: stearoyl-CoA desaturase-1, SK6 kidney cells, transfection, palmitoleic acid

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0765 Gene expression profiling and fatty acid composition in muscle during growth of Yanbian Yellow Cattle. X. Li*[1], C. Yan[1], S. Choi[2], J. Shin[3], and S. B. Smith[4], *[1]Yanbian University, Yanji, P. R. China, [2]Chungbuk National University, Chengju, the Republic of Korea, [3]Kongwon National University, Chuncheon, the Republic of Korea, [4]Texas A&M University, College Station*.

We hypothesized that gene expression and fatty acid composition would differ among different muscle depots and over time on a finishing diet. The present study was conducted with 16 Yanbian Yellow cattle steers (approximately 8 mo of age). Yanbian Yellow cattle are genetically similar to Korean Hanwoo and Japanese Wagyu cattle. Steers were fed a corn-based diet and were randomly assigned to 4 sampling groups. Five consecutive biopsy samples were taken from the chuck, loin, and round muscle at age 12, 16, 20, and 24 mo. Fat content in each muscle increased from 12 to 24 mo of age and the order of fat content in muscles was loin > round > chuck at 12, 16, 20, and 24 mo of age. There were significant differences in the concentrations of stearic acid (18:0), oleic acid (18:1*n*-9), linoleic acid (18:2*n*-6), SFA, MUFA, and the MUFA:SFA ratios with age. At the earliest sampling period, muscle lipids had low MUFA:SFA ratios (0.9 to 1.1), and the muscle lipid MUFA:SFA ratios were highest at 24 mo of age (1.29 to 1.41). There were significant depot effects for stearic acid, linoleic acid, SFA, MUFA, PUFA, and the MUFA:SFA ratio across muscles. Expression of *SREBP1*, *A-FABP*, *SCD1*, *ACC*, and *LPL* in the muscle biopsy samples increased with age, whereas the expression of *PPARγ* and *FAS* decreased with age ($P < 0.05$). The presence of adipogenic gene expression indicated that the muscle biopsy samples also contained intramuscular adipose tissue. Between 12 and 24 mo of age, stearic acid decreased from approximately 16 to 10%, whereas oleic acid increased from approximately 34 to 45% of total muscle fatty acids. Correspondingly, *SCD1* gene expression increased approximately 4-fold between 12 and 24 mo of age. There also were significant muscle main effects for gene expression. Gene expression in biopsies from the loin exhibited the highest expression of all adipogenic genes included in this study; conversely, samples from the chuck had the lowest adipogenic gene expression ($P < 0.05$ for all genes). These results were consistent with loin biopsy samples having the highest fat content. The findings of this study support our hypothesis that adipogenic gene expression varies across muscles and across time on feed and provide novel information about the development and composition of marbling in Yanbian Yellow cattle.

Key Words: Yanbian Yellow cattle, fatty acids, gene expression

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0766 α-Chaconine induces myogenesis of bovine satellite cells isolated from semimembranosus and longissimus muscle tissue. K. Y. Chung*, S. C. Jang, E. M. Lee, S. H. Yang, and E. G. Kwon, *Hanwoo Research Institute, NIAS, RDA, Pyeongchang, the Republic of Korea*.

α-Chaconine is a steroidal glycoalkaloid that found in leaves, fruit, and tubers of the solanaceae family such as potato, tomato, and eggplant. Alkaloid poisoning of potato plant was reported in various animal models such as mice, rabbit, and chicken. However, it is also used as a treatment for human asthma. Some medicine used for treating human asthma has been used to induce myogenesis of bovine skeletal muscle. We hypothesized that α-chaconine may affect myogenesis of bovine satellite cells isolated from different muscle depots. Bovine satellite cells were pronase-liberated from semimembranosus (SM) and longissimus dorsi (LD) muscle tissues of three newborn Hanwoo calves. Bovine SM and LD satellite cells were incubated with Dulbecco's modified Eagle medium (DMEM) with 10% fetal bovine serum for proliferation and induced differentiation with DMEM with 3% horse serum. Bovine satellite cells were treated with various levels of α-chaconine (control and 0.001, 0.01, 0.1, 1, and 10 μ*M*). Messenger RNA abundance for myosin heavy chain 1 (MHC1), MHC2X, glucose transporter 4 (GLUT4), myogenin, G-coupled protein receptor 43 (GPR43), and β2-adrenergic receptor (β2-AR) were measured by real-time quantitative PCR. Data were analyzed as a completely randomized design using the MIXED model, with each treatment performed in triplicated. Means were considered different at $P < 0.05$. Relative MHC2X mRNA abundance was increased at dose-dependent levels in both SM and LD satellite cells with α-chaconine treatments compared with the control ($P < 0.05$). However, MHC2X and GLUT4 levels were decreased in 10 μ*M* treatments ($P < 0.05$). Relative level of MHC2X and β2-AR were greater in LD satellite cell compared with SM satellite cells ($P < 0.05$). There was no tissue × dose interaction among MHC1 mRNA concentration ($P > 0.05$). These results indicated that α-chaconine has a dose-dependent effect on MHC2X mRNA but did not affect to MHC1 mRNA in bovine satellite cells.

Key Words: α-chaconine, Hanwoo, semimembranosus, longissmus dorsi, satellite cells

0767 Vitamin C supplement increased intramuscular adipose tissues but not affect myogenic development of Hanwoo steers. S. C. Jang, K. Y. Chung*, E. M. Lee, S. H. Yang, and E. G. Kwon, *Hanwoo Research Institute, NIAS, RDA, Pyeongchang, the Republic of Korea*.

Vitamin C (VC) supplements have been used for enhancing marbling fat in high-quality beef cattle. However, mode of action of vitamin C was not clearly studied for long time. The aim of this experiment was to determine the effect of additional saturated parm-oil coated VC supplement compare to a control diet (saturated parm-oil only) on the level of adipogenic and myogenic gene expressions at liver (LV), subcutaneous adipose tissue (SC), perirenal adipose tissue (PR), and longissimus dorsi muscle (LD). A 2 × 4 factorial arrangement (control, VC, and LV, SC, PR, and LD tissues) was used to feed 10 Hanwoo steers. Two steers were fed in same pen and 5 pens were used for treatment. Tissues were collected within 10 min of harvest for analysis of PPARγ, SCD, GLUT4, MHC1, MHC2X, and GPR43 mRNA abundance. Real-time RT-PCR was used to measure the quantity of respective mRNA relative to a ribosomal protein subunit 9 (RPS9) mRNA. Data were analyzed as a completely randomized design using the MIXED model. Difference between the control and treatments were determined using the LSD procedure. Overall ADG did not differ between VC supplement and the control ($P > 0.05$). Marbling score was greater in the VC treatment than in the control ($P < 0.05$). Lipid percentage tended to greater ($P = 0.084$) in the VC treatment but share force tended to be lower in the VC treatment ($P = 0.068$). Real-time quantitative PCR revealed that the mRNA content of SCD in PR from VC supplement cattle increased ($P < 0.05$) compared with the control. There was no mRNA effect at MUS in cattle. However, mRNA level of GLUT4 and GPR43 were increased at LV tissues in VC-treated cattle ($P > 0.05$). These data indicated that VC supplement increased relative mRNA level of GLUT4 and SCD in SC and LV tissue but not affect myogenic gene expression on final fattening periods of Hanwoo steers.

Key Words: Hanwoo, adipogenic, myogenic, |gene expression

0768 Chromium propionate supplementation alters feedlot performance and GLUT4 activity in feedlot steers. J. O. Baggerman*[1], Z. K. F. Smith[1], A. J. Thompson[1], J. Kim[1], P. W. Rounds[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Kemin Industries, Inc., Des Moines, IA*.

The objective was to evaluate the effects of increasing concentrations of chromium propionate (CrP) on feedlot performance, blood parameters, carcass characteristics, and skeletal muscle changes over time in feedlot steers. Crossbred steers ($n = 32$, 16 pens, 2 hd/pen) were blocked by BW, and each pen was randomly assigned to one of four treatments: control, 150 ppb supplemental CrP (KemTRACE Chromium, 0.04%; Kemin Industries, Des Moines, IA), 300 ppb supplemental CrP, and 450 ppb supplemental CrP. Steers were fed 1x daily ad libitum a steam-flaked corn–based diet, and the treatment was top-dressed at the time of feeding. Body weights, blood samples, and skeletal muscle biopsies were collected before time of feeding on d 0, 28, 56, 91, 119, and 147. Blood sera were harvested for analysis of glucose, insulin, serum urea nitrogen, and NEFA concentrations. Skeletal muscle biopsy samples were used for immunohistochemical analysis. Data was analyzed using the GLIMMIX procedure of SAS 9.4, with pen as the experimental unit for live and carcass data and steer as the experimental unit with day as a repeated measure for laboratory analysis. Starting on d 56 through the end of the trial, cattle fed the 450-ppb treatment were the heaviest ($P < 0.05$). A linear effect ($P < 0.05$) of treatment on BW and ADG was observed starting on d 56 until the end of the trial. For HCW, there was also a linear effect of treatment, with the greatest HCW in the cattle fed the 450-ppb treatment ($P < 0.05$). There was no effect of treatment on any blood parameter measured ($P > 0.05$). For skeletal muscle fiber cross-sectional area, there was a treatment × day interaction ($P < 0.05$), with the greatest increase in the 450-ppb treatment group. Density of total GLUT4 decreased over time for all treatments ($P < 0.05$), with the treatments receiving CrP having less of a decrease than the control group ($P < 0.05$). Internalization of GLUT4 was increased in the 300-ppb and 450-ppb treatments ($P < 0.05$). For total nuclei density and myonuclei density, there were treatment × day interactions ($P < 0.05$), where the 450-ppb treatment exhibited a greater density of total nuclei and myonuclei on d 147. These results indicated supplementation of 450 ppb CrP increases HCW, possibly due to changes in GLUT4 activity in skeletal muscle.

Key Words: beef cattle, growth, muscle

0769 Feeding five percent grass hay or wheat straw with high-starch, textured diets to weaned dairy calves between eight and sixteen weeks of age. F. X. Suarez-Mena*, T. S. Dennis, T. M. Hill, J. D. Quigley, and R. L. Schlotterbeck, *Provimi, Brookville, OH*.

This research had the objective to determine if changing diet forage fiber concentration by feeding different forages affected BW gain and structural growth of dairy calves from 8 to 16 wk of age. Male Holstein calves (24 per treatment in 6 pens with 4 calves/pen) initially 76 ± 1.6 kg BW were fed a common, textured grain-based concentrate (95% of the total mixed ration; 37% whole corn, 25% whole oats, 35% protein supplement pellet, and 3% molasses; 22% CP, 40% starch, 9% ADF, and 16% NDF) with either 5% chopped grass hay (13% CP, 40% ADF, and 67% NDF) or 5% chopped wheat straw

(2% CP, 48% ADF, and 80% NDF). During the previous nursery phase, calves were fed 0.66 kg DM from milk replacer (25% CP and 17% fat) and weaned at 42 d. Calves were also fed a similar textured, grain-based concentrate and water ad libitum. Calves remained in the nursery after weaning for 14 d. Calves were weighed and scored for body condition, and hip widths were measured initially (8 wk) and at 12 and 16 wk (periods 1 and 2; 56-d trial). Body condition score was a 5-point system (1 being thin and 5 being obese). Treatments were analyzed as a completely randomized design with repeated measurements. Initial BW, hip width, and BCS did not differ ($P > 0.10$) among treatments. The hay diet contained 3.3% NDF from forage whereas the straw diet contained 4.0% NDF from forage. There tended ($P < 0.09$) to be an interaction of treatment with 4-wk period for DMI as a percent of BW (2.87 vs. 2.76% BW in period 1 and 2.87 vs. 2.93% BW in period 2 for hay vs. straw, respectively), but there were no interactions ($P > 0.10$) for other measurements. Overall BW gain tended ($P < 0.07$) to be greater for calves fed hay vs. straw (1.04 vs. 0.97 kg/d). Change in hip width (5.0 vs. 4.6 cm) and feed efficiency (0.350 vs. 0.334 BW gain/feed) were greater ($P < 0.05$) for calves fed hay vs. straw. Change in BCS was 0.5 points for each treatment. These results further suggest that BW and structural growth in Holstein calves less than 16 wk of age is very sensitive to forage fiber concentration.

Key Words: forage, calves, growth

0770 Effects of a milk balancer protein supplement on growth and performance of dairy calves.

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In Argentina, dairy calves are commonly fed 4 L/d of milk plus starter pelleted feed containing 20% of CP during the first 8 wk of life. The objective of the study was to evaluate the effect of a milk balancer protein supplement on growth and performance of dairy calves during the first 30 d of this period. Fourteen newborn calves were randomly assigned to one of two treatments: 1) control (fed 4 L/d of raw milk) and 2) supplement (SUP; fed 4 L/d of raw milk and 0.2 kg/d of supplement). All calves had access to water and were individually offered starter feed. Body weight and body measurements (withers and hip height, thoracic diameter, and body length) were taken weekly and every 2 wk, respectively. Intake of starter feed was calculated daily based on offered and remaining feed, and total DMI was calculated taking into account milk, supplement, and starter feed intake. Milk, starter feed, and milk balancer were sampled weekly and chemically characterized. The data was analyzed as a randomized complete block design and the statistical model included treatment, time (repeated), sex, and interactions. Body measurements and weight at calving were used as a covariate. Compared with the control, calves fed SUP had greater total DMI (0.83 vs. 0.65 kg/d; SEM = 0.04) and thoracic diameter (0.83 vs. 0.85 cm; SEM = 0.01). No effect of supplement was observed on starter intake (0.14 vs. 0.15 kg/d; SEM = 0.05), daily gain (0.51 vs. 0.44 kg/d; SEM = 0.04), feed efficiency (0.61 vs. 0.67; SEM = 0.04), withers (0.80 vs. 0.81; SEM = 0.006) and hip heights (0.83 vs. 0.84; SEM = 0.007), or body length (0.73 vs. 0.73; SEM = 0.007). In conclusion, the use of the milk balancer supplement increased intake but did not significantly improve growth during the first month of age. Considering that under normal conditions, calves lose weight during the first 2 wk, it would be important to carry out a new trial considering the total 8 wk that calves are kept in the calf unit.

Key Words: calves, growth, milk supplement

0771 Effects of *trans*-10, *cis*-12 conjugated linoleic acid on gene expression and lipid content of adipocytes derived from lactating dairy cows.

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The antilipogenic effects of *trans*-10, *cis*-12 CLA are widely reported across monogastric species. However, abomasal infusions of this CLA isomer have been shown to increase expression of lipogenic genes in the adipose of lactating dairy cows. It is not clear if this is a result of energy repartitioning due to a decrease in milk fat synthesis or a direct effect of *trans*-10, *cis*-12 CLA on adipocytes. Our objective was to examine the effects of *trans*-10, *cis*-12 CLA on cultured adipocytes derived from subcutaneous adipose of lactating dairy cows ($n = 4$). Adipose samples were digested with collagenase type II and cells from the stromal vascular fraction were cultured in DMEM/F12 supplemented with 10% fetal bovine serum. Preadipocytes were obtained from outgrowth of plastic adherent cells and seeded in assay plates. After reaching confluence, cells were induced to differentiate and maintained in the plates for 10 d. From d 2 to 10, the medium was supplemented with one of two treatments: 50 μ*M trans*-10, *cis*-12 CLA (T10C12) or 50 μ*M cis*-9, *trans*-11 CLA (C9T11). On d 10, intracellular triglyceride was quantified using an AdipoRed assay and RNA was extracted to analyze gene expression using RT-qPCR. Statistical analysis was performed using linear mixed models. Fold changes (FC) in gene expression are presented relative to the C9T11 treatment. Conjugated linoleic acid supplementation did not affect triglyceride content of the adipocytes ($P = 0.47$), but the ratio of triglyceride content of adipocytes to preadipocytes indicated differentiation occurred in both treatment groups (T10C12 = 60.0 and C9T11 = 55.0). T10C12 decreased expression of the lipogenic genes ACACA (FC = 0.75; $P = 0.01$), ELOVL6 (FC = 0.73; $P = 0.03$), and SCD1 (FC = 0.52; $P = 0.03$). Expression of C/EBPβ, FAS, GAPDH, LPL, and PPARγ were not affected by treatment ($P \geq 0.43$). In contrast to what has been observed in murine-derived 3T3-L1 cells, T10C12 increased the expression of the

fatty acid transport gene FABP4 (FC = 2.06; $P = 0.01$) and tended to increase the expression of DGAT1 (FC = 1.07; $P = 0.06$), which is associated with triglyceride synthesis. Although *trans*-10, *cis*-12 CLA decreased the expression of several lipogenic genes, it did not inhibit lipid accumulation. This suggests that cultured adipocytes derived from dairy cows respond differently to *trans*-10, *cis*-12 CLA than those derived from monogastric species.

Key Words: adipocyte, conjugated linoleic acid, lipogenesis

0772 Effects of maternal exercise on postnatal growth and carcass characteristics of swine.

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Our laboratory has previously reported that pregnant swine allowed to exercise during mid to late gestation have increased umbilical blood flow to the piglets. Our objective was to determine how maternal exercise would impact postnatal growth and carcass parameters of their offspring at 6 mo of age. Yorkshire gilts were paired to either remain in their individual stall from d 40 to term (CON; $n = 4$) or exercise for 30 min 3 times per week from mid to late gestation (EX; $n = 4$). Within 12 h postpartum, litter size was normalized within a pair of gilts. Pigs were weighed monthly. Upon reaching an average BW of 58.1 kg, loin muscle area (LMA) and backfat were obtained every 28 d via ultrasonography. Pigs were harvested at 118 kg with organ masses recorded and carcass composition and meat quality determined. Data were analyzed with sow as the experimental unit. Maternal treatment did not impact ADG or LMA, but there was greater ($P = 0.03$) backfat in female piglets from EX dams compared with CON and male piglets from CON dams compared with EX. Backfat in female-EX and male-CON was similar. Although there were limited organ and muscle mass differences due to maternal treatment, pigs from EX dams had an increased ($P \leq 0.05$) longissimus muscle pH at 24 h (5.36 vs. 5.27 ± 0.03), decreased drip loss (6.31 vs. 4.54 ± 0.48%), and increased L* (55.73 vs. 52.40 ± 0.74) compared with CON. Maternal activity during gestation appears to have limited impacts on gross body measurements but may be advantageous to carcass quality of their offspring. Future studies are needed to confirm that the increased meat quality relates to better pork for consumers.

Key Words: carcass, maternal activity, pigs

0773 The effect of phase feeding on feed cost, growth, and performance of calves fed milk replacer.

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Ninety-six 3- to 10-d-old Holstein bull calves with an average initial BW of 44.1 kg (SD 1.67) were shipped from Wisconsin to the Land O'Lakes Research Facility in northwest Iowa. The objective of this study was to evaluate the use of phase feeding with a milk replacer (MR) containing only milk protein in the first phase and a MR using hydrolyzed soy protein modified (HSPM) in the second phase of calf rearing. Calves were randomly assigned according to BW and blood γ globulin to one of four MR diets offered in a 15% solution: 1) 27% CP containing only milk protein, 10% fat (control); 2) phase feeding, 28% CP, 20% fat in Phase 1 and 22% CP, 15% fat with HSPM in Phase 2; 3) phase feeding, 28% CP, 20% fat in Phase 1 and 25% CP, 15% fat with HSPM in Phase 2; and 4) phase feeding, 28% CP, 20% fat in Phase 1 and 28% CP, 15% fat with HSPM in Phase 2. Calves were fed to provide 816 g DM/d during Days 1 to 6 and 1,135 g DM/d during Days 7 to 41, in 2 feedings at 0600 and 1515 h. Calves were offered 567.5 g in one feeding at 0600 h during the last week. Calf starter (22% CP, as-fed basis) was offered ad libitum throughout this 48-d trial. Data were analyzed by Mixed procedures of SAS. Total weight gain, MR consumption, feed:gain ratio, and starter intake did not differ ($P > 0.05$) among treatments. Total feed costs over the 7-wk trial were significantly lower ($P < 0.05$) for the three phase-feeding treatments. Calves on the three phase-fed diets performed equally to calves on the control-fed diets and the feed costs were significantly reduced, making this a viable option where applicable.

Key Words: calf, milk replacer, phase feeding

0774 The effect of weaning over a fourteen-day versus a twenty-one-day period on the performance of calves fed milk replacer on a controlled ad libitum curve through an automatic feeder.

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Thirty-eight 3- to 10-d-old Holstein bull calves with an average initial BW of 39.2 kg (SD 1.12) were shipped from Wisconsin to the Land O'Lakes Research Facility in northwest Iowa. The objective of this study was to better understand

the impact of weaning period on the performance of calves fed a 26% CP, 20% fat milk replacer (MR) on a controlled ad libitum curve (40FIT Technology, Foerster-Technik, Engen, Germany) through an automatic feeder. Calves were randomly assigned according to BW and blood γ globulin to either a 14-d or a 21-d weaning period. Calves were limited to meal size, but not number of meals, before the start of weaning. Weaning began at either Day 29 (21-d weaning) or Day 36 (14-d weaning), offering 1.65 kg of MR DM on Day 1 of weaning and gradually decreasing MR offering daily to 0.299 kg of MR DM on the day of weaning. Milk replacer was offered in a 13.0% solids solution throughout the 49-d milk feeding phase. All calves were followed for 5 wk after weaning to monitor starter intake and growth. Calf starter (22% CP, as-fed basis) was fed ad libitum throughout this 84-d trial. Data were analyzed by Mixed procedures of SAS. There were no statistical differences ($P > 0.05$) in total BW gain or MR consumption between treatments. Calves fed according to the 21-d weaning period schedule appeared to consume more starter over the 12 wk trial compared with the calves fed according to the 14-d weaning period schedule (140.9 vs. 129.9 kg, respectively); however, due to group feeding of starter and no individual starter intake values, no statistical analysis could be performed. Either a 14-d or 21-d weaning period could be successfully used for calves fed on a controlled ad libitum curve through an automatic feeder.

Key Words: automatic milk replacer feeder, calf, weaning

0775 Effects of maternal dietary restriction during the second trimester on offspring growth and feedlot performance. S. M. Quarnberg*, J. F. Legako, J. M. Gardner, D. R. ZoBell, C. E. Carpenter, K. A. Rood, and K. J. Thornton, *Utah State University, Logan*.

This study determined the impacts of maternal dietary insult during the second trimester on offspring growth and early feedlot performance. Angus-influenced commercial cows ($n = 34$) were naturally bred to a purebred Angus sire. During preparturition, individual cow served as the experimental unit for one-way ANOVA. During 84 d of mid gestation, cows were stratified into two groups, maintenance ($n = 16$) and restricted ($n = 18$), by initial weights ($P = 0.804$) and BCS ($P = 0.723$). Restricted cows were provided with lower forage biomass (1,662 kg/ha, DM) in comparison with maintenance (2,309 kg/ha, DM). Following the insult period, restricted cows had a mean BCS 1.55 lower ($P = 0.001$) than maintenance cows and a BW difference of 85.3 kg ($P = 0.024$). Dams were commingled and uniformly managed following mid gestation. Calves were weaned approximately 215 d of age and placed on a background diet for 7 wks before entering the feedlot phase where calves were kept in individual pens and fed a grower ration ad libitum. Calves BW were measured at birth, weaning, and every 28 d of the feedlot phase. Ultrasound was used for measurement of BF and REA during the feedlot phase. Calf temperament was evaluated at weaning and during the feedlot phase. Serum glucose, insulin, IGF-1, and cortisol were determined for calves at weaning, 1 wk before the feedlot phase, and the last day of the feeding trial. One-way ANOVA was used to determine impacts of fetal programming on calves. Individual calf served as the experimental unit. Calf BW at birth, weaning, and during feeding showed no differences ($P \geq 0.245$). No differences were determined for ADFI ($P \geq 0.428$), ADG ($P \geq 0.338$), G:F ($P \geq 0.273$), REA ($P \geq 0.285$), or BF ($P \geq 0.416$) during the feedlot stage. Concentrations of glucose ($P \geq 0.504$), insulin ($P \geq 0.224$), IGF-1 ($P \geq 0.107$), and cortisol ($P \geq 0.709$) were found to be similar at all time points. Restricted calves were found to be more excitable, with greater temperament scores at weaning ($P = 0.026$). Recent work has indicated that fetal programming alters progeny carcass characteristics. However, concerns for negative impacts on performance of progeny exist. This study determined little impact on calf performance during early feedlot stages.

Key Words: feedlot performance, fetal programming, temperament

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0776 Neonate immunity, growth, and puberty in dairy calves: Influence of dietary conjugated linoleic acid supplementation of the dam. C. L. Cardoso*[1], D. Somwe[2], and G. Esposito[3,4], *[1]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa, [2]Department of Animal and Wildlife Science, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa, [3]Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Pretoria, South Africa, [4]Institute of Food, Nutrition and Well-Being, University of Pretoria, Pretoria, South Africa*.

Colostrum provides the calf with maturational, immune-modulatory, and antimicrobial factors. Feeding isomers of CLA reportedly increase immunoglobulin production in rats and circulating IGF-I levels in cows. The objective of the study was to evaluate the effect of CLA dietary supplementation of the dam on colostrum quality, calves immune system, growth, and attainment of puberty. Forty Holstein cows blocked by parity, BW, and BCS were randomly assigned to two groups: control (CTL; 100 g/cow per day of Ca salts) and CLA (100 g/cow per day of CLA). Individual top-dressed supplementation started 20 ± 7 d before calving until 35 d in milk. From Day 0 to 4, each calf was fed its mother's colostrum. The latter was sampled for IgG quantification. Calves were bled every other day from 0 to 15 d for IgG and total protein (TP) levels. Weekly, from Day 0 to 35, body measurements and weight were recorded for growth rate; furthermore, calves were bled

for GH and IGF-I quantification. Attainment of puberty was monitored from the age of 180 d. Monthly, body measurements and weight were recorded. Semen collection by electroejaculation was performed in males with scrotal circumference ≥23 cm for semen parameters evaluation (volume, color, mass/individual motility, and concentration). Puberty was declared with concentration of 50 million spermatozoa/ejaculate with at least 10% progressive motility. Females were bled fortnightly for progesterone levels, whereas ovarian activity was monitored by ultrasonography. Puberty was attained with progesterone levels ≥1 ng/mL and the presence of a corpus luteum. Growth rate, blood, and colostrum parameters were analyzed by ANOVA for repeated measures using the GLM procedure. Age at puberty was compared by one-way ANOVA. No differences between groups were observed for blood and colostrum IgG levels, blood GH levels, and attainment of puberty. Treatment showed decreased levels of IGF-I ($P < 0.05$) compared with the control. A trend for higher TP levels (treatment × age, $P = 0.079$) and overall ADG ($P = 0.1$), calculated from Day 0 to 300, was observed in CLA calves. However, from Day 0 to 35, growth rate was significantly higher in CLA females (treatment × age, $P < 0.05$) and lower in CLA males (treatment, $P < 0.05$) compared with the CTL. These differences were not observed from 180 to 300 d. Colostrum from CLA supplemented dams showed a gender and time-dependant effect on calf's growth; however, it did not alter immune response and attainment of puberty. Further investigation is needed to unveil CLA's possible mechanism of action.

Key Words: conjugated linoleic acid, growth, immunoglobulin G

0777 Repeatability of residual feed intake and indices of body composition in growing Columbia ewes fed the same diet. K. A. Perz*, J. G. Berardinelli, L. N. Park, R. K. Pollard, C. M. Page, W. C. Stewart, and J. M. Thomson, *Montana State University, Bozeman*.

Residual feed intake (RFI), an efficiency measurement based on the difference in expected feed intake for a given weight and growth rate and actual feed intake, is used to improve production efficiency of domestic ruminants. The purpose of this study was to evaluate the repeatability of RFI of sheep measured for two consecutive years and to investigate the relationship between indices of body composition and RFI in yearling ewes. Two trials, using the same Columbia ewe lambs ($n = 17$ per trial), were conducted in consecutive years. Ewes were individually fed for 47 and 45 d, respectively, beginning in September of each year. The diet, an alfalfa–barley pellet, was the same composition and batch for both years. Residual feed intake was calculated for each ewe in each year. Ewe was the experimental unit. Residual feed intake and performance data were analyzed using ANOVA. Residual feed intake did not differ ($P > 0.05$) between years, indicating that on the same diet and environmental conditions, RFI does not appear to change with age. Ewes were categorized into 3 RFI classes (efficient, average, and inefficient) based on RFI values 1 SD below and above the yearly average. In 2014, initial and final liveweights, ADG, and DMI did not differ due to RFI classification ($P > 0.05$). In 2015, DMI was greater for inefficient ewes ($P < 0.05$), but there was no difference in initial and final liveweights or ADG ($P > 0.05$). Ultrasound data were analyzed using ANOVA with repeated measures. Rib eye area (REA; cm^2) and backfat thickness (BF; cm) were measured by ultrasound on Day 0, 17, and 45 in 2015. These variables were used to calculate estimates of final body composition: whole-body muscle mass, intramuscular fat, empty BW, empty BW DM, empty BW fat, empty BW protein, carcass weight, carcass weight DM, carcass weight fat, and carcass weight protein. Residual feed intake classification did not affect REA or BF ($P > 0.05$). Regression analysis indicated that both REA and BF increased ($P < 0.05$) from Day 0 to 17 and BF increased ($P < 0.05$) again from Day 17 to 45. No body composition estimates were affected by RFI classification ($P < 0.05$). Results suggest that RFI is repeatable; however, indices of body composition seem to be independent of RFI in Columbia ewes fed the same diet under similar conditions.

Key Words: residual feed intake, repeatability, body composition

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0778 A new view on the growth of pigs in relation to frequent body weight monitoring. A. H. Stygar*[1], K. A. Dolecheck[2], and A. R. Kristensen[1], [1]*University of Copenhagen, Department of Large Animal Sciences, Frederiksberg, Denmark,* [2]*University of Kentucky, Lexington*.

Frequent BW monitoring of growing pigs can be useful for identifying production (e.g., feeding), health, and welfare problems. However, to construct a tool that will properly recognize abnormalities in pigs' growth, a precise description of the growth process should be used. In this study, we proposed a new model of pig growth accounting for daily fluctuations in BW. Data on BW measurements of 1,710 pigs (865 gilts and 843 barrows) originating from 5 consecutive batches from one Danish commercial farm was collected. Pigs were inserted into a large pen (maximum capacity = 400) between November 2014 and September 2015. On average, each pig was observed for 42 d and weighed 3.6 times a day when passing from the resting to the feeding area. Altogether, 243,160 BW measurements were recorded. To properly account for the diurnal pattern, the time of BW measurements was corrected for daylight saving time. A multilevel model of pig growth was constructed and fitted to available data. The BW of pigs was modeled as a quadratic function of time. A diurnal pattern was incorporated into the model by a cosine wave with known length (24 h). The model included pig effect, which was defined as a random autoregressive process

with exponential correlation. Variance of within-pigs error was assumed to increase with time. The intercept, time, square value for time, and cosine wave were significant fixed effects ($P < 0.0001$). Additionally, the interaction between these fixed effect elements and each batch was determined to be significant ($P < 0.0001$). The gender effect was not significant and was removed from the final model ($P = 0.52$). According to results, pigs were lighter in the morning and heavier in the evening (the minimum BW was obtained around 1000 h and the maximum was obtained around 2200 h). However, the exact time of obtaining maximum and minimum BW during the day differed between batches. Pigs had access to natural light, and therefore, existing differences could be explained by varying daylight level during observation periods. Because the diurnal amplitude for pig growth ranged between batches from 0.9 to 1.4 kg, BW monitoring tools based on frequent measurements should account for diurnal variation in BW of pigs. This proposed description of growth was built into a monitoring tool (a dynamic linear model) consisting of an updating, forecasting, and filtering procedure. The constructed monitoring tool will be applied to farm data in future studies.

Key Words: body weight, pigs, diurnal pattern

0779 Effect of prior fiber consumption on diet-induced obesity susceptibility and metabolic health indicators in Ossabaw pigs. V. V. Almeida[1] and K. M. Ajuwon*[2], [1]*Purdue University, West Lafayette, IN,* [2]*Department of Animal Sciences, Purdue University, West Lafayette, IN*.

Sixty-three mixed-sex pigs (28 d of age and 5.63 ± 0.20 kg BW) were used to evaluate the effects of dietary fiber source and fat level on growth performance, backfat thickness (BF), and metabolic status. Pigs were blocked by BW and allotted by sex and litter to 1 of 4 treatments with 8 pens per treatment and 2 pigs per pen. Treatments were arranged in 2 × 2 factorial with 2 fiber sources (inulin and cellulose) and 2 fat levels (5 and 15%, as-fed basis, for the low-fat diet [LF] and high-fat diet [HF], respectively). Pigs received diets containing 4% of either inulin or cellulose on an as-fed basis for the first 56 d (nursery phase) and thereafter were fed LF and HF containing no added fiber source from d 56 to 140 (growing phase). On d 140, BF was measured by ultrasound and jugular blood samples were taken for insulin, glucose, and triglyceride (TAG) analyses. Data were analyzed using the MIXED procedure of SAS. There were fiber × fat interactions for final BW ($P = 0.02$) and G:F ($P = 0.01$), as pigs receiving cellulose had greater ($P < 0.05$) final BW (63.96 and 70.31 ± 1.15 kg for LF and HF, respectively) and G:F (0.136 and 0.157 ± 0.003 for LF and HF, respectively) when fed HF diet than pigs fed LF. Feeding HF, regardless of fiber source, tended to increase ADG (0.432 and 0.464 ± 0.01 kg for LF and HF, respectively; $P = 0.07$) and reduce ADFI (3.184 and 3.013 ± 0.05 kg for LF and HF, respectively; $P = 0.07$). Moreover, HF, regardless of fiber source, resulted in higher BF (13.41 and 18.18 ± 0.12 mm for LF and HF, respectively; $P < 0.01$). There was a tendency for a fiber × fat interaction ($P = 0.07$) for serum TAG concentration, as pigs receiving cellulose had greater serum TAG (0.264 and 0.392 ± 0.02 mg/mL for LF and HF, respectively; $P < 0.05$) when fed HF than pigs fed LF. Pigs fed HF, regardless of fiber source, had greater ($P < 0.01$) insulin (0.014 and 0.016 ± 0.001 mg/L for LF and HF, respectively) and glucose (100.89 and 125.03 ± 4.39 mg/dL for LF and HF, respectively) concentrations in the serum. In summary, dietary cellulose inclusion during the early life of pigs increased susceptibility to obesity and metabolic syndrome in the future, whereas dietary inulin inclusion prevented future metabolic disorders.

Key Words: early nutrition, fiber metabolic disorders, pig model

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0780 Body composition at first heat of gilts exposed to three different feeding regimens. S. Van Vliet[1], T. S. Bruun[2], J. Hales[3], C. F. Hansen[3], and P. K. Theil*[1], [1]*Aarhus University, DK-8830 Tjele, Denmark,* [2]*SEGES Pig Research Centre, 1609 Copenhagen V, Denmark,* [3]*University of Copenhagen, DK-1870 Fredriksberg C, Denmark*.

This study was conducted to evaluate the possibility of increasing body fatness of gilts by nutritional means during rearing. Forty-eight gilts (Danish Landrace × Yorkshire [LY]) with an initial BM of 62 ± 2 kg were selected from 16 litters (3 littermates from each).Gilts were fed individually with one of three diets from 62 to 105 kg LW and then transferred to diets lower in CP and Lys. Littermates stratified for BM were randomly allocated to one of three dietary regimens: low protein ad libitum (LPAD) (4.3/3.5 g SID Lys/kg feed), moderate protein restriction (MPRE) (5.4/4.3 g SID Lys/kg feed), or high protein ad libitum (HPAD) (7.0/5.4 g SID Lys/kg feed). The experiment was designed to limit growth by lysine (LPAD), energy (MPRE), or the growth potential of gilts (HPAD). Body water content was measured using the deuterium oxide dilution technique before the dietary intervention were initiated ($n = 9$) and at first heat ($n = 47$). Body contents of fat, protein, and ash were calculated using prediction equations developed for LY gilts by Rozeboom and coworkers and back fat depth was measured at the P2 site. Statistical analysis of fixed effect of treatment was performed using a mixed model to account for repeated measurements. Initially, no differences were observed in body water content or derived contents of fat, protein, or ash ($P > 0.20$). On average, gilts initially contained 61.2% water, 11.2% fat, 17.9% protein, and 3.4% ash. At first heat, the measured water content was lowest in LPAD, highest in MPRE, and intermediate in HPAD gilts ($P < 0.001$), whereas the body fat content was changed inversely, as LPAD (26.6%), MPRE (23.1%), and HPAD gilts (25.3%) had highest, lowest, and intermediate body fat contents ($P < 0.001$), respectively. The

protein and ash contents were lowest ($P < 0.001$) in LPAD fed gilts (15.5 and 2.8%, respectively), highest in MPRE fed gilts (16.1 and 3.0%, respectively), and intermediate in HPAD fed gilts (15.8 and 2.9%, respectively). The change in body fatness was supported by measurements of back fat depth, which at first heat was highest ($P < 0.001$) in LPAD gilts (15.1 mm), lowest in MPRE gilts (11.8 mm), and intermediate in HPAD sows (14.3 mm). In conclusion, body fatness of gilts can be considerably increased through dietary means even in breeds that thoroughly have been genetically selected for leanness.

Key Words: body condition, body fatness, dietary composition, gilt rearing, growth performance

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0781 Preweaning diet and exogenous estrogen alter mammary epithelial cell proliferation and progesterone and estrogen receptor expression.

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Preweaning diet and estrogen treatment alters mammary development. Our objectives were to study the effects of diet and estrogen on mammary histology, proliferation, and expression of estrogen (ESR1) and progesterone (PR) receptors. Thirty-six Holstein heifer calves were reared on 1) a control milk replacer (MR) fed at 454 g powder/d (R; 20% CP and 20% fat) or 2) an enhanced MR fed at 1,135 g powder/d (E; 28% CP and 25% fat). Milk replacer was fed for 8 wk. At weaning, a subset of calves were sacrificed ($n = 6$/diet). Remaining calves received E_2 implants and were sacrificed at wk 10. Treatments were 1) R, 2) R + E_2 (R-E2), 3) E, and 4) E + E_2 (E-E2). One day before harvest, calves were given bromodeoxyuridine (BrdU; 5 mg/kg). At sacrifice, parenchyma (PAR) was removed and fixed. Sections from lower, middle, and distal zones were stained with H and E and antibodies to measure expression of ESR1, PR, and BrdU. Comparisons with PROC GLIMMIX in SAS on a per-area and per-cell basis were similar. At wk 8, R-fed calves had more ($P < 0.01$) PR-expressing cells in distal PAR. But PR expression intensity was greater ($P < 0.01$) in E-fed calves. The proportion of cells expressing ESR1 was not affected by diet, but expression intensity was increased for E-fed calves across all zones (62 to 81%; $P < 0.01$). Percent BrdU-positive cells was 2- and 0.5-fold greater ($P < 0.01$) for E-fed calves in zone 2 and 3, respectively. At wk 10, calves treated with estrogen had 3.9-fold greater PR expression intensity. The intensity and percent of cells expressing ESR1 was lowest in estrogen-treated calves. Overall, estrogen-treated calves had the most proliferating cells ($P < 0.01$). However, in zone 3, E-E2 calves had a higher percentage of proliferating cells than calves on all other treatments ($P < 0.01$). Results indicate both diet and estrogen administration alter proliferation rates of the mammary epithelium and that changes in expression of ESR1 and PR are at least partially responsible for changes in mammary PAR development associated with enhanced preweaning feeding of dairy calves. However, furthermore, more detailed analyses are needed to fully understand mechanisms at play.

Key Words: estrogen receptor, progesterone receptor, mammary gland

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0782 In vivo knockdown of FGFR2 and MET mRNA in trophectoderm of ovine conceptuses retards their development via abrogation of MAPK and MTOR pathways.

X. Wang*, K. A. Dunlap, M. C. Satterfield, G. Wu, and F. W. Bazer, *Texas A&M University, College Station*.

The paradigm of downregulation of progesterone receptor in uterine epithelia before implantation is common to sheep, cow, pigs, rhesus monkey, women, and mice. Therefore, progestamedins, which derive from PGR-positive uterine stromal cells and include hepatocyte growth factor (HGF), fibroblast growth factor 7 (FGF7) and FGF10, regulate uterine luminal (LE), superficial glandular (sGE), and glandular (GE) epithelia during the estrous cycle/early pregnancy. Previous studies with sheep demonstrated the existence of receptors for HGF (HGFR; encoded by MET) as well as FGF7 and FGF10 (FGFR2) in conceptus trophectoderm (Tr). However, the biological roles of progestamedins in conceptus development are unknown. In this study, we conducted an in vivo morpholino antisense oligonucleotide (MAO)–mediated knockdown of translation of *FGFR2* and *MET* mRNA in ovine conceptus Tr. Normality of data and homogeneity of variance were tested using the Shapiro–Wilk test and the Brown–Forsythe test, respectively, in SAS. Data were analyzed by least squares one-way ANOVA and post hoc analysis (the Fisher LSD), with each ewe/conceptus as an experimental unit. $P < 0.05$ was considered significant. Translational knockdown of MET mRNA severely retarded conceptus development whereas translational knockdown of FGFR2 mRNA resulted in small, thin, and less elongated conceptuses compared with MAO control conceptuses. Both MAO-MET and MAO-FGFR2 conceptuses were functionally abnormal based on lower ($P < 0.05$) production of interferon tau, the pregnancy recognition signal in sheep. Quantitative immunofluorescence (IF) analysis demonstrated that MAO were evenly delivered ($P > 0.05$) into Tr but not uterine LE, sGE, and GE and that the abundance of both MET and FGFR2 proteins in Tr was decreased ($P < 0.01$) by 83.3 and 93.3%, respectively. Western blot analysis using ovine Tr cells treated with respective MAO also validated knockdown efficiencies of both MAO-MET and MAO-FGFR2. Further quantitative IF revealed that compared with MAO control, active caspase-3 in Tr of MAO-MET and MAO-FGFR2 conceptuses was increased ($P < 0.01$) by 4.5- and 6.5-fold, respectively. Moreover, phosphorylation of P38 was decreased ($P < 0.01$) by 68.7 and 84.4% in MAO-MET and MAO-FGFR2, respectively, compared with MAO control, whereas phosphorylation of MTOR was decreased ($P < 0.01$) by 75.0

and 83.3% in MAO-MET and MAO-FGFR2 conceptuses, respectively. Interestingly, phosphorylation of TSC2 was decreased ($P < 0.01$) by 79.2% in Tr of MAO-MET compared with MAO control but was no different ($P > 0.05$) between MAO-FGFR2 and MAO control conceptuses. Collectively, these results demonstrate critical roles for progestamedins (i.e., HGF, FGF7, and FGF10) in ovine conceptuses that are mediated via their receptors (MET and FGFR2) and activation of MAPK and MTOR pathways and that translational knockdown of *MET* and *FGFR2* mRNA increased apoptosis and retarded conceptus development during early pregnancy.

Key Words: progestamedin, trophectoderm, MTOR, MAPK, sheep

GROWTH AND DEVELOPMENT SYMPOSIUM: NEW -OMICS TECHNOLOGIES TO UNDERSTANDING THE BIOLOGICAL PROCESSES AND NETWORK PATHWAYS ASSOCIATED WITH CATTLE GROWTH AND HEALTH

0783 Objective-oriented genomic relationship matrices.

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The advent of affordable high-density SNP genotyping platforms has boosted the implementation of genomic selection program in many livestock species. However, large reference populations are required to accurately compute genomic predictions of breeding value (GEBV). Combining information from (seemingly independent) separate populations has been highlighted as a beneficial strategy and methods to adjust the realized genomic relationship matrix (GRM) to accommodate the heterogeneity in allele frequencies have been proposed. Simulation studies based on real sequence data have shown the importance of using only variants as close as possible or identical to the causative mutations. Recently, we showed that data from reference populations from two distinct breeds can be merged to generate GEBV, provided the SNP used to build the GRM are carefully selected based on their significance and direction of the effect associated to the phenotype. We show that this approach can optimize the genomic correlation for the phenotype of interest in the two populations. We further show how a "hybrid" GRM permits the linking of genotypic data of pooled DNA samples of commercial cattle pooled according to phenotype with individual DNA samples from animals available for selection. Our examples are concerned with beef cattle raised extensively in tropical and subtropical regions of Australia. We anticipate that the use of traditional "one size fits all" relationship matrices, based on pedigree information only, is coming to an end and predict the time has come for "objective-oriented" GRM purpose built for a specific breeding objective.

Key Words: genomic selection, genomic predictions, genomic relationship matrix

0784 Multi-omics data resources and use in genetic improvement of cattle growth and health.

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Interactions of growth and health influence the progression of cattle to maturity. Growth and carcass traits typically have moderate to high heritability ($h^2 = 0.2–0.5$), whereas pathogen-disease related health traits tend to have low heritability ($h^2 \leq 0.2$). Genetic improvement in beef cattle involves selection with EPD predicted from multitrait, and often multibreed, models that incorporate genomic data derived from SNP chips. Available genotyping platforms have genomewide distance gaps of 49.4 (BovineSNP50) and 3 kb (BovineSNPHD). Genetic prediction accuracy can be improved with use of genomic data; however, process varies greatly depending on trait heritability and quality–quantity of data. Because most economically relevant traits are polygenic and single SNP within a positional-candidate gene explain limited variation, there is great interest in discovery and use large numbers of causal-mutation SNP in genetic prediction. These SNP will likely be located within nodes and hubs of gene networks and can be added to the current chips to improve their effect. Various "omics" tools evaluating transcriptome, proteome, and metabolome assist with discovery of coding and tag SNP. Differentially expressed targets from the latter two tools reveal gene products closely associated with an animal's physiologic phenotype, which can correlate with gene expression levels observed in RNA. Concordant results and enrichment analyses from these tools yield confidence to analyze target sequence, either DNA or RNA, to discover functional SNP. However, transcript splicing, peptide processing, and post-translational modifications complicate comparing results from the various approaches. The animal's epigenome and microbiome also influence phenotype. To identify functional SNP, RNA must be harvested from tissues of animal models designed to be informative for a trait collected from large breeding populations. Case versus control or comparisons of cattle from the tails of the quantitative trait distribution curves have proven useful strategies in several multi-omics growth and health studies of which pulmonary arterial pressure (PAP; $h^2 = 0.2–0.4$), an indicator of hypoxia-induced pulmonary hypertension, is an example. Here, cardiopulmonary tissues were collected from high- and low-PAP Angus steers ($n = 10$/group) with sire-pedigree diversity to growing seed stock bulls. Transcript abundance was assessed and differential expression results were obtained and are being merged with QTL and whole-genome sequence information to discover SNP genotypes for incorporation into a PAP EPD, a tool for selecting cattle for high elevation tolerance. Therefore,