T121 Effect of residual feed intake on hypothalamic gene expression and meat quality in heat-stressed Angus-sired cattle. C. N. Key,* S. D. Perkins, C. F. Garrett, C. D. Foradori, C. L. Bratcher, L. A. Kriese-Anderson, and T. D. Brandebourg, *Auburn University, Auburn, AL.*

Residual feed intake (RFI) is a heritable feed efficiency measure. The relationship between RFI, heat stress and meat quality is unknown. To address these issues, 48 Angus-sired steers were trained to the Calan Gate (Northwood, NH) system. Daily feed intake and RFI were assessed during a 70 d feeding trial conducted July through September. The test diet was 50% balage consisting of a winter annual mix, 50% grain (2.9 Mcal ME/kg DM). Feed intake was recorded daily while body weights and hip heights were recorded at 14 d intervals. Ultrasound measurements of rib eye area (REA) and backfat (BF) were recorded initially and before slaughter. RFI was calculated for each animal as the difference between actual dry matter intake and the expected intake to create 2 divergent cohorts consisting of High (H) and Low (L) RFI individuals. At slaughter, hypothalamic tissue samples were collected to facilitate gene studies into the mechanisms underlying variation in RFI. After chilling for 24 h post harvest, carcass characteristics were measured. Carcass and growth data were analyzed using a mixed model with RFI level (L, H) as the independent variable (SAS, 2002). Means were separated using lsmeans at a significance level of $P < 0.05$. The lsmeans for RFI were −1.2 and 0.99 respectively for the L and H cohorts ($P < 0.0001$) and were greater than 2 standard deviations apart. As expected dry matter intake was higher for the H individuals versus the L steers ($P < 0.0001$) while on-test gain was not different between groups. Marbling score was greater in L than H steers ($P < 0.05$). However there were no differences in objective color measures L*, a*, and b*, adjusted back fat, ribeye area or yield grade between L and H cohorts. Real-time PCR studies in the arcuate nucleus indicate that neuropeptide Y (NPY) and agouti related protein (AgRP) mRNA were expressed 2.8-fold and 1.85-fold greater while Pro-opiomelanocortin (POMC) mRNA was expressed 1.6-fold lesser in L than H animals. These data suggest there is no relationship between RFI and meat quality while surprisingly the mRNA expression of neuropeptides that stimulate feed intake were increased in efficient animals during heat-stressed conditions.

Key Words: RFI, meat quality, heat stress

T122 Effect of residual feed intake on meat quality and hypothalamic gene expression in Angus-sired cattle. S. D. Perkins,* C. N. Key, C. F. Garrett, C. D. Foradori, C. L. Bratcher, L. A. Kriese-Anderson, and T. D. Brandebourg, *Auburn University, Auburn, AL.*

Residual feed intake (RFI) is a heritable feed efficiency measure. Mechanisms underlying RFI are poorly understood while the relationship between RFI and meat quality is unknown. To address these issues, 48 Angus-sired steers were trained to the Calan Gate (Northwood, NH) system. Daily feed intake and RFI were assessed during a 70 d feeding trial. The test diet was 50% sorghum-sudan silage, 50% grain (2.9 Mcal ME/kg DM). Feed intake was recorded daily while body weights and hip heights were recorded at 14 d intervals. Ultrasound measurements of rib eye area (REA) and backfat (BF) were recorded initially and before slaughter. RFI was calculated for each animal as the difference between actual dry matter intake and the expected intake to create 2 divergent cohorts consisting of High (H) and Low (L) RFI individuals. Steers were humanely harvested and hypothalamic tissue (HT) samples were collected to facilitate gene studies into the mechanisms underlying variation in RFI. After chilling for 24 h post harvest, carcass characteristics were measured. Carcass and growth data were analyzed using a mixed model with RFI level (L, H) as the independent variable (SAS, 2002). Means were separated using lsmeans at a significance level of $P < 0.05$. The lsmeans for RFI were −1.3 and 1.5 respectively for the L and H cohorts ($P < 0.001$) and were greater than 2 standard deviations apart. As expected dry matter intake was higher for the H individuals versus the L steers ($P < 0.001$) while on test gain was not different between the 2 groups. There were no differences in marbling score, objective color measures L*, a*, and b*, adjusted back fat, ribeye area or yield grade between L and H cohorts suggesting there is no relationship between RFI and meat quality. Initial targeted gene expression studies in the arcuate nucleus indicate that neuropeptide Y (NPY) mRNA is expressed 2.7-fold lower and pro-opiomelanocortin (POMC) mRNA is expressed 3.6-fold higher in L than H animals. This suggests differences in neuropeptide expression in part underlie differences in feed efficiency observed in growing cattle during conditions of thermoneutrality.

Key Words: RFI, meat quality, neuropeptide Y

T123 Serum IGFI and hepatic *IGFI* mRNA levels in feedlot cattle infected with bovine respiratory disease. C. A. Gifford*[1], B. Wilson[1], C. Maxwell[1], D. M. Hallford[2], and C. R. Krehbiel[1], *[1]Oklahoma State University, Stillwater, [2]New Mexico State University, Las Cruces.*

Bovine respiratory disease (BRD) is a leading cause of feedlot morbidity and mortality. Calves treated for BRD exhibit decreased growth, but mechanisms responsible for BRD-induced impaired growth are still unknown. The objectives of these studies were to evaluate serum IGFI and hepatic *IGFI* mRNA levels in BRD-infected calves. In study 1, serum samples were collected from control calves (CONT1; n = 5) and calves receiving a single treatment for BRD (1TRT1; n = 5) at arrival, at time of treatment, and on d 33, and serum IGFI levels were quantified via RIA. Serum IGFI or relative fold change of *IGFI* mRNA was tested against treatment, day, and treatment × day using the GLM procedure of SAS and means were separated using PDIFF when appropriate. There was not a treatment x day interaction ($P > 0.10$), but overall means of IGFI were greater ($P < 0.05$) for CONT1 (100.1 ± 8.6 ng/mL) than 1TRT1 (55.6 ± 9.4 ng/mL). Serum IGFI was low at arrival (39.6 ± 3.4 ng/mL) and increased ($P < 0.05$) to 152.7 ± 12.4 ng/mL on d 33 for both groups. In study 2, serum and peripheral blood leukocytes (PBL) were collected from calves chronically infected with BRD (CHRON; n = 6) and controls (CONT2; n = 6). Serum IGFI levels decreased ($P < 0.05$) in CHRON (65.3 ± 46.0 ng/mL) compared with CONT2 (236.5 ± 46.0). In PBL, *IGFI* mRNA was present but similar ($P > 0.10$) in CHRON and CONT2. In study 3, hepatic mRNA was collected from controls (CONT3; n = 6), calves treated once for BRD (1TRT3; n = 6), calves treated twice (2TRT3; n = 5), and calves treated 3 times (3TRT3; n = 6). Relative abundance for *IGFI* mRNA was quantified, and, relative to CONT3, 1TRT3 exhibited similar ($P > 0.10$) *IGFI* mRNA levels. However, 2TRT3 and 3TRT3 *IGFI* levels were approximately 2.5-fold below CONT3 ($P < 0.05$). These results demonstrate that serum IGFI is reduced at time of arrival and in calves chronically infected with BRD. In calves treated once for BRD, reduced feed intake might account for a reduction in IGFI without affecting growth. However, calves treated

multiple times for BRD exhibit alteration in hepatic synthesis of *IGFI* mRNA possibly leading to long-term growth suppression.

Key Words: bovine respiratory disease, IGFI, growth

T124 Relationship between carcass traits and tenderness with residual feed intake and residual average daily gain of Brahman steers. F. Rouquette Jr.*[1], R. Randel[1], J. Paschal[2], T. Machado[3], and C. Long[1], *[1]Texas AgriLife Research and Extension Center, Overton, [2]Texas AgriLife Extension Service, Corpus Christi, [3]Texas A&M University-Kingsville, Kingsville.*

Residual feed intake (RFI) and residual average daily gain (RADG) indices have been used to assess an efficiency rating to cattle. The objectives of this 3-year experiment were to determine the relationship between RFI and RADG groupings on carcass traits and tenderness. After weaning, yearling Brahman bulls were fed a growing ration via calan gates in drylot during 3 consecutive years, (2008, n = 56; 2009, n = 47; 2010, n = 34). Bulls were phenotyped for RFI and RADG and sorted into 4 efficiency groups: 1 = more than 0.5 standard deviation (SD) below the mean (most efficient); 2 = less than 0.5 SD below the mean; 3 = less than 0.5 SD above the mean; and 4 = more than 0.5 SD deviation above the mean (least efficient). Following the drylot period, bulls were stocked on bermudagrass pastures during the summer, castrated in the fall, and transported to a commercial feedlot for finishing to an approximate 1.0 cm backfat. After harvest, standard carcass traits were taken. Year was an independent variable and with an interaction for year and RFI and RADG, carcass trait relationships were assessed by year using Proc Mixed. Steers that were sorted into most efficient group had higher ($P < 0.05$) dressing % (2008, 2010), liveweight and hot carcass weights (2009), backfat (2010), and USDA Yield grade (2008, 2009, and 2010). Steers sorted into the least efficient group had higher ($P < 0.05$) marbling score (2009) and quality grade (2009). Steers harvested in 2010 were assessed for tenderness using Warner-Bratzler shear force. The shear force values for the 4 efficiency groupings were different when using either RFI ($P = 0.078$) or RADG ($P < 0.001$). For both efficiency rankings, the least efficient steers (group 4) had the highest scores (least tender) of 4.29 kg (RFI) and 4.33kg (RADG). These carcass traits indicated a general lack of relationship for either RFI or RADG groups. However, the most tender steaks were in Group 3 (RFI) and Group 2 (RADG).

Key Words: residual feed intake, residual average daily gain, carcass

T125 Adipocyte location and anabolic implant alter adipocyte transcriptome in steers. S. K. Duckett,* J. W. Long, M. D. Owens, S. E. Ellis, and S. L. Pratt, *Clemson University, Clemson, SC.*

The accumulation of excess fat results in economic loss in beef production. However, understanding how lipid is accumulated at different depots could lead to strategies reducing financial loss by targeting specific sites for lipid deposition. The objectives of this study were to: 1) determine if location of fat depot alters adipocyte gene expression and 2) evaluate the impact anabolic implants have on adipocyte's transcriptome in 2 separate adipose depots. Angus x Hereford steers (n = 24; BW = 488 kg) were randomly allotted to non-implant (CON) or implant (IMP) treatments. Steers were individually fed a high concentration diet for 72 d and IMP steers received a single Revalor-S (24 mg estradiol, 124 mg trenbolone acetate) at time of allotment. At slaughter, adipose tissue samples were collected from subcutaneous (SQ) and mesenteric (MS) depots, flash-frozen, and stored at −80°C for RNA extraction. Total cellular RNA was isolated using the mirVana miRNA Isolation Kit (Ambion, Austin, TX). The cleared homogenate was loaded on to the binding matrix by vacuum and the column washing and elution of bound tcRNA were performed per manufacturer's protocol. Four pools of tcRNA were generated for SQ-CON, SQ-IMP, MS-CON and MS-IMP. The samples were subjected to RNA sequencing (LC Sciences, Houston, TX) using the Illumina high-throughput sequencing technology. Data were analyzed by LC Sciences using Bowtie, Tophat, and Cufflinks statistical analysis software systems. The number of mappable reads ranged from 87,387,760 to 91,927,097 for all tissue-treatment combinations. This resulted in 32,493 to 35,030 predicted messenger RNA transcripts for all tissue-treatment combinations. Gene expression differences were compared between data sets of MS-CON vs MS-IMP, MS-CON vs SQ-CON, MS-IMP vs SQ-IMP, and SQ-CON vs SQ-IMP. Of differentially expressed genes identified, 95 were differentially expressed due to adipose depot ($P < 0.05$) and 36 were differentially expressed due to IMP ($P < 0.05$). Therefore, adipocyte gene expression is impacted by both location and anabolic steroid treatment, which suggests that strategies/treatments could be developed to adjust lipid accumulation based on location and exogenous hormonal treatment.

Key Words: beef, implants, gene expression

T126 Subcutaneous adipose tissue gene expression in bulls fed ergot alkaloid-containing fescue seed. T. A. Burns,* M. C. Miller, H. M. Stowe, S. M. Calcatera, S. L. Pratt, J. G. Andrae, and S. K. Duckett, *Clemson University, Clemson, SC.*

Grazing toxic endophyte-infected tall fescue (E+) is a common practice in the southeastern US and is associated with decreased performance and adipose tissue necrosis. The objective of this study was to determine the effects of E+ on male adipose tissue gene expression. In addition, isolation of adipose tissue is inherently difficult due to the abundance of lipid; therefore, a secondary objective of this work was to identify a RNA isolation method that efficiently isolated RNA of good quality. Eight beef bulls approximately 12 to 16 mo of age were stratified by breed, weight, and BCS and then assigned to 1 of 2 treatment groups receiving 4.2 g/kg of BW per day of E+ or endophyte-free fescue (E-) seed in a total mixed ration. After a feeding period of 126 d, bulls were slaughtered and tissues snap frozen for gene expression analysis. Four commercially available kits were used to isolate RNA according to manufacturer's instructions: mirVana miRNA Isolation Kit (Invitrogen; Grand Island, NY), Direct-zol RNA MiniPrep (Zymo Research; Irvine, CA), RNeasy Lipid Tissue Midi Kit (Qiagen; Valencia, CA), and PureYield RNA Midiprep System (Promega; Madison, WI). Data were analyzed using the Proc GLM procedure of SAS 9.2. Quality of RNA, assessed by 260/280 absorbance ratio, was acceptable for all isolation methods and was greatest ($P < 0.05$) for RNA isolated using Direct-zol, but only mirVana and RNeasy RNA had a consistently acceptable 18S/28S ribosomal band ratio. Efficiency of extraction (μg RNA/g tissue) was greatest ($P < 0.05$) for mirVana isolations. Therefore, real time PCR was performed on *stearoyl-CoA desaturase* (*SCD1*) and *cytochrome P450 subfamily 3A* (*CYP3A*) genes with reference gene *glyceraldehyde-3-phosphate dehydrogenase* from mirVana-isolated RNA. Subcutaneous adipose tissue of E+ bulls had downregulated expression ($P < 0.05$) of *SCD1* indicating a reduction in fatty acid desaturation compared with E-. Associated with animal metabolism of ergot alkaloids present in toxic fescue, *CYP3A* expression was not different ($P > 0.05$) in E+ compared with E- bulls. Therefore, expression of *SCD1* mRNA isolated from subcutaneous adipose tissue of bulls is affected by E+ fescue.

Key Words: bovine, fescue, RNA isolation

T127 Growth performance of Mahabadi goat kids fed different levels organic trivalent chromium. A. Emami, A. Zali, M. Ganjkhanlou,* A. Hojabri, and A. Akbari, *University of Tehran, Tehran, Iran.*

This study was carried out to determine the effects of supplementing chromium-methionine (Cr-Met) on performance in Mahabadi goat kids. Thirty-two male kids (average initial BW of 22 ± 2 kg, 4mo) were used in a completely randomized design with 4 treatments: 1) control (without Cr), 2) 0.5, 3) 1.0 and 4) 1.5 mg Cr as Cr-Met/animal/d. Diets were formulated to meet NRC requirements with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Diets were the same except for top-dress addition of Cr-Met and fed in 2 equal meals (0800 and 1600 h) and orts were collected before morning meal. Animals were kept in individual pens with self-mangers. Experimental period was 90 d. Animals were weighed at 21 d intervals. Feed conversion ratio (FCR) was calculated according to FCR = DMI (Dry matter intake) (kg)/Average daily gain (ADG) (kg). DMI, ADG and FCR data were analyzed using MIXED procedure of SAS 9.1. The Tukey test was used for comparison of treatment means. ADG was not affected by the Cr-Met ($P > 0.05$). Also DMI and FCR were not affected by the chromium supplementation ($P > 0.05$). These results indicated that dietary supplementation of Cr-Met failed to significantly affect growth performance of Mahabadi goat kids.

Table 1. DMI, ADG, and FCR of kids fed different levels of organic chromium

	Treatment (mg of Cr)				
Trait	Control	0.5	1.0	1.5	SEM
DMI(kg/d)	1.01	1.00	1.03	1.07	0.04
ADG	0.14	0.14	0.15	0.17	0.01
FCR	7.55	7.48	6.95	6.44	0.47

Key Words: feed intake, daily gain, feed conversion ratio

T128 Postweaning feed restriction effects on steer feedlot performance and carcass characteristics. R. L. Endecott*[1], B. L. Shipp[2], M. D. MacNeil[2], L. J. Alexander[2], and A. J. Roberts[2], *[1]Department of Animal and Range Sciences, Montana State University, Miles City, [2]USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.*

The objective was to evaluate effects of 2 levels of supplemental feed provided to cows during late gestation and 2 levels of feed provided to their sons during postweaning development on subsequent feedlot performance and carcass characteristics. Bull calves (n = 56 in 2010; n = 51 in 2011) were born from dams receiving adequate (1.8 kg/d) or marginal (1.2 kg/d) winter supplementation. After weaning, bulls were developed on ad-libitum (Control) or 27% less feed (Restricted) for ~140 d. Bulls were then band-castrated and placed on an 80% corn finishing diet ad libitum. Individual intakes were measured with a GrowSafe system for the final 100–150 d of the finishing period. Cattle were harvested at a commercial packing plant and carcass data were collected. Dam winter supplementation effects were not detected ($P \geq 0.22$). Postweaning phase ADG exhibited a postweaning treatment × year interaction ($P < 0.01$). Restricted calves had similar ADG in both years (0.64 vs 0.68 ± 0.03 kg/d) and gained less than Control calves. Control calves had greater ADG in 2010 than in 2011 (1.16 vs 1.03 ± 0.03 kg/d). Postweaning treatment did not affect feed intake during the finishing phase ($P = 0.29$; 13.0 vs 12.8 ± 0.22 kg/d for Restricted vs Control; as-fed basis). During the finishing phase, ADG exhibited a postweaning treatment × year interaction ($P < 0.01$). Restricted steers had similar ADG in both years (1.25 vs 1.27 ± 0.05 kg/d) and gained more than Control steers. Control steer ADG was less in 2010 than in 2011 (0.92 vs 1.13 ± 0.05 kg/d). Compared with Control steers, Restricted steers had lower ($P \leq 0.08$) final BW (603 vs 623 ± 9 kg), HCW (357 vs 373 ± 6 kg), and yield grade (2.71 vs 2.89 ± 0.10). However, back fat thickness (1.09 vs 1.14 ± 0.05 cm), ribeye area (85.4 vs 85.8 ± 0.98 cm^2), and marbling score (5.59 vs 5.50 ± 0.12) were not different ($P \geq 0.34$). Calves restricted during postweaning development gained more efficiently, and when harvested on a common date, had lower carcass weights and yield grade, but similar fat thickness, ribeye area and quality grade compared with their ad libitum-fed counterparts.

Key Words: postweaning development, uterine programming, finishing

T129 Stearoyl-CoA desaturase (SCD1) localization and intensity in bovine adipose and muscle tissues from implanted and non-implanted steers. M. Wilder, S. Safayi, S. E. Ellis, and S. K. Duckett,* *Clemson University, Clemson, SC.*

Anabolic steroids are commonly used during the finishing phase to increase weight gain and feed efficiency. The objective of this study is to assess the localization and relative amount of stearoyl-CoA desaturase (SCD1) in mesenteric adipose tissues (MS), subcutaneous adipose tissue (SC), and longissimus muscle (LM) of implanted and non-implanted steers. Stearoyl-CoA desaturase is the rate-limiting enzyme involved in fatty acid metabolism, which converts saturated fatty acid to monounsaturated fatty acid. In this experiment, 12 steers (448kg) were implanted with Revalor-S (24 mg estradiol, 124 mg trenbolone acetate) and 12 steers were not implanted. All steers were fed a high concentrate diet for 72 d before slaughter. Fat and muscle samples were removed at slaughter, immediately flash-frozen, and stored at −80°C for subsequent cyrosectioning and immunofluorescent staining. Cryosections were stained with POPO-1 iodide, a high-affinity blue nucleic acid stain, and green fluorescent phalloidin, an F-actin stain. Cryosections were also incubated overnight with SCD-1 antibody (4 μg/mL) and stained with AlexaFluor 594 secondary antibody. Micrographs were collected with the Nuance Multispectral imaging system using a consistent exposure and illumination protocol. SCD1 staining intensity was most obvious in the perinuclear region, but was also visible through the cytoplasm. SCD1 staining was visible in adipocytes, muscle cells, endothelial cells and schwann cells. Discrete cell populations were manually traced in each micrograph to assess the recorded fluorescent staining intensity in regions and cells of interest. Average intensities in each group of cells were analyzed to estimate the relative abundance of SCD1 protein. There was a tissue by treatment interaction ($P < 0.05$). Adipose tissues from SC and MS had greater SCD1 intensity than LM, regardless of treatment. The SCD1 staining intensity was reduced in MS from implanted steers relative to MS of non-implanted and SC of both non-implanted and implanted. Using immunofluorescent staining, we were able to visualize SCD-1 localization in various adipose tissues and determine changes in SCD-1 relative amounts due to implant treatment.

Key Words: beef, adipose tissues, SCD

T130 Body′s growth curve and shape of grazing young bulls, receiving concentrate supplementation with different protein profiles. H. J. Fernandes*[1,2], A. G. da Silva[2], M. F. Paulino[2], S. A. Lopes[2], L. O. Tedeschi[4], J. A. G. Azevêdo[3,2], and A. Aguiar[5], *[1]State University of Mato Grosso do Sul, Aquidauana, MS, Brazil, [2]Federal University of Viçosa, Viçosa, MG, Brazil, [3]State University of Santa Cruz, Ilhéus, BA, Brazil, [4]Texas A&M University, College Station, [5]University of Florida, Gainesville.*

The objectives of this study were to analyze and compare full body weight (FBW) and body measurements (BM) growth of crossbred bulls

grazing *Brachiaria decumbens* Stapf. pastures over 430 d. Twenty bulls with initial FBW of 129 ± 28.1 kg, were divided in 4 groups, receiving either mineral supplement *ad libtum* (control) or 0.5% of FBW of one of the concentrate supplementation rations (26.7% CP), identified as T1 (high urea level), T2 (low urea level), and T3 (no urea). The FBW and the BM were recorded every 28 d. The BM included hooks width (HW), pins width (PW), pelvic girdle length, rump height (HeR), abdomen width, body length (BL), height at withers (HeW), and rib depth (RiD). The first and the second canonical variables were estimated using all BM by PROC CANDISC of SAS. A growth multiphase model with 3 phases was adjusted using PROC NLIN of SAS. The phases of the model corresponded to a first rainy season, a dry season (the feed restriction season in the year to grazing animals) and a second rainy season. Growth models and their parameters were compared using a dummy variable. The main BM to describe the differences between animal body shape (explaining 73.1% of the differences) were RiD, PW, HeR, and HeW. Animals in control group tend to be shorter and wider. There were no differences ($P > 0.05$) in the growth curves of FBW between the concentrate supplemented treatments. The growth curves of FBW of the control and the supplemented animals differs in days in the experiment at which the animals respond to feed restriction in dry season (82 and 113.3 d, $P = 0.047$), in the growth rate during this phase (0.141 and 0.328 kg/d, $P = 0.006$), and in days in the experiment at which the animals respond to the end of this phase (314 and 292 d, $P = 0.006$). These parameters could explain the greater mature weight ($P = 0.003$) of the supplemented animals. The main differences ($P < 0.05$) between the supplemented and the control animals in the growth curves of BM were the greater mature HeW, HeR, RiD, and BL in the supplemented group. The protein patterns of the concentrate affected ($P < 0.05$) the growth of the HeW, RiD, and HW.

Key Words: biometrics, cattle, modeling

T131 Mathematical models to describe growth of grazing beef cattle. H. J. Fernandes*[1], V. S. Siquiera[1], G. C. Z. N. de Oliveira Coelho[1], A. L. B. Netto[2], K. O. De Barros[1], A. Aguiar[3], L. M. Paiva[1], and J. C. de Souza[2], *[1]State University of Mato Grosso do Sul, Aquidauana, MS, Brazil, [2]Federal University of Mato Grosso do Sul, Aquidauana, MS, Brazil, [3]University of Florida, Gainesville.*

The objective of this study was to evaluate the use of different mathematical models to describe growth of grazing beef cattle. Ten Nellore castrated males and 10 females, with initial age and weight of 16 ± 1.27 mo and 224 ± 18.5 kg, respectively, were grazing *Brachiaria decumbens* Stapf. pasture and received mineral supplement ad libitum, for 16 mo. Every 28 d, animals were weighed and biometric measures (including hook width, pin width, pelvic girdle length, rump depth, rump height, abdomen width, body length, height at withers, rib depth, and girth circumference) were taken to develop growth curves of the animals. Six mathematical models were evaluated to describe animal growth: multiphase (with 3 phases), linear, quadratic, exponential, monomolecular, and Richards. Assessment of adequacy of the models was performed using coefficient of determination (R^2), simultaneous *F*-test for identity of parameters, concordance correlation coefficient (CCC), and partition of the mean square error of prediction (MSEP). The analysis of paired mean square error of prediction and delta information criterion of Akaike were used to compare the models for accuracy and precision. Based on the simultaneous *F*-test for identity of parameters, monomolecular and Richards models produced estimates different ($P < 0.05$) of the observed growth data. Linear and exponential models presented low R^2 (49.3 and 52.6%) and CCC <0.800. The quadratic model had R^2 = 70.0% and CCC = 0.826 and partitioning of the MSEP of this model showed more than 99% of deviations observed were attributed to the random errors. The best fit was the multiphase model (R^2 = 82.5% and CCC = 0.906), and it was the most ($P < 0.05$) accurate and precise model. Best performance of the multiphase model can be attributed to the fact that this model is able to separate animal growth in 3 phases, best describing the seasonal environmental changes that grazing animals are subject to during the year.

Key Words: modeling, Nellore, tropical environment

T132 Dietary fat content and fiber type influence adiposity, lipid oxidative genes and cecal volatile fatty acid concentrations in pigs. H. Yan,* V. Almeida, H. Lu, T. Stewart, A. Schinckel, and K. Ajuwon, *Purdue University, West Lafayette, IN.*

The interactive effect of fat level and dietary fiber type on performance, backfat thickness and expression of key transcripts involved in energy metabolism was evaluated. Growing pigs (n = 32, initial BW = 10.2 ± 0.15 kg) were allocated randomly to 4 treatments with 2 dietary fat levels; low fat (LF, 3%) and high fat (HF, 17.5%) swine grease as fat source and 2 fiber types (inulin and solka floc, 4% inclusion) in a 2 X 2 factorial design. There were 2 replicates per treatment and 4 pigs per replicate. Pigs were fed ad libitum for 6 wks. At slaughter, liver and mesenteric adipose tissues were collected for gene expression quantification of peroxisome proliferator-activated receptorγ co-activator (PGC1α), peroxisome proliferator-activated receptor α (PPARα), acyl-coA oxidase (ACO) and carnitine palmitoyltransferase 1(CPT1α) via real time PCR. Fecal samples were analyzed for the concentration of key volatile fatty acids. Gene expression data are expressed as normalized values to 18s. There were no interactions between fat level and fiber type for final BW, ADG and G:F ($P > 0.05$). There was an increase in ADG and G:F and a trend ($P = 0.06$) toward increased final BW in HF- than LF-treated pigs. However, no effect of fiber type was found ($P > 0.05$). Pigs fed HF diet had greater ($P < 0.01$) backfat thickness than LF-treated pigs. Inulin reduced the subcutaneous fat deposit in the HF diet pigs ($P < 0.05$). High fat diet also resulted in lower ($P < 0.05$) concentrations of acetate, butyrate and propionate. Inulin tended ($P < 0.07$) to increase propionate concentration compared with cellulose. Expression of PGC1α and PPARα in liver was unaffected by fat level and fiber type ($P > 0.05$). In the liver, Inulin led to increased ($P = 0.04$) expression of ACO expression compared with solka floc (1.53 ± 0.22 vs. 1.10 ± 0.23, respectively). However, no effect of fat level was observed ($P > 0.05$). Pigs fed HF diet had greater ($P = 0.002$) expression of CPT1α in liver tissue than LF diet (1.65 ± 0.20 vs. 0.83 ± 0.18, respectively). High dietary fat level led to a tendency ($P = 0.07$) toward increased CPT1α mRNA abundance in mesenteric fat compared with LF-treated pigs (1.55 ± 0.25 vs. 1.03 ± 0.24, respectively), whereas no effect of fiber type was detected ($P > 0.05$). This study shows that dietary fatty acid and fiber type have a profound influence on adiposity and level of fermentation end products in the hind gut which may affect fatty acid oxidation in distant organs such as the liver.

Key Words: dietary fat, fiber, oxidation

T133 Factors affecting serum IGF-1 and triiodothyronine concentrations as related to fat deposition in feedlot lambs. F. A. Rodriguez-Almeida*[1], D. M. Hallford[2], J. A. Grado-Ahuir[1], D. Briones[1], and E. Flores[1], *[1]Universidad Autónoma de Chihuahua, Chihuahua, México, [2]New Mexico State University, Las Cruces.*

To identify factors affecting serum IGF-1 and T3 concentrations after weaning and their relationship to fat deposition, 115 F_1 lambs (males

and females) weaned at 90 d (BW = 17 ± 3.7 kg), sired by Charollais (CH), Dorper (DP), Hampshire (HM), Suffolk (SF) and Texel (TX) rams bred to estrus synchronized-Pelibuey (PB) and Blackbelly (BB) ewes, were utilized. Lambs were individually fed an ad libitum mixed ration in 80 pens (1.25 × 2.45 m) and 35 stalls (0.5 × 1.45 m) and weighed every 14 d until they reached a minimum BW of 42 kg for males and 40 kg for females. Serum concentrations of IGF-1 and T3 at d 14, 42, and 70 of the feeding trial were quantified by RIA. Log-transformed hormone concentrations were analyzed with PROC MIXED of SAS, fitting a linear model with fixed effects of breed of sire (SB), breed of dam (DB), sex, number weaned, management (pen *vs* stall), day of blood sampling, 2-way interactions, and BW at sampling as first and second order covariates. Sire within SB was fitted as a random effect and repeated measures within animal were assumed correlated with an ARH(1) covariance structure. There were management and sex by day and SB by DB interactions ($P < 0.05$) for IGF-1. IGF-1 concentrations were greater ($P < 0.05$) for lambs in pens than for lambs in stalls later on the trial and increased ($P < 0.05$) with time for males but not for females. Lambs from the CH × PB cross had the lowest ($P < 0.05$) IGF-1 concentrations. Pearson correlations ($P < 0.05$) for IGF-1 at d 14, 42, and 70 were −0.42, −0.47 and −0.42 with back fat; −0.54, −0.65 and −0.51 with kidney fat (KF); and −0.36, −0.43 and −0.26 with percent of total carcass fat (PTCF). There were day main effects and sex by management and sex by SB interactions effects ($P < 0.05$) for T3. Mean was greatest ($P < 0.05$) at d 70 and was greater ($P < 0.05$) in females than in males in stalls but not in pens. Also, T3 concentrations were greater ($P < 0.05$) in females than in males for the CH, DP and SF sired breeds, but not for HM and TX. Pearson correlations for T3 were important ($P < 0.05$) only at d 70 with KF (0.23) and at d 14 and 70 with PTCF (−0.40 and −0.21). Serum IGF-1 concentrations in lambs, more than T3, are related to fat deposition as affected by sex, breed, management and days on feed.

Key Words: IGF-1, triiodothyronine, sheep breeds