302 Economic analysis of cost, rewards and trade-offs of alternative forage management strategies. G. A. Benson*, *North Carolina State University, Raleigh*.

Farm financial performance and cost of production data show a wide variation in revenue, expense and net returns per for individual cattle operations within regions as well as among average performance among regions. In addition, the producers' goals likely vary among farms. Therefore, few general recommendations can be made about production practices. One general recommendation is that producers keep adequate records to measure animal performance, cost of production, revenue, and net income. Estimates of the amount of forage produced that is lost and wasted during harvesting, storage and feeding total as much as 50%. Changes in management practices can reduce losses. The adoption of rotational or strip grazing can increase utilization by half, allowing increases in animal performance or stocking rate. Added costs include increases in labor and equipment use. New investments in grazing infrastructure may be needed. The cost of stored forages includes harvesting, storage, feeding out, and losses. The effective cost can be double that of comparable grazed forages. Extending the grazing season through modifications to fertilizer applications and stockpiling can be profitable alternatives to stored forages in some circumstances. Risk is inherent to rainfed forage production systems and includes reduced forage production and livestock performance and input price risk. Risk management options include carrying reserves of stored forages, purchasing forages, and purchasing forage extenders, all of which incur cost. Budgeting tools, including partial and enterprise budgets and sensitivity analysis can be used to evaluate alternative forage production practices and risk management scenarios. Case study examples based on Mid-Atlantic conditions demonstrate a substantial profit potential for low cost storage systems for hay and for intensively managed stockpiled forages for producers with the requisite management skill, interest and time.

Key Words: forage economics, beef cattle

Growth and Development: Physiology of Growth In Vivo and In Vitro

303 Modeling lifetime growth and feed efficiency in pigs. A. B. Strathe*[1], A. Danfaer[1], and E. Kebreab[2], [1]*University of Copenhagen, Copenhagen, Denmark*, [2]*University of Manitoba, Winnipeg, Manitoba, Canada*.

Animal genetic selection programs have improved growth rates, feed efficiency and produced leaner pigs at time of slaughter. These programs were based on analysis of data collected from 20 to 120 kg pigs with little or no information given on growth patterns beyond this point. Thus, a growth study was setup to obtain information on growth and feed efficiency patterns in Danish meat type pigs from birth to maturity. A total of 40 pigs (Landrace-Yorkshire × Duroc crossings) originating from 17 litters and of 3 genders were fed 7 diets in the period of 0 to 1007 days of age. Weekly BW and feed consumption data was collected. The BW vs. age data was subjected to analysis using 4 different growth functions i.e. Gompertz, Logistic, Bridges and Lopez. The BW vs. cumulative feed intake (CFI) was modeled using the monomolecular function. All mathematical functions were implemented in multilevel nonlinear mixed effect framework where nested random effects were included i.e. pig within litter. The statistical models where further updated to include a first order continuous autoregressive process and variance weights for modeling the error structure. The Lopez function was best suited to modeling the BW vs. age relations and estimated the maximum rate of growth to occur at 151.2 (SE=4.38), 163.6 (SE=3.67) and 133.0 (SE=3.49) days of age which corresponds to 117.0 (SE=4.47), 134.6 (SE=4.06) and 96.1 (SE=3.35) BW for barrows, boars and gilts, respectively. The feed efficiency curve was obtained as the derivative of monomolecular function with respect to CFI. The results showed that gilts had a distinct feed efficiency pattern when compared to the boars and barrows ($P < 0.001$). These data suggests that growth capacity in boars and barrows is not maximized in the standard growth period which may influence decisions on the time of slaughter.

Key Words: nonlinear mixed model, growth curves, pigs

304 Stimulation of skeletal muscle protein synthesis in neonatal pigs by long-term infusion of leucine is amino acid dependent. F. A. Wilson, A. Suryawan, M. C. Gazzaneo, R. A. Orellana, H. V. Nguyen, and T. A. Davis*, *USDA/ARS Children's Nutrition Research Center, Critical Care Med. Div., Dept. Pediatrics, Baylor College of Medicine, Houston, TX*.

Infusing leucine for 1 h increases skeletal muscle protein synthesis in neonatal pigs, but this is not sustained for 2 h unless the leucine-induced fall in amino acids is prevented. We aimed to determine whether continuous leucine infusion can stimulate protein synthesis for a prolonged period when baseline amino acids are maintained and to identify signalling mechanisms involved. Overnight fasted 7-d-old pigs were infused for 24 h with saline, leucine (400 $\mu mol \cdot kg^{-1} \cdot h^{-1}$), or leucine with replacement amino acids (n=6/group). Fractional protein synthesis and translation control mechanisms were examined in skeletal muscle. Amino acid replacement prevented the leucine-induced fall in plasma amino acids. Leucine stimulated muscle protein synthesis ($P<0.05$), but only when replacement amino acids were infused to maintain fasting levels. Leucine had no effect on phosphorylation of protein kinase B, AMP-activated protein kinase, tuberous sclerosis complex 2, signalling proteins upstream of mammalian target of rapamycin (mTOR). Leucine also did not alter phosphorylation of raptor or PRAS40 nor the association of mTOR with raptor, GβL, or rictor, regulators of mTOR. Phosphorylation of mTOR, as well as its downstream targets that regulate translation initiation, eukaryotic initiation factor (eIF) 4E binding protein (4EBP1) and ribosomal protein S6 kinase, as well as eIF4E•eIF4G association were increased, and eIF2α phosphorylation was reduced by leucine, in the absence and presence of replacement amino acids ($P<0.05$). Thus, prolonged infusion of leucine activates mTOR and its downstream targets that regulate translation in skeletal muscle, irrespective of the circulating levels of the other amino acids. However, the ability of leucine to stimulate muscle protein synthesis is dependent upon amino acid availability. *Supported by Ajinomoto Amino Acid Research Program and USDA/ ARS 6250510000-43.*

Key Words: muscle, amino acids, protein synthesis

305 Dietary starch effects on metabolic gene networks in *longissimus lumborum* of early–weaned angus steers. D. E. Graugnard*, L. L. Berger, D. B. Faulkner, and J. J. Loor, *University of Illinois, Urbana*.

Post–weaning evaluation of gene expression networks driving adipogenesis and energy metabolism provides a means to examine long–term effects of nutrition on *longissimus* muscle development. Angus steer calves (155 ± 10 d age, n = 7/diet) were fed high–starch (HiS) or low–starch (LoS) diets for 112 d followed by a common finishing diet

for an additional 112 d. *Longissimus lumborum* was biopsied at 0, 56, 112, and 224 d for transcript profiling via quantitative PCR of 24 genes associated with aspects of adipogenesis and energy metabolism. Expression of *PPARG* and its target genes *FABP4* and *SCD* increased (time $P < 0.05$) through 112 d. Whereas *PPARG* was greater (diet × time $P < 0.05$) on d 112, *FABP4* and *SCD* were greater at 56 d in steers fed HiS vs. LoS. Interactions during the growing phase also were observed for *THRSP*, *SREBF1*, and *DGAT2* such that feeding LoS resulted in greater ($P < 0.05$) expression at d 112. Among genes involved in driving the lipogenic program, carryover effects of HiS-feeding were reflected by greater (diet × time $P < 0.05$) expression at 224 d of *SREBF1*, the lipogenic genes *ACLY*, *ACSM1*, and *LPIN2*, and the insulin/Akt-signaling gene *IRS1*. Similar carryover effects were observed for genes involved in calcium signaling (*ATP2A2)* , control of glucose oxidation (*PDK4*), and transcriptional control of fatty acid oxidation (*PPARD*, *PPARGC1A*). *FASN*, *GPAM*, *G6PD*, and *ADIPOQ* increased regardless of diet through 224 d. However, HiS led to greater (diet × time $P < 0.05$) expression of FASN and ADIPOQ between 112 and 224 d. Steers fed LoS vs. HiS had greater (diet × time $P < 0.05$) serum NEFA throughout the growing phase as well as a marked increase in insulin by day 224 d all of which were suggestive of insulin resistance. Overall, mRNA abundance provided evidence of greater intramuscular adipose tissue differentiation due to high–starch diets during the growing phase.

Key Words: early weaning, adipogenesis, genomics

306 Effect diet composition on precocious puberty and concentrations of IGF–1 in beef heifers. M. Maquivar*[1], L. A. Souto[1], D. E. Grum[1], D. M. Hallford[2], S. C. Loerch[1], A. V. Pires[3], and M. L. Day[1], [1]*The Ohio State University*, *Columbus*, [2]*New Mexico State University*, *Las Cruces, NM*, [3]*University of Sao Paulo*, *Piracicaba, Sao Paulo, Brazil*.

Feeding a high concentrate diet to heifers weaned at 3 months of age induces precocious puberty (before 300 d of age) in a high proportion of animals. The objectives of the present study were to determine if a diet that had similar energy content but lower starch content would induce precocious puberty, and to compare metabolic responses between diets. Heifers (n=33) weaned at 76 ± 11 d of age received 1 of 3 diets beginning at 98 ± 11 d of age. The control diet (C, n=12) was hay-based and formulated for ADG of 0.75 kg/d. Experimental diets, formulated for ADG of 1.5 kg/d but differing in starch (S) content were designated as H-S (46.4% starch, 50% corn, n=10) and L–S (14.48% starch, 47% dried distillers grain and soyhulls, n=12). Jugular blood was collected weekly to be analyzed for progesterone concentrations, at 174, 184, 212, 239, 269, 297 and 323 d of age for quantification of IGF–1 concentrations and at h 0, 1, 2, 3, 4, and 6 after feeding at 239 d of age for insulin concentration determination. The L–S and H–S treatments did not differ for ADG (1.21 ± 0.34 vs. 1.27 ± 0.39 kg/d respectively) and were greater ($P<0.05$) than the C treatment (0.77 ± 0.41 kg/d). Concentrations of insulin did not differ between treatments at h 0 but were greater in the H–S and L–S than the C treatment from h 2 to 6 (trt x h, $P = 0.06$). Concentrations of IGF–1 were greater in the H–S and L–S than in the C treatment from d 174 to 239, were greater ($P<0.05$) in the H–S than L–S on d 212 and 269 and did not differ between treatments on d 297 or 323 (trt x age, $P<0.01$). Precocious puberty was induced in 42% (5/12) and 60% (6/10) of heifers in the L–S and H–S and in no heifers in the C treatment. Age at puberty was greater ($P<0.05$) in the C (377 ± 26 d) than L–S (269 ± 69 d) and H–S (262 ± 56 d) treatments. Across H–S and L–S treatments, heifers that experienced precocious puberty had greater ($P<0.05$) IGF–1 concentrations from d 174 to 239 than those that did not reach precocious puberty. These data suggest a role of IGF–1 in precocious puberty and support the conclusion that high dietary starch is not essential to induce precocious puberty in early weaned heifers.

Key Words: puberty, IGF–1, heifers

307 Effect of nutrition and chronic infusion of leptin on sexual maturation of *Bos indicus* heifers. M. V. Carvalho*, J. D. Magalhães, L. U. Gimenes, and L. F. P. Silva, *Universidade de São Paulo*, *Pirassununga, São Paulo, Brazil*.

In order to test if increase in leptin concentration is capable of inducing puberty in *Bos indicus* heifers, thirty-six prepubertal Nelore heifers, 18 to 20 months-old, 275.8±17.2kg BW and BCS of 5±0.5 (1 to 9 scale) were randomly assigned to each of three treatments (n=12): H (high energy diet), L (low energy diet), and LL (low energy diet + oLeptin). Diets were formulated to promote weight gain of 0.4kg/day (groups L and LL) or 1.2kg/day (H group). Heifers were fed *ad libitum* once a day, they were weighed and had their BCS evaluated twice weekly. After 21 days of adjustment, heifers in LL group received subcutaneous injections of oLeptin at 4.8µg/kg BW twice a day, for 56 days. Groups H and L received similar injections of 2ml saline solution. Age at puberty was considered to be the age on first detection of a *corpus luteum* by twice weekly transrectal ultrasonography, confirmed by plasma concentrations of progesterone of > 1ng/ml. The mean diameter of the greater follicle in each ovary was also measured. Heifers in H group were younger at ovulation ($P<0.05$) than L group, and did not differ from LL group. Groups L and LL were not different. The H group tended ($P=0.09$) to be heavier at ovulation (357.9±11.4kg BW) than the LL group (331.2±10.2kg BW, and did not differ from L group. As expected, group H had higher ADG (1.3kg/d) than the other two (0.53kg/d for L group and 0.57kg/d for LL group). Also, heifers in high energy diet ovulated with higher BCS ($P<0.05$) then the other two groups. Although there was little difference among groups concerning the time of puberty, there were significant differences in follicle diameters ($P<0.05$), mostly at the beginning of hormonal treatment. Group H had the greatest follicles (1.09cm), group LL was intermediate (0.97cm) and group L had the smallest ones (0.92cm). In summary, exogenous infusion of leptin increased follicle diameters of heifers in low energy diet, although it had no effect on the onset of puberty. Higher energy intake increased BCS at ovulation and tended to increase BW.

Key Words: beef heifers, leptin, puberty

308 Physiological drivers of variation in feed efficiency in Red Angus-sired calves. C. M. Welch*[1], J. K. Ahola[1], J. B. Hall[1], J. I. Szasz[1], L. Keenan[2], and R. A. Hill[1], [1]*University of Idaho*, [2]*Red Angus Association of America*.

Residual feed intake (RFI) is becoming a well-accepted approach to determine variation in feed efficiency in beef cattle. Thirty-five to 40 percent of this variation is due to differences in basal metabolism (Richardson and Herd, 2004). To gain a clearer understanding of the mechanisms that drive this relationship between feed efficiency and metabolic rate, a number of molecular and genomics-based approaches have been suggested (Hill and Azain, 2008). In the present study, forty-two progeny (25 steers, 17 heifers) of red angus bulls divergent for maintenance energy (ME) EPD were RFI-tested in an 84 day post-weaning period. For steers and heifers ADG was 1.24 and 1.06 kg/d,

respectively. RFI was determined as the difference between expected and actual feed consumption for a given growth rate and the ranges were -1.17 to 2.43 and -0.86 to 2.30 kg/day for steers and heifers, respectively. Partial correlations were determined as follows: RFI:ADG, 0.00 (P = 1) for both steers and heifers; RFI:DMI, 0.75 and 0.81 (P < 0.0001) and ADG:FCR, - 0.67 and -0.75 (P < 0.001) for steers and heifers, respectively. Although variation in RFI may be partially driven by differences in maintenance requirements, it is a complex trait that is, as yet, poorly understood. As greater numbers of progeny (also representing a greater number of bulls) are characterized for RFI and physiological data are determined for this population, the relationship between RFI and a range of physiological parameters including ME EPD will be characterized. Variation in RFI in red angus cattle is comparable with other breeds determined to date. Hill, R. A., and M. Azain. 2008. Growth and development symposium: The molecular basis for feed efficiency. J. Anim. Sci. (jas.2008-1418v1-20081418) doi: 10.2527/jas.2008-1418 [Epub ahead of print]. Richardson, E. C., and R. M. Herd. 2004. Biological basis for variation in residual feed intake in beef cattle. 2. Synthesis of results following divergent selection. Australian Journal of Experimental Agriculture 44: 431-440.

Key Words: residual feed intake, feed efficiency, beef cattle

309 Effect of the beta-agonist RU-42173 on growth and body composition of bulls. D. P. D. Lanna*[1], P. R. Leme[2], F. G. F. Castro[1], A. C. Vieira[1], V. M. Quecini[1], L. O. Tedeschi[3], and L. L. Coutinho[1], [1]*ESALQ/USP*, *Piracicaba, SP, Brazil*, [2]*FZEA/USP*, *Pirassununga, SP, Brazil*, [3]*Texas A&M University*, *College Station*.

This study was conducted to determine the effects of the beta-agonist RU-42173 (Hoechst-Roussel) on growth and body composition of bulls. The 2x3 factorial included control or β-agonist and three breed groups (purebred Nellore, Nellore × Marchigiana, and Nellore × Holstein). The 72 bulls came from pasture with an average initial BW of 406 kg. Bulls were fed, three per pen, a 60:40 corn silage:concentrate diet with 15.7% CP. After 28 d of adaptation, RU-42173 was added at 6 ppm to the treated group diet for a 47 d experimental period (actual intake 0.16 mg/kg BW). Results are presented in the table below. There was no hormone × breed interaction (P>0.10). The addition of RU-42173 during the last 47 d before slaughter had positive effects on ADG (P<0.01) and feed efficiency (P<0.01). The decrease in DMI as a percentage of BW (P<0.05), was consistent with the decrease in the deposition of internal fat and the lower fat content of the 9-11th rib cut. Carcass quality characteristics were not affected by treatments.

Table 1. Results

Variables (^{ab}P<0.01 ^{AB}P<0.05)	Control	β-agonist	Change, %	SEM
ADG, kg/d	1.79^{b}	2.02^{a}	13	0.06
DMI, %BW/d	2.53^{A}	2.42^{B}	-4	0.03
Feed efficiency, ADG/DMI	0.157^{a}	0.182^{b}	16	0.004
9-11th rib section physical fat, %	25.1^{A}	23.6^{B}	-6	0.42
9-11th rib section lipid, %	23.2^{a}	19.9^{b}	-14	0.56
Hot carcass weight, kg	282^{b}	298^{a}	6	3.86
Dressing, %	57.7^{b}	59.2^{a}	3	0.003
Ribeye area, cm^2	64.5^{b}	73.5^{a}	14	1.38
Fat thickness, mm	3.1	3.2	3	0.14
Warner-Bratlzer *Longissimus*, kg	3.9	4.1	5	0.09
Warner-Bratlzer *Semimem*, kg	5.0	5.1	2	0.07

Key Words: beef cattle, β-agonist, body composition

310 Effects of ractopamine and gender on serum hormones and skeletal muscle gene expression in finishing steers and heifers. D. K. Walker*[1], E. C. Titgemeyer[1], T. J. Baxa[1], K. Y. Chung[1], D. E. Johnson[1], S. B. Laudert[2], and B. J. Johnson[1], [1]*Kansas State University*, *Manhattan*, [2]*Elanco Animal Health*, *Greenfield, IN*.

We compared growth–related responses to ractopamine (RAC) in steers and heifers. Angus steers (n=16; 512 kg, SD=21) and heifers (n=16; 473 kg, SD=18) in individual pens were used in a complete block design. At 90 to 97 d prior to the experiment, steers were implanted with 120 mg trenbolone acetate and 24 mg estradiol–17β, and heifers were implanted with 140 mg trenbolone acetate and 14 mg estradiol–17β. Treatments were arranged as a 2 × 2 factorial (gender × 0 or 200 mg/d ractopamine–HCl). Cattle were fed a diet based on steam–flaked corn once daily. Blood and longissimus (LM) and biceps femoris (BF) biopsy samples were collected on d 0 (before RAC) and after 14 and 28 d of RAC feeding. Serum insulin was not affected by RAC or gender. Serum insulin–like growth factor (IGF)–I was greater in steers than heifers (P<0.001), and steers demonstrated greater IGF–I mRNA expression (measured by real-time qPCR) in BF than heifers (P=0.05). RAC numerically decreased serum IGF–I concentrations in heifers on d 14 and 28 and in steers on d 14, but increased serum IGF–I concentrations in steers on d 28 (gender × RAC × day; P=0.03). RAC did not affect (P≥0.17) mRNA expression of IGF–I, IGFBP–3, or calpastatin in BF or LM. In LM, RAC increased mRNA expression of IGFBP–5 in heifers but decreased it in steers (gender × RAC, P=0.04). In BF, IGFBP–5 mRNA responded similarly to that in LM, but the gender × RAC interaction was not significant (P=0.17). RAC decreased myosin heavy chain IIA mRNA expression in BF (P=0.02) but not in LM (P=0.72). RAC decreased β2–receptor mRNA expression in LM of steers on d 14, but numerically increased it in steers on d 28; in contrast, expression of β2–receptor mRNA in LM of heifers was not affected by RAC (gender × RAC × day interaction; P=0.03). Although RAC led to a few differences in response between steers and heifers, there were no striking disparities to suggest that effectiveness of RAC markedly differs between genders.

Key Words: ractopamine

311 Bovine satellite cells contain three distinct subpopulations in young and adult cattle. D. K. Walker*, J. Li, M. J. Hersom, and S. E. Johnson, *University of Florida*, *Gainesville*.

Satellite cells (SC) are a heterogenous population of cells that lie adjacent to muscle fibers that are identified by their expression of Pax7 and Myf5. In mice, Pax7+/Myf5– SC undergo asymmetric division producing daughter cells that differentially express Myf5. Pax7+/Myf5+ progenitors proliferate and give rise to myoblasts that fuse into muscle fibers. The diverse populations of bovine SC were characterized by Pax7 and MRF expression in vitro. Satellite cells from young calves (<10 d) and adults (30–32 mo.) were isolated and cultured for 4 d. Cultures were pulsed labeled with 10 uM bromodeoxyuridine (BrdU) for two h prior to fixation at 24 h time intervals. The cells were immunostained for Pax7, Myf5, MyoD and BrdU. Results indicate the percentage of Pax7+/Myf5– cells were not different between young (5%) and adult (6%) animals (P = 0.63). Pax7+/Myf5+ adult cell isolates were not different at 24, 48, 72, and 96 h in culture (79, 70, 78, and 75%, respectively), but decreased from 24 to 96 h in young calves (72, 59, 54, and 19%, respectively; age × time in culture interaction, P = 0.008). Adult SC displayed similar numbers of Pax7–/Myf5+ cells from 24 to 96 h in culture (9, 23, 13, and 13%, respectively), but cells isolated from young calves displayed an increase in Pax7–/Myf5+cells (15, 27, 29, and 48%, respectively; age

× time in culture interaction, P = 0.05). MyoD+ cells were present at 48 h in young calf isolates and at 72 h in adult isolates; MyoD+ numbers increased over time in culture (P < 0.0001). Unlike rodents, the time course of activation did not differ between young and adult SC isolates. Both groups entered S-phase within 48 h and the numbers of BrdU+ cells increased over time in culture (P < 0.0001). Our data demonstrate distinct differences in the percentage of progenitors (Pax7+/Myf5+) and myoblasts (Pax7–/Myf5+) between young and adult animals. Importantly, our data demonstrate clear differences in gene expression and activation kinetics between cattle and rodent SC.

Key Words: bovine, Pax7, satellite cells

312 Abundance of growth hormone secretagogue receptor in adipose tissue from beef cattle undergoing compensatory growth. J. S. Jennings*, J. A. Clapper, A. D. Weaver, and A. E. Wertz-Lutz, *South Dakota State University*, *Brookings*.

We hypothesized that growth hormone secretagogue-receptor (GHS-R) abundance in adipose tissue would be decreased in cattle fed to achieve a faster rate of fat deposition. Beef steers (n=72) of similar age, weight (292±1.44 kg), and genetic background were used to determine the effects of growing diet (high forage vs. high concentrate) on GHS-R abundance in subcutaneous adipose tissue. At trial initiation (d 0), 8 steers were harvested for initial adipose tissue collection. The remaining 64 steers were allotted, by weight, to pen and treatment was assigned randomly. Treatments were 1) 60% forage; 40% concentrate diet fed during the growing period (112 d) followed by 10% forage; 90% concentrate diet during the finishing period (113-209 d) (GRW-FNSH) or 2) 10% forage; 90% concentrate diet fed for the duration of the experiment (0-209 d) (FNSH-FNSH). Steers were allowed ad libitum consumption regardless of dietary treatment. Eight steers per treatment were harvested on d 88, 116, 165, and 209. Subcutaneous adipose tissue samples were collected from each steer and immediately immersed in liquid nitrogen. Proteins were separated and quantified using SDS-PAGE and Western blotting techniques. Abundance of GHS-R was detected using the LI-COR ® system and standardized to β-Actin. Protein abundance data were analyzed statistically using the MIXED procedure of SAS to evaluate effects of diet, harvest date, and their interaction. A significant interaction (P≤0.05) resulted between dietary treatment and harvest date. At the final harvest, carcass weight was not different between treatments, but FNSH-FNSH steers had more (P≤0.01) subcutaneous fat and higher (P≤0.001) marbling scores compared with GRW-FNSH steers. Receptor abundance in the GRW-FNSH was greatest (P≤0.05) on d 84 whereas GHS-R abundance for the FNSH-FNSH treatment was greatest (P≤0.05) at the end of the finishing period (d 209). These data are not consistent with the hypothesis that GHS-R abundance decreases in beef cattle with greater fat deposition.

Key Words: adipose tissue, compensatory growth, GHS-R

313 Effect of Sirt1 on lipolysis and gene expression of adipose triglyceride lipase (ATGL) in porcine adipocytes. Y. Wang*, T. Shan, J. Guo, T. Wu, and C. Liu, *The Key Laboratory of Molecular Animal Nutrition, Ministry of Education. Institute of Feed Science, Zhejiang University*, *Hangzhou, Zhejiang, China*.

Sirt1 is a nicotinamide adenine dinucleotide (NAD)-dependent deacetylase that plays an important role in fat metabolism. To investigate whether Sirt1 could affect the lipolysis and adipose triglyceride lipase (ATGL) gene expression, we treated porcine adipocytes with the general Sirt1 inhibitor nicotinamide (NAM), the Sirt1 activator resveratrol (RES), and knockdown of Sirt1 by Sirt1-specific siRNA. The results showed that treatment with NAM decreased glycerol release (P < 0.05) and the levels of Sirt1 mRNA in porcine adipocytes. Compared with the control (0 μM), treatment with 100 or 150 μM NAM decreased the Sirt1 mRNA levels by 10.76% (P < 0.05), 36.05% (P < 0.01) and 28.58% (P < 0.01), respectively. Meanwhile, treatment with 100 or 150 μM NAM also decreased the mRNA levels of ATGL by 24.65% (P < 0.01) and 14.49% (P < 0.05). Furthermore, treatment with 100 μM NAM for 24, 48, or 72 h significantly decreased glycerol release (P < 0.05) and the mRNA expression of Sirt1 and ATGL. Exposure of cultured adipocytes to Sirt1 agonist (RES) increased (P < 0.01) glycerol release and the mRNA levels of Sirt1 and ATGL. Furthermore, knockdown with Sirt1-siRNA significantly inhibited (P < 0.01) Sirt1 mRNA expression, further decreased ATGL mRNA levels and reduced glycerol release. These results revealed that Sirt1 could promote lipolysis and up-regulate the expression of the ATGL gene. The results add to our understanding of the role of Sirt1 in adipose mobilization and as a potential target for regulating fat metabolism and metabolic disorders such as type 2 diabetes.

Key Words: adipose triglyceride lipase, pig, Sirt1

314 Breed difference and regulation of porcine adipose triglyseride lipase (pATGL) and hormone sensitive lipase (HSL) by TNFα and insulin. T. Shan*, Y. Wang, T. Wu, C. Liu, and J. Guo, *The Key Laboratory of Molecular Animal Nutrition, Ministry of Education. College of Animal Science, Zhejiang University*, *Hangzhou, China*.

Adipose triglyceride lipase (ATGL) and hormone sensitive lipase (HSL) are major novel triglyceride lipases in animals. The aim of this study was to determine if there are differences in the porcine ATGL (pATGL) and HSL between Jinhua pigs (a fatty breed) and Landrace pigs (a leaner breed). In addition, the effect of TNFα and insulin on the expression of pATGL and HSL mRNA levels in porcine adipocytes was also examined. The results showed that the body weight (BW) of Jinhua pigs was lower (P < 0.01), while intramuscular fat content (in the longissimus dorsi muscle), as well as the back fat thickness and body fat content were higher (P < 0.01) compared to Landrace pigs. Compared with Landrace pigs, the expression of pATGL and HSL mRNA in Jinhua pigs was lower (P < 0.01) in subcutaneous adipose tissue, and higher (P < 0.01) in longissimus dorsi muscle. In vitro treatment of porcine adipocytes with TNFα and insulin decreased (P < 0.01) the glycerol release and the gene expression of pATGL and HSL in porcine adipocytes. Compared with the control (0 ng/mL), treatment with 1, 12.5, 25, or 50 ng/mL TNFα signficantly decreased (P < 0.01) the mRNA levels of pATGL by 32.06%, 28.27%, 50.54% and 28.54% respectively, and decreased (P < 0.01) the mRNA levels of HSL by 28.02%, 17.40%, 25.22% and 18.34%, respectively. Furthermore, treatment with 25 ng/mL TNFα for 12, 24, 36, 48 h decreased (P < 0.01) the glycerol release and the gene expression of pATGL and HSL. Exposure of cultured adipocytes to 10, 50 and 100 nM insulin decreased (P < 0.01) the glycerol release and the mRNA levels of pATGL and HSL. Treatment with 50 nM insulin for 12, 24, 36, and 48 h, the glycerol release and the mRNA levels of pATGL and HSL were also decreased (P < 0.01). These results provide useful information to further the understanding of the function of pATGL and HSL in porcine lipid metabolism, which should have applicability to regulation of fat deposition and improvement of meat quality.

Key Words: adipose triglyceride lipase (ATGL), hormone sensitive lipase (HSL), pig

315 Effects of plane of nutrition and bioavailable trace minerals on claw growth and wear in transported male dairy calves. J. S. Osorio*[1], J. K. Drackley[1], R. L. Wallace[1], D. Rincker[1], D. J. Tomlinson[2], M. T. Socha[2], and T. J. Earleywine[3], [1]*University of Illinois, Urbana*, [2]*Zinpro Performance Minerals, Eden Prairie, MN*, [3]*Land O'Lakes Animal Milk Products Inc., Madison, WI.*

Data are limited on how claw development early in life will affect the susceptibility to lameness and claw disorders later in life. Adequate nutrition and bioavailable trace minerals might enhance claw development by ameliorating various stressors early in life. Ninety Holstein bull calves <1 wk old were purchased in 3 groups and transported to the Illinois research facility from Wisconsin. Calves were randomly assigned to treatments in a 2x2 factorial arrangement of plane of nutrition (PN) and trace mineral source (TM). Conventional PN received a fixed amount (568 g/d) of milk replacer (22% CP, 20% fat) plus ad libitum starter (18% CP) and were weaned at 6 wk; they received ad libitum starter to wk 12 and 0.5 kg/d of hay wk 10-12. During wk 13-20 calves were fed 3.2 kg/d of grower (16% CP) plus chopped hay ad libitum. Intensified PN received variable amounts (810, 1136, and 568 g/d for wk 1, 2 to 6, and 7, respectively) of milk replacer (28% CP, 20% fat) plus ad libitum starter (22% CP), were weaned at 7 wk, were fed ad libitum starter to wk 12, and fed ad libitum grower plus 0.5kg/d hay wk 13-20. Feeds contained either inorganic sulfates of Fe, Cu, Zn, and Mn or bioavailable sources (Zinpro Performance Minerals, Eden Prairie, MN). Calves were individually housed in hutches bedded with straw through wk 9 and group-housed by diet wk 10-20. Calves had free access to water. Claws were measured at wk 0, 5, 10, 15, and 20. Calves were born with uneven claw length (P<0.001), with rear and medial claws longer than front and lateral claws. Organic TM tended to increase claw length (P=0.105) after wk 15. Net growth increments were established after wk 5 regardless of treatment, which could be associated with complete establishment of corium tissue and physiological changes such as rumination and thermoregulation. Rear medial claws had more growth and wear (P<0.05) regardless of treatment. Intensified PN increases biological value of organic TM reflected by enhanced hoof dynamics and body growth.

Key Words: trace minerals, claw growth, calves

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316 Gene expression profile research of dairy goat mammary gland by Long-SAGE. H. Yan, C. Li, Q. Li*, and X. Gao, *Northeast Agricultural University, Harbin, China*.

Serial analysis of gene expression (SAGE) is a high-throughput, sensitive and efficient method for global expression profiles analysis that allows the quantitative and simultaneous analysis of large-scale transcripts under different conditions or in certain tissues. The Long-SAGE technique, developed from original SAGE, generates longer tags (21bp) than typical 14bp tags, which are more unambiguous in uniquely identifying with corresponding genes. Therefore, Long-SAGE technique was chosen to study gene expression profile of lactating dairy goat mammary gland, to find candidate genes that could control or regulate function of mammary gland.An improved protocol of Long-SAGE, considering characters of mammary gland, was applied to construct Long-SAGE libraries. Briefly, mRNA were isolated and synthesized into double-strand cDNA (ds cDNA), concatemers were formed by linking tags randomly which were extracted from ds cDNA through a series of restriction enzyme cleaving and ligating processes, sequenced the positive clones of concatemers to get information of tags. An extra heating process was necessary to increase cloning efficiency of concatemers.7 Long-SAGE libraries of different lactation stages (initiation, peak, stabilization and involution) of healthy dairy goat lactating mammary gland were successfully constructed. Over 21 thousands Long-SAGE tags were obtained by sequencing 7 thousands positive clones of concatemers. Removing the of duplicated and invalid tags, there're about 10 thousands of 17bp unique Long-SAGE tags, only 12% tags were matched to UniGene data according to limited genome resources. Further gene expression profile research of dairy goat mammary gland is still going on.

Key Words: gene expression profile, mammary gland, Long-SAGE

317 Selection of key gene related to development of mammary gland in dairy goat. C. Li, H. Yan, Q. Li*, and X. Gao, *Northeast Agricultural University, Harbin, China*.

To identify key genes involved in the initiation and development of mammary gland in dairy goat, we analyzed the global gene expression profiles of 7 different developmental stages using long serial analysis of gene expression (LongSAGE). We performed LongSAGE in healthy dairy goat mammary at seven different developmental stages (early puberty, late puberty, early pregnancy, late pregnancy, middle lactation, early involution and late involution). Computational analysis was carried out to identify differentially expressed genes in mammary gland between early puberty and late puberty, early pregnancy and late pregnancy which were further validated by real-time quantitative RT-PCR. Approximately 8,000 clones were sequenced for the seven libraries. Totally, 104,995 valid LongSAGE tags were obtained with 12,574 unique tags. Compared with the gene expression profile of early puberty mammary gland, 404 genes were identified to be differentially expressed in late puberty. 83 genes were high-abundance expressed in late pregnancy and early pregnancy contrast with late puberty. These diversely expressed genes were related to cell proliferation, biosynthesis, signal transduction, and cellular transport. In this study, seven LongSAGE libraries of different developmental stages of dairy goat mammary gland were successfully constructed. The genes expression profiles of these seven developmental stages were depicted on a genome-wide scale. For the restriction of annotation databases, we provided novel candidate genes that might be related to mammary gland development.

Key Words: dairy goat, mammary gland, LongSAGE

318 Epigenetic changes during functional differentiation of the mammary gland. M. Rijnkels*, C. Freeman-Zadrowski, and J. Hernandez, *USDA/ ARS Children's Nutrtion Research Center, Baylor College of Medicine, Houston, TX*.

The packaging of the DNA that surrounds a gene, the conformation of chromatin, is an integral part of gene regulation. Chromatin conformation is determined by DNA methylation, the post-translational modifications of the core histones and the proteins that bind to this. Hypermethylated DNA is usually associated with silent genes, whereas actively transcribed genes are hypomethylated. Different histone modifications are associated with open (active) or closed (inactive) chromatin. DNAseI hypersensitivity (DHS) indicates an open chromatin conformation and is often associated with regulatory elements. To identify a role for chromatin