521 Warner-Bratzler and slice shear force measurements of three beef muscles in response to various aging periods following anabolic implant and zilpaterol hydrochloride supplementation of finishing beef steers. A. J. Garmyn*[1], L. F. Hightower[1], J. C. Brooks[1], B. J. Johnson[1], S. L. Parr[1], R. J. Rathmann[1], J. D. Starkey[1], D. A. Yates[2], J. M. Hodgen[2], J. P. Hutcheson[2], and M. F. Miller[1], *[1]Texas Tech University, Lubbock, [2]Intervet/Schering-Plough Animal Health, DeSoto, KS.*

Our objectives were to determine the effects of zilpaterol hydrochloride (ZH) and the payout pattern of trenbolone acetate and estradiol-17β on Warner-Bratzler shear force (WBSF) and slice shear force (SSF) of longissimus lumborum (LL) and the WBSF of gluteus medius (GM) and psoas major (PM) in response to various aging periods. British × Continental steers (n = 168) were assigned to treatments in a 3 × 2 factorial. The main effects of treatment were implant [no implant (NI); Revalor-S (REV-S), Revalor-XS (REV-XS)] and ZH (0 or 8.3 mg/kg of DM for 20 d). Harvest group was included as a random effect to account for the variation in days on feed (153 or 174 d). Loins (n = 96) were fabricated to obtain strip loin, top sirloin butt, and tenderloin subprimals. Five 2.54-cm steaks were cut from each subprimal and assigned to 1 of 5 aging periods (7, 14, 21, 28, or 35 d postmortem). Feeding ZH increased ($P < 0.01$) LL WBSF and SSF values at each aging period compared with controls. Implanting increased ($P < 0.05$) LL WBSF values at 14 and 21 d, but did not affect LL SSF values ($P > 0.05$). Only REV-S increased WBSF values at 28 and 35 d compared with NI or REV-XS. The percentage of LL steaks with a WBSF value <4.6 kg did not differ ($P > 0.05$) between ZH supplementation or implant strategy at any aging period, and by d 28 over 99% of LL steaks registered WBSF values <4.6 kg. Feeding ZH increased ($P < 0.05$) GM WBSF values only on d 21. Implant had no effect ($P > 0.05$) on GM WBSF values. The percentage of GM steaks with a WBSF value <4.6 kg did not differ ($P > 0.05$) between ZH supplementation or implant strategy at any aging period. Neither ZH nor implant strategy affected PM WBSF values ($P > 0.05$). All PM WBSF values were <4.6 kg on d 7. The results of this study indicated feeding ZH increased WBSF and SSF of LL steaks, regardless of aging period; however, the percentage of steaks with WBSF <4.6 kg did not differ due to ZH or implant. Implanting increased LL WBSF, but not SSF values.

Key words: anabolic implant, shear force, zilpaterol hydrochloride

522 The effects of anabolic growth implant and restricted feed intake on proliferation of bovine primary skeletal muscle cells. T. L. Lee*, D. U. Thomson, B. W. Wileman, L. K. Mamedova, B. J. Bradford, and C. D. Reinhardt, *Kansas State University, Manhattan.*

Sixteen crossbred steers (BW 293 ± 19.3 kg) were used to evaluate the impact of a steroid implant and nutrient intake on nutrient metabolism and muscle cell growth of steers. Steers were trained to Calan gates and randomly assigned to 1 of 4 groups: (1) implant (Revalor XS; 200 mg trenbolone acetate, 40 mg estradiol), high intake (2 × ME for maintenance); (2) implant, restricted intake (1 × ME for maintenance; (3) no implant, high intake; and (4) no implant, restricted intake. Serum was collected on d 0, 14, and 28 for application to satellite cells (previously isolated from non-study steers and frozen). Satellite cells were incubated with serum treatments (20% of total media) for 72 h. Protein abundance of myosin heavy chain (MYH; d 0, 14, and 28), phosphorylated extracellular signal related kinase (pERK; d 0 and 28), and phosphorylated mammalian target of rapamycin (pmTOR; d 0 and 28) were analyzed in differentiated satellite cells to determine effects of implant, intake, and their interaction (applied via the serum). MYH is used as a marker of myotube formation, and pERK and pmTOR are growth factor protein indicators of cell proliferation. Intake had no effect on MYH but implant increased MYH abundance ($P < 0.01$). There was no interaction between intake and implant on MYH abundance. Implant increased the abundance of pERK ($P < 0.01$), but intake had no effect, and there was no interaction between intake and implant on pERK. At high intake, implant increased abundance of pmTOR ($P = 0.02$) but implant had no effect on pmTOR at restricted intake ($P = 0.21$, interaction $P < 0.01$). These results demonstrate that a circulating factor in implanted cattle promotes satellite cell differentiation, possibly mediated by ERK phosphorylation.

Key words: implant, satellite cells, nutrient

523 Identification of tough beef carcasses from epigenetic changes detectable in blood. M. S. Updike*, C. Zhao, Y. Yu, F. Tian, and J. Song, *University of Maryland, College Park.*

For decades, inconsistency in beef tenderness has been a major problem identified by consumers. Currently a variety of methods to segregate palatable carcasses from unpalatable carcasses such as quality grade and camera technologies are used. Much of the research has focused upon changes in the muscle as this will become the beef. By taking a step back and asking what are some of the reasons that muscle can turn into tough beef, other methods may be identified. One factor that has previously been identified as causing tougher beef is stress on the live cattle such as that from hardware disease. To mimic hardware disease in this study, yearling Wye Angus cattle were surgically implanted with cannulas into the rumen. The cattle were fed a pelleted forage diet sufficient for maintenance, but not growth. Two months after the surgery, the cattle were serially slaughtered. Blood was collected during exsanguination and longissimus dorsi samples were collected 24 h after harvest, vaccum packed, aged for 14 d and then frozen. The steaks underwent Warner Bratzler shear force (WBS) analysis. The blood was used to detect epigenetic changes in the CpG islands of promoter regions of selected genes. As expected, the steaks from the negative control were more tender than the steaks from the treatment group. However, of greater interest was the bimodal distribution of tenderness within the stress group. Some stressed cattle were relatively tender while other stressed cattle had very tough beef. We also found that the methylation levels of NAALAD2, a member of the N-acetylated α-linked acidic dipeptidase (NAALADase) gene family, significantly increased in stress groups in blood samples ($P < 0.05$), compared with the non-stress group, although the methylation change is higher in the tender-stress group than in the tough-stress group, indicating that the methylation variation of the gene in blood mainly relates to stress stimuli.

Key words: epigenetics, stress, tenderness

524 Carcass and production characteristics of grass-fed Angus cattle through spring, summer, winter and fall. C. Zhao, J. Song, B. Bequette, and M. S. Updike*, *University of Maryland, College Park.*

Consumers are demanding that grass fed beef be available year round. This can pose challenges for grass fed beef producers as feeding harvested forages is one of the most expensive aspects of grass fed beef

production. Some producers choose not to finish cattle on forages over the winter due to increased costs. To examine the effects of seasonal effects, including feeding harvested forages during the winter, the production and carcass characteristics of Angus cattle finished on grass were examined. The Wye Angus based Angus cattle were rotationally grazed on 100% Alflalfa pasture, when available, during the spring, summer and fall. During the winter, the cattle were fed ad libitum alfalfa baylage. Cattle were harvested based upon both demand for additional beef and visual appraisal for degree of finish. Longissimus dorsi samples were aged for 14 d and then frozen before Warner Bratzler shear force (WBS) analysis. Season had no effect on any of the production or carcass characteristics of these grass fed Angus cattle ($P > 0.5$). The mean age at slaughter was 22.5 mo, the mean carcass weight was 291.3 kg, 62% of the carcasses graded choice, and the mean WBS was 2.9 kg.

Key words: grass-fed, beef, tenderness

525 Withdrawn

526 Effect of castration and slaughter ages on animal performance and meat quality of Holstein bulls fed high-concentrate diets. S. Marti*[1], C. E. Realini[2], A. Bach[3,1], M. Perez-Juan[2], and M. Devant[1], *[1]Department Ruminant Production, IRTA, Barcelona, Spain, [2]Carcass Quality Subprogram, IRTA, Girona, Spain, [3]ICREA, Barcelona, Spain.*

The aim of this study was to evaluate the effect of castration and slaughter ages on performance and meat quality of Holstein bulls fed a high-concentrate diet. One hundred and 20 4 animals (97 ± 2.4 d of age) were randomly allocated in 6 pens following a 3x3 factorial arrangement of treatments. Three castration ages (bulls: INT, 116 ± 3.7 kg; castration at 3 mo: CAS3, 115 ± 3.7 kg; and castration at 8 mo of age: CAS8, 117 ± 3.7 kg) and 3 slaughter ages (10, 12, and 14 mo of age) were evaluated. Animal intake was recorded daily using a computerized concentrate feeder, and BW was recorded every 14 d. The 9–10–11th rib section was removed at 24 h post-mortem and dissected into lean, fat and bone, and meat quality evaluated on the Longissimus thoracis. Data were analyzed using a mixed-effects model including castration and slaughter ages and their 2-way interaction as fixed effects, and initial BW as a covariate. Castration, at 3 or 8 mo of age, reduced animal growth and muscle pH, and increased marbling, and tenderness ($P < 0.001$). As slaughter age increased, feed efficiency was reduced ($P < 0.001$), and carcass weight, marbling and tenderness increased ($P < 0.001$). An interaction ($P = 0.01$) between castration and slaughter ages affected percentage of subcutaneous fat. The percentage of subcutaneous fat was greater in castrated animals and increased between 10 (INT: 3.7 ± 0.75%; CAS8: 5.7 ± 0.75%; CAS3: 7.6 ± 0.75%) and 12 mo at slaughter age (INT: 8.3 ± 0.75%; CAS8: 10.9 ± 0.75%; CAS3: 13.2 ± 0.75%). However, subcutaneous fat percentage decreased in animals slaughtered at 14 mo of age (INT: 7.0 ± 0.75%; CAS8: 9.7 ± 0.75%; CAS3: 7.5 ± 0.75%) and was similar for rib-sections from INT and CAS3. Interactions between castration age and slaughter age tended to be significant for intermuscular ($P = 0.07$) and intramuscular fat ($P = 0.06$). Castration at 3 or 8 mo of age reduces ADG and improves meat tenderness. As slaughter age increases feed efficiency decreases and carcass weight and meat tenderness increases, and depending on castration age increases or decreases subcutaneous, intermuscular and intramuscular fat percentages.

Key words: beef, castration, meat quality

527 Establishing a molecular fingerprint of high versus low-quality beef carcasses. K. J. Thornton*, K. Chapalamadugu, and G. K. Murdoch, *University of Idaho, Moscow.*

Beef cattle raised in the US exhibit undesirable carcass variability, despite similar production practices. Given that "uniformity" is one of the primary areas of improvement identified by the NCBA Beef Quality Audit, carcass characteristic variability observed in the northwest is less than ideal. In accordance with improved uniformity, producers are driven to select for less variance and higher quality animals. Therefore, it is important that underlying physiological causes for carcass quality differences are identified. To address this, post-mortem longissimus dorsi samples were collected from a random population of 500 cattle from different producers in the northwest, for the purpose of identifying key carcass characteristics that vary across this population. The whole transcriptome and proteome of the top 5% (high quality carcass grade) and bottom 5% (low quality carcass grade) of samples were analyzed using custom Nimblegen bovine microarrays and 2D proteomics, respectively. A total of 48 samples were evaluated representing 4 different groups: high-quality steers (HS, n = 12), low-quality steers (LS, n = 12), high-quality heifers (HH, n = 12), and low-quality heifers (LH, n = 12). The protein samples were pooled by group for proteome analysis, whereas microarray studies were conducted using individual samples balanced across the 12-plex microarray. When HS and LS were compared, 52 unique proteomic features differed by at least a 1.25 fold change in protein expression. Similar analysis between HH and LH showed that 61 proteins differed by at least a 1.25 fold change of expression. Differentially expressed proteins between the high and low quality groups are involved in pathways that regulate anabolism such as myogenesis and adipogenesis. Protein and mRNA differences between the 2 groups will provide insight into the molecular pathways contributing to high-quality cattle. In conclusion, we are generating a combined transcriptome and proteome fingerprint for high vs. low-quality beef carcasses. This may allow producers to employ altered management and genetic selection practices that promote greater uniformity with respect to carcass quality.

Key words: beef quality, proteome, muscle

528 Localization and abundance of DLK1 in skeletal muscle of cattle. E. Albrecht*[1], J. Kuzinski[1], T. Gotoh[2], and S. Maak[1], *[1]Leibniz Institute for Farm Animal Biology, Muscle Biology and Growth, Dummerstorf, Germany, [2]Kyushu University, Kuju Agricultural Research Center, Kuju-cho, Oita, Japan.*

The delta-like 1 homolog (DLK1), also known as preadipocyte factor 1 (PREF1), is a transmembrane protein involved in the differentiation of several cell types including adipocytes. Cell culture models demonstrated high expression in preadipocytes and complete disappearance during differentiation to adipocytes. Consequently, it can be expected that DLK1 expression decreases during life of cattle with increasing fat deposition. Furthermore, cattle which exploited their full potential for intramuscular fat (IMF) deposition are expected to have low DLK1 expression, independent of the final IMF content. We therefore investigated the localization and protein abundance of DLK1 in skeletal muscle of steers, known to have different capabilities to store IMF, in comparison with newborn calves and fetal muscle tissue. Six Japanese Black (JB), 5 Holstein (HS), and 6 Charolais (CH) steers were fed a high energy diet to maximize IMF deposition. When slaughtered at 26 mo of age, the IMF content in longissimus muscle was 34.3%, 20.4%, and 6.4% for JB, HS, and CH, respectively. Immunohistochemistry showed that DLK1 was localized in the cytoplasm of cells in muscle

perimysium. Many DLK1-positive cells were detected in fetal and newborn calf muscles, but only few in adult muscles. The abundance of DLK1 protein, determined by Western blot analysis, was accordingly lower in adult muscle tissue. A specific ~50 kDa band showed high variability between animals and reflected well the immunohistochemical results. The protein abundance and the number of DLK1-positive cells in a muscle cross section were highest in HS ($P < 0.05$), but similar in JB and CH ($P > 0.05$). Differences in mRNA abundance were not significant between breeds. According to our hypothesis, the results suggest that JB and CH, rather than HS steers, have widely exhausted their potential to generate new adipocytes or clusters of adipocytes growing to visible marbling flecks. This may indicate a more advanced maturity state of intramuscular adipose tissue in JB and CH steers at 26 mo of age.

Key words: intramuscular fat, cattle, preadipocyte