
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% bagage 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. 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 Ismeans 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 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 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


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 Ismeans 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, heat stress
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. Randel1, J. Paschal2, T. Machado3, and C. Long1. 1Texas A&M University-Kingsville, Kingsville, TX, 2Texas AgriLife Research and Extension Center, Overton, TX, 3Texas AgriLife Extension Service, Corpus Christi, TX

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 canan 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 the least efficient group had lower 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) dressing % (2008, 2010), liveweight 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 and RNeasy RNA isolations. Therefore, real time PCR was performed on stearyl-CoA desaturase (SCD1) and cytochrome P450 subfamily 3A4 (CYP3A4) 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, CYP3A4 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
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 cryosectioning 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

T128 Postweaning feed restriction effects on steer feedlot performance and carcass characteristics. R. L. Endecott*1, B. L. Shipp2, M. D. MacNeil3, L. J. Alexander2, and A. J. Roberts2, 1Department of Animal and Range Sciences, Montana State University, Miles City, 2USDA-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 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>
<thead>
<tr>
<th>Trait</th>
<th>Treatment (mg of Cr)</th>
<th>Control</th>
<th>0.5</th>
<th>1.0</th>
<th>1.5</th>
<th>SEM</th>
</tr>
</thead>
<tbody>
<tr>
<td>DMI(kg/d)</td>
<td>1.01</td>
<td>1.00</td>
<td>1.03</td>
<td>1.07</td>
<td>0.04</td>
<td></td>
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<tr>
<td>ADG</td>
<td>0.14</td>
<td>0.14</td>
<td>0.15</td>
<td>0.17</td>
<td>0.01</td>
<td></td>
</tr>
<tr>
<td>FCR</td>
<td>7.55</td>
<td>7.48</td>
<td>6.95</td>
<td>6.44</td>
<td>0.47</td>
<td></td>
</tr>
</tbody>
</table>

Key Words: feed intake, daily gain, feed conversion ratio
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 (R²), 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 R² (49.3% and 52.6%) and CCC ≤ 0.800. The quadratic model had R² = 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 (R² = 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
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